UNIVERSIDADE ESTADUAL PAULISTA
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Bioprospecção de compostos bioativos: descoberta de peptídeos inovadores presentes na fauna acompanhante

Dissertação apresentada ao programa de Pós-graduação em Doenças Tropicais da Faculdade de Medicina, Universidade Estadual Paulista “Júlio de Mesquita Filho”, Campus de Botucatu, para obtenção do título de Mestre em Doenças Tropicais.

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"When the last tree has fallen and the rivers are poisoned, you cannot eat money"

(Aurora Aksnes)

RESUMO

A fauna acompanhante está presente nas atividades pesqueiras realizadas por meio da rede de arrasto e na maioria dos casos, somam cerca de 50% da captura. Por não representar valor econômico, esta é comumente descartada de volta ao mar morta ou moribunda, causando ainda um grande desequilíbrio no ecossistema marinho local. Devido ao declínio mundial das populações de peixes, ao aumento da poluição e ao reconhecimento da limitação dos recursos biológicos, a necessidade de utilizar o *bycatch* de forma consciente torna-se indispensável. Atualmente, este material tem fomentado o interesse biotecnológico por meio de sua utilização para a identificação de compostos bioativos com atividades analgésicas, antioxidantes, antimicrobianas, imunorreguladoras, entre outras. As amostras presentes neste estudo foram coletadas em Ubatuba, São Paulo, Brasil, e revelaram que, naquela área, o *Paralonchurus brasiliensis, o Micropogonias furnieri* e o *Hepatus pudibundus* são as espécies mais abundantes no *bycatch* proveniente da pesca de camarão sete-barbas. Após a hidrólise das amostras, estas apresentaram uma alta capacidade antioxidante e potencial para ser uma ferramenta biotecnológica no combate ao estresse oxidativo. Portanto, o presente estudo teve como objetivo caracterizar compostos expressos em animais presentes na fauna acompanhante, a fim de identificar compostos bioativos, investigar atividades biológicas e possíveis meios de utilização dessa fauna descartada, visando potenciais farmacológicos e nutracêuticos. Para isso, foram realizadas diversas análises proteômicas. Dessa maneira a efetividade da digestão pelas hidrólises com Alcalase e Protamex foi comprovada, bem como sua eficácia na obtenção de peptídeos complexos. A maioria dos peptídeos são polares com potencial nutracêutico, já que são facilmente diluídos. Vale ressaltar que esses peptídeos possuem também um potencial de utilização como modelos para a produção de peptídeos sintéticos devido às suas ações biológicas, sendo estes peptídeos análogos – que possuem maior permeabilidade de membrana e maior sobrevida. Com o resultado obtido pelo banco de dados BioPep foi possível prever diversas atividades bioativas, como atividade antioxidante, inibidora de alfa-glicosidase, inibidora de enzima conversora de angiotensina, antiamnésica, antitrombótica, hipertensora, neuropeptídica, entre outras, ressaltando seu potencial visando questões de saúde pública. O *bycatch* pode, portanto, representar uma fonte de peptídeos únicos com inúmeras utilizações como bioprodutos comerciais, sendo assim, há uma ampla gama de possibilidades para trabalhar com essa fauna inexplorada.

Palavras-chave: *Paralonchurus brasiliensis*, *Micropogonias furnieri*, *Hepatus pudibundu*s, peptídeos, antioxidantes, *bycatch*, fauna acompanhante, bioprospecção.

ABSTRACT

The bycatch is present in the fishing by means of the trawl and in most cases, they are about 50% of the catch. As they have no economic value, this is commonly discarded back into the sea dead or dying, causing a major imbalance in the local marine ecosystem. Due to the worldwide decline in fish populations, the increase in pollution and the recognition of the limitation of biological resources, it is essential to use bycatch consciously. Currently, this material has fostered biotechnological interest for its use in the bioprospecting of bioactive compounds with analgesic, antioxidant, antimicrobial, immunoregulatory activities, among others. The samples present in this study were collected in Ubatuba, São Paulo, Brazil, and revealed that, in that area, Paralonchurus brasiliensis, Micropogonias furnieri and Hepatus pudibundus are the most abundant species in the bycatch from the seven-barb shrimp fishery. After hydrolysis of the samples, they showed a high antioxidant capacity and potential to be a biotechnological tool in the fight against oxidative stress. Therefore, the present study aimed to characterize compounds expressed in animals present in bycatch and, in order to identify bioactive compounds, investigate biological activities and possible ways of using this discarded fauna, aiming at pharmacological and nutraceutical potential. For this, several proteomic analyzes were performed. In this way, the effectiveness of the digestion performed by the hydrolysis with Alcalase and Protamex was proven, as well as its effectiveness in obtaining complex peptides. Most peptides are polar with nutraceutical potential, as they are easily diluted. It is worth mentioning that these peptides also have the potential to be used as models for the production of synthetic peptides due to their biological actions, which are analogous peptides - which have greater membrane permeability and greater survival. Several bioactive activities were found, such as antioxidant activity, alpha-glucosidase inhibitor, angiotensin-converting enzyme inhibitor, antiamnesic, antithrombotic, hypertensive, neuropeptide, among others, highlighting its potential for public health issues. Therefore, bycatch represents a source of unique peptides with numerous uses as commercial bioproducts, thus, there is a wide range of possibilities for using this unexplored fauna.

Key words: *Paralonchurus brasiliensis*, *Micropogonias furnieri*, *Hepatus pudibundu*s, peptides, antioxidants, *bycatch*, bioprospecting, proteomics.

Sumário

1. INTRODUÇÃO

1.1 MEIO AMBIENTE MARINHO

O Brasil é privilegiado em termos de possíveis explorações racionais de recursos marinhos, com uma costa litorânea que se estende cerca de 8 mil quilômetros, é considerado o segundo país com a maior costa contínua do mundo[1]. Os oceanos cobrem cerca de 70,8% da superfície da Terra, neles se concentram a maior parte de vida do planeta, consequentemente, a maior parte das riquezas naturais[2]. O ambiente marinho representa cerca de 98% da biosfera e possui profundidade média de 3.800m [2]. Devido às limitações técnicas, apenas 5% desse meio foi explorado e menos de 0,01% foi amostrado em detalhes, portanto, grande parte desse ambiente permanece subutilizado e inexplorado[2].

A biodiversidade presente nos oceanos abriga a maioria dos filos, sendo considerado o ambiente com maior número de organismos[3]. No Quadro 1 está a classificação da fauna e flora marinha, a qual excede um total de 230.000 espécies conhecidas[3], com uma previsão de 2 milhões de espécies não descobertas[4].

Quadro 1 – Classificação dos organismos marinhos de acordo com Blunt e Munro[3].

Archea e Eubacteria	*Cyanobacteria*	*Chlorophyta*	*Rhodophyta*	*Phaeophyta*	*Bacillariophyta Chrysophyta, Haptophyta*	*Fungi*
~ 1000 espécies	~ 7000 espécies	~ 2000 espécies	~ 6000 espécies	~ 1500 espécies	~ 50 000 espécies	~ 1000 espécies
Dinoflagellata	*Porifera*	*Cnidaria*	*Platyelmintes*	*Annelida*	*Bryozoa*	*Mollusca*
~ 200 espécies	~ 8000 espécies	~ 11 000 espécies	~ 18 000 espécies	~ 10 000 espécies	~ 5700 espécies	~ 90 000 espécies

Echinodermata	*Crustácea*	*Hemichordata*	*Phorochordata*	*Pisces*	Total
~ 7000 espécies	~ 60 000 espécies	~ 100 espécies	~ 3000 espécies	~ 16 000 espécies	**Mais de 230 000 espécies**

O ecossistema marinho possui uma complexa e eficiente conectividade entre os organismos, nesse meio encontra-se grandes variações de fatores bióticos e abióticos (temperatura, calor, pressão, luz, nutrientes e salinidade), diferenciando-o fundamentalmente do ambiente terrestre[5]. Para sobreviverem nesse ambiente específico e peculiar, os diferentes tipos de organismos marinhos realizam estreitas associações entre si, como por exemplo, as anêmonas, corais e esponjas que abrigam peixes e microrganismos, servindo de proteção uns aos outros[5,6].

Essas variações nos habitats influenciam diretamente na natureza química dos organismos, exigindo que estes apresentem mecanismos especiais de adaptação, como a produção de metabólitos primários e secundários biologicamente ativos[2,6]. Portanto, as variações interespecíficas são responsáveis por produzir diferenças nas estruturas químicas dos compostos e suas concentrações em diferentes ambientes marinhos[2,7]. Nos organismos marinhos, os metabólitos são utilizados para controlar as relações ecológicas, as quais envolvem funções de sinalização intra e interespecífica, supressão de competidores, dissuasão de predadores, inibição de invasão bacteriana e fúngica, proteção contra radiação UV, entre outros[5,7].

Por possuir uma grande variedade de macro e microrganismos que diferem em sua capacidade de adaptação e fisiologia fazendo com que deem origem a estruturas química incomparáveis, o ambiente marinho é considerado um meio promissor para a exploração de novos fármacos[6,5].

1.2 A PESQUISA E O AMBIENTE MARINHO

Os produtos naturais marinhos estão sendo mais explorados nas últimas décadas devido às variedades de atividades biológicas apresentadas por eles[7]. Tais atividades biológicas podem ter um importante papel no desenvolvimento de medicamentos voltados para a saúde pública[7]. Devido às peculiaridades do ambiente e dos organismos marinhos, seus compostos bioativos possuem alta atividade biológica e estruturas químicas exclusivas, se mostrando atualmente uma área de estudo que promete grandes descobertas[8].

Alguns dos organismos mais explorados nessa área desde 1990 são as esponjas, os fungos, as algas e os corais[8]. Os micróbios, bactérias e cianobactérias, que vivem em associações com estes e outros organismos, são considerados uma fonte prolífica de compostos naturais bioativos. Sendo assim, os estudos com esses organismos e microrganismos vem aumentando a cada ano[9,10].

É ampla a gama de utilização dos compostos encontrados no ambiente marinho, podendo ser nutracêuticos, cosméticos e até mesmo fármacos. Já foram encontradas bioatividades antibacterianas[11,12], antioxidantes[13,14], antitumorais[15], anticâncer[16,17], imunomoduladoras[18,19], antifúngicas[20–22], antiinflamatórias[23], antimicrobianas[24–26], analgésicas[27], antimaláricas[28–30], entre outros. Há ainda, em andamento, um estudo para o tratamento de Alzheimer[31] e outros estudos antivirais específicos para o COVID-19[32,33].

Dessa maneira, pode-se dizer que a ênfase das pesquisas no ambiente marinho está na descoberta de novas moléculas – desde 2008, mais de 1200 novos compostos são relatados por ano[34] – e, consequentemente, a bioprospecção de moléculas e compostos bioativos provenientes deste ambiente também está em ascensão[35–37]. De acordo com o banco de dados MarinLit[38] (http://pubs.rsc.org/marinlit/) e com o Dicionário de Produtos Naturais Marinhos[34], mais de 37.000 compostos de origem marinha estão listados no momento[39].

Com base nesses dados, espera-se que o ambiente marinho seja cada vez mais uma fonte de inspiração para descoberta de novos meios de pesquisas relacionadas com a área de saúde pública[39].

1.3 BIOPROSPECÇÃO E FÁRMACOS PROVENIENTES DO AMBIENTE MARINHO

A bioprospecção pode ser utilizada na pesquisa de vários tipos de produtos, tais como, farmacêuticos, nutracêuticos, anti-incrustantes e adesivos, biocombustíveis, biocatalizadores (enzimas), cosméticos, entre outros[40]. Para a realização de uma busca química guiada de novos compostos e detecção de atividades biológicas, são utilizadas técnicas de espectrometria de massas e cromatografia líquida combinadas com análises nos bancos de dados adequados[7,41,42].

O desenvolvimento de fármacos de origem marinha é bem antigo. Na década de 1940, perto de Sardenha, nas águas do mar Mediterrâneo, encontra-se o fungo *Acremonium chysogenum* que produz a cefalosporina C e é considerado o ponto de partida para o desenvolvimento da classe de antibióticos de cefalosporinas[42].

Posteriormente, com o surgimento das bibliotecas de compostos combinatórios sintéticos, que eram mais simples e econômicos para a triagem de alto rendimento, as principais empresas farmacêuticas acabaram interrompendo os investimentos em compostos marinhos por alguns anos40. Entretanto, a abordagem química combinatória não surtiu os efeitos desejados, fazendo com que surgissem empresas biotecnológicas que investem em pesquisa e comercialização de fármacos de origem marinha[42].

A tabela 1 foi criada por pesquisadores de Farmacologia Marinha da Universidade de Midwestern, Illinois (EUA), atualizada em 15 de setembro de 2021, possui a relação de fármacos provenientes de compostos marinhos já aprovados pela FDA (Food and Drugs Administration)[43]:

Tabela 1 – Fármacos derivados de compostos marinhos já aprovados pela FDA

Efermidade	Nome do composto	Organismo marinho	Classificação química	Alvo molecular	Marca comercial	Ano de aprovação FDA
Câncer (carcinoma, gástrico, mama)	Disitamab vedotin (RC48)	Molusco/ Cianobactéria	Conjugado anticorpo-droga	HER3	Aidixi™	2021
Câncer (mieloma)	Belantamab Mafodotin-blmf	Molusco/ Cianobactéria	Conjugado anticorpo-droga	BCMA	Blenrep™	2020
Câncer (de pulmão)	Lubinectedin	Tunicado	Alcalóide	RNA Polimerase II	Zepzelca™	2020
Câncer (urotelial metastático)	Enfortumab Vedotin-ejfv	Molusco/ Cianobactéria	Conjugado anticorpo-droga	Nectin-4	PADCEV™	2019
Câncer (linfoma)	Polatuzumab vedotin (DCDS-4501A)	Molusco/ Cianobactéria	Conjugado anticorpo-droga	CD76b e microtúbulos	Polivy™	2019
Câncer (mieloma, leucemia, linfoma)	Plitidepsin	Tunicado	Depsipeptídeo	eEF1A2	Aplidin®	2018
Câncer (mieloma múltiplo)	Panobinostat	Esponja	Ácido hidroxâmico	Histona deacetilase	Farydak®	2015
Câncer (sarcoma e ovário)	Trabectedin (ET-743)	Tunicado	Alcalóide	Sulco menor do DNA	Yondelis®	2015
Hipertrigliceridemia	Omega-3-carboxilic acid	Peixe	Ácidos gordurosos de Ômega-3	Enzimas que sintetizam triglicerídeos	Epanova®	2014
Hipertrigliceridemia	Eicosapentaenoic acid ethyl ester	Peixe	Ácidos gordurosos de Ômega-3	Enzimas que sintetizam triglicerídeos	Vascepa®	2012
Câncer (linfoma)	Brentuximab vedotin (SGN-35)	Molusco/ Cianobactéria	Conjugado anticorpo-droga	CD30 e microtúbulos	Adcetris®	2011
Câncer (de mama)	Eribulin Mesylate (E7389)	Esponja	Macrolídeo	Microtúbulos	Halaven®	2010
Dor crônica	Ziconotide	Caracol cone	Peptídeo	Canal de Cálcio tipo-N	Prialt®	2004
Antivírus – Herpes	Vidarabine (Ara-A)	Esponja	Nucleosídeo	DNA polimerase viral	Arasena A®	1976
Câncer – Leucemia	Cytarabine (Ara-C)	Esponja	Nucleosídeo	DNA polimerase	Cytosar-U®	1969

Fonte: *https://www.marinepharmacology.org/*

De acordo com os dados levantados na Tabela 1, o câncer é tido como o principal alvo dos medicamentos derivados de organismos marinhos. Sendo o primeiro a ser aprovado pela FDA em 1969, com o composto Cytarabine (Ara-C) – um nucleosídeo que age no DNA polimerase, utilizado para tratamento de leucemia. O medicamento mais recente foi aprovado em 2021 e é voltado para o tratamento de câncer, utilizando o conjugado anticorpo-droga Disitamab vedotin (RC48), que age no HER3[43].

Nas tabelas 2 e 3, também criadas pelos pesquisadores de Farmacologia Marinha da Universidade de Midwestern, Illinois (EUA), possui um levantamento dos medicamentos oriundos de compostos marinhos em fase clínica 2 e 3, respectivamente[43].

Tabela 2 – Fármacos derivados de compostos marinhos em fase clínica 2

Enfermidade	Nome do composto	Organismo marinho	Classificação química	Alvo molecular
Esquizofrenia, Alzheimer, Déficit de Atenção, Hiperatividade	GTS-21 (DMXBA)	Poliqueta (verme)	Alcaloide	Receptor nicotínico de acetilcolina α7
Câncer (tumores sólidos)	Procabulin (PM184)	Esponja	Policetídeos	Sulco menor do DNA
Câncer (de ovário, cérvix, próstata, cabeça e pescoço, pulmão)	Tisotumab Vedotin	Molusco/ Cianobacteria	Conjugado anticorpo-droga	Fator tecidual e microtúbulos
Câncer de mama	Ladiratuzumab vedotin (SGN-LIV1A)	Molusco/ Cianobacteria	Conjugado anticorpo-droga	LIV-1 e microtúbulos
Alzheimer	Bryostatin	Briozoário	Macrolídeo lactona	Proteina quinase C
Câncer (tumores sólidos)	Telisotuzumab vedotin (ABBV-399)	Molusco/ Cianobacteria	Conjugado anticorpo-droga	c-Met
Câncer (tumores sólidos)	CAB-ROR2 (BA-3021)	Molusco/ Cianobacteria	Conjugado anticorpo-droga	ROR2
Câncer (de cabeça, pescoço, pâncreas, pulmão)	CX-2029 (ABBV-2029)	Molusco/ Cianobacteria	Conjugado anticorpo-droga	CD71
Câncer (tumores sólidos com metástase avançada)	W0101	Molusco/ Cianobacteria	Variante de auristatina	IGF-R1

Fonte: *https://www.marinepharmacology.org/*

Tabela 3 – Fármacos derivados de compostos marinhos em fase clínica 3 – atualizada em 30 de abril de 2021:

Enfermidade	Nome do composto	Organismo marinho	Classificação química	Alvo molecular
Câncer (de pulmão e cérebro)	Plinabulin (NPI-2358)	Fungo	Dicetopiperazina	Microtúbulos
Dor crônica	Tetrodoxin	Peixe (Baiacu)	Alcaloide guanidínico	Canais de sódio
Câncer (de ovário e mama)	Lurbinectedin (PM01183)	Tunicado	Alcaloide	Inibidor de transcrição oncogênica
Câncer (de pulmão, pâncreas, melanoma, linfoma, mieloma múltipla)	Marizomib (Salinosporamide A; NPI-0052)	Bactéria	β-lactoma γ-lactama	20S Proteasoma
Coronavirus	Plitidepsin	Tunicado	Depsipeptídeos	eEF1A2

Fonte: *https://www.marinepharmacology.org/*

Observa-se nas tabelas 2 e 3 que, os estudos realizados com compostos marinhos estão também abrangendo outras áreas, como neurológicas e virais. Diante deste cenário, é possível notar que, mesmo perante a algumas adversidades existentes, os estudos e a aprovação de produtos farmacêuticos provenientes do ambiente marinho vêm crescendo nos últimos anos[37].

O conjunto destas informações nos faz refletir e concluir que a ampla variedade das bioatividades dos metabólitos primários e secundários provenientes desse meio, bem como os produtos naturais já existentes, possuem alto valor de interesse para aplicações na indústria farmacêutica, fazendo com que o investimento neste campo cresça cada vez mais[6,36].

1.4 A FAUNA ACOMPANHANTE – “BYCATCH”:

A prática de pesca de camarões é corriqueira e abundante no mundo, sendo muito comum em zonas litorâneas. Uma das maneiras de captura mais eficiente e, portanto, a mais utilizada é a rede de arrasto[44].

De acordo com o último Relatório Anual da Organização das Nações Unidas de Alimentação e Agricultura (FAO) foi constatado que, no mundo, 178,5 milhões de toneladas de peso vivo são capturados por ano, tal estimativa inclui a aquicultura, a pesca marinha e interior[45]. Deste montante, cerca de 156,4 milhões de toneladas são destinadas ao consumo humano e 22,2 milhões de toneladas para consumo indireto. O consumo indireto inclui a produção de farinha e óleo de peixe, onde os resíduos da produção de óleo são utilizados para a fabricação da farinha[45].

Em uma pesca do camarão sete-barbas por rede de arrasto, estima-se que cerca de 46% da captura é descartada como não comestíveis[45]. Esse descarte recebe o nome de subprodutos ou resíduos de processamento – carcaças, ossos, pele, entre outros[45]. Segundo questões logísticas, somente os subprodutos oriundos do processamento direto podem ser capturados e processados, o que leva a cerca de 60% da coleta (107,1 milhões de toneladas) a ser viável para fins alimentares, resultando em 27,85 milhões de toneladas de descartes a nível global[45,46].

Os animais capturados acidentalmente são chamados de fauna acompanhante ou *bycatch* e, por muitas vezes não possuem valor comercial, são frequentemente descartados de volta ao mar, mortos ou moribundos[47,48].

Por mais que a pesca por rede de arrasto seja voltada a uma espécie alvo, e essa prática seja uma atividade socioeconômica importante, sempre afetará muitas outras espécies, podendo ser problemática para o meio ambiente[48]. A frequência dos descartes pode causar várias alterações na biodiversidade marinha, no ecossistema e na cadeia alimentar, comprometendo também os estoques pesqueiros[59,60], as relações predador-presa, além de causar a destruição de organismos e de regiões bentônicas[47,49].

Diante deste cenário, a necessidade de uma utilização mais consciente e aprimorada da fauna acompanhante e dos subprodutos da pesca, vem sendo cada vez mais ressaltada através do declínio mundial das populações de peixes, do aumento da poluição ambiental e do reconhecimento da limitação dos recursos biológicos[49,51,52].

Dentro dessa fauna associada à pesca camaroeira existe uma grande quantidade de biodiversidade, em sua maioria, peixes demersais – são considerados demersais os peixes que vivem a maior parte da sua vida em associação com o substrato, mesmo tendo capacidade de natação ativa[44,53]. No litoral brasileiro, os animais mais comuns e abundantes capturados por *bycatch* são o *Paralonchurus* brasiliensis (Steindachner, 1875)[53], conhecido popularmente como Maria-Luísa[50,61], o *Micropogonias furnieri* (Desmarest, 1823)[62] e o crustáceo mais abundante é o *Hepatus pudibundus* (Herbst, 1785)[63].

O *Paralonchurus brasiliensis* é um peixe teleósteo, Sciaenidae, encontrado na zona litorânea, em profundidades inferiores a 100 metros – abundantes em profundidades até 20 metros – em fundos lodosos, arenosos ou lamosos. Ocorre na América Central (costa Atlântica do Panamá) até a América do Sul (Argentina, Uruguai, Venezuela e Brasil), normalmente se alimenta de poliquetas e crustáceos e é considerada uma espécie-chave associada a águas rasas[53].

O M*icropogonias furnieri* também é encontrado na zona litorânea, abundantes na faixa de 20 a 40 metros. Ocorrem do Atlântico Ocidental ao Sudoeste, passando pelas Grandes Antilhas, Costa Rica à Argentina, Nicarágua e Brasil. Alimentam-se de crustáceos, moluscos, bentos e, ocasionalmente, outros peixes[54].

O crustáceo *Hepatus pudibundus* faz parte da família *Aethridae* e habita águas rasas e profundas – 10 a 100 metros – comumente encontrado em fundos duros de rochas e cascalhos, são onívoros e se alimentam de sedimento, moluscos, crustáceos peneídeos e pequenos peixes. Podem ser encontrados no Atlântico Ocidental, do Caribe ao Brasil[55].

Mesmo sendo espécies tão frequentes na fauna acompanhante e sabendo da desestruturação que o descarte indevido causa no ecossistema marinho, existem poucos trabalhos sobre bioprospecção e os possíveis usos desses animais. Portanto, é de suma importância conhecer melhor seus potenciais e valores biológicos.

1.5 A PESQUISA E O POTENCIAL DA FAUNA ACOMPANHANTE:

Com o objetivo de aprimorar o aproveitamento da fauna acompanhante, o setor da biotecnologia marinha vem crescendo e a obtenção de ingredientes ativos provenientes de subprodutos da pesca vem sendo de grande anseio, portanto, há um amplo potencial para essas moléculas promissoras[56,57]. O avanço de técnicas e da biotecnologia, tais como espectrometria de massas e cromatografia líquida têm se mostrado muito úteis na prospecção e caracterização de compostos bioativos com atividade biológica terapêutica relacionadas a várias doenças consideradas problemas de saúde pública[58].

Para que possa se tornar possível a produção diversificada e de produtos com diferentes finalidades, as proteínas de pescado precisam, primeiramente, ser processadas por meio de técnicas de hidrólise e análises dos componentes. Os hidrolisados enzimáticos fornecem peptídeos com uma composição bem definida, fazendo com que a absorção pelo organismo seja mais efetiva[59,60].

De acordo com estudos realizados, foram revelados que a fauna acompanhante pode ser fonte de diversas moléculas bioativas, tais como peptídeos, ácidos graxos poliinsaturados, colágeno, quitina, compostos antioxidantes, entre outros[36]. Alguns estudos realizados com essa fauna mostraram que, após serem processadas por procedimentos químicos, é possível obter compostos com efeitos antioxidantes[61], antimicrobianos[26], imunomoduladores[19], anticâncer[62], entre outros. A atividade antioxidante é de grande interesse de estudo, tendo em vista que a oxidação é um processo vital em todos os organismos vivos e, em desequilíbrio pode causar efeitos colaterais, como a produção excessiva de radicais livres[18,63].

As espécies reativas do oxigênio (ERO), tais como ânion superóxido, radical hidroxila e peróxido de hidrogênio são normalmente produzidas nos organismos vivos durando o metabolismo, e estão relacionadas com muitas doenças como, diabetes, hipertensão, doenças cardiovasculares e câncer[64]. Uma das defesas mais eficazes contra diversas doenças é a remoção de radicais livres e das espécies reativas do oxigênio, assim, o papel dos antioxidantes naturais tem recebido muita atenção[14].

Outra bioatividade de grande interesse é a antimicrobiana, tendo em vista que bactérias patogênicas resistentes aos antibióticos tem se tornado um grande problema de saúde pública. Os compostos antimicrobianos são essenciais ao sistema imune inato, podendo apresentar atividade microbicida rápida e potente contra um amplo espectro de microrganismos[65].

Para a obtenção de informações relativas aos componentes de uma amostra, é necessária a realização de alguns processos químicos. A hidrólise é realizada em condições controladas, garantindo assim um perfil peptídico definido – de possível reprodução[57]. Também melhoram as propriedades funcionais e permitem a liberação de peptídeos de diversos tamanhos com diferentes bioatividades, além de garantir a manutenção da qualidade dos compostos14,64. Após a hidrólise, é realizada a liquefação, onde serão obtidas duas frações: a fração solúvel (mais aquosa, composta por polipeptídios) que contém as proteínas hidrolisadas; e a fração insolúvel retém os lipídeos e fosfolipídios, cujo rendimento pode variar de acordo com a enzima escolhida para hidrólise, e forma uma emulsão, o que sugere regiões hidrofóbicas partindo dos peptídeos produzidos[66,67].

Com a necessidade de caracterização, isolamento e sequenciamento dos compostos, são realizados os processos de eletroforese, cromatografia líquida e espectrometria de massas[68]. Esses processos são realizados para a identificação e caracterização de todas as proteínas expressas por um genoma ou tecido, auxilia a compreensão de como essas proteínas funcionam – sozinhas ou em conjunto – dentro de um organismo através do uso de um conjunto de tecnologias analíticas capazes de analisar amostras de alta complexidade simultaneamente[69].

O presente estudo consiste na bioprospecção de moléculas bioativas expressas no músculo de *Paralonchurus brasiliensis, Micropogonias furnieri* e *Hepatus pudibundus*, a fim de identificar e investigar suas atividades biológicas, potencial bioquímico e possíveis meio de utilização.

2. OBJETIVOS

2.1. OBJETIVO GERAL

Realizar a caracterização de compostos expressos no músculo de *Paralonchurus brasiliensis, Micropogonias furnieri* e *Hepatus pudibundus*, a fim de melhor compreender seus valores biológicos, bioquímicos, terapêuticos e nutricionais, visando possíveis usos correlacionados aos problemas de saúde pública.

2.2. OBJETIVOS ESPECÍFICOS:

- Realizar eletroforese para comprovação da eficiência das hidrólises realizadas com Alcalase e com Protamex;
- Traçar o perfil das amostras de *Paralonchurus brasiliensis, Micropogonias furnieri* e *Hepatus pudibundus* a fim de caracterizar os compostos presentes nas mesmas;
- Isolar e identificar os compostos utilizando análises proteômicas;
- Estabelecer a existência de potencial aplicabilidade de tais compostos como nutracêuticos e/ou fármacos.

3. MATERIAL E MÉTODOS

3.1. OBTENÇÃO DAS AMOSTRAS

As amostras foram obtidas por meio de coletas realizadas pela doutoranda Tavani Rocha Camargo, orientanda do Prof. Dr. Wagner Cotroni Valenti do Centro de Aquicultura da Unesp (CAUnesp) de Jaboticabal, as coletas ocorreram na praia de Ubatuba, São Paulo, e foi dividida em duas partes, uma no período de 30/08 a 02/09 em 2017 e outra no período de 01 a 05/03 de 2018. O *Paralonchurus brasiliensis* e o *Micropogonias furnieri* foram os peixes mais abundantes em ambas as coletas.

Foram realizadas algumas análises de composição proximal química dos músculos e brânquias das espécies coletadas (*Paralonchurus brasiliensis, Micropogonias furnieri, Hepatus pudibundus* e *Callinectes ornatus*). Amostras de músculo dos peixes (100g) foram trituradas em liquidificador e homogeneizados com água destilada na proporção 1:2. Antes do processo de hidrólise, as enzimas endógenas contidas nas amostras foram inativadas em banho a 80°C por 20 min[70–72].

3.1.1. HIDRÓLISE

Para a realização da hidrólise, foram utilizadas, separadamente, as enzimas Alcalase e Protamex, ambas são tidas como enzimas com alto potencial de recuperação de proteínas[73]. A Alcalase é uma endopeptidase serina de *Bacillus licheniformis*, fornece informações sobre a estrutura catalítica, conhecida pela tríada catalítica clássica de aminoácidos, sendo a serina uma delas. Também cliva proteínas no meio da cadeia de aminoácidos[73]. A Protamex é uma endoprotease que promove uma hidrólise extensa, consiste em uma mistura de proteases microbianas produzida com enzimas de *Bacillus licheniformis* e *Bacillus amyloliquefaciens*.

A reação de hidrólise se realizou em um reator de vidro, de parede dupla, conectado a um banho termostatizado (MARCONI), utilizando a enzima Alcalase e Protamex de acordo com as condições ótimas de cada enzima (Alcalase: pH 8.0; 50

°C; Protamex: pH 7.0; 50 °C). A proporção enzima e substrato proteico foi de 1:10 (U/g de proteína). O grau de hidrólise (GH) foi monitorado ao longo do processo, e foi determinado de acordo com a fórmula abaixo:

$$GH\ (\%) = [(B \times Nb) / MP] \times (1 / \alpha) \times (1/htot) \times 100$$

Sendo: htot é o número de ligações peptidicas (moles equiv/kg) para pescado (8,6 moles equiv/kg); B é o volume da base consumida durante a hidrólise para manter o pH constante (mL); Nb é a normalidade da base; MP é a massa de proteína (g, determinado em N x fator de Kjeldahl); e α é o grau de dissociação. O grau de dissociação α é calculado segundo a equação:

$$\alpha = (10pH\text{-}pK) / (1+ 10pH\text{-}pK)$$

Sendo: pH é o pH durante a hidrólise e pK é a constante de dissociação. Quando o grau de hidrólise se tornou constante, a reação foi interrompida pela inativação da enzima (90 °C/10 min) em banho termostatizado (Marconi). Após o resfriamento, à temperatura ambiente, as amostras foram centrifugadas (3220 x g por 20 min) (Biosystems MPW-350/350-R - Brasil) no Laboratório de Enzimologia Aplicada (LEA) da Faculdade de Ciências Agrárias e Veterinárias de Jaboticabal. O sobrenadante foi armazenado no ultrafreezer (-80oC) do Centro de Aquicultura da UNESP para posterior liofilização[70–72].

As liofilizações foram realizadas no Setor de Avicultura da Unesp, sob a coordenação da Profa. Dra. Nilva Kazue Sakomura. Após as liofilizações, os hidrolisados foram armazenados em temperatura -18 ± 2 °C. Todo o processo de hidrólise tem duração de aproximadamente quatro horas, pois optou-se por alcançar o GH máximo de cada amostra. Para as análises estatísticas os registros com resíduos studentizado menores que -3 e maiores que 3 desvios-padrão foram retirados do conjunto de dados, assim como valores influentes. Após a retirada dos valores discrepantes, os resíduos atenderam as pressuposições de homocedasticidade e a normalidade, verificadas pelos testes de boxcox e Cramer-von Mises, respectivamente[70–72].

A análise de variância (ANOVA) e o teste de comparação de médias (Tukey) ao nível de significância média (P < 0,05) foi realizada por meio do pacote agricolae (Mendiburu, 2017) no software R (R Core Team, 2017) [70–72].

A Figura 1 mostra um esquema visual das análises realizadas até a obtenção dos hidrolisados proteicos.

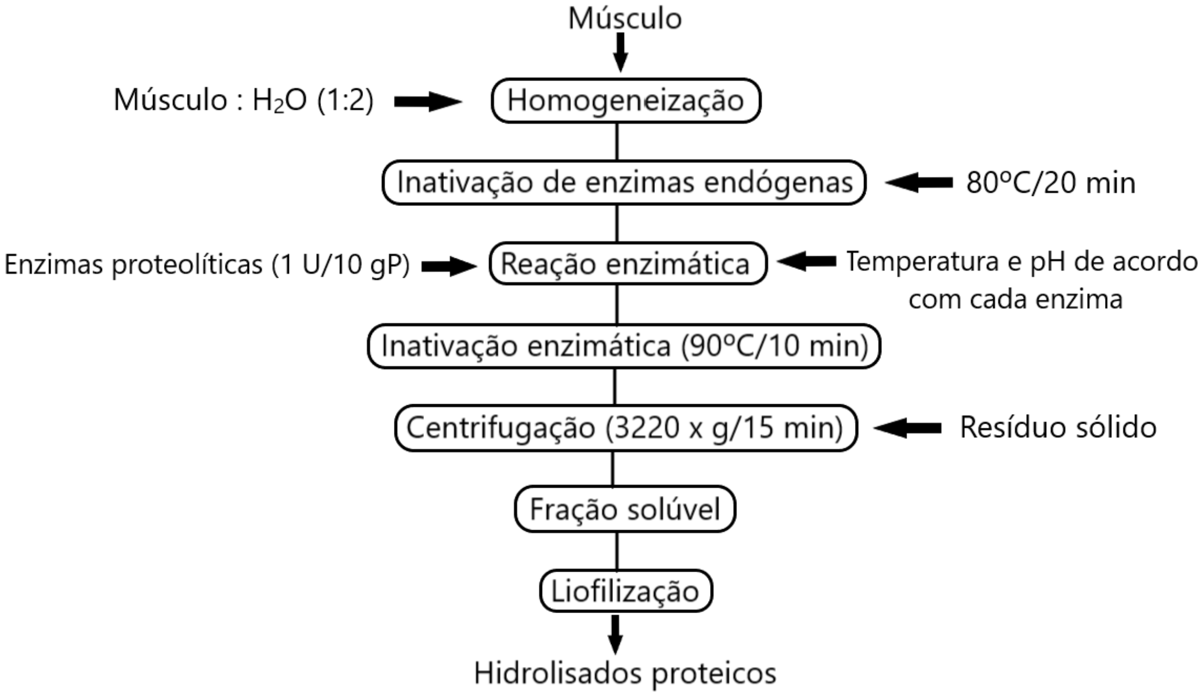


Figura 1: Esquema explicativo das fases do processo de hidrólise realizada nas amostras de músculo dos peixes.

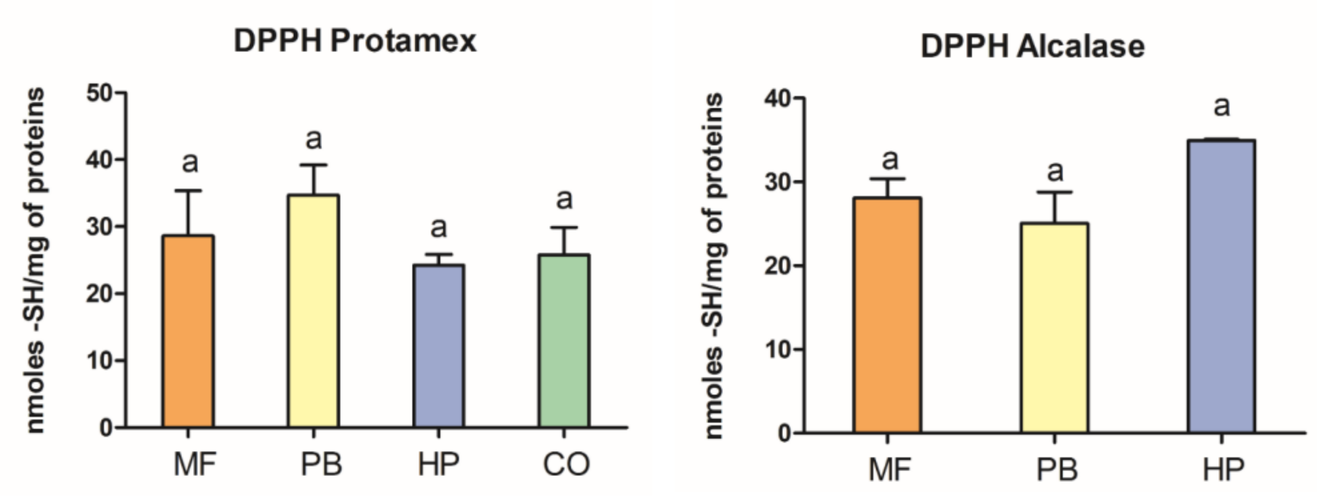
3.1.2. ANÁLISES ANTIOXIDANTES

Após a hidrólise, foram realizados testes para avaliar a capacidade antioxidante dos hidrolisados através de três métodos: capacidade antioxidante total contra radicais peroxil, capacidade antioxidante total pelo método de DPPH e dosagem dos grupos sulfidrilas[70–72].

O método DPPH baseia-se na transferência de elétrons de um composto antioxidante para um oxidante, dessa maneira, o antioxidante em estudo reage com o radical DPPH convertendo-o em sua forma reduzida. É possível notar tal mudança pela coloração que inicialmente é violeta e torna-se mais clara, podendo chegar a tons amarelados. O grau deste descoramento indica a habilidade do antioxidante em sequestrar o radical livre.

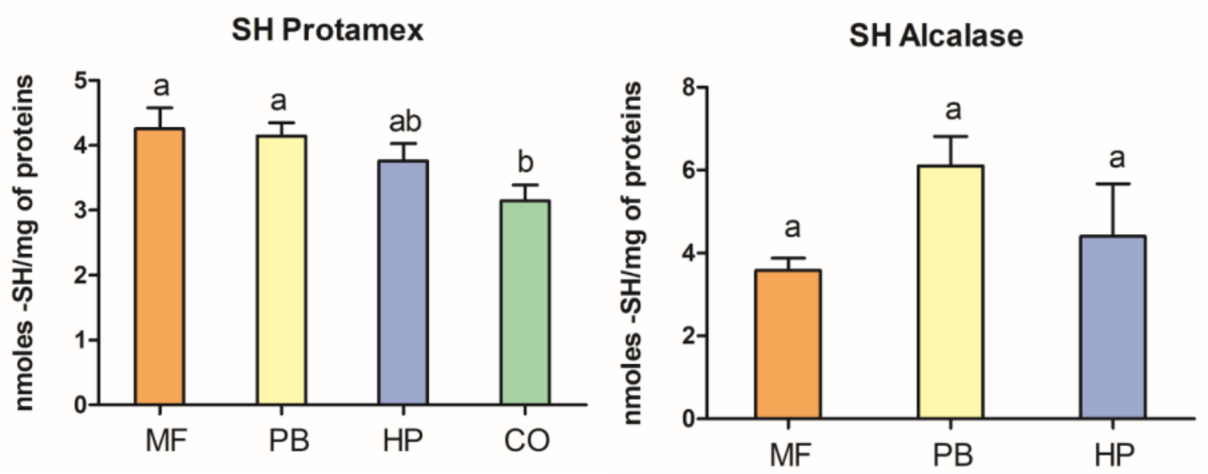
A capacidade antioxidante contra radicais peroxil (ACAP) baseia-se na detecção de espécies reativas de oxigênio (ERO) por flourometria e foi realizado de acordo com Amado *et al*. (2009)[74] e Zamora-Sillero *et al*. (2018)[75] com algumas modificações. E para a realização do teste de dosagem dos grupos sulfidrilas foram utilizados os compostos tiólicos (glutationa, cisteina e proteínas tiólicas) são antioxidantes que contêm em sua estrutura o grupamento -SH e estão envolvidos no sequestro de radicais livres, sendo capazes de quebrar íons metálicos danosos, desempenhando uma importante função na defesa antioxidante (Hermes-Lima, 2004). O teor total dos grupos sulfidrila (T-SH) foi determinado baseado em White *et al*. (2003)[76] com modificações.

Os resultados de capacidade dos hidrolisados em sequestrar o radical livre DPPH indicaram que as quatro espécies estudadas possuem capacidade de eliminar o radical DPPH, sendo assim, podem ter em sua composição peptídeos que atuam como doadores de elétrons que reagem com os radicais livres para transformá-los e moléculas estáveis. Nos hidrolisados obtidos com a enzima Protamex (Figura 2), embora sem diferenças significativas (P > 0,05), pode-se observar que *P. brasiliensis* apresentou maior atividade antioxidante contra radicais DPPH, seguido de *M. furnieri*, *H. pudibundus* apresentou menor atividade antioxidante. Já nas amostras hidrolisadas com a enzima Alcalase (Figura 3), *H. pudibundus* apresentou maior atividade antioxidante.



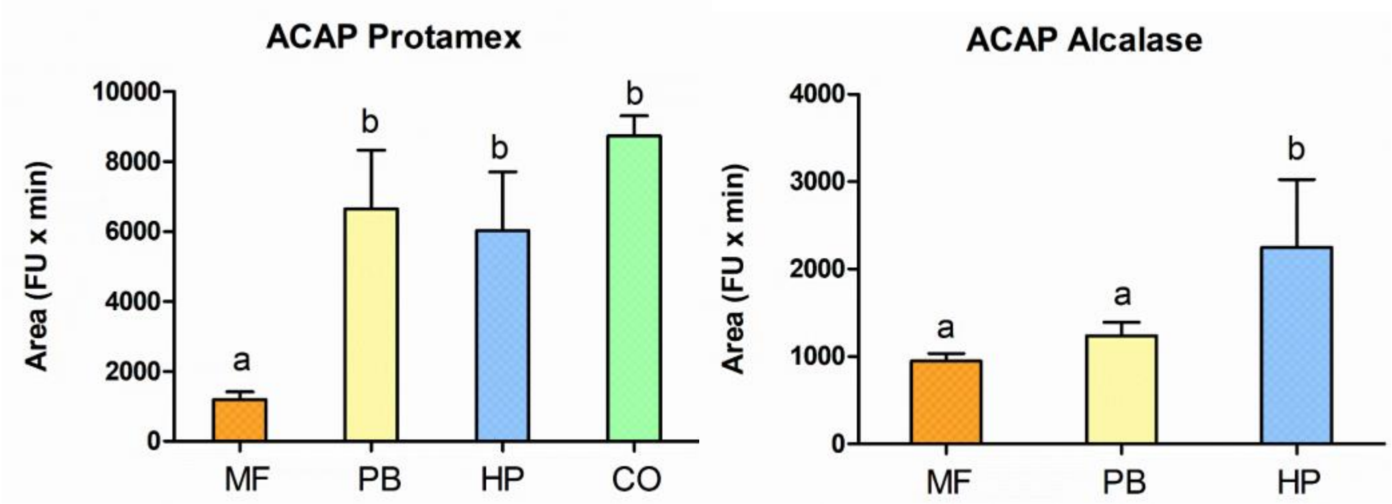
Figuras 2 e 3: Capacidade dos hidrolisados em sequestrar o radical livre DPPH. Dados expressos como média (n=6). Letras idênticas indicam ausência de diferenças estatísticas (P > 0.05). CO= *Callinectes ornatus*; HP= *Hepatus pudibundus*; MF= *Micropogonias furnieri*; PB= *Paralonchurus brasiliensis*.

Com os resultados da dosagem dos grupos sulfidrilas é possível observar que as amostras de *P. brasiliensis e M. furnieri* hidrolisadas com Protamex (Figura 4) apresentaram as maiores concentrações de grupos sulfidrilas, seguidas dos crustáceos *H. pudibundus* e *C. ornatus* com as menores concentrações. Os hidrolisados com a enzima Alcalase (Figura 5) não apresentaram diferenças estatísticas, porém os hidrolisados de *P. brasiliensis* exibiram a maior concentração de -SH, o que também se observa quando comparado com os resultados de *M. furnieri*.



Figuras 4 e 5: Concentração de grupos sulfidrilas das diferentes amostras obtidas pelo processo de hidrolise enzimática com as enzimas Protamex e Alcalase. Dados expressos como média (n=6). Letras idênticas indicam ausência de diferenças estatísticas (P > 0.05). CO= *Callinectes ornatus*; HP= *Hepatus pudibundus*; MF= *Micropogonias furnieri*; PB= *Paralonchurus brasiliensis*.

Com relação aos resultados obtidos da capacidade dos hidrolisados proteicos das quatro espécies estudadas para redução de radicais peroxil, a amostra de *Micropogonias furnieri* hidrolisada com a enzima Protamex (Figura 6) apresentou a menor capacidade antioxidante em comparação com *C. ornatus, H. pudibundus* e *P. brasiliensis* quando hidrolisados com a mesma enzima. Nas amostras hidrolisadas com a enzima Alcalase (Figura 7), *H. pudibundus* apresentou a maior capacidade antioxidante. De uma maneira geral, pode-se observar que os resultados com a enzima Protamex foram melhores do que com a enzima Alcalase.



Figuras 6 e 7: Capacidade antioxidante total contra radicais peroxil dos hidrolisados proteicos hidrolisados obtidos com as enzimas Alcalase e Protamex. Dados expressos como média (n=6). Letras idênticas indicam ausência de diferenças estatísticas (P > 0.05). CO= *Callinectes ornatus*; HP= *Hepatus pudibundus*; MF= *Micropogonias furnieri*; PB= *Paralonchurus brasiliensis*.

Os resultados das análises de antioxidantes descritos acima por Camargo *et al*.[70–72], indicam que os hidrolisados proteicos dos músculos das quatro espécies do bycatch estudadas possuem propriedade antioxidante. Entretanto, os hidrolisados proteicos de *P. brasiliensis* apresentaram maior capacidade antioxidante *in vitro*, evidenciado pela sua grande concentração de grupos sulfidrilas e pela eliminação de radicais DPPH. De uma maneira geral, houve poucas diferenças entre os músculos hidrolisados com a enzima Alcalase e Protamex, porém *Paralonchurus brasiliensis* apresentou a maior concentração de grupos sulfidrilas quando hidrolisado com a enzima Alcalase[70–72].

3.1.3. ARMAZENAMENTO DAS AMOSTRAS

As amostras utilizadas pela doutora Tavani Rocha Camargo foram enviadas para o Departamento de Química e Bioquímica no Campus da Unesp em Botucatu, onde alunos do professor Willian Fernando Zambuzzi realizaram análises para avaliar se os hidrolisados eram citotóxicos para as células ou se interferiam no processo de adesão. Logo após, foram recolhidas e encaminhadas ao Centro de Estudo de

Animais Peçonhentos – CEVAP/UNESP onde foram conservadas em geladeira a 4ºC de acordo com as recomendações.

3.2. ELETROFORESE EM SDS-PAGE

As amostras foram separadas, pesadas (100µL), diluídas em tampão de amostra (0,06M Tris; 2% SDS; 10% Glicerol; 0,025% Azul de Bromofenol; pH 6,8) e aquecidas durante 5 minutos à 70ºC em banho-maria.

O gel, devidamente polimerizado, foi montado em cuba de eletroforese vertical Mini Protean II (Bio-Rad Laboratories), contendo tampão Tris Glicina-SDS, com pH 8,3. 50µg da amostra diluído em tampão de amostra (0,06 M Tris; 2%SDS; 10% Glicerol; 0,025% Azul de Bromofenol; pH 6,8) foram aplicados, em cada poço do gel. Para a separação das proteínas, a eletroforese foi efetuada com voltagem contínua de 150V por 12 minutos, para alinhar as proteínas, em seguida efetuamos um aumento na voltagem para 200 V por 40 minutos.

Quando o indicador azul de bromofenol atingiu a porção inferior do gel, a fonte foi desligada e o gel transferido à um recipiente com solução corante Coomassie Briliant Blue R250 0,025% (Sigma Chem. Co). O gel foi corado por 40 minutos e descorado em solução Destain (etanol 30% [v/v] e ácido acético 10%[v/v]) até o background do gel (plano de fundo das proteínas) alcançar a transparência.

Para separação de moléculas com tamanhos e cargas diferentes foram realizados quatro géis de poliacrilamida, dois a 12% e dois a 20% preparados com tampão Tris-HCl pH 8,8; SDS (Dodecil sulfato de sódio) (Sigma Chem. Co) à 10% (m/v); Acrilamida: Bis 30, 0:0,8 (Sigma Chem. Co); persulfato de amônio (Sigma Chem. Co) 10% (v/v) e Temed (N´, N´, N´, N´- tetrametilenodiamino) (Sigma Chem. Co), podendo assim separar as amostras de Alcalase e Protamex.

Após a corrida eletroforética, corado em Solução de Comassie Blue R-250, durante 30 minutos. A descoloração do gel foi efetuada em banhos sucessivos com solução de ácido acético-etanol-água (10:30:60). Após a descoloração, foi feira a captura de imagem do gel.

3.3. CROMATOGRAFIA LÍQUIDA DE ALTA EFICIÊNCIA / FASE REVERSA (CLAE/FR)

Para o conhecimento do perfil cromatográfico das amostras de *Paralonchurus brasiliensis, Micropogonias furnieri* e *Hepatus pudibundus* hidrolisados tanto com Alcalase quanto com Protamex, foi utilizado um sistema de HPLC Shimadzu® modelo LC-20AT, equipado com detector de luz ultravioleta do tipo arranjo de diodos modelo SPD-M20A, constituído por duas bombas LC-20AT (bombas A e B), injetor automático modelo SIL-20AC HT, com um coletor automático modelo FRC-10A e um sistema controlador modelo CBM-20AT.

O controle de aquisição de dados foi feito através do software LC Solution. Todos os solventes orgânicos utilizados foram de grau HPLC e a água Milli-Q obtida em ultrapurificador de água Milipore®.

O cromatograma foi obtido sob fase reversa, utilizando uma coluna analítica C-18 (4,6 X 250 mm) (Wakopak®). As amostras liofilizadas, na concentração de 0,5 mg / 0,5 mL de Ácido trifluoroacético (TFA) 0,1% (v/v) foram injetadas manualmente no sistema. A eluição das amostras foi feita através de dois solventes: (A) TFA 0,1% (v/v) e (B) TFA 0,1% (v/v) e Acetonitrila 90% (v/v), através de um gradiente de 0 a 100% do solvente B por 20 minutos. O fluxo utilizado foi de 1 mL/min e a eluição foi monitorada na absorbância de 214nm.

Este procedimento foi realizado para todas as amostras. Esta metodologia foi desenvolvida pela área laboratorial do Centro de Estudos de Venenos e Animais Peçonhentos (CEVAP) – UNESP.

3.4. Espectrometria de Massas (MALDI-TOF)

A espectrometria de massa tipo MALDI-TOF, foi realizada no Departamento de Bioquímica do Instituto Butantan.

As análises foram realizadas em um instrumento Axima Performance MS/MS (Shimadzu®). As amostras, em solução, foram misturadas na proporção 1:1 (v:v) com uma solução supersaturada de matriz recomendada para a análise de peptídeos (ácido cinâmico), proteínas (ácido sinápico) ou para baixa massa molecular (DHB), conforme o caso e a mistura foi depositada sobre a placa de amostragem (0,4-0,8 µL) para evaporação dos solventes.

Foi utilizado o modo automático de controle do equipamento e aquisição de dados via software de controle do equipamento (Launchpad, Shimadzu Biotech®).

3.5. Espectrometria de Massas (LC/MS)

A espectrometria de massas LC/MS foi realizada no Departamento de Bioquímica do Instituto Butantan.

As amostras previamente secas foram dissolvidas em 0,1% ácido fórmico e depositadas no amostrador do auto injetor. 20 µL de amostra foram injetadas em um sistema de HPLC/Espectrometria de Massas (LC/MS) tipo IT-TOF (Shimadzu®) sob fluxo constante de 0.2mL/min, e submetida a uma separação cromatográfica por fase reversa em coluna Kinetex C18 (2.1 x 50 mm), utilizando como solventes A: ácido fórmico 0,1% e solvente B: ACN: H2O:ácido fórmico/900:100:0,1 e um programas de gradiente linear de 0 a 100% de B em 30 minutos.

O controle do instrumento, a aquisição e o processamento de dados foram realizados pelo pacote de programas LCMSolution (Shimadzu®).

3.6. Espectrometria de Massas (LC-MSMS)

A análise proteômica LC-MSMS também foi realizada no Departamento de Bioquímica do Instituto Butantan.

As amostras foram então analisadas em sistema de cromatografia líquida-espectrometria de massas em equipamento ESI-IT-TOF acoplado a UFLC (20A Prominence, Shimadzu®). Cada amostra foi injetada em uma coluna C18 (Kinetex C18, 5 µm; 50 × 2,1 mm) em um sistema de solvente binário: (A) água : ácido (999 : 1) e (B) ACN : água : ácido (900 : 99: 1). Um gradiente de eluição de 0-100% de solvente B foi utilizado por 35 minutos a um fluxo constante de 0,2 mL.min-1. As amostras foram monitoradas por um detector Shimadzu® SPD-M20A PDA antes de serem injetadas no espectrômetro de massa.

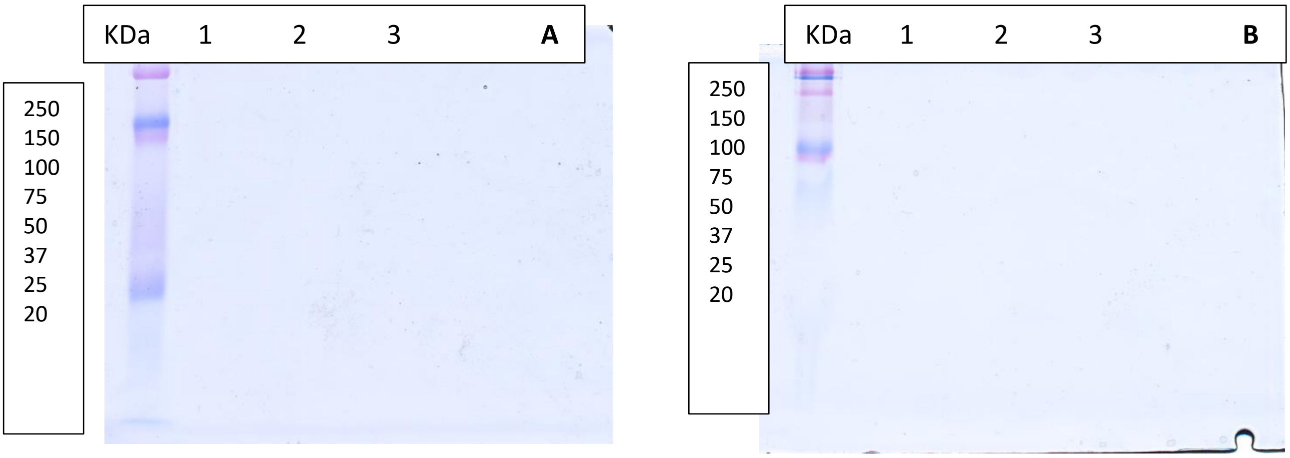
A tensão da interface foi de 4,5 kV; a tensão capilar de 1,95 kV, a 200ºC; e a fragmentação induzida por uma colisão de argônio, com 55% de "energia". Os espectros de MS foram adquiridos no modo positivo, na faixa de m / z de 350-1400 e os espectros de MS / MS foram coletados na faixa de 50 a 1950 m / z.

Os arquivos LCD foram convertidos em arquivos MGF pela ferramenta Shimadzu® LCMSolution e carregados no Peaks Studio V7.0 (BSI, Canadá). Os dados foram processados de acordo com os seguintes parâmetros: MS e massa de erro MS / MS foram 0,1 Da; oxidação de metionina e carbamidometilação como modificação variável e fixa, respectivamente; tripsina como enzima de clivagem; clivagens perdidas máximas (3), PTMs variáveis máximas por peptídeos (3) e clivagem não específica (ambas); a taxa de descoberta falsa foi ajustada para ≤0,5%; apenas proteínas com pontuação 20 e contendo pelo menos 1 peptídeo único foram consideradas neste estudo.

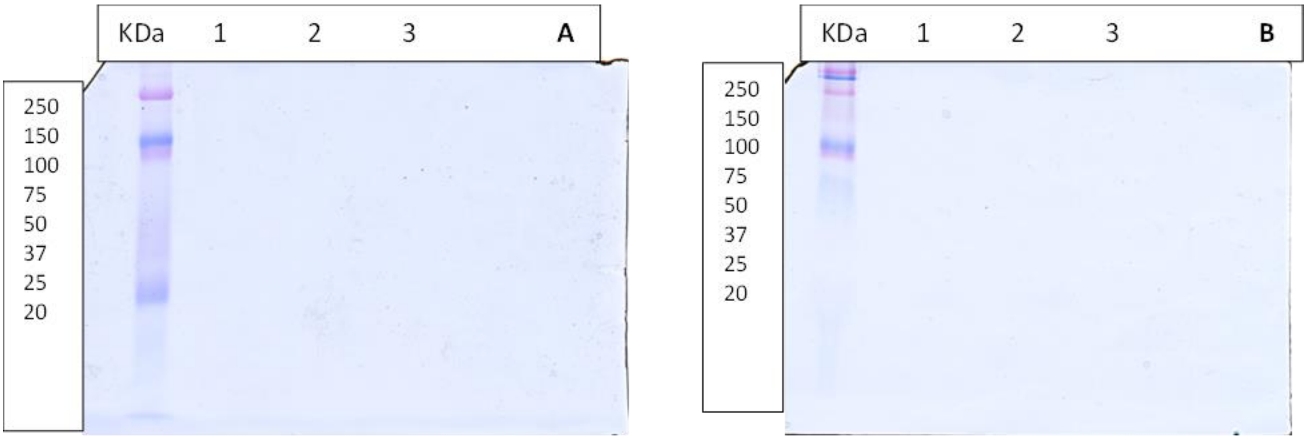
4. RESULTADOS

4.1 ELETROFORESE SDS-PAGE

Os resultados obtidos pela eletroforese SDS-PAGE revelaram que as hidrólises foram concluídas com êxito, podendo ser observados nas Figuras 8 a 11. A ausência de bandas proteicas nos géis de malha 12% e 20% representam a efetividade das hidrólises, representando amostras sem proteínas intactas, apenas com peptídeos.



Figuras 8 e 9: Eletroforese SDS-PAGE realizada com géis de malha 12% (**A**) e 20% (**B**), respectivamente, das amostras de *Paralonchurus brasiliensis* (**1**)*, Micropogonias furnieri* (**2**) *e Hepatus pudibundus* (**3**) hidrolisadas com Alcalase. As bandas marcadas à esquerda dos géis representam o padrão de massa molecular.



Figuras 10 e 11: resultado da eletroforese SDS-PAGE realizada com géis de malha 12% (**A**) e 20% (**B**), respectivamente, das amostras de *Paralonchurus brasiliensis* (**1**)*, Micropogonias furnieri* (**2**) *e Hepatus pudibundus* (**3**) hidrolisadas com Protamex. As bandas marcadas à esquerda dos géis representam o padrão de massa molecular.

4.2 CROMATOGRAFIA LÍQUIDA DE ALTA EFICIÊNCIA COM DETECTOR UV (CLAE)

A cromatografia foi utilizada para se obter uma caracterização geral das amostras e visualizar qual seria o perfil dos compostos existentes, relacionando a complexidade e a polaridade.

Quanto mais próximo do início da corrida, significa que os compostos encontrados são mais hidrofílicos, ou seja, possuem maior interação com a água. Os compostos que surgem em picos mais próximos ao final da corrida, são os mais hidrofóbicos, ou seja, possuem maior interação com o composto orgânico (acetonitrila), portanto, são apolares.

As amostras de *Paralonchurus brasiliensis* indicaram poucas diferenças de picos ao comparar a amostra hidrolisada com Alcalase (Figura 12) com a hidrolisada Protamex (Figura 13), sendo possível notar a semelhança dos perfis na Figura 14.

Em ambos os perfis cromatográficos de *Paralonchurus brasiliensis* os picos começaram a surgir em aproximadamente 9,2 minutos de corrida e eluiram a 45% de acetonitrila, portanto, é uma amostra com picos intermediários a apolares.

É possível observar que a amostra hidrolisada com Alcalase obteve quatro picos majoritários, sendo três com polaridade intermediária e um apolar, enquanto a amostra hidrolisada com Protamex apresentou apenas três picos majoritários com polaridade intermediária.

Figura 12: Perfil cromatográfico da amostra de *Paralonchurus brasiliensis* hidrolisado com Alcalase.

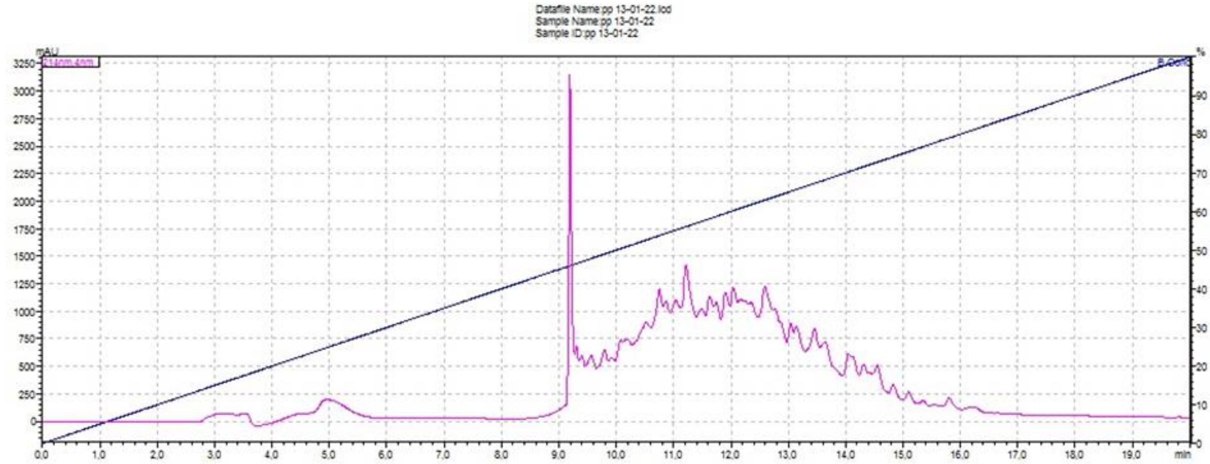


Figura 13: Perfil cromatográfico da amostra de *Paralonchurus brasiliensis* hidrolisado com Protamex.

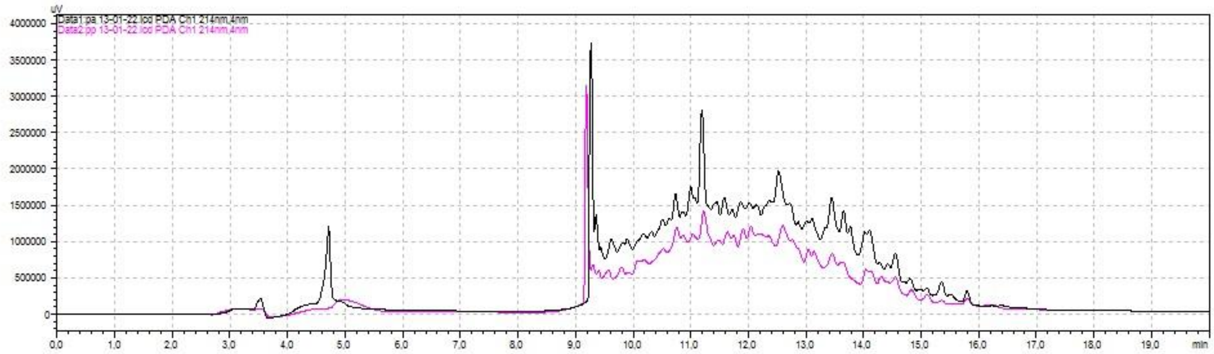


Figura 14: Perfil cromatográfico da amostra de *Paralonchurus brasiliensis* hidrolisado com Alcalase (cor preta) e Protamex (cor rosa).

As amostras de *Micropogonias furnieri* apresentaram perfis peptídicos mais similares, onde os picos estão regulares em relação a amplitude e espaçamento, tendo como diferencial apenas o tempo de início dos picos, sendo 9,2 minutos na amostra hidrolisada com Alcalase (Figura 15) e 9,6 minutos na amostra hidrolisada com Protamex (Figura 16), porém ambos são classificados como polaridade intermediária a apolar devido a porcentagem de eluição começar em 45 a 50%.

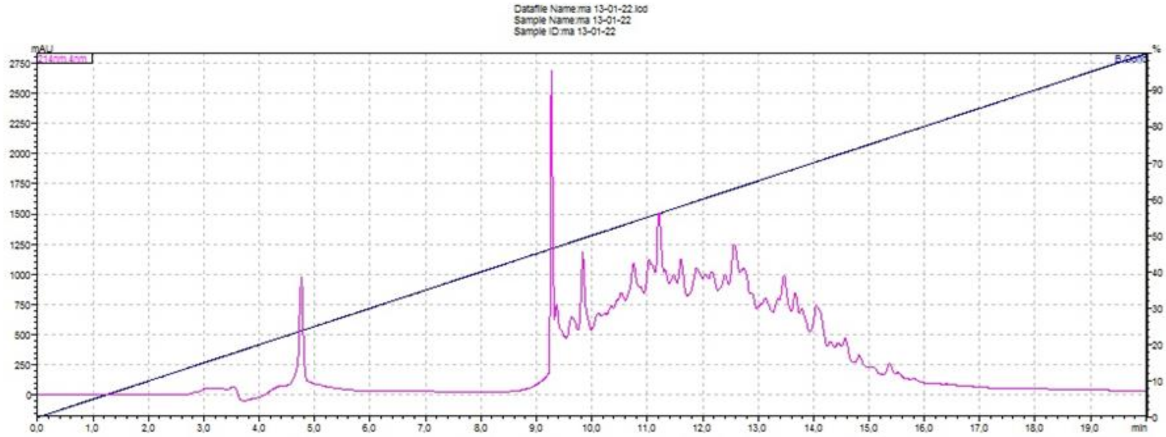


Figura 15: Perfil cromatográfico da amostra de Micropogonias furnieri hidrolisado com Alcalase.

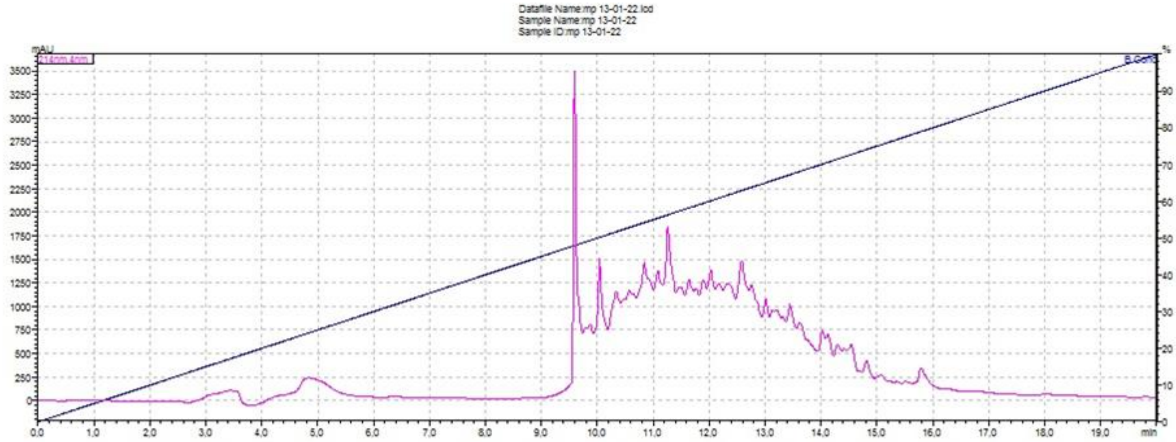


Figura 16: Perfil cromatográfico da amostra de *Micropogonias furnieri* hidrolisado com Protamex.

Na figura 17 é possível observar a semelhança do perfil peptídico de ambas as amostras e a diferença de amplitude do primeiro pico. Na amostra hidrolisada com Alcalase foram encontrados seis picos majoritários, portanto seis produtos principais da digestão, e quatro picos majoritários da amostra hidrolisada com Protamex.

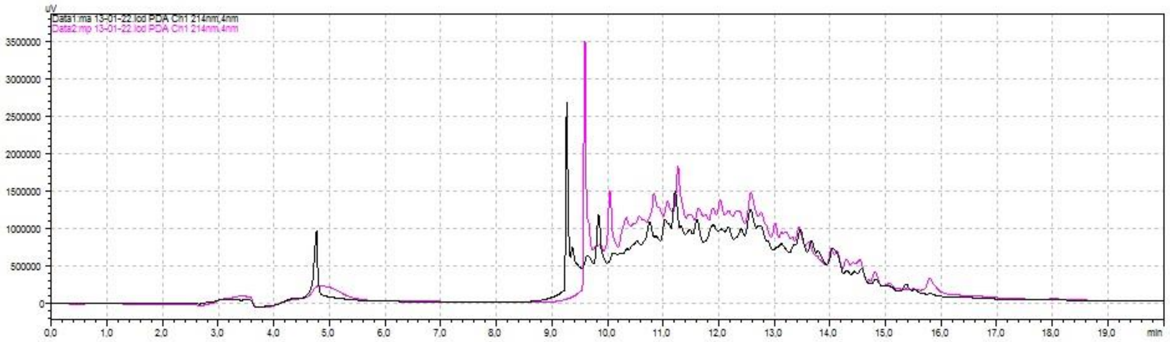


Figura 17: Perfil cromatográfico da amostra de *Micropogonias furnieri* hidrolisado com Alcalase (cor preta) e Protamex (cor rosa).

A maioria dos picos majoritários encontrados possuem polaridade intermediária contendo apenas um pico majoritário polar na amostra com Protamex. E ambas as amostras possuem pequenos picos apolares. As amostras de *Micropogonias furnieri* apresentam polaridades similares se comparadas com as amostras de *Paralonchurus brasiliensis.* As amostras de *Hepatus pudibundus* (crustáceo) se mostraram mais peculiares do que as de *Paralonchurus brasiliensis* e *Micropogonias furnieri* (peixes) tendo grande diferença entre os perfis.

É possível observar que na amostra hidrolisada com Alcalase (Figura 18) foram obtidos sete picos majoritários, onde quatro possuem polaridade intermediária e três são apolares, em contrapartida, na amostra com Protamex (Figura 19), foram obtidos apenas três picos majoritários, sendo dois polares e um apolar. Na Figura 20 fica nítida a diferença dos perfis peptídicos das amostras hidrolisadas com diferentes enzimas. Valendo ressaltar que a amostra hidrolisada com Alcalase mostrou mais resultado relacionado com a polaridade dos compostos.

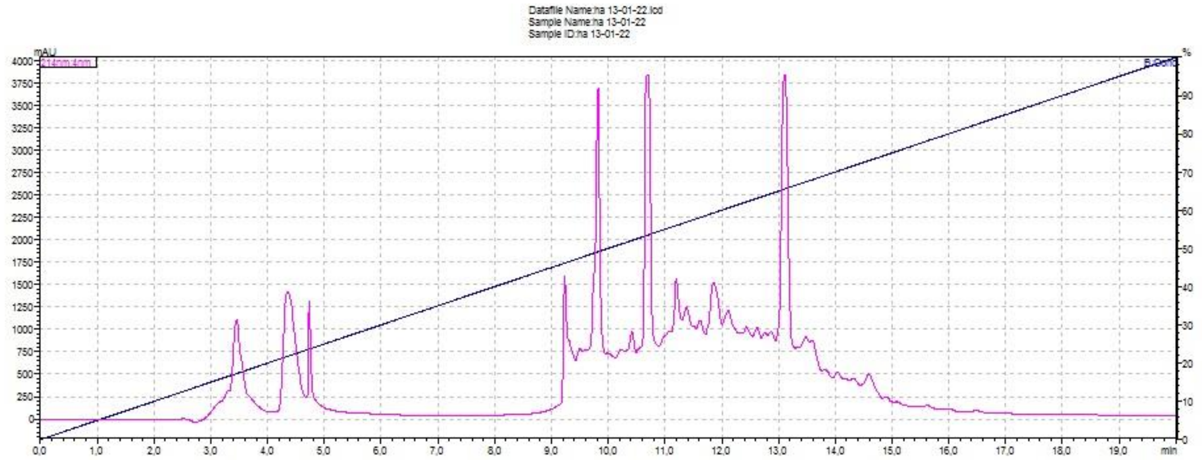


Figura 18: Perfil cromatográfico da amostra de *Hepatus pudibundus* hidrolisado com Alcalase.

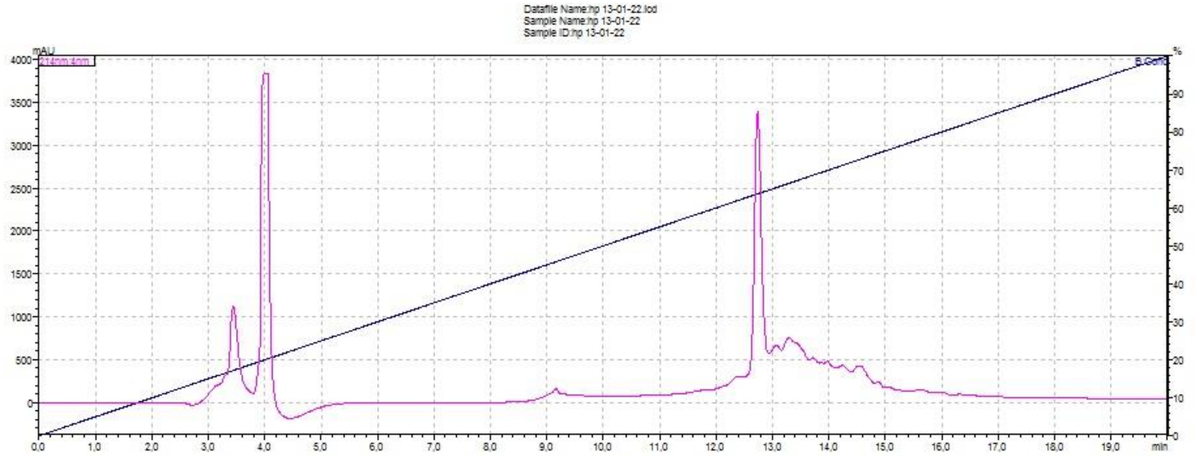


Figura 19: Perfil cromatográfico da amostra de *Hepatus pudibundus* hidrolisado com Protamex.

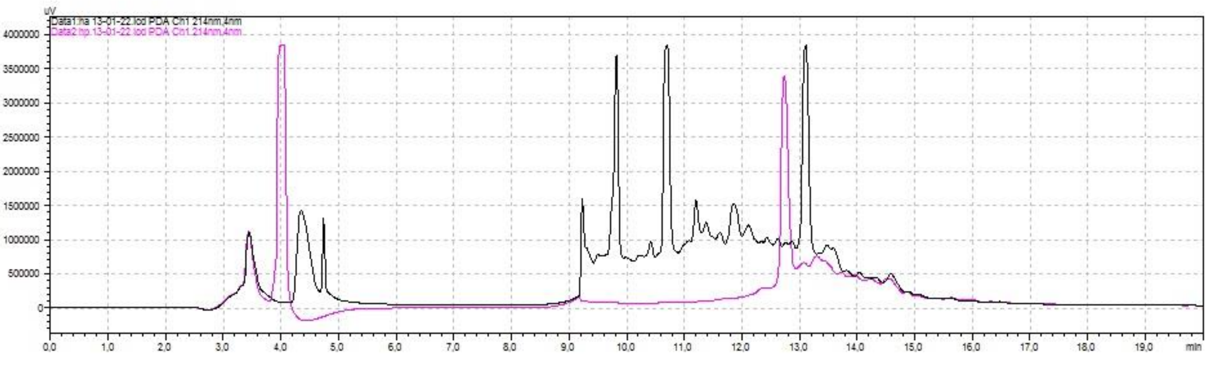


Figura 20: Perfil cromatográfico da amostra de *Hepatus pudibundus* hidrolisado com Alcalase (cor preta) e Protamex (cor rosa).

4.3 ESPECTROMETRIA DE MASSAS TIPO MALDI-TOF

A espectrometria de massas tipo MALDI-TOF forma espectros de massa de acordo com sua razão massa/carga (m/z), os picos correspondem a massa molecular e indicam a quantidades de variáveis de cada substância analisada. Esse tipo de espectrometria é muito utilizado em análises de misturas e, portanto, foi um dos métodos escolhidos na realização do presente estudo.

A Figura 21 mostra o perfil da amostra de *Paralonchurus brasiliensis* hidrolisado com Alcalase, é possível observar um pico principal com uma massa de 1181,40 Da, sendo este constituído por 11 aminoácidos. Foram encontrados seis picos com 15 a 27 aminoácidos, com massas entre 1554,4 Da a 2774,5 Da.

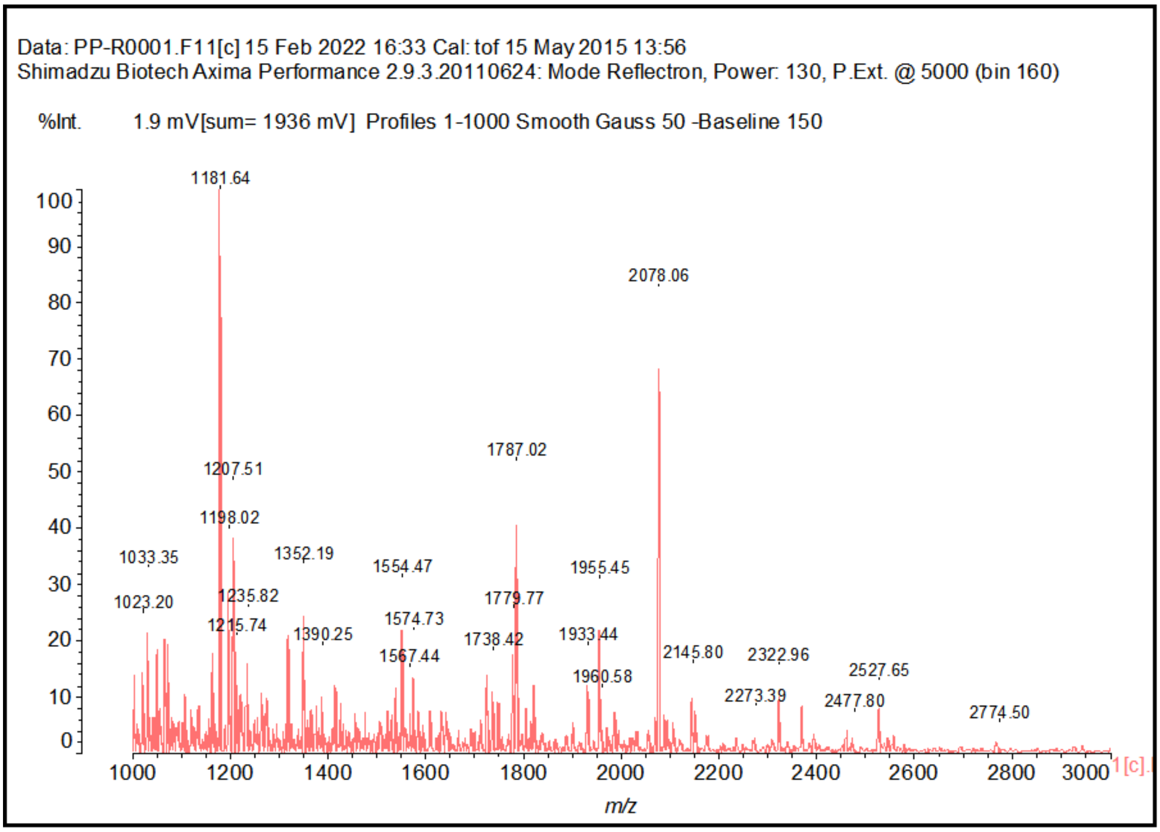
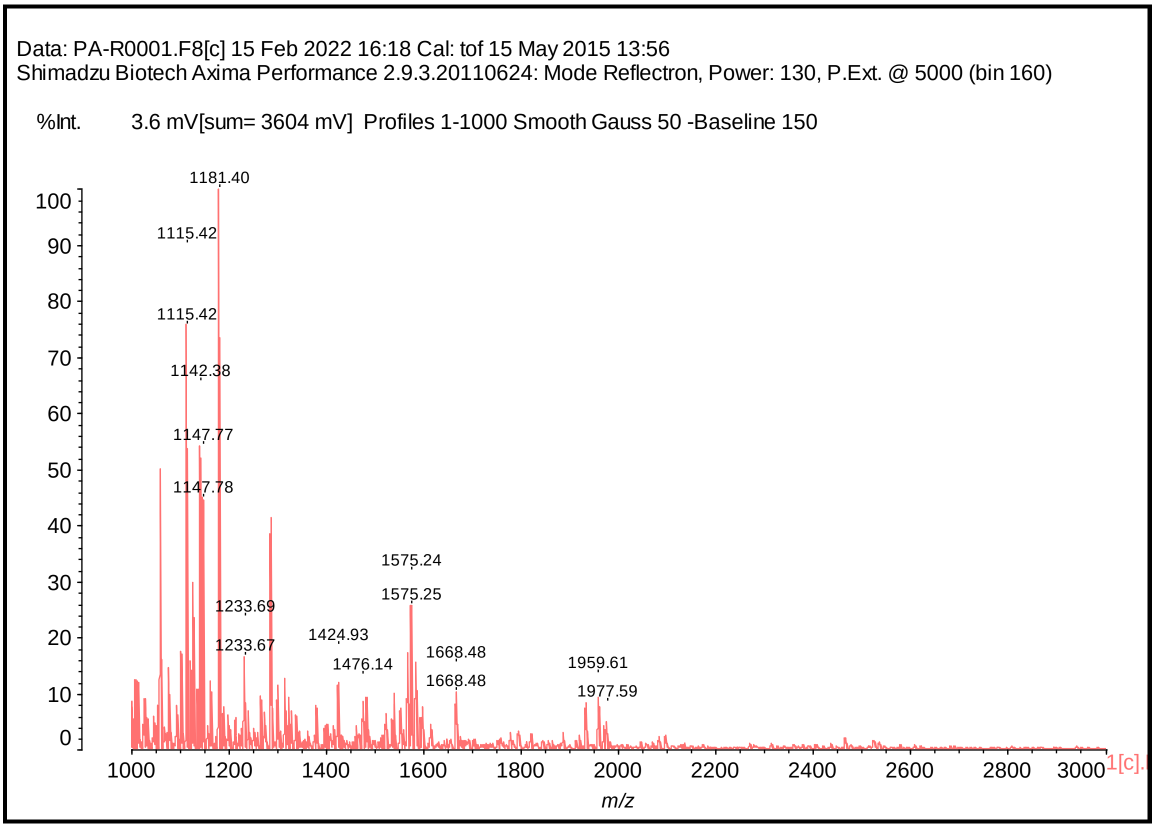


Figura 21: Resultado da análise de espectrometria de massas tipo MALDI-TOF gerado a partir da amostra de *Paralonchurus brasiliensis* hidrolisado com a enzima Alcalase.

Enquanto na amostra de *Paralonchurus brasiliensis* hidrolisado com Protamex os resultados foram mais promissores, tendo em vista que houve dezesseis picos de peptídeos com potencial atividade biotecnológica contendo entre 11 a 20 aminoácidos, sendo o de maior massa 1977,5 Da, contendo de 19 a 20 aminoácidos em sua cadeia (Figura 22).



Data: PA-R0001.F8[c] 15 Feb 2022 16:18 Cal: tof 15 May 2015 13:56
Shimadzu Biotech Axima Performance 2.9.3.20110624: Mode Reflectron, Power: 130, P.Ext. @ 5000 (bin 160)

%Int. 3.6 mV[sum= 3604 mV] Profiles 1-1000 Smooth Gauss 50 -Baseline 150

Figura 22: Resultado da análise de espectrometria de massas tipo MALDI-TOF gerado a partir da amostra de *Paralonchurus brasiliensis* hidrolisado com a enzima Protamex.

Na amostra de *Micropogonias furnieri* hidrolisada com Alcalase, o pico com maior intensidade possui massa de 1102,98 Da, ao total foram dezoito picos de interesse, onde nove possuem cadeias com 15 a 25 aminoácidos (Figura 23). Por outro lado, a amostra hidrolisada com Protamex apresentou o maior pico com massa equivalente a 1181,60 Da, um total de vinte e dois picos, sendo treze com cadeias de 15 a 26 aminoácidos (Figura 24).

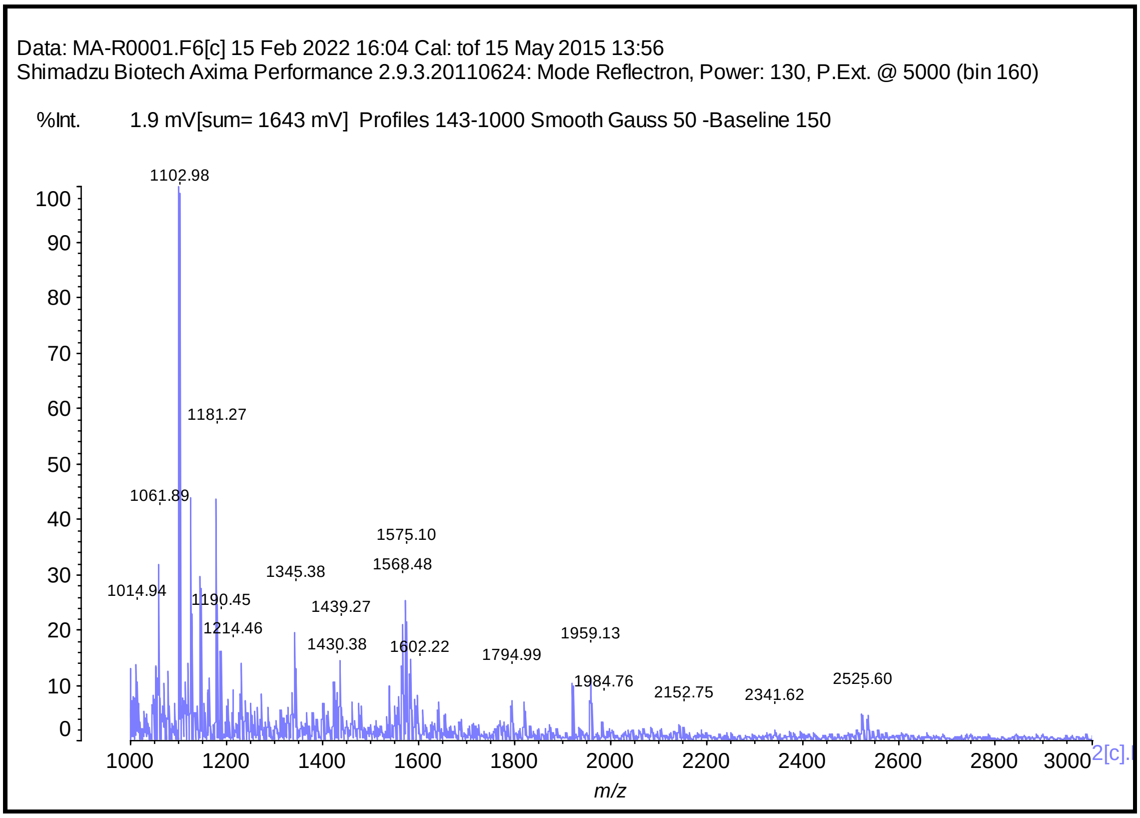


Figura 23: Resultado da análise de espectrometria de massas tipo MALDI-TOF gerado a partir da amostra de *Micropogonias furnieri* hidrolisado com a enzima Alcalase.

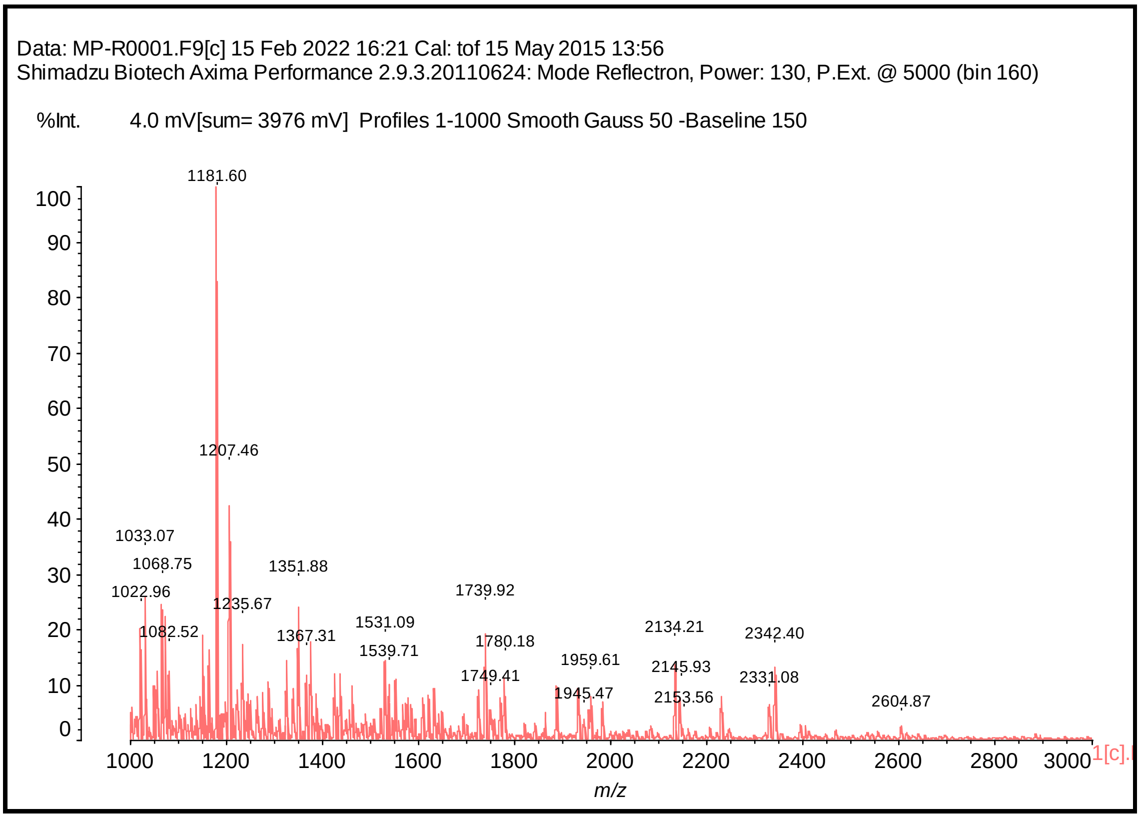


Figura 24: Resultado da análise de espectrometria de massas tipo MALDI-TOF gerado a partir da amostra de *Micropogonias furnieri* hidrolisado com a enzima Protamex.

A análise das amostras de *Hepatus pudibundus* se mostraram mais peculiares e com grande potencial. Na amostra hidrolisada com Alcalase (Figura 25), foram reconhecidos vinte e três picos, onde treze estão no parâmetro de cadeias com 16 a 29 aminoácidos, a maior massa molecular encontrada foi de 2939,54 Da e o pico com maior interação possui 1686 Da. Na amostra hidrolisada com Protamex (Figura 26) foram constatados treze picos de peptídeos com 16 a 27 aminoácidos e um total de vinte e um picos. O pico com maior interação possui massa molecular de 1685,97 Da.

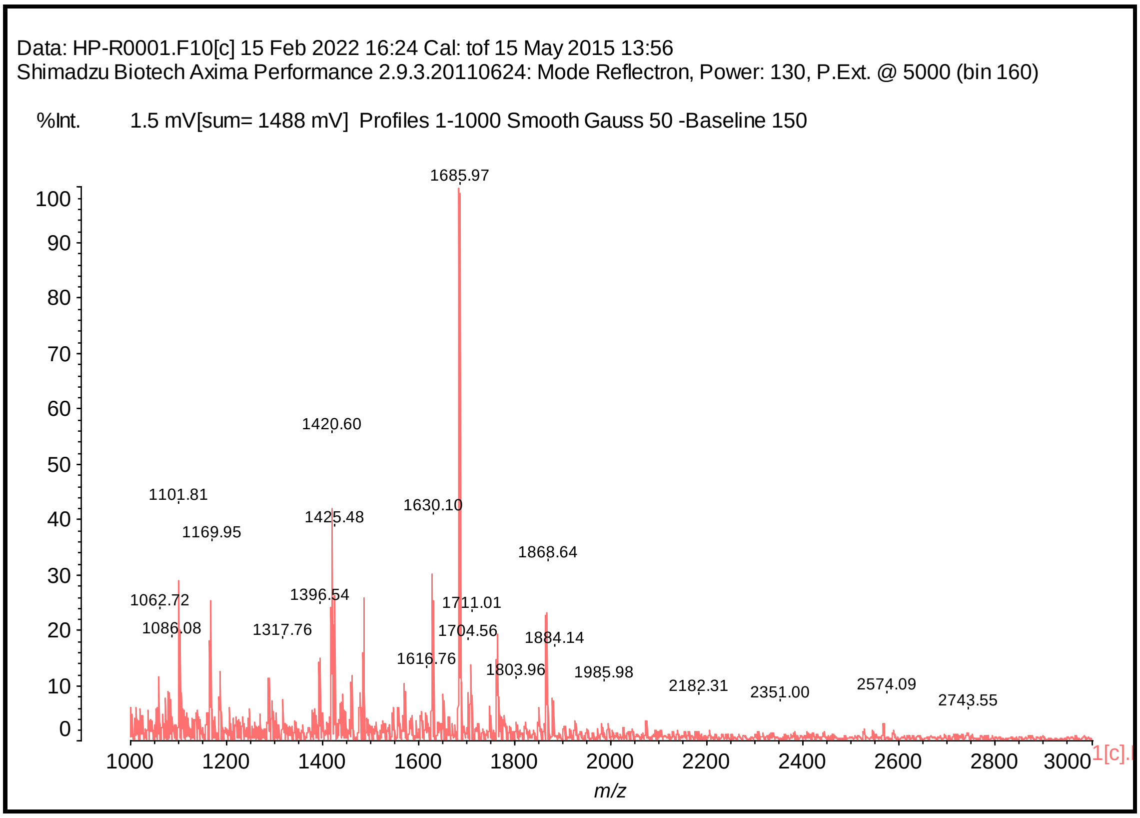


Figura 25: Resultado da análise de espectrometria de massas tipo MALDI-TOF gerado a partir da amostra de *Hepatus pudibundus* hidrolisado com a enzima Alcalase.

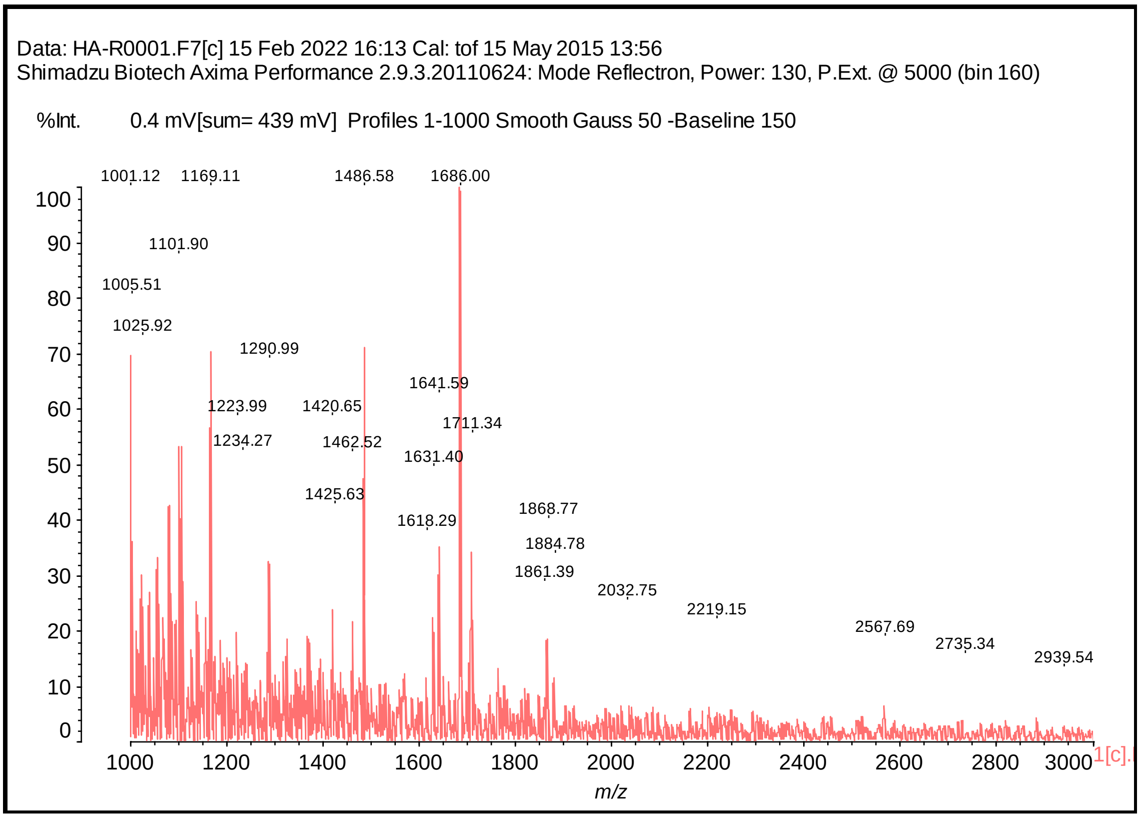


Figura 26: Resultado da análise de espectrometria de massas tipo MALDI-TOF gerado a partir da amostra de *Hepatus pudibundus* hidrolisado com a enzima Protamex.

4.4 CROMATOGRAFIA LÍQUIDA ACOPLADA À ESPECTROMETRIA DE MASSAS – LC/MS

A análise de cromatografia líquida acoplada à espectrometria de massas (LC/MS) foi realizada a fim de tentar entender a aparente divergência entre a riqueza de moléculas obtidas nas análises de espectrometria de massas MALDI-TOF e na quantidade de picos obtidos pela cromatografia líquida com detecção UV (CLEA).

Na figura 27 consta o perfil encontrado na análise LC/MS realizada no peixe *Paralonchurus brasiliensis* hidrolisado com Alcalase. Nesse perfil é possível notar que o pico majoritário se encontra em 9,35 minutos de corrida e os outros dois picos majoritários foram obtidos em 7,14 minutos e 8,17 minutos.

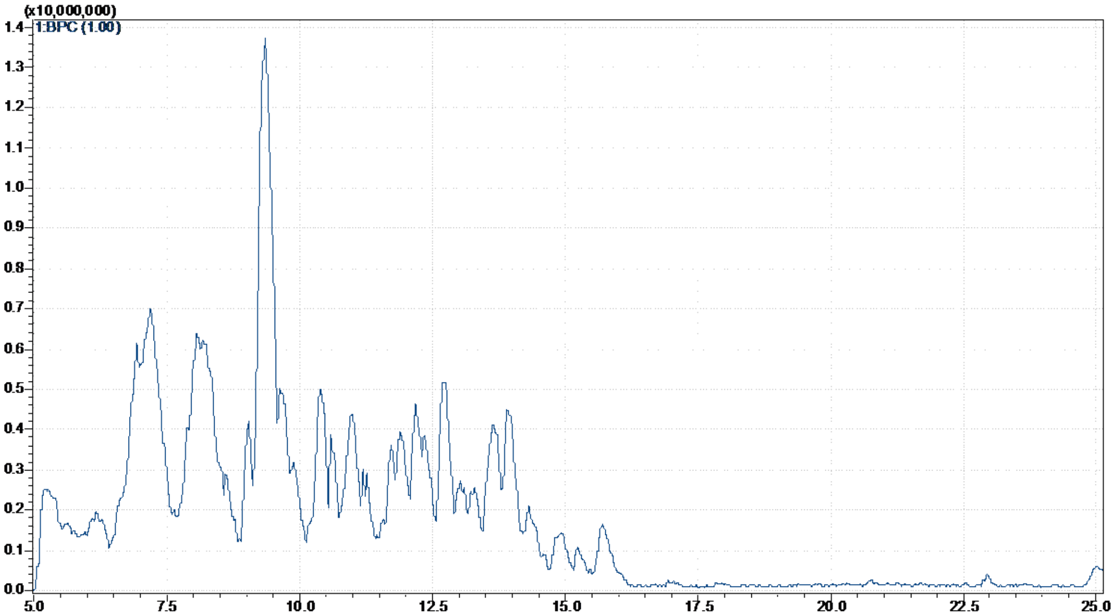


Figura 27: Resultado do perfil peptídico total da amostra de *Paralonchurus brasiliensis* hidrolisado com a enzima Alcalase obtido pela análise LC/MS, sendo uma amostra polar.

É possível notar os picos majoritários presentes nos tempos de retenção de 7,14 minutos, 8,17 minutos e 9,35 minutos os quais foram ampliados e os resultados estão apresentados nas Figuras 28, 29 e 30, respectivamente. O pico com maior interação no tempo de retenção de 7,14 minutos, possui massa molecular de 401,23 Da – não visto no MALDI-TOF devido a sua baixa massa – e picos medianos com massas entre 263 Da a 554,3 Da. Nesse tempo de corrida a amostra também apresenta pequenos picos com massas que variam de 657,3 Da a 332,4 Da.

No tempo de 8,17 minutos (Figura 29), o pico de maior interação tem massa molecular de 401,27 Da, sendo semelhante ao tempo de 7,14 minutos. O número de aminoácidos presentes nos peptídeos também é parecido, de 3 a 7 aminoácidos, com pequenos picos com maior massa molecular.

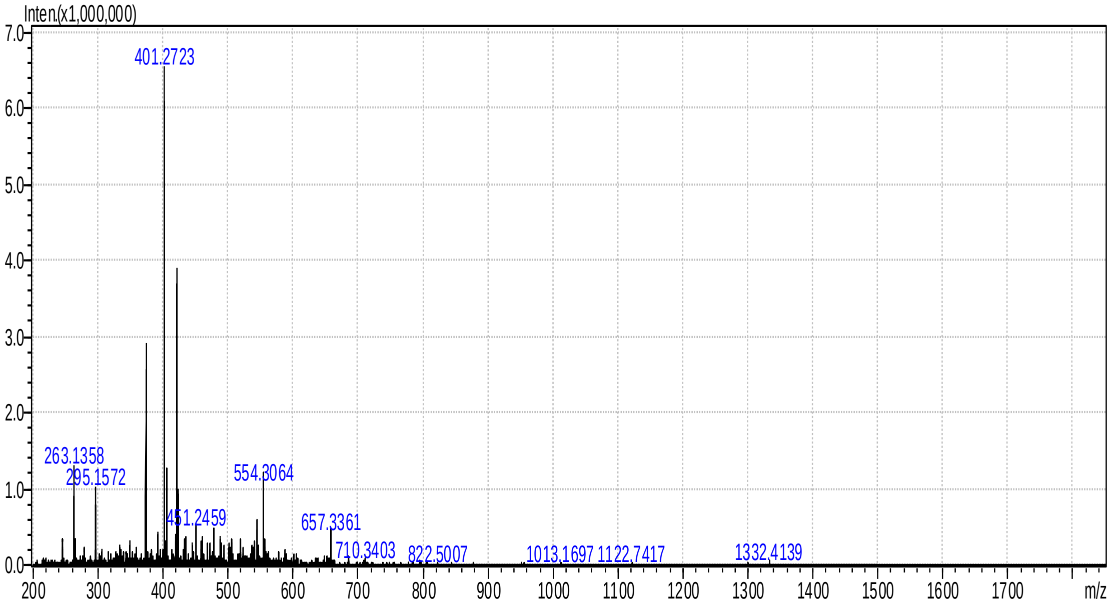


Figura 28: Massas moleculares obtidas por LC/MS realizado na amostra de *Paralonchurus brasiliensis* hidrolisado com a enzima Alcalase no tempo de 7,14 minutos.

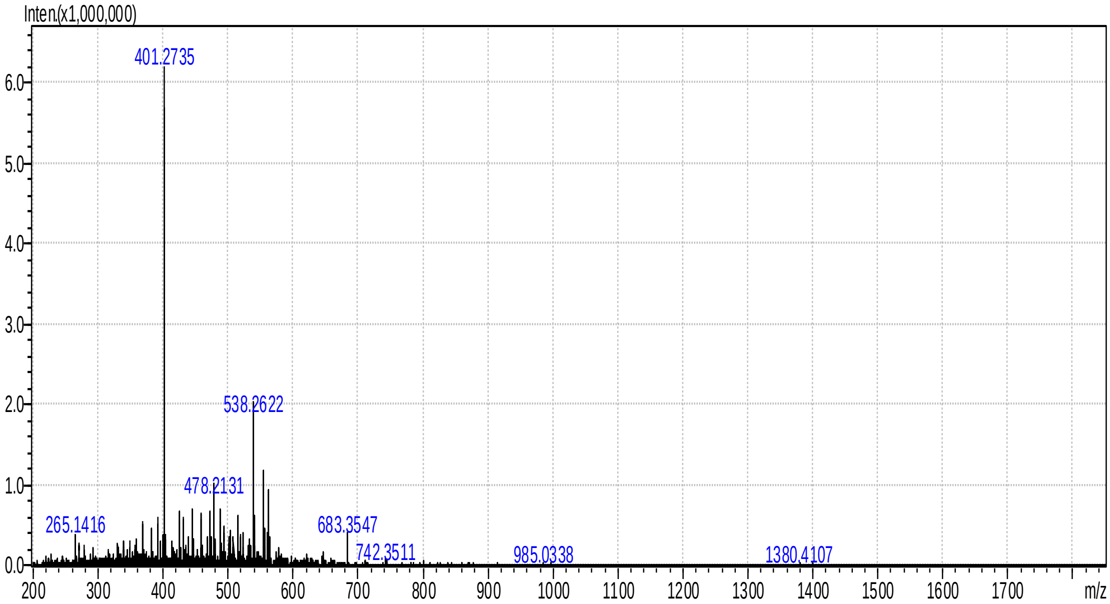


Figura 29: Massas moleculares obtidas por LC/MS realizado na amostra de *Paralonchurus brasiliensis* hidrolisado com a enzima Alcalase no tempo de 8,17 minutos.

Já no tempo de 9,35 minutos (Figura 30), o pico com maior interação possui 554,3 Da de massa molecular, já os outros picos são poucos e bem menores, contendo de 2 a 6 aminoácidos. Portanto, pode-se concluir que nos picos de 7,14 minutos, 8,17 minutos e 9,35 minutos predominam os peptídeos com 3 a 6 aminoácidos.

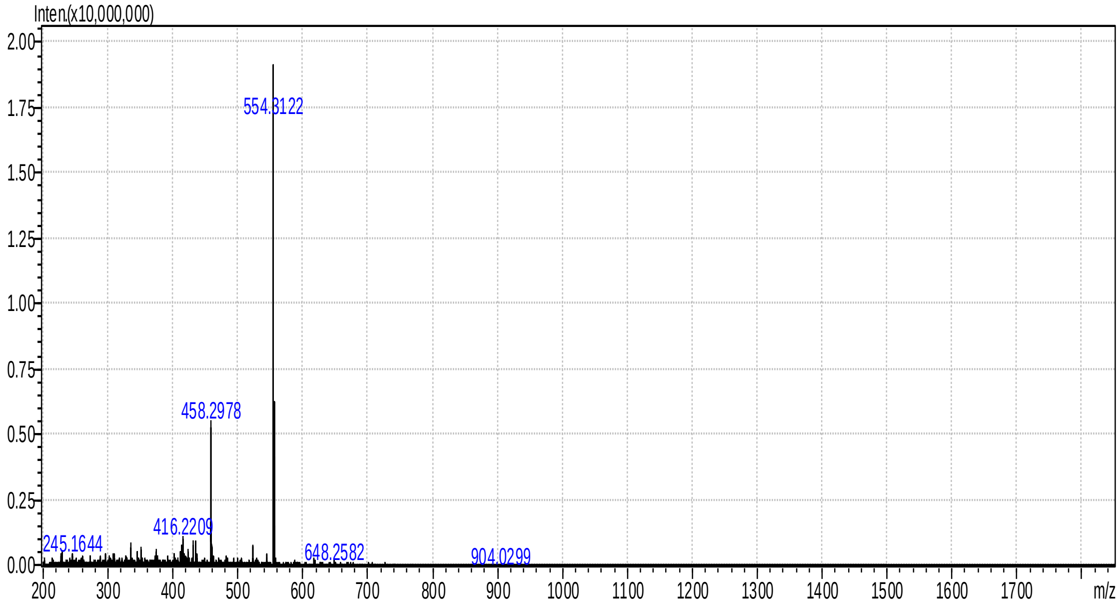


Figura 30: Massas moleculares obtidas por LC/MS realizado na amostra de *Paralonchurus brasiliensis* hidrolisado com a enzima Alcalase no tempo de 9,35 minutos.

A amostra de *Paralonchurus brasilensis* hidrolisada com Protamex mostrou um perfil mais diverso (Figura 31) com picos significantes nos tempos de retenção de 8,94 minutos, 9,54 minutos, 11,35 minutos e 15,41 minutos. Além disso, a amostra se mostrou mais polar, tendo em vista que os picos foram surgindo no começo da corrida.

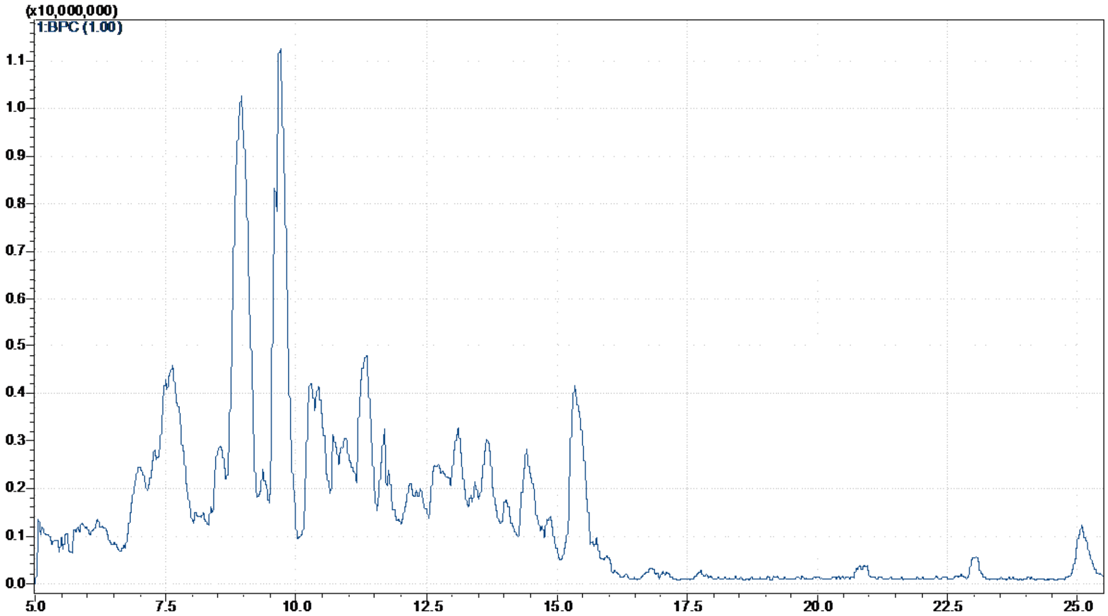


Figura 31: Resultado do perfil peptídico total da amostra de *Paralonchurus brasiliensis* hidrolisado com a enzima Protamex obtido pela análise LC/MS, sendo uma amostra polar.

Ao ampliar o pico de 8,94 minutos (Figura 32), é possível observar que o pico com maior interação obteve 508,27 Da, possuindo 5 aminoácidos e não identificado por MALDI-TOF, e o pico de maior massa é de 1016,37 Da, contendo 10 aminoácidos.

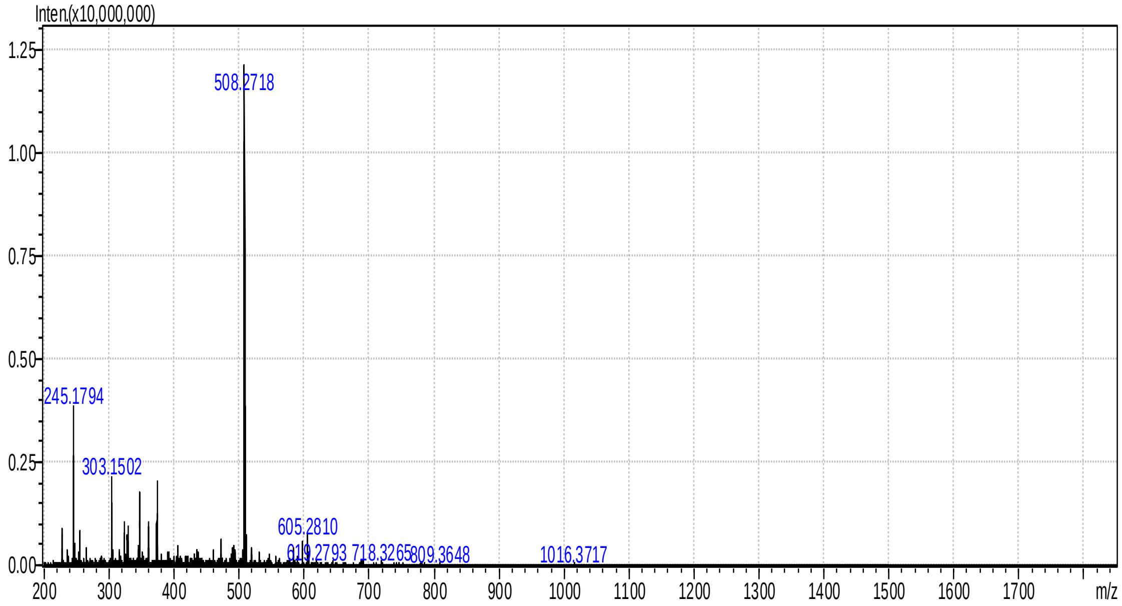


Figura 32: Massas moleculares obtidas por LC/MS realizado na amostra de *Paralonchurus brasiliensis* hidrolisado com a enzima Protamex no tempo de 8,94 minutos.

No tempo de 11,35 minutos (Figura 33), o maior pico encontrado possui massa de 585,3 Da, contendo 5 ou 6 aminoácidos e o de maior massa é de 1118,4 Da, possuindo 11 aminoácidos e já observado em MALDI-TOF. Em 15,41 minutos (Figura 34) foi encontrado um pico com 776,3 Da, sendo este o de maior interação e um pico de 1317,6 Da, possuindo a maior massa encontrada nesse tempo de retenção.

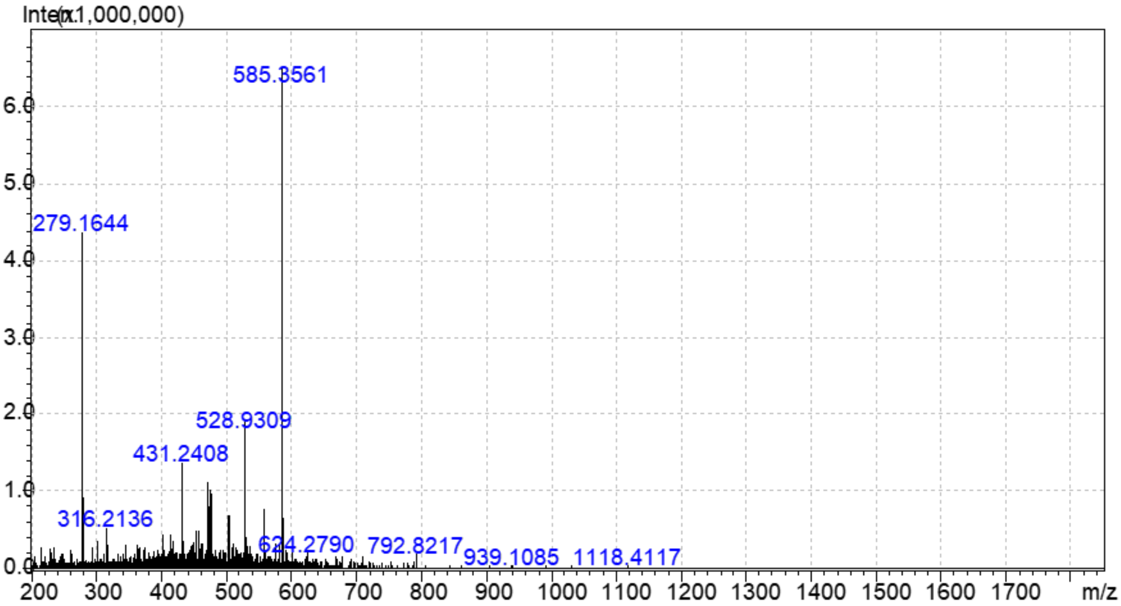


Figura 33: Massas moleculares obtidas por LC/MS realizado na amostra de *Paralonchurus brasiliensis* hidrolisado com a enzima Protamex no tempo de 11,35 minutos.

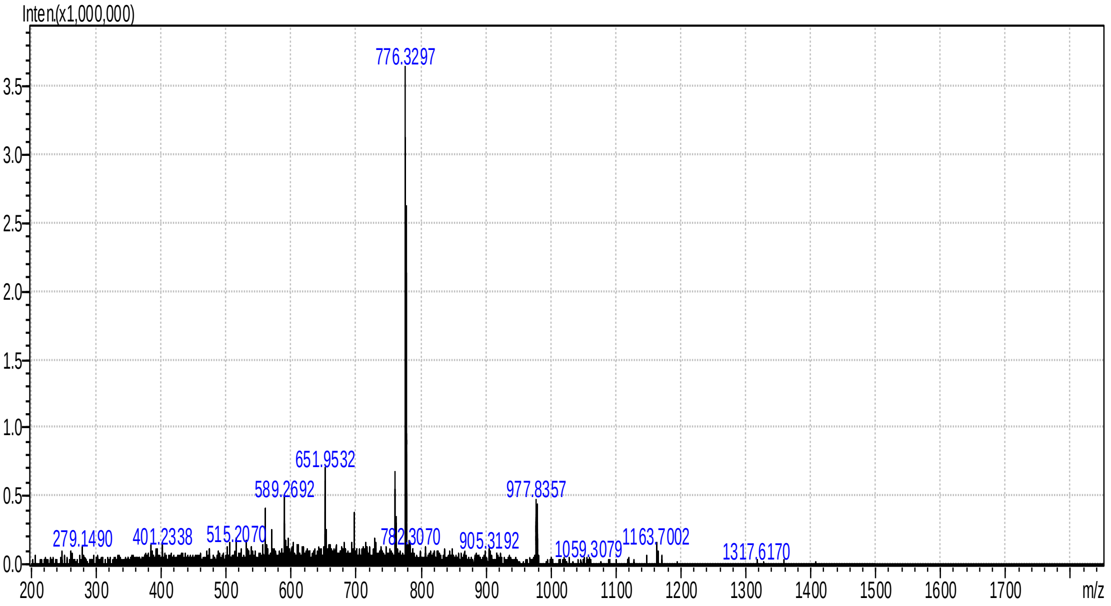


Figura 34: Massas moleculares obtidas por LC/MS realizado na amostra de *Paralonchurus brasiliensis* hidrolisado com a enzima Protamex no tempo de 15,41 minutos.

As amostras de *Micropogonias furnieri* mostraram perfis parecidos com os de *Paralonchurus brasiliensis*, o gráfico correspondente ao perfil da amostra hidrolisada com Alcalase é mostrada na Figura 35.

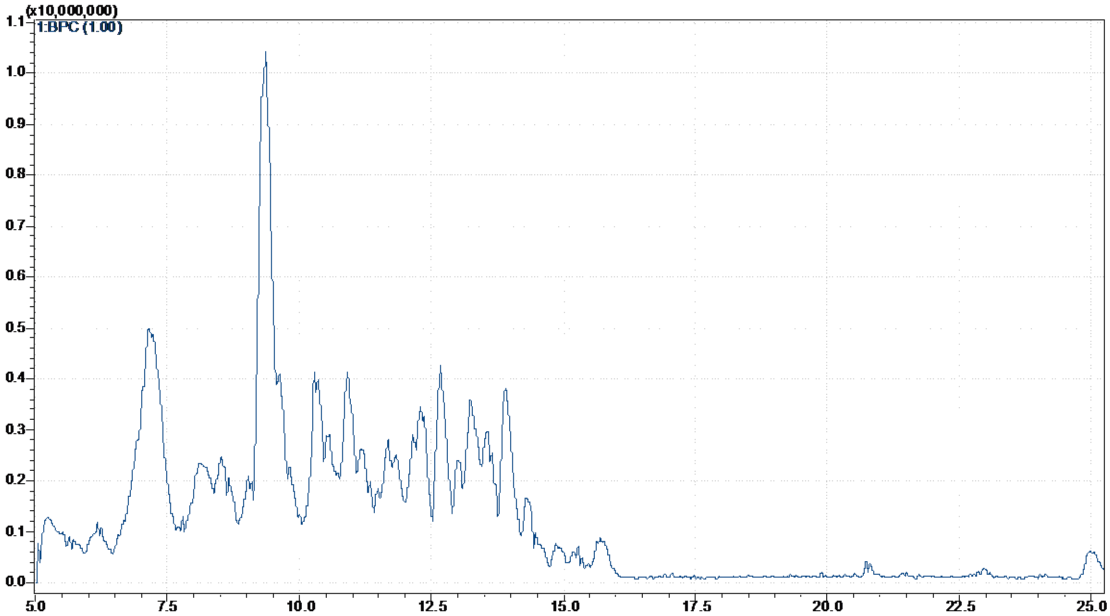


Figura 35: Resultado do perfil peptídico total da amostra de *Micropogonias furnieri* hidrolisado com a enzima Alcalase obtido pela análise LC/MS, onde é possível notar a polaridade da amostra.

A amostra é predominantemente polar, possuindo alguns compostos intermediários e poucos apolares, nos picos principais foram encontrados compostos de baixa massa molecular. No tempo de retenção de 7,15 minutos (Figura 36) está o pico de maior retenção, onde o íon principal foi de 401 Da – também não identificado pelo MALDI-TOF. A maioria possui massa molecular entre 263 Da a 700 Da, o composto de maior massa corresponde a 1402 Da, possuindo 14 aminoácidos em sua cadeia. No total foram registrados onze picos.

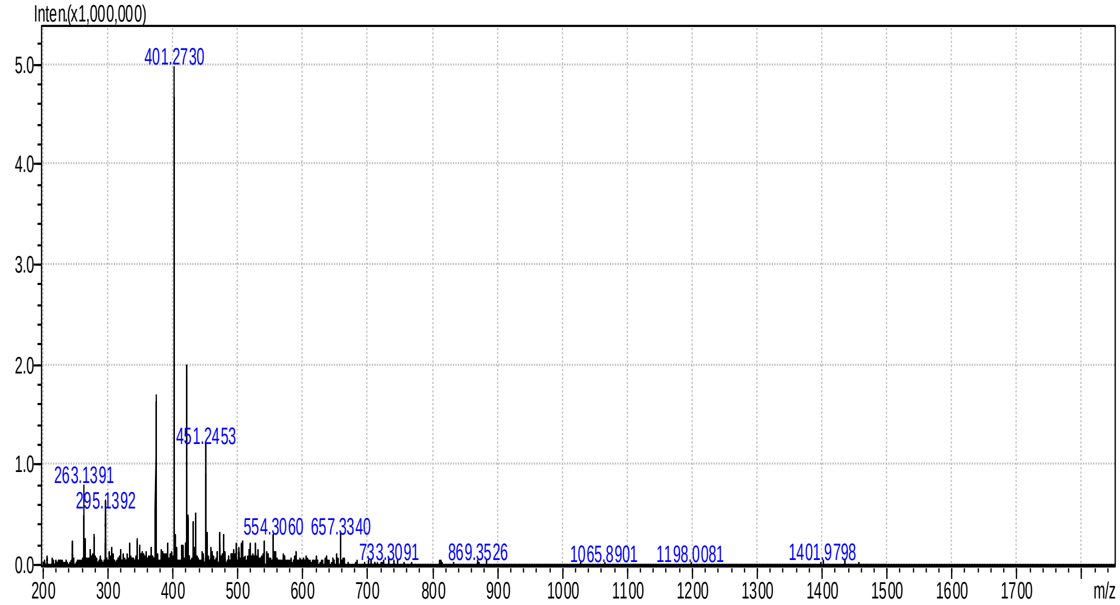


Figura 36: Massas moleculares obtidas por LC/MS realizado na amostra de *Micropogonias furnieri* hidrolisado com a enzima Alcalase no tempo de 7,15 minutos.

No tempo de 9,35 minutos (Figura 37), os picos de principais possuem massa de 554 Da, 5 aminoácidos e 456 Da, 4 aminoácidos, em um total de sete picos, os compostos se concentram em massas entre 245,1 Da e 648,2 Da. O pico com maior massa molecular registrado foi de 1028,55 Da, possuindo 10 aminoácidos em sua cadeia.

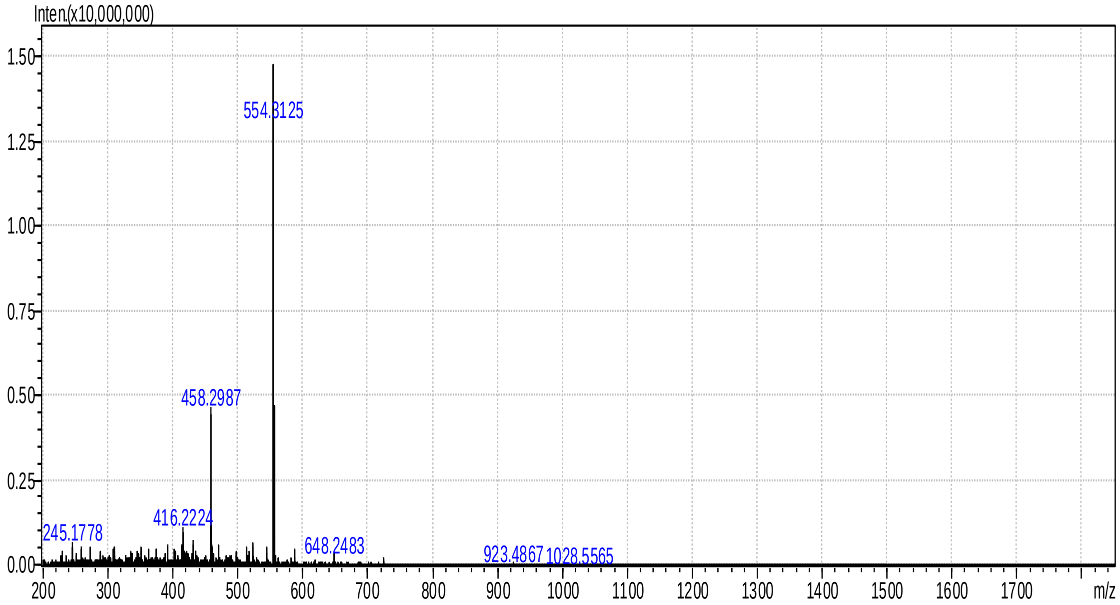


Figura 37: Massas moleculares obtidas por LC/MS realizado na amostra de *Micropogonias furnieri* hidrolisado com a enzima Alcalase no tempo de 9,35 minutos.

Os peptídeos encontrados no tempo de retenção de 12,67 minutos (Figura 38) se mostraram com picos menores, possuindo o pico de maior interação com 467 Da, e o pico de maior massa molecular com 1278 Da, ou seja, 12 ou 13 aminoácidos em cadeia. Lembrando que um pico não necessariamente indica apenas uma molécula.

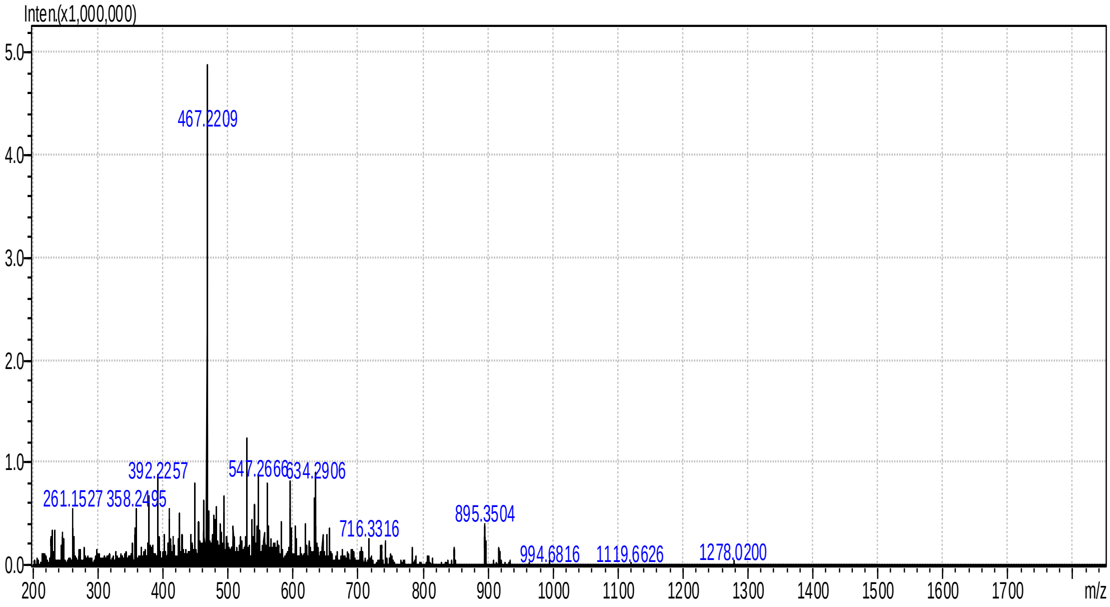


Figura 38: Massas moleculares obtidas por LC/MS realizado na amostra de *Micropogonias furnieri* hidrolisado com a enzima Alcalase no tempo de 12,67 minutos.

A amostra de *Micropogonias furnieri* hidrolisada com a enzima Protamex (Figura 39) possui um perfil cromatográfico polar, com três picos principais, no tempo de retenção de 7,5 minutos, 8,9 minutos e 9,65 minutos. Nos três tempos é possível observar que há apenas um pico com grande interação, sendo os outros significativamente menores.

No tempo de 7,5 minutos (Figura 40) o maior pico possui massa de 444,27 Da, ou seja, 4 aminoácidos na cadeia, já a maior massa registrada nesse tempo de retenção é de 1487,8 Da, 14 ou 15 aminoácidos, de um total de doze picos. Em 8,9 minutos (Figura 41), foram registrados apenas seis picos, sendo o de maior interação com massa 508,27 Da e o de maior massa 635,28 Da, contendo 5 e 6 aminoácidos respectivamente, portanto nesse tempo de retenção foram obtidos apenas peptídeos com baixa massa molecular.

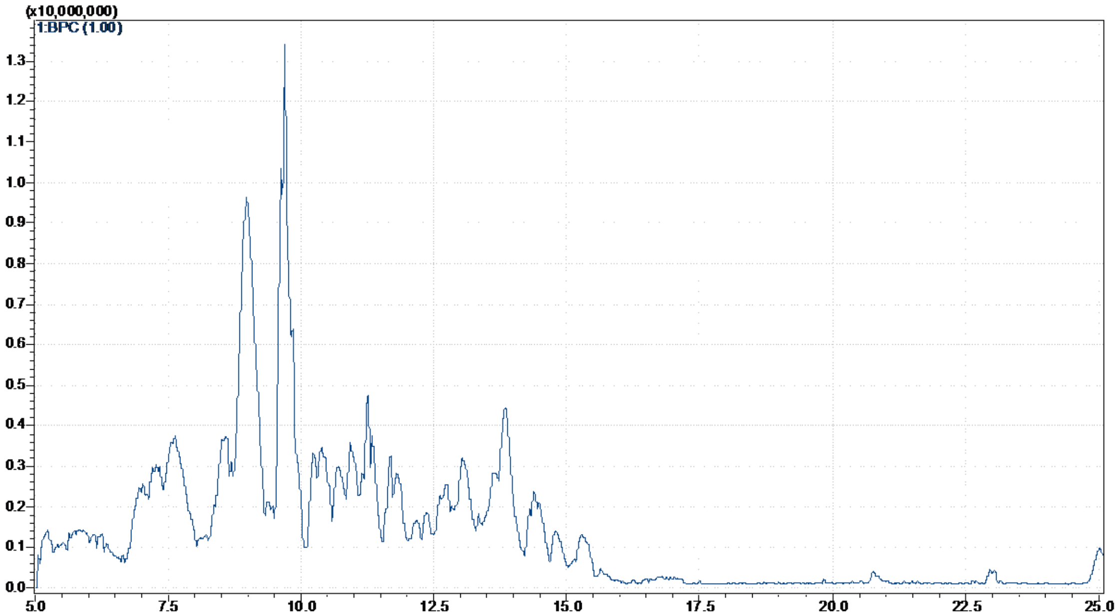


Figura 39: Resultado do perfil peptídico total da amostra de *Micropogonias furnieri* hidrolisado com a enzima Protamex obtido pela análise LC/MS.

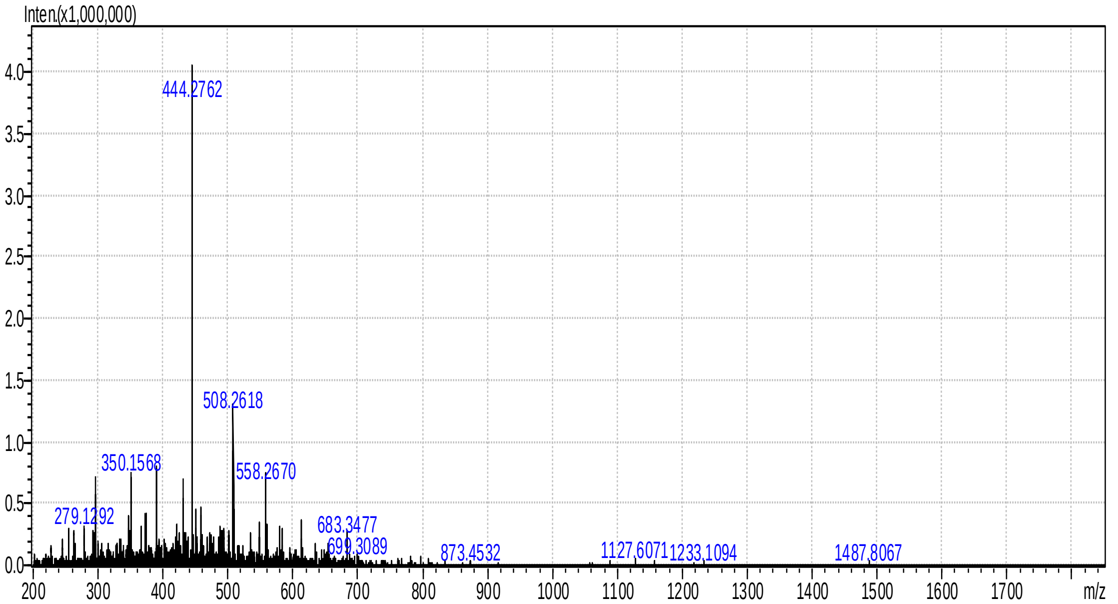


Figura 40: Massas moleculares obtidas por LC/MS realizado na amostra de *Micropogonias furnieri* hidrolisado com a enzima Protamex no tempo de 7,5 minutos.

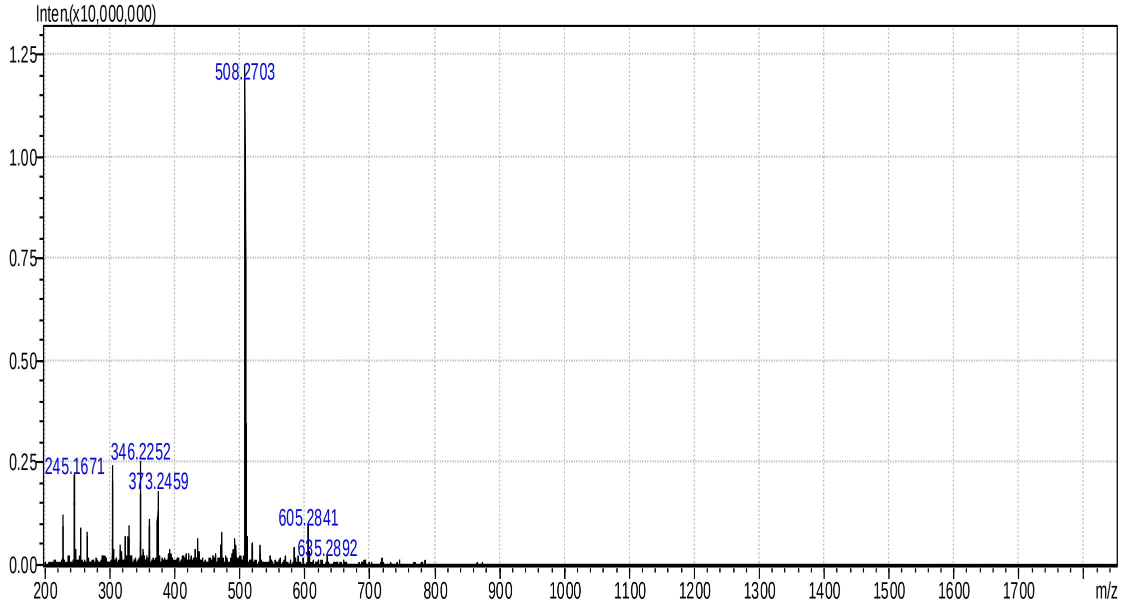


Figura 41: Massas moleculares obtidas por LC/MS realizado na amostra de *Micropogonias furnieri* hidrolisado com a enzima Protamex no tempo de 8,9 minutos.

O tempo de retenção de 9,65 minutos (Figura 42) também não registrou muitos peptídeos, sendo sete picos no total, onde o de maior interação possui massa de 245.17 Da, 2 aminoácidos na cadeia e o de maior massa 976,63 Da, contendo 9 ou 10 aminoácidos.

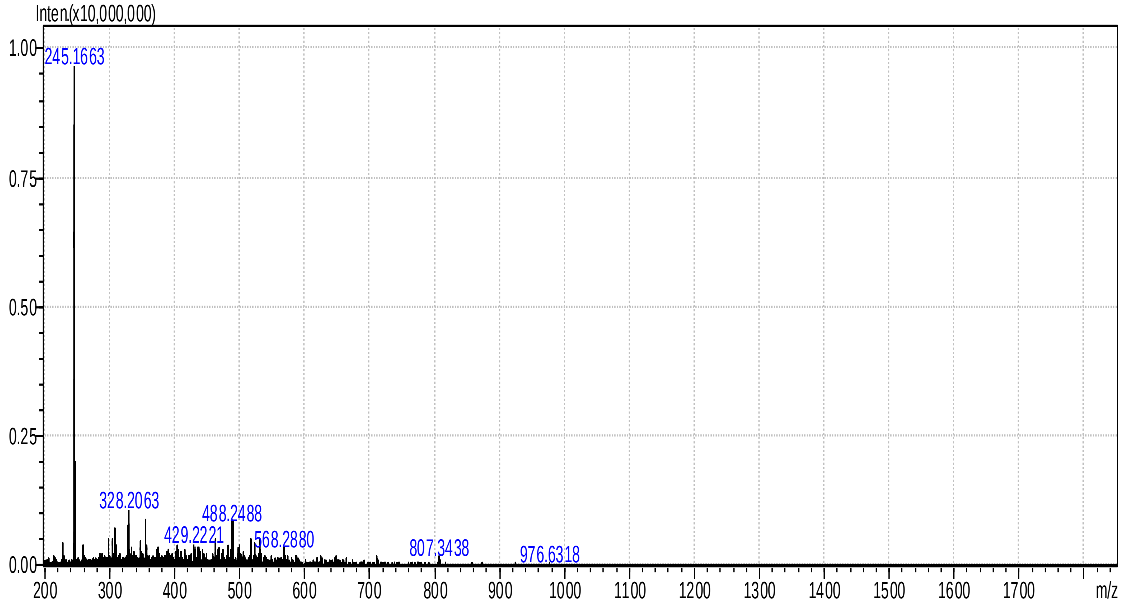


Figura 42: Massas moleculares obtidas por LC/MS realizado na amostra de *Micropogonias furnieri* hidrolisado com a enzima Protamex no tempo de 9,65 minutos.

Com essas informações podemos dizer que a amostra de *Micropogonias furnieri* hidrolisada com Protamex obteve peptídeos com menores massas moleculares, já que a média de aminoácidos em cadeia foi de 4 a 9.

A amostra do crustáceo *Hepatus pudibundus* hidrolisada com Alcalase (Figura 43) é considerada polar, com apenas dois pequenos picos com apolares. Seus três picos principais estão no tempo de retenção de 10,34 minutos, 11,73 minutos e 12,3 minutos. No tempo de retenção de 10,34 minutos (Figura 44), no geral, foram obtidos pequenos picos, onde o de maior interação possui massa molecular de 391,88 Da, ou seja, 3 ou 4 aminoácidos na cadeia e o de maior massa foi de 1362,33 Da, portanto, 13 aminoácidos, que já havia sido registrado com o MALDI-TOF. Os picos menores variam de 2 a 8 aminoácidos na cadeia, tanto esses, quanto o de maior interação não foram registrados no MALDI-TOF.

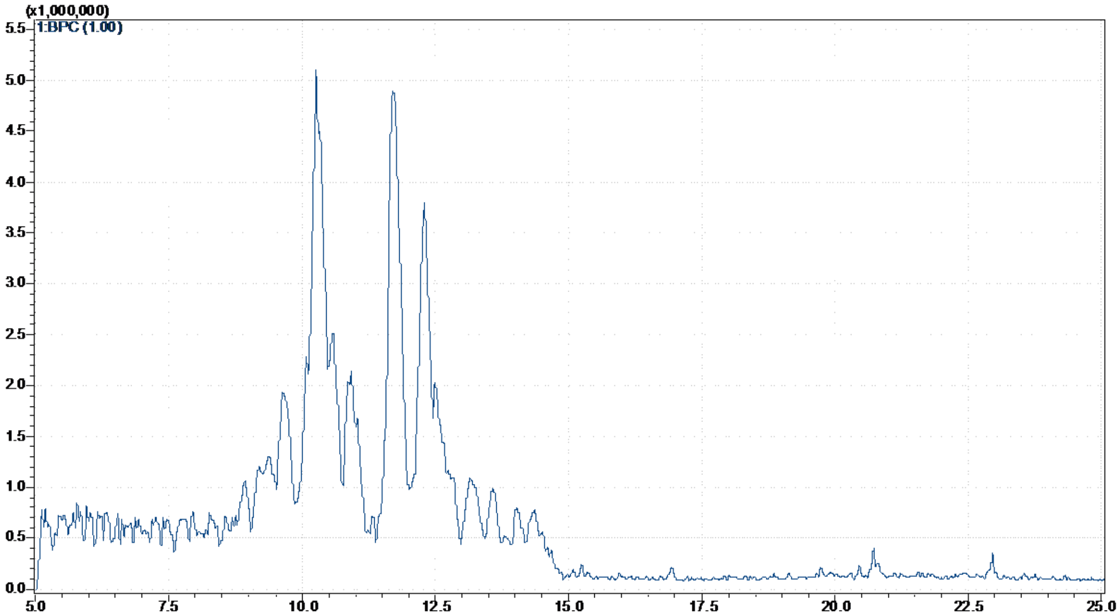


Figura 43: Resultado do perfil peptídico total da amostra de *Hepatus pudibundus* hidrolisado com a enzima Alcalase obtido pela análise LC/MS, onde é possível notar que se trata de uma amostra polar.

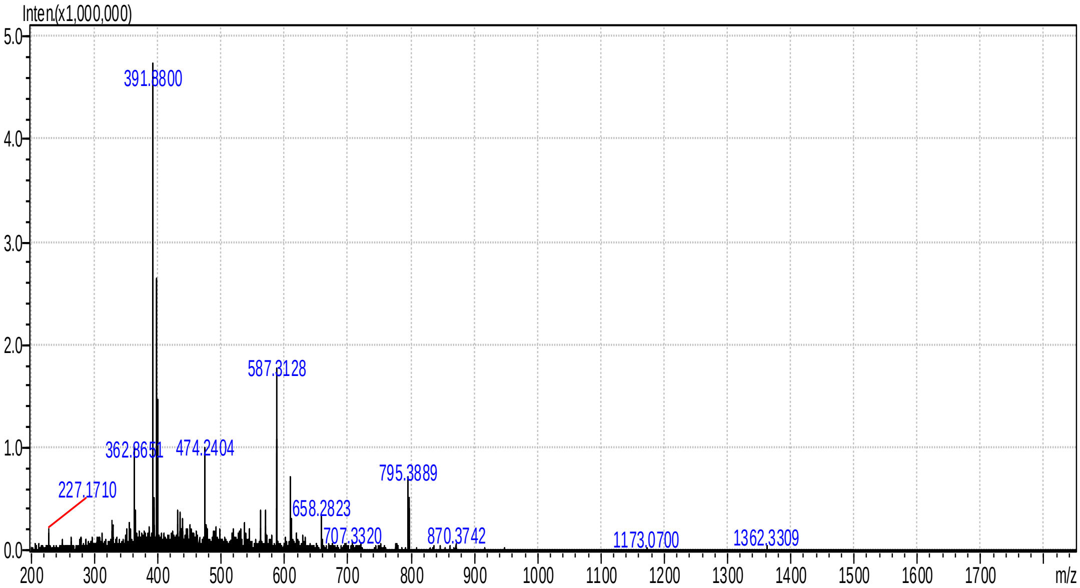


Figura 44: Massas moleculares obtidas por LC/MS realizado na amostra de *Hepatus pudibundus* hidrolisado com a enzima Alcalase no tempo de 10,34 minutos.

Observando o gráfico do tempo de retenção de 11,73 (Figura 45) foram obtidos apenas cinco picos existentes, sendo o de maior intensidade o pico de massa 620,3 Da, contendo 6 aminoácidos na cadeia e o de maior massa 719,3 Da, portanto, 7 aminoácidos.

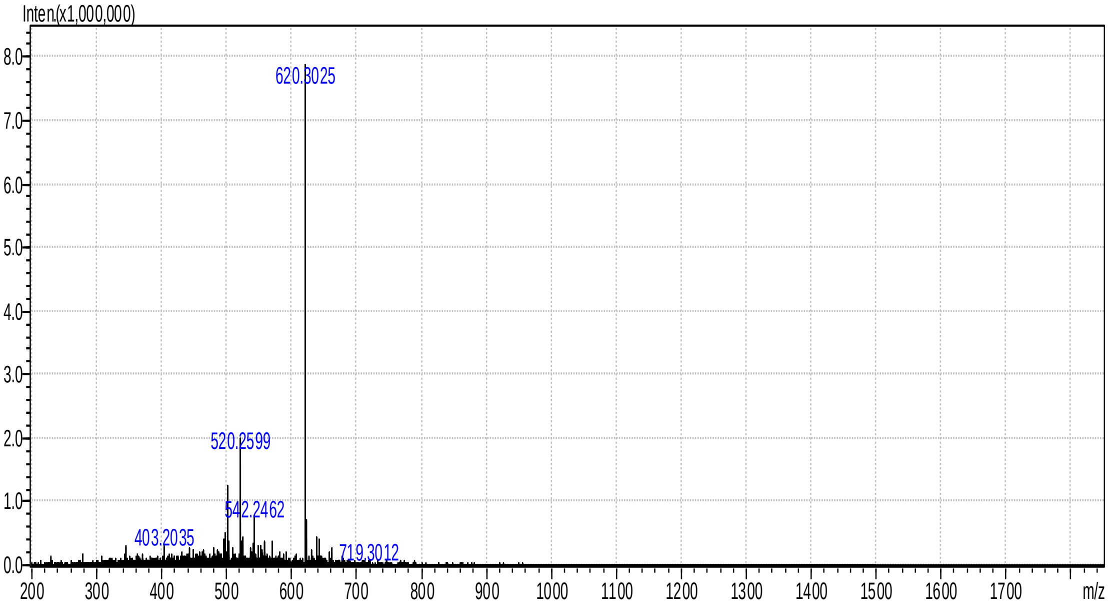


Figura 45: Massas moleculares obtidas por LC/MS realizado na amostra de *Hepatus pudibundus* hidrolisado com a enzima Alcalase no tempo de 11,73 minutos.

Dos outros três picos encontrados dois possuem 5 aminoácidos na cadeia e um possui 4 aminoácidos. Dessa maneira, o gráfico do tempo de retenção citado revela um pequeno arranjo de peptídeos com baixa massa molecular que não foram detectados pelo MALDI-TOF.

No tempo de retenção de 12,30 (Figura 46) minutos nota-se poucos picos com vários peptídeos de baixa massa, sendo nove picos variando de 270,1 Da a 908,3 Da, onde o de maior interação com 401,2 Da, além de um pequeno pico maior de 1230,7 Da, sendo este com 12 aminoácidos. No geral, este tempo de retenção revelou picos com uma variação de 3 a 9 aminoácidos em cadeia, considerados peptídeos de baixa massa molecular.

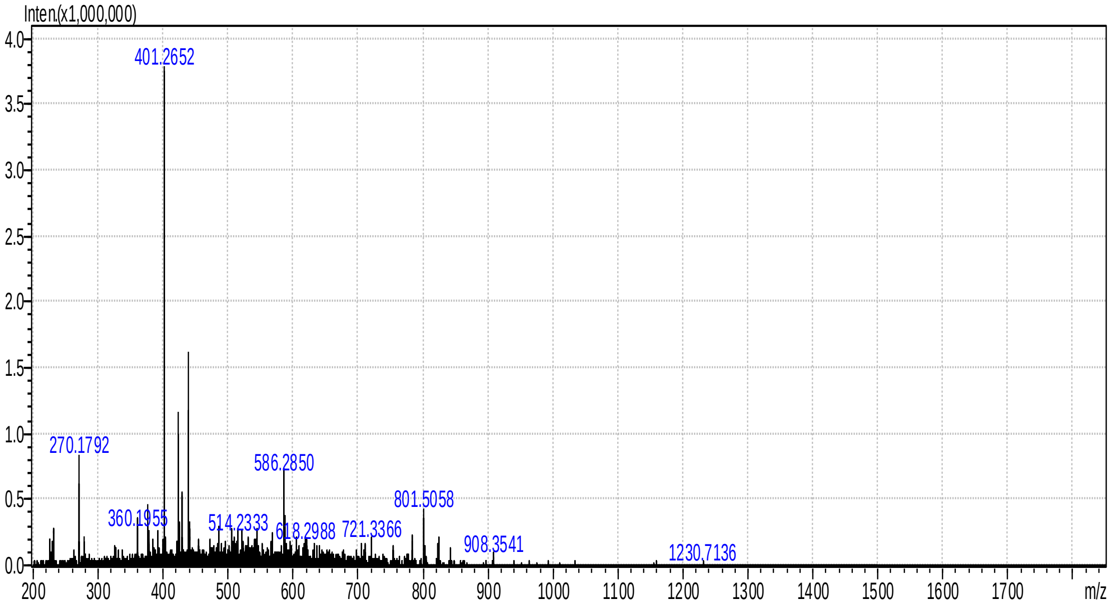


Figura 46: Massas moleculares obtidas por LC/MS realizado na amostra de *Hepatus pudibundus* hidrolisado com a enzima Alcalase no tempo de 12,3 minutos.

A amostra do crustáceo *Hepatus pudibundus* hidrolisada com Protamex (Figura 47) é considerada polar a intermediária, os picos considerados principais foram encontrados nos tempos de retenção de 6,63 minutos, 10,44 minutos e 11,79 minutos.

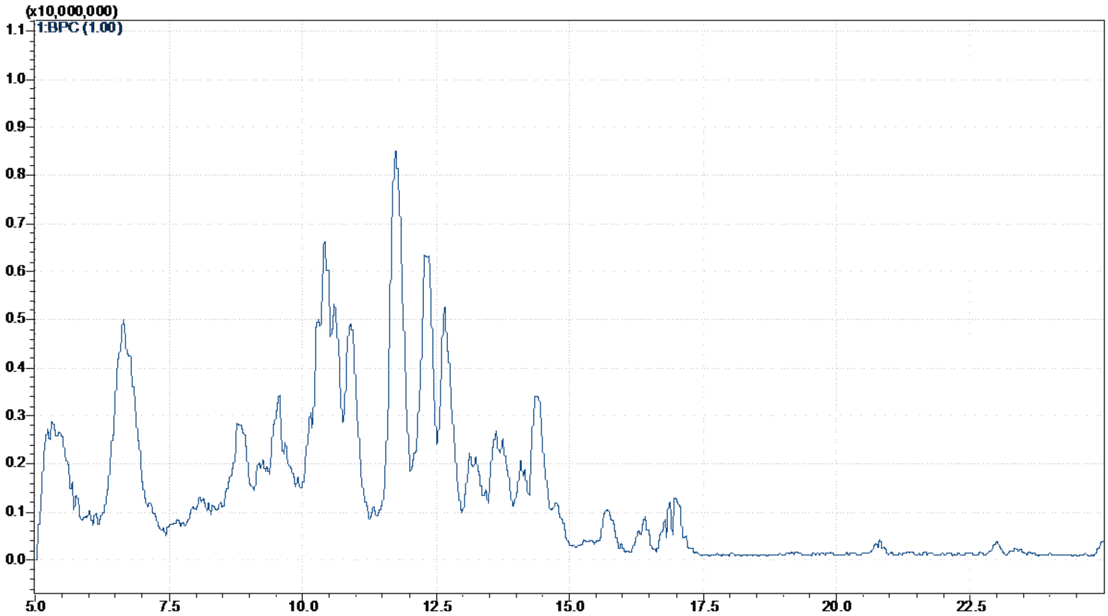


Figura 47: Resultado do perfil peptídico total da amostra de *Hepatus pudibundus* hidrolisado com a enzima Protamex obtido pela análise LC/MS, onde é possível notar que se trata de uma amostra polar a intermediária.

O perfil relacionado ao tempo de retenção de 6,63 (Figura 48) minutos apresentou treze picos, dos quais o de maior intensidade possui 437,23 Da, ou seja, 4 aminoácidos e o de maior massa molecular aproximadamente 1500 Da, 15 aminoácidos. A maior parte dos peptídeos estão entre 279,14 Da e 626,36 Da.

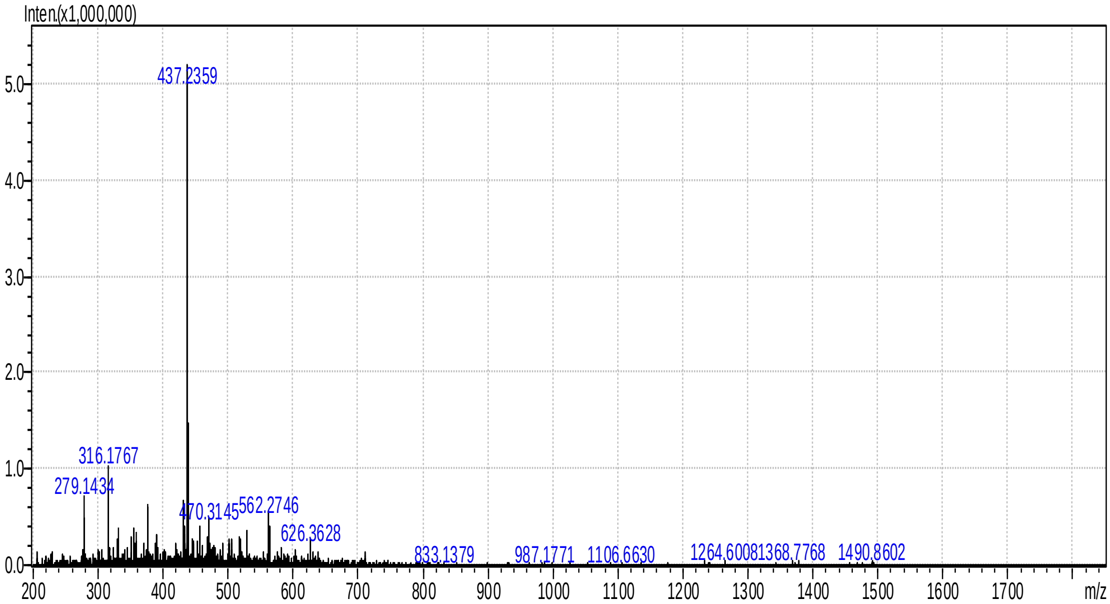


Figura 48: Massas moleculares obtidas por LC/MS realizado na amostra de *Hepatus pudibundus* hidrolisado com a enzima Protamex no tempo de 6,63 minutos.

Foram registrados dez picos no tempo de retenção de 10,44 minutos (Figura 49), onde a maioria se encontra entre 227,14 Da e 867,35 Da, portanto, possuem de 2 a 8 aminoácidos, compondo peptídeos de baixa massa molecular que não foram registrados por MALDI-TOF. O peptídeo de maior massa molecular possui 1074,72 Da, com 10 aminoácidos em sua cadeia. No tempo de retenção de 11,79 minutos (Figura 50) também constatou peptídeos de baixa massa molecular, em um total de sete picos, os peptídeos são de 229,15 Da a 848,44 Da, portanto de 2 a 8 aminoácidos. A maior interação está no pico com 620,3 Da, contendo 6 aminoácidos em sua cadeia.

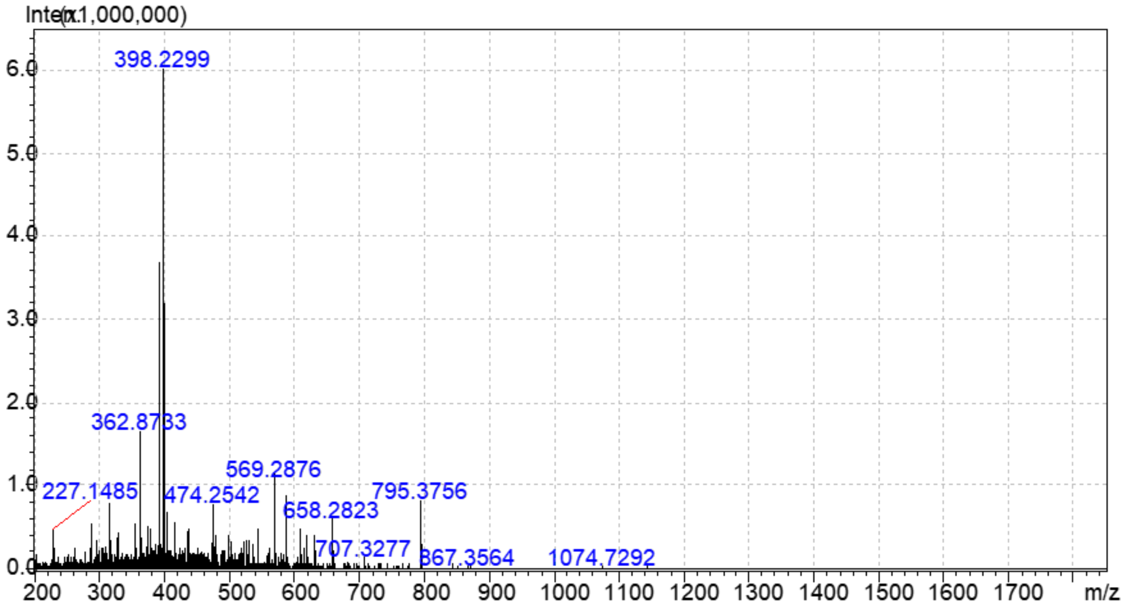


Figura 49: Massas moleculares obtidas por LC/MS realizado na amostra de *Hepatus pudibundus* hidrolisado com a enzima Protamex no tempo de 10,44 minutos

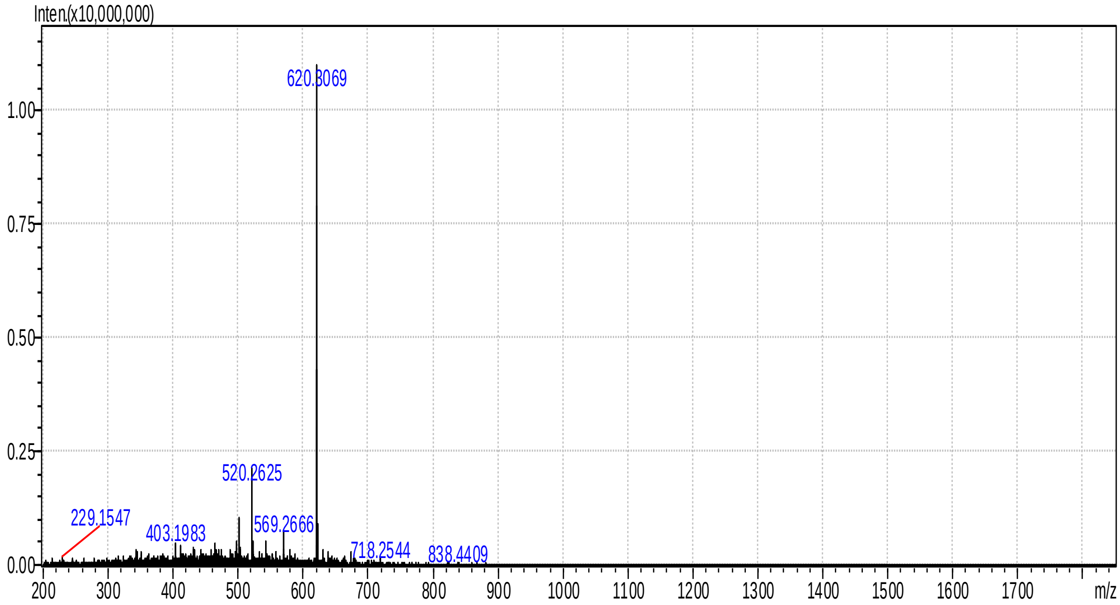


Figura 50: Massas moleculares obtidas por LC/MS realizado na amostra de *Hepatus pudibundus* hidrolisado com a enzima Protamex no tempo de 11,79 minutos

4.5 CROMATOGRAFIA LÍQUIDA ACOPLADA À ESPECTROMETRIA DE MASSAS SEQUENCIAL – LS/MSMS

A cromatografia líquida acoplada à espectrometria de massas sequencial ou LS/MSMS realiza as estatísticas da análise, onde os padrões de peptídeos são colocados para saber quais proteínas originaram os peptídeos existentes nas amostras e qual foi a relevância da clivagem realizada. Foram várias proteínas descritas nas listas, porém foi necessária a utilização do banco de dados de *Teleostei* para os peixes e *Arthropoda* para o crustáceo. Os resultados obtidos pelas análises proteômicas estão disponíveis em Anexo.

Essa análise foi imprescindível para o controle de qualidade da amostra, comprovando que o preparo da amostra foi eficiente, tendo em vista que as proteínas que originaram os peptídeos encontrados são todas de origem muscular, como actina, miosina e beta-actina. Dessa maneira, o controle de qualidade foi positivo comprovando que não houve contaminação de outros tecidos e órgãos.

4.6 SEQUENCIAMENTO DE NOVO

No caso de organismos que não tenham o genoma sequenciado e, portanto, possuem poucas proteínas que constam nos bancos de dados, a abordagem de sequenciamento de novo é essencial. Nele os peptídeos são sequenciados por massa independente de banco de dados ou análises proteômicas. Dessa maneira, esse sequenciamento foi realizado no parâmetro de até 85% de confiança para o score de novo, os resultados completos estão em anexo. Nas Tabelas 4 e 5 estão descritos os peptídeos com confiança média até 90% encontrados nas amostras de *Paralonchurus brasiliensis* hidrolisadas com Alcalase e com Protamex, respectivamente.

O programa de alinhamento BLAST[77] foi utilizado na busca em bancos de dados de ácidos nucléicos e proteínas por sequências homólogas e para a realização do alinhamento local por pares de sequências. Dessa maneira, essa ferramenta permitiu uma análise individual das sequências peptídicas com confiança média geral (ALC) até 90%. Os resultados estão apresentados nas Tabelas 6 e 7, sendo amostras hidrolisadas com Alcalase e Protamex, respectivamente.

Já as Tabelas 8 e 9 representam as bioatividades já encontradas presente nos peptídeos registrados no banco de dados BioPep[78], sendo a Tabela 8 as amostras hidrolisadas com Alcalase e Tabela 9 as amostras hidrolisadas com Protamex, permitindo assim, uma comparação dos peptídeos gerados pelas duas hidrólises.

Tabela 4: Peptídeos encontrados na amostra de *Paralonchurus brasiliensis* hidrolisada com Alcalase pelo sequenciamento de novo, com confiança média geral até 90%. Onde, ALC = confiança média geral, RT = tempo de retenção, ppm = chance de erro na identificação da sequência peptídica.

Peptídeo	ALC (%)	Massa	RT	ppm
LLAPPE	97	638.36	11.09	-0.8
YEKK	96	566.30	0.69	0.1
LVYPSV	94	676.37	13.97	-31.2
VKLPKL	94	696.48	11.25	-0.6
LKYPLE	94	761.43	11.22	-0.8
LDFDEFLMK	94	1156.54	14.85	0.7
LLDQDKSGFLE	93	1263.63	11.60	5.2
SERRLL	93	772.45	11.54	-15.0
EYKK	92	566.30	7.02	0.0
LLVYPW	91	789.44	14.90	-0.4
TGPLKF	91	661.37	11.39	-0.8
VDLVSFK	91	806.45	13.15	-26.9
QDDKLKDK	91	988.51	8.10	-0.5
VGADKK	90	616.35	2.03	-1.3
VVDRLK	90	728.45	11.18	-16.1

Tabela 5: Peptídeos encontrados na amostra de *Paralonchurus brasiliensis* hidrolisada com Protamex pelo sequenciamento de novo, com confiança média geral até 90%. Onde, ALC = confiança média geral, RT = tempo de retenção, ppm = chance de erro na identificação da sequência peptídica.

Peptídeo	ALC (%)	Massa	RT	ppm
LEEEELKLF	97	1148.59	13.44	-0.4
EYKK	95	566.30	2.46	-0.3
VDLWFK	95	806.43	13.17	-0.9
LKLFL	94	632.42	13.64	-0.4
LEDDLVALK	92	1014.55	12.13	5.3
VGDEAKSQ	91	832.39	8.15	0.1
VDLWFKA	90	877.46	13.37	-1.1
TVDDKVELE	90	1046.51	11.30	-0.4
LVVDRKL	90	841.53	12.90	-14.4
LLDKNRDGLLSQ	90	1370.75	10.32	4.4
EARE	90	503.23	4.23	-0.1
QGREK	90	616.32	4.94	0.1

Tabela 6: Análise individual das sequências peptídicas encontradas na amostra de *Paralonchurus brasiliensis* hidrolisada com Alcalase, visando alinhamento e consequência pelo banco de dados BLAST[77], descrição das dez primeira sequencias peptídicas. Sendo Query cover = porcentagem da sequência enviada conseguiu realizar um alinhamento, E value = possibilidade de o alinhamento ter sido realizado ao acaso (quanto mais perto do valor 0, maior é a confiabilidade) e Seq ID = identificação da sequência peptídica.

Peptídeo	Massa	Query cover	E value	Seq. ID	Descrição	Espécie
LLAPPE	638.36	100%	520	TSK3760.1	Roquin-1	*Hemibagrus wyckioides*
YEKK	566.30	100%	19223	TSR51413.1	Titina	*Bagarius yarrelli*
LVYPSV	676.37	100%	367	XP_043868191.1	Proteína dedo de zinco	*Solea senegalensis*
VKLPKL	696.48	100%	738	XP_035982871.1	Isoforma de proteína ANHAK associada à diferenciação de neuroblastos	*Fundulus heteroclitus*
LKYPLE	761.43	100%	182	RXN10808.1	Miosina	*Labeo rohita*
LDFDEFLMK	1156.54	100%	1.9	XP_042563305.1	Proteína de ligação ao cálcio	*Clupea harengus*
LLDQDKSGFLE	1263.63	100%	0.52	TSK14644.1	Parvalbumina	*Bagarius yarrelli*
SERRLL	772.45	100%	520	XP_024127336.1	Ubiquitina-ligase	*Oryzias melastigma*
EYKK	566.30	100%	19233	TSR51413.1	Titina	*Bagarius yarrelli*
LLVYPW	789.44	100%	33	XP_028311025.1	Hemoglobina beta-A-like	*Gouania willdenowi*

Tabela 7: Análise individual das sequências peptídicas encontradas na amostra de *Paralonchurus brasiliensis* hidrolisada com Protamex, visando alinhamento e consequência pelo banco de dados BLAST[77], descrição das dez primeira sequencias peptídicas.

Peptídeo	Massa	Query cover	E value	Seq. ID	Descrição	Espécie
LEEEELKLF	1148.59	100%	1.4	P86432.1	Parvalbumina	*Oncorhynchus mykiss*
EYKK	566.30	100%	19223	TSR51413.1	Titina	*Bagarius yarrelli*
VDLWFK	806.43	100%	46	XP_021169181.2	Nucleosídeo difosfato quinase B	*Fundulus heteroclitus*
LKLFL	632.42	100%	4595	XP_023808923.1	Nesprina-1	*Oryzias latipes*
LEDDLVALK	1014.55	100%	5.6	KAF6714773.1	Serina beta-lactamase- like LACTB. mitocondrial	*Oryzias melastigma*
VGDEAKSQ	832.39	100%	855	XP_020777739.1	Serotransferrina-like	*Boleophthalmus pectinirostris*
VDLWFKA	877.46	100%	7.3	XP_021169181.2	Nucleosídeo difosfato quinase B	*Fundulus heteroclitus*
TVDDKVELE	1046.51	88%	22	XP_040927192.1	Cadeia pesada de miosina	*Betta splendens*
LVVDRKL	841.53	100%	473	XP_016302193.1	WD repeat-containing protein 3-like	*Sinocyclocheilus anshuiensis*
LLDKNRDGLLSQ	1370.75	100%	0.89	XP_022539758.1	Proteína de ligação ao cálcio	*Astyanax mexicanus*

Tabela 8: Bioatividades encontradas nos peptídeos presentes na amostra de *Paralonchurus brasiliensis* hidrolisada com Alcalase através da utilização do banco de dados BioPep[78], apenas as sequencias com confiança média geral (ALC) até 90% foram descritas.

Peptídeo	Massa	Sequência	Bioatividades
LLAPPE	638,36	**LAP, AP, LA, PP**	Inibidor da Enzima Conversora da Angiotensina
		PP, LA, AP, LL, LLAP	Inibidor da Dipeptidil Peptidase IV
		PP, PE	Inibidor de alfa-glicosidase
		LA, PE	Inibidor da Dipeptidil Peptidase III
YEKK	566,3	**EK, YE**	Inibidor da Enzima Conversora da Angiotensina
		KK	Ligante de permease bacteriana
		EK, KK, YE	Inibidor da Dipeptidil Peptidase IV
LVYPSV	676,37	**LVYP, VY, VYP, YP, LVY**	Inibidor da Enzima Conversora da Angiotensina
		VY	Antioxidante
		YP, LV, OS, SV, VY	Inibidor da Dipeptidil Peptidase IV
		YP	Inibidor de alfa-glicosidase
		VY	Inibidor da Dipeptidil Peptidase III

VKLPKL	696,48	**VK, KL, KLP, LP**	Inibidor da Enzima Conversora da Angiotensina
		VKL	Antioxidante
		LP, PK, VK	Inibidor da Dipeptidil Peptidase IV
LKYPLE	761,43	**YP, PL, KY**	Inibidor da Enzima Conversora da Angiotensina
		LK	Antioxidante
		YP, PL, KY	Inibidor da Dipeptidil Peptidase IV
		YPL, YP	Inibidor de alfa-glicosidase
LDFDEFLMK	1156,54	**DF, EF**	Inibidor da Enzima Conversora da Angiotensina
		FL, LM, MK	Inibidor da Dipeptidil Peptidase IV
		FL	Inibidor da Dipeptidil Peptidase III
		EF	Inibidor de renina
LLDQDKSGFLE	1263,6	**GF, SG**	Inibidor da Enzima Conversora da Angiotensina
		GFL	Imunoestimulante
		LL, FL, DQ, GF, KS, QD	Inibidor da Dipeptidil Peptidase IV
		FL, GFL	Inibidor da Dipeptidil Peptidase III
SERRLL	772,45	**RL, RR, ER**	Inibidor da Enzima Conversora da Angiotensina
		LL, RL, RR	Inibidor da Dipeptidil Peptidase IV
		RR	Inibidor da Dipeptidil Peptidase III
EYKK	566,3	**YK, EY**	Inibidor da Enzima Conversora da Angiotensina
		KK	Ligante de permease bacteriana
		EY, KK, YK	Inibidor da Dipeptidil Peptidase IV
		YK	Inibidor da Dipeptidil Peptidase III
LLVYPW	789,44	**LVYP, VY, VYP, YP, LVY**	Inibidor da Enzima Conversora da Angiotensina
		PW, VY, YPW	Antioxidante
		LL, YP, LV, PW, VY	Inibidor da Dipeptidil Peptidase IV
		YP	Inibidor de alfa-glicosidase
		VY, LVYPW	Inibidor da Dipeptidil Peptidase III
TGPLKF	661,37	**GP**	Atividade anti-amnésica
		GPL, GP, PL, TG, KF, TGP	Inibidor da Enzima Conversora da Angiotensina
		GP	Antitrombótica
		LK	Antioxidante
		GP, PL, KF, TG	Inibidor da Dipeptidil Peptidase IV
		KF	Inibidor de renina
VDLVSFK	806,45	**SF**	Inibidor da Enzima Conversora da Angiotensina
		LV, SF, VD, VS	Inibidor da Dipeptidil Peptidase IV
		SF	Inibidor de renina
QDDKLKDK	988,51	**KL**	Inibidor da Enzima Conversora da Angiotensina
		KD, LK	Inibidor da Dipeptidil Peptidase IV
		QD	Antioxidante
VGADKK	616,35	**VG, GA**	Inibidor da Enzima Conversora da Angiotensina
		KK	Ligante de permease bacteriana
		GA, AD, KK, VG	Inibidor da Dipeptidil Peptidase IV
		AD	Inibidor de alfa-glicosidase

Tabela 9: Bioatividades encontradas nos peptídeos presentes na amostra de *Paralonchurus brasiliensis* hidrolisada com Protamex através da utilização do banco de dados BioPep[78], apenas as sequencias com confiança média geral (ALC) até 90% foram descritas.

Peptídeo	Massa	Sequência	Bioatividades
LEEEELKLF	1148.59	**LKL, LF, KL, LEE**	Inibidor da Enzima Conversora da Angiotensina
		EL, LK	Antioxidante
EYKK	566.30	**YK, EY**	Inibidor da Enzima Conversora da Angiotensina
		KK	Ligante de permease bacteriana
		EY, KK, YK	Inibidor da Dipeptidil Peptidase IV
		YK	Inibidor da Dipeptidil Peptidase III
VDLWFK	806.43	**LW**	Inibidor da Enzima Conversora da Angiotensina
		LWF, LW	Antioxidante
		LW, WF, VD	Inibidor da Dipeptidil Peptidase IV
		LW	Inibidor da Dipeptidil Peptidase III
		LW	Inibidor de renina
LKLFL	632.42	**LKL, LF, KL**	Inibidor da Enzima Conversora da Angiotensina
		LK	Antioxidante
		FL	Inibidor da Dipeptidil Peptidase IV
		FL	Inibidor da Dipeptidil Peptidase III
LEDDLVALK	1014.55	**LK**	Antioxidante
		VA, AL, LV	Inibidor da Dipeptidil Peptidase IV
VGDEAKSQ	832.39	**VG, GD, EA**	Inibidor da Enzima Conversora da Angiotensina
		EAK	Antioxidante
		KS, VG	Inibidor da Dipeptidil Peptidase IV
		EA	Inibidor de alfa-glicosidase
VDLWFKA	877.46	**LW, KA**	Inibidor da Enzima Conversora da Angiotensina
		LWF, LW	Antioxidante
		KA, LW, WF, VD	Inibidor da Dipeptidil Peptidase IV
		LW, KA	Inibidor da Dipeptidil Peptidase III
		LW	Inibidor de renina
TVDDKVELE	1046.51	**VE**	Inibidor da Enzima Conversora da Angiotensina
		EL	Antioxidante
		KV, TV, VD, VR	Inibidor da Dipeptidil Peptidase IV
		VE	Inibidor de alfa-glicosidase
LVVDRKL	841.53	**KL, DR**	Inibidor da Enzima Conversora da Angiotensina
		VV, DR, LV, RK, VD	Inibidor da Dipeptidil Peptidase IV
LLDKNRDGLLSQ	1370.75	**GL, DG, DGL**	Inibidor da Enzima Conversora da Angiotensina
		LL, GL, NR	Inibidor da Dipeptidil Peptidase IV
		NR	Inibidor de renina
EARE	503.23	**EA, AR**	Inibidor da Enzima Conversora da Angiotensina
		EA	Inibidor de alfa-glicosidase
QGREK	616.32	**GR, QG, EK**	Inibidor da Enzima Conversora da Angiotensina
		EK, QG	Inibidor da Dipeptidil Peptidase IV

Nas Tabelas 10 e 11 estão descritas as amostras de *Micropogonias furnieri* hidrolisadas com Alcalase e com Protamex, respectivamente, de acordo com os dados que foram obtidos a partir do no sequenciamento de novo. Os resultados obtidos pelo programa de alinhamento BLAST[77] realizado nas sequencias peptídicas com confiança média geral (ALC) até 90%, estão representados nas Tabelas 12 e 13, sendo amostras hidrolisadas com Alcalase e Protamex, respectivamente. Já nas Tabelas 14 e 15 estão descritas as bioatividades presentes nos peptídeos registrados pelo banco de dados BioPep[78], sendo a Tabela 14 as amostras hidrolisadas com Alcalase e Tabela 15 as amostras hidrolisadas com Protamex, permitindo assim, uma comparação dos peptídeos gerados pelas duas hidrólises.

Tabela 10: Peptídeos encontrados na amostra de *Micropogonias furnieri* hidrolisada com Alcalase pelo sequenciamento de novo, com confiança média geral até 90%. Onde, ALC = confiança média geral, RT = tempo de retenção, ppm = chance de erro na identificação da sequência peptídica.

Peptídeo	ALC (%)	Massa	RT	ppm
LDEVLKFF	95	1009.54	14.37	-0.4
LEHEE	95	655.28	8.51	3.2
LNNLL	93	585.34	11.73	-37.8
TKTPGLME	93	875.44	10.50	-1.2
KLKKK	93	643.47	0.94	0.5
MKFLW	92	723.37	13.84	-1.8
LKYPLE	92	761.43	11.25	-1.5
APPHLF	91	680.36	11.68	-1.5
LLAPPEVGKY	91	1085.61	10.01	8.3
VVDGVKL	91	728.44	11.24	-1.5
WLDPDDFPLLLFS	91	1576.78	15.34	5.8
FLFGSKDKDPP	90	1249.63	11.36	-14.3
AGDDAPVK	90	771.37	8.96	-33.0
LLVYPW	90	789.44	14.89	0.0
KKTSPAE	90	759.41	1.29	14.0
FDDLQVR	90	891.44	11.05	-1.5
KDLLMVLTHSK	90	1283.72	12.36	-15.7
KFLVLADLW	90	1103.63	13.30	2.2

Tabela 11: Peptídeos encontrados na amostra de *Micropogonias furnieri* hidrolisada com Protamex pelo sequenciamento de novo, com confiança média geral até 90%. Onde, ALC = confiança média geral, RT = tempo de retenção, ppm = chance de erro na identificação da sequência peptídica.

Peptídeo	ALC (%)	Massa	RT	ppm
LEEEELKLF	97	1148.59	13.44	-0.3
FLDLDQDKKFEE	94	1525.73	12.66	-0.7
LVLHL	93	593.39	12.64	-1.2
VLDQDKSGFLE	93	1249.61	11.38	-0.4
LEKERL	93	786.45	11.42	-37.0
LVLDAGDRTH	92	1095.56	11.28	-10.2
LVEELPARW	92	1111.60	13.24	22.3
LHDQH	92	648.29	3.70	0.3
VGDEAQSK	92	832.39	8.09	0.0
VMLKQ	91	617.35	5.47	-31.3
FSVDEEFPDLSQH	91	1548.67	13.11	1.0
LEDQYSELK	91	1123.53	10.84	-0.3
DVEEFPDLSHQ	90	1314.57	12.03	-0.7
FAGDDAPRAL	90	1031.50	11.22	-0.9
LKEAETR	90	845.46	8.38	0.1

Tabela 12: Análise individual das sequências peptídicas encontradas na amostra de *Micropogonias furnieri* hidrolisada com Alcalase, visando alinhamento e consequência pelo banco de dados BLAST[77], descrição das dez primeiras sequências peptídicas.

Peptídeo	Massa	Query cover	E value	Seq. ID	Descrição	Espécie
LDEVLKFF	1009.54	100%	1.6	XP_034043238.1	ATPase 2-like	*Thalassophryne amazonica*
LEHEE	655.28	100%	1610	XP_036065667.1	Titina	*Oryzias melastigma*
LNNLL	585.34	100%	4594	XP_029692942.1	Titina-like	*Takifugu rubripes*
TKTPGLME	875.44	100%	2.2	TWW70116.1	Cadeia pesada de miosina	*Takifugu rubripes*
KLKKK	643.47	100%	9253	XP_046728865.1	Nesprina-2	*Silurus meridionalis*
MKFLW	723.37	100%	141	KAA0719128.1	Proteína dedo de zinco	*Sinocyclocheilus rhinocerous*
LKYPLE	761.43	100%	182	RXN10808.1	Miosina-Vc não convencional	*Labeo rohita*
APPHLF	680.36	100%	182	XP_029608157.1	Metilcitosina dioxigenase	*Salmo trutta*
LLAPPEVGKY	1085.61	100%	56	XP_013882412.1	Tomoregulina-1	*Austrofundulus limnaeus*
VVDGVKL	728.44	100%	116	TSK22821.1	Creatina kinase	*Bagarius yarrelli*

Tabela 13: Análise individual das sequências peptídicas encontradas na amostra de *Micropogonias furnieri* hidrolisada com Protamex, visando alinhamento e consequência pelo banco de dados BLAST[77], descrição das dez primeiras sequências peptídicas.

Peptídeo	Massa	Query cover	E value	Seq. ID	Descrição	Espécie
LEEEELKLF	1148.59	100%	2.0	TWW69872.1	Parvalbumina Beta 2	*Takifugu flavidus*
FLDLDQDKKFEE	1525.73	100%	7.2	XP_016411869.1	Ubiquitina carboxil-hidrolase	*Sinocyclocheilus rhinocerous*
LVLHL	593.39	100%	4595	XP_023807343.1	Nesprina-1	*Oryzias latipes*
VLDQDKSGFLE	1249.61	100%	0.066	TSK77154.1	Parvalbumina Beta	*Bagarius yarrelli*
LEKERL	786.45	100%	366	XP_041932362.1	Nesprina-1	*Alosa sapidissima*
LVLDAGDRTH	1095.56	100%	28	XP_028972366.2	Glicogenina-2	*Esox lucius*
LVEELPARW	1111.60	100%	16	XP_035995563.1	Titina	*Fundulus heteroclitus*
LHDQH	648.29	100%	1137	TWW70116.1	Cadeia pesada de miosina	*Takifugu flavidus*
VGDEAQSK	832.39	100%	8.7	ABP97428.1	Beta actina	*Rhinichthys cataractae*
VMLKQ	617.35	100%	1610	XP_041932362.1	Nesprina-1	*Alosa sapidissima*

Tabela 14: Bioatividades encontradas nos peptídeos presentes na amostra de *Micropogonias furnieri* hidrolisada com Alcalase através da utilização do banco de dados BioPep[78], apenas as sequencias com confiança média geral (ALC) até 90% foram descritas.

Peptídeo	Massa	Sequência	Bioatividades
LDEVLKFF	1009.54	**KF, EV, FF**	Inibidor da Enzima Conversora da Angiotensina
		LK	Antioxidante
		EV, KF, VL, FF	Inibidor da Dipeptidil Peptidase IV
		KF	Inibidor de renina
LEHEE	655.28	**EH, HE**	Inibidor da Dipeptidil Peptidase IV
LNNLL	585.34	**LN**	Inibidor da Enzima Conversora da Angiotensina
		LL, LN, NL, NN	Inibidor da Dipeptidil Peptidase IV
TKTPGLME	875.44	**PGL, GL, PG, ME, TP**	Inibidor da Enzima Conversora da Angiotensina
		PG	Atividade anti-amnésica
		PG	Antitrombótica

		TP, GL, KT, LM, ME, PG, TK	Inibidor da Dipeptidil Peptidase IV
KLKKK	643.47	**KL**	Inibidor da Enzima Conversora da Angiotensina
		LK	Antioxidante
		KK, KKK	Ligante de permease bacteriana
		KK	Inibidor da Dipeptidil Peptidase IV
MKFLW	723.37	**LW, KF**	Inibidor da Enzima Conversora da Angiotensina
		LW	Antioxidante
		FL, LW, KF, MK	Inibidor da Dipeptidil Peptidase IV
		LW, FL	Inibidor da Dipeptidil Peptidase III
		LW, KF	Inibidor de renina
LKYPLE	761.43	**YP, PL, KY**	Inibidor da Enzima Conversora da Angiotensina
		LK	Antioxidante
		YP, PL, KY	Inibidor da Dipeptidil Peptidase IV
		YPL, YP	Inibidor de alfa-glicosidase
APPHLF	680.36	**LF, AP, HL, PP, PH, APPH**	Inibidor da Enzima Conversora da Angiotensina
		HL, PHL	Antioxidante
		PP, AP, HL, PH	Inibidor da Dipeptidil Peptidase IV
		PP	Inibidor de alfa-glicosidase
		HL	Inibidor da Dipeptidil Peptidase III
LLAPPEVGKY	1085.61	**LAP, AP, LA, VG, GK, KY, EV, PP**	Inibidor da Enzima Conversora da Angiotensina
		LA	Ativador da Proteólise Mediada por Ubiquitina
		PP, LA, AP, LL, LLAP, EV, KY, VG	Inibidor da Dipeptidil Peptidase IV
		PP, PE	Inibidor de alfa-glicosidase
		LA, PE	Inibidor da Dipeptidil Peptidase III
VVDGVKL	728.44	**VK, GV, DG, KL**	Inibidor da Enzima Conversora da Angiotensina
		VKL	Antioxidante
		VV, GV, VD, VK	Inibidor da Dipeptidil Peptidase IV
WLDPDDFPLLLFS	1576.78	**FP, LF, PL, LLF, DF, WL**	Inibidor da Enzima Conversora da Angiotensina
		LL, FP, PL, WL, DP	Inibidor da Dipeptidil Peptidase IV
FLFGSKDKDPP	1249.63	**LF, FG, GS, PP**	Inibidor da Enzima Conversora da Angiotensina

		KD	Antioxidante
		PP, FL, DP, SK	Inibidor da Dipeptidil Peptidase IV
		PP	Inibidor de alfa-glicosidase
		FL	Inibidor de renina
AGDDAPVK	771.37	**VK, AP, AG, DA, GD**	Inibidor da Enzima Conversora da Angiotensina
		AP, AG, PV, VK	Inibidor da Dipeptidil Peptidase IV
		DA	Inibidor da Dipeptidil Peptidase III
LLVYPW	789.42	**LVYP, VY, VYP, YP, LVY**	Inibidor da Enzima Conversora da Angiotensina
		PW, VY, YPW	Antioxidante
		LL, YP, LV, PW, VY	Inibidor da Dipeptidil Peptidase IV
		YP	Inibidor de alfa-glicosidase
		VY, LVYPW	Inibidor da Dipeptidil Peptidase III
KKTSPAE	759.41	**KK**	Ligante de permease bacteriana
		PA, SP, AE, KK, KT, TS	Inibidor da Dipeptidil Peptidase IV
FDDLQVR	891.44	**VR, LQ**	Inibidor da Enzima Conversora da Angiotensina
		VR, QV	Inibidor da Dipeptidil Peptidase IV
KDLLMVLTHSK	1283.72	**VL, LL**	Estimulador da captação de glicose
		KD	Antioxidante
		LL, HS, LM, LT, MV, SK, TH, VL	Inibidor da Dipeptidil Peptidase IV
KFLVLADLW	1103.63	**LW, LVL, LA, KF**	Inibidor da Enzima Conversora da Angiotensina
		VL, LV	Estimulador da captação de glicose
		LW	Antioxidante
		LA	Ativador da Proteólise Mediada por Ubiquitina
		LA, FL, LW, AD, KF, LV, VL	Inibidor da Dipeptidil Peptidase IV
		AD	Inibidor de alfa-glicosidase
		LW, LA, FL	Inibidor da Dipeptidil Peptidase III
		LW, KF	Inibidor de renina

Tabela 15: Bioatividades encontradas nos peptídeos presentes na amostra de *Micropogonias furnieri* hidrolisada com Protamex através da utilização do banco de dados BioPep[78], apenas as sequencias com confiança média geral (ALC) até 90% foram descritas.

Peptídeo	Massa	Sequência	Bioatividades
LEEEELKLF	1148.59	**LKL, LF, KL, LEE**	Inibidor da Enzima Conversora da Angiotensina
		EEE, EE	Estimulador da liberação de substâncias vasoativas
		EL, LK	Antioxidante
FLDLDQDKKFEE	1525.73	**KF**	Inibidor da Enzima Conversora da Angiotensina
		EE	Estimulador da liberação de substâncias vasoativas
		KK	Ligante de permease bacteriana
		FL, DQ, KF, KK, QD	Inibidor da Dipeptidil Peptidase IV
		FL	Inibidor da Dipeptidil Peptidase III
		KF	Inibidor de renina
LVLHL	593.39	**LVL, HL**	Inibidor da Enzima Conversora da Angiotensina
		VL, LV	Estimulador da captação de glicose
		LH, HL, LHL	Antioxidante
		HL, LH, LV, VL	Inibidor da Dipeptidil Peptidase IV
		HL	Inibidor da Dipeptidil Peptidase III
VLDQDKSGFLE	1249.61	**GF, SG**	Inibidor da Enzima Conversora da Angiotensina
		VL	Estimulador da captação de glicose
		GFL	Imunoestimulante
		FL, DQ, GF, KS, QD, VL	Inibidor da Dipeptidil Peptidase IV
		GF, FL, GFL	Inibidor da Dipeptidil Peptidase III
LEKERL	786.45	**RL, EK, KE, LEK, ER**	Inibidor da Enzima Conversora da Angiotensina
		EK, KE, RL	Inibidor da Dipeptidil Peptidase IV
LVLDAGDRTH	1095.56	**LVL, AG, DA, GD, DR**	Inibidor da Enzima Conversora da Angiotensina
		VL, LV	Estimulador da captação de glicose
		AG, DR, LV, TH, VL	Inibidor da Dipeptidil Peptidase IV
		DA	Inibidor da Dipeptidil Peptidase III
LVEELPARW	1111.60	**RW, AR, LVE, VE, LP**	Inibidor da Enzima Conversora da Angiotensina
		LV	Estimulador da captação de glicose
		EL, RW	Antioxidante
		PA, LP, LV, RW, VE	Inibidor da Dipeptidil Peptidase IV
		VE	Inibidor de alfa-glicosidase
		RW	Inibidor da Dipeptidil Peptidase III

LHDQH	648.29	**LH, LHD**	Antioxidante
		DQ, HD, LH, QH	Inibidor da Dipeptidil Peptidase IV
VGDEAQSK	832.39	**VG, GD, EA**	Inibidor da Enzima Conversora da Angiotensina
		QS, SK, VG	Inibidor da Dipeptidil Peptidase IV
		EA	Inibidor de alfa-glicosidase
VMLKQ	617.35	**VM**	Inibidor da Enzima Conversora da Angiotensina
		LK	Antioxidante
		ML, VM	Inibidor da Dipeptidil Peptidase IV
FSVDEEFPDLSQH	1548.67	**FP, EF**	Inibidor da Enzima Conversora da Angiotensina
		DEE	Antitrombótico
LEDQYSELK	1123.53	**FP, QH, SV, VD**	Inibidor da Dipeptidil Peptidase IV
		EF	Inibidor de renina
		EF	Hipolipidêmica
DVEEFPDLSHQ	1314.57	**FP, VE, EF**	Inibidor da Enzima Conversora da Angiotensina
		FP, SH, VE	Inibidor da Dipeptidil Peptidase IV
		VE	Inibidor de alfa-glicosidase
		EF	Inibidor de renina
		EF	Hipolipidêmica
FAGDDAPRAL	1031.50	**AGDDAPR**	Inibidor de alfa-amilase
		PR, AP, RA, AG, GD, AGDDAPR	Inibidor da Enzima Conversora da Angiotensina
		AGDDAPR	Antioxidante
		RA	Ativador da Proteólise Mediada por Ubiquitina
		FA, AP, RA, AG	Inibidor da Dipeptidil Peptidase IV
		PR, DA, FA	Inibidor da Dipeptidil Peptidase III
		AGDDAPR	Inibidor de lipase pancreática
LKEAETR	845.46	**EA, KE**	Inibidor da Enzima Conversora da Angiotensina
		EAE	Imunoestimulante
		LK	Antioxidante
		AE, ET, KE, TR	Inibidor da Dipeptidil Peptidase IV
		EA	Inibidor de alfa-glicosidase

Os resultados do sequenciamento de novo realizado nas amostras de *Hepatus pudibundus* hidrolisadas com Alcalase e com Protamex estão descritos nas Tabelas 16 e 17, respectivamente. Nas Tabelas 18 e 19 estão os resultados obtidos de acordo com o programa de alinhamento BLAST[77], utilizado na busca em bancos de dados de ácidos nucléicos e proteínas por sequências homólogas e para a realização do alinhamento local por pares de sequências dos peptídeos com confiança média geral (ALC) até 90%, a Tabela 18 representa os resultados da amostra hidrolisada com Alcalase e na Tabela 19 a amostra hidrolisada com Protamex. Já os resultados obtidos pelo banco de dados BioPep[78] podem ser vistos nas Tabelas 20 e 21, sendo amostra hidrolisada com Alcalase e Protamex, respectivamente. O banco de dados BioPep[78] é uma ferramenta utilizada para a identificação das bioatividades existentes nos peptídeos encontrados nas amostras.

Tabela 16: Peptídeos encontrados na amostra de *Hepatus pudibundus* hidrolisada com Alcalase pelo sequenciamento de novo, com confiança média geral até 90%. Onde, ALC = confiança média geral, RT = tempo de retenção, ppm = probabilidade de erro da sequência peptídica.

Peptídeo	ALC (%)	Massa	RT	ppm
LTKLL	97	5.864.054	11.72	-0.5
LPTKF	95	6.043.584	10.77	2.1
VVAKKPQE	95	8.975.283	10.02	19.8
KLHWH	94	7.193.867	8.76	0.1
VHLKLPK	94	8.335.486	10.05	-0.7
MLSLKEM	93	8.504.293	12.91	17.1
WPGPLNF	92	8.294.122	12.89	-18.2
FGDKFT	92	7.133.384	10.67	-0.4
LDAPSQPEDF	91	11.174.927	9.53	2.6
VVLPKNME	91	9.285.052	13.61	23.4
DFDLSLMFM	91	11.174.824	13.92	26.0
ELLPNTDAGDY	90	12.065.405	10.23	11.7
VGDEAKTN	90	8.323.926	7.67	0.0
YPGLADTW	90	9.214.232	11.25	15.5
VSVGDKLPAMP	90	11.125.898	11.82	16.1
VGDEAQSK	90	8.323.926	7.39	0.0

Tabela 17: Peptídeos encontrados na amostra de *Hepatus pudibundus* hidrolisada com Alcalase pelo sequenciamento de novo, com confiança média geral até 90%. Onde, ALC = confiança média geral, RT = tempo de retenção, ppm = probabilidade de erro da sequência peptídica.

Peptídeo	ALC (%)	Massa	RT	ppm
LKYPLE	95	7.614.323	11.29	0.0
VNVDPDGKF	94	9.894.818	11.26	-0.2
LPDWHPMDR	93	11.655.339	10.20	1.9
VHLKLPK	93	8.335.486	10.11	-0.2
LDKFF	91	6.683.533	13.73	0.2
MLSLQFL	91	8.504.622	13.21	-21.8
VDFLGTFLYEYSR	90	16.087.825	15.06	0.1
LKMPL	90	6.003.669	11.28	29.2
LDAPSKPEDM	90	11.015.012	10.72	-0.1
LHLML	89	6.253.621	12.98	-5.6
TLKLL	89	5.864.054	11.93	-1.2
LLAPPERQHL	89	11.726.665	10.19	-10.2
APNELLAMK	88	9.855.266	10.82	18.0
VFAALVT	88	7.194.218	13.67	-13.8
YPGLADWT	88	9.214.232	11.49	15.1
SPGVLDAGLVMH	88	11.946.067	12.56	-0.9
LLAPLLVGQY	88	10.856.484	10.38	-24.2
AKLPKW	88	7.414.537	11.01	-0.9
LDNLFR	88	7.764.180	11.80	-0.3

Tabela 18: Análise individual das sequências peptídicas encontradas na amostra de *Hepatus pudibundus* hidrolisada com Alcalase, visando alinhamento e consequência pelo banco de dados BLAST[77], descrição das dez primeiras sequências peptídicas.

Peptídeo	Massa	Query cover	E value	Seq. ID	Descrição	Espécie
LEEEELKLF	1148.59	100%	1.5	P86432.1	Parvalbumina beta 2	*Oncorhynchus mykiss*
FLDLDQDKKFEE	1525.73	100%	15	XP_016411870.1	Ubiquitina carboxil-terminal hidrolase	*Sinocyclocheilus rhinocerous*
LVLHL	593.39	100%	4595	XP_023807343.1	Nesprina-1	*Oryzias latipes*
VLDQDKSGFLE	1249.61	100%	0.047	P86432.1	Parvalbumina beta 2	*Oncorhynchus mykiss*
LEKERL	786.45	100%	366	XP_041932362.1	Nesprina-1	*Alosa sapidissima*
LVLDAGDRTH	1095.56	100%	28	XP_028972366.2	Glicogenina-2	*Esox lucius*
LVEELPARW	1111.60	100%	16	XP_035995563.1	Titina	*Fundulus heteroclitus*
LHDQH	648.29	100%	1137	TWW70116.1	Cadeia pesada de miosina	*Takifugu flavidus*
VGDEAQSK	832.39	100%	8.7	ABP97428.1	Beta Actina	*Rhinichthys cataractae*
VMLKQ	617.35	100%	1610	XP_041932362.1	Nesprina-1	*Alosa sapidissima*

Tabela 19: Análise individual das sequências peptídicas encontradas na amostra de *Hepatus pudibundus* hidrolisada com Protamex, visando alinhamento e consequência pelo banco de dados BLAST[77], descrição das dez primeiras sequências peptídicas.

Peptídeo	Massa	Query cover	E value	Seq. ID	Descrição	Espécie
LLAPPE	638.36	100%	544	MBN3292205.1	Roquin-1	*Oncorhynchus mykiss*
YEKK	566.30	100%	20098	TRS51413.1	Titina	*Bagarius yarrelli*
LVYPSV	676.37	100%	384	XP_043868191.1	Dedo de zinco	*Solea senegalensis*
VKLPKL	696.48	100%	772	XP_017578900.2	Proteína AHNAK associada à diferenciação de neuroblastos	*Pygocentrus nattereri*
LKYPLE	761.43	100%	190	XP_0411101389.1	Proteína âncora A-quinase	*Polyodon spathula*
LDFDEFLMK	1156.54	100%	2.0	XP_042563305.1	Proteína de ligação ao cálcio	*Clupea harengus*
LLDQDKSGFLE	1263.63	100%	0.049	P86432.1	Parvalbumina beta 2	*Oncorhynchus mykiss*
SERRLL	772.45	100%	543	XP_024127336.1	Ubiquitina E3 ligase	*Oryzias melastigma*
EYKK	566.30	100%	20098	TSR51413.1	Titina	*Bagarius yarrelli*
LLVYPW	789.44	100%	191	XP_014836463.1	Tirosina neuronal	*Poecilia mexicana*

Tabela 20: Bioatividades encontradas nos peptídeos presentes na amostra de *Hepatus pudibundus* hidrolisada com Alcalase através da utilização do banco de dados BioPep[78], apenas as sequencias com confiança média geral (ALC) até 90% foram descritas.

Peptídeo	Massa	Sequência	Bioatividades
LTKLL	586.40	**KL**	Inibidor da Enzima Conversora da Angiotensina
		LL	Estimulador da captação de glicose
		LL, LT, TK	Inibidor da Dipeptidil Peptidase IV
LPTKF	604.35	**KF, PT, LP**	Inibidor da Enzima Conversora da Angiotensina
		LP, KF, PT, TK	Inibidor da Dipeptidil Peptidase IV
		KF	Inibidor de renina
VVAKKPQE	897.52	**AKK, KP, PQ**	Inibidor da Enzima Conversora da Angiotensina
		KP	Antioxidante
		KK	Ligante de permease bacteriana
		VA, VV, KP, KK, PQ, QE	Inibidor da Dipeptidil Peptidase IV
KLHWH	719.38	**KL**	Inibidor da Enzima Conversora da Angiotensina

		LH, HWH, LHW	Antioxidante
		HW, LH, WH	Inibidor da Dipeptidil Peptidase IV
VHLKLPK	833.54	**LKL, HL, KL, LKLP, LP**	Inibidor da Enzima Conversora da Angiotensina
		HL, LK	Antioxidante
		LP, HL, PK, VH	Inibidor da Dipeptidil Peptidase IV
		HL	Inibidor da Dipeptidil Peptidase III
MLSLKEM	850.42	**KE**	Inibidor da Enzima Conversora da Angiotensina
		SL	Regulador da atividade da fosfoglicerato quinase
		LK	Antioxidante
		SL, KE, ML	Inibidor da Dipeptidil Peptidase IV
WPGPLNF	829.41	**PGP, PG, GP**	Anti-amnésica
		GPL, GP, PL, PG, NF, LN, LNF	Inibidor da Enzima Conversora da Angiotensina
		GP, PGP, PG	Antitrombótica
		GP, PG, PGP	Regulador da atividade da membrana mucosa do estômago
		PGP	Inibidor de secreção de insulina
		PGP	Quimiotático
		GP, WP, PL, LN, NF, PG	Inibidor da Dipeptidil Peptidase IV
FGDKFT	713.33	**FG, GD, KF**	Inibidor da Enzima Conversora da Angiotensina
		KF	Inibidor da Dipeptidil Peptidase IV
		FT, KF	Inibidor de renina
LDAPSQPEDF	1117.49	**AP, DA, DF, QP**	Inibidor da Enzima Conversora da Angiotensina
		AP, QP, OS	Inibidor da Dipeptidil Peptidase IV
		PE	Inibidor de alfa-glicosidase
		DA, PE	Inibidor da Dipeptidil Peptidase III
VVLPKNME	928.50	**VLP, ME, VVL, LP**	Inibidor da Enzima Conversora da Angiotensina
		VL	Estimulador da captação de glicose
		LP, VV, ME, NM, PK, VL	Inibidor da Dipeptidil Peptidase IV
DFDLSLMFM	1117.48	**MF, DF**	Inibidor da Enzima Conversora da Angiotensina
		SL	Regulador da atividade da fosfoglicerato quinase
		SL, LM, MF	Inibidor da Dipeptidil Peptidase IV
		FM	Inibidor da Dipeptidil Peptidase III
ELLPNTDAGDY	1206.54	**LLP, AG, DA, GD, DY, LP**	Inibidor da Enzima Conversora da Angiotensina
		LL	Estimulador da captação de glicose
		DY	Regulador de fluxo de íons
		EL	Antioxidante

		LP, LL, AG, NT, PN, TD	Inibidor da Dipeptidil Peptidase IV
		DA	Inibidor da Dipeptidil Peptidase III
VGDEAKTN	832.39	**VG, GD, EA**	Inibidor da Enzima Conversora da Angiotensina
		EAK	Antioxidante
		KT, TN, VG	Inibidor da Dipeptidil Peptidase IV
		EA	Inibidor de alfa-glicosidase
YPGLADTW	921.42	**PG**	Antiamnésica
		YP, PGL, LA, GL, PG, YPG	Inibidor da Enzima Conversora da Angiotensina
		PG	Antitrombótica
		PG	Regulador da atividade da membrana mucosa do estômago
		TW	Antioxidante
		LA	Ativador de proteólise mediado por Ubiquitina
		LA, YP, GL, AD, PG, TW	Inibidor da Dipeptidil Peptidase IV
		YP, YPG, AD	Inibidor de alfa-glicosidase
		LA	Inibidor da Dipeptidil Peptidase III
VSVGDKLPAMP	1112.58	**VG, GD, KL, KLP, LP**	Inibidor da Enzima Conversora da Angiotensina
		MP, PA, LP, SV, VG, VS	Inibidor da Dipeptidil Peptidase IV
VGDEAQSK	832.39	**VG, GD, EA**	Inibidor da Enzima Conversora da Angiotensina
		QS, SK, VG	Inibidor da Dipeptidil Peptidase IV
		EA	Inibidor de alfa-glicosidase

Tabela 21: Bioatividades encontradas nos peptídeos presentes na amostra *Hepatus pudibundus* hidrolisada com Protamex através da utilização do banco de dados BioPep[78], sequencias com confiança média geral (ALC) até 88%.

Peptídeo	Massa	Sequência	Bioatividades
LKYPLE	761.43	**YP, PL, KY**	Inibidor da Enzima Conversora da Angiotensina
		LK	Antioxidante
		YP, PL, KY	Inibidor da Dipeptidil Peptidase IV
		YPL, YP	Inibidor de alfa-glicosidase
VNVDPDGKF	989.48	**GK, DG, KF**	Inibidor da Enzima Conversora da Angiotensina
		DP, KF, NV, VD, VN	Inibidor da Dipeptidil Peptidase IV
		KF	Inibidor de renina
LPDWHPMDR	1165.33	**HP, DR, LP**	Inibidor da Enzima Conversora da Angiotensina
		LP, HP, DR, PM, WH	Inibidor da Dipeptidil Peptidase IV
		HP	Inibidor da Dipeptidil Peptidase III
VHLKLPK	833.48	**LKL, HL, KL, LKLP, KLP, LP**	Inibidor da Enzima Conversora da Angiotensina
		HL, LK	Antioxidante
		LP, HL, PK, VH	Inibidor da Dipeptidil Peptidase IV

		HL	Inibidor da Dipeptidil Peptidase III
LDKFF	668.35	**KF, FF**	Inibidor da Enzima Conversora da Angiotensina
		KF, FF	Inibidor da Dipeptidil Peptidase IV
		KF	Inibidor de renina
MLSLQFL	850.46	**LQ**	Inibidor da Enzima Conversora da Angiotensina
		SL	Regulador da atividade da fosfoglicerato quinase
		FL, SL, ML, QF	Inibidor da Dipeptidil Peptidase IV
		FL	Inibidor da Dipeptidil Peptidase III
		QF	Inibidor de renina
VDFLGTFLYEYSR	1608.78	**LY, GT, LG, EY, DF, YE**	Inibidor da Enzima Conversora da Angiotensina
		LY, YEY	Antioxidante
		FL, EY, TF, VD, YE, YS	Inibidor da Dipeptidil Peptidase IV
		TF, FL	Inibidor da Dipeptidil Peptidase III
		LY, TF	Inibidor de renina
LKMPL	600.36	**PL**	Inibidor da Enzima Conversora da Angiotensina
		LK	Antioxidante
		MP, PL	Inibidor da Dipeptidil Peptidase IV
LDAPSKPEDM	1101.50	**AP, DA, KP, DM**	Inibidor da Enzima Conversora da Angiotensina
		KP	Antioxidante
		AP, KP, PS, SK	Inibidor da Dipeptidil Peptidase IV
		PE	Inibidor de alfa-glicosidase
		DA, PE	Inibidor da Dipeptidil Peptidase III
LHLML	625.36	**HL**	Inibidor da Enzima Conversora da Angiotensina
		LH, HL, LHL	Antioxidante
		HL, LH, LM, ML	Inibidor da Dipeptidil Peptidase IV
		HL	Inibidor da Dipeptidil Peptidase III
TLKLL	586.40	**LKL, KL**	Inibidor da Enzima Conversora da Angiotensina
		LL	Estimulador da captação de glicose
		LK	Antioxidante
		LL, TL	Inibidor da Dipeptidil Peptidase IV
LLAPPERQHL	1172.66	**LAP, AP, LA, HL, PP, ER**	Inibidor da Enzima Conversora da Angiotensina
		LL	Estimulador da captação de glicose
		HL	Antioxidante
		LA	Ativador de proteólise mediado por Ubiquitina
		PP, LA, AP, LL, HL, LLAP, QH	Inibidor da Dipeptidil Peptidase IV
		PP, PE	Inibidor de alfa-glicosidase
		HL, LA, PE	Inibidor da Dipeptidil Peptidase III
APNELLAMK	985.52	**AP, LA**	Inibidor da Enzima Conversora da Angiotensina
		LL	Estimulador da captação de glicose
		EL	Antioxidante
		LA	Ativador de proteólise mediado por Ubiquitina
		LA, AP, LL, MK, NE, PN	Inibidor da Dipeptidil Peptidase IV

		LA	Inibidor da Dipeptidil Peptidase III
VFAALVT	719.42	**VF, AA**	Inibidor da Enzima Conversora da Angiotensina
		LV	Estimulador da captação de glicose
		AA	Hipotensor
		FA, AL, AA, LV, VF, VT	Inibidor da Dipeptidil Peptidase IV
		FA	Inibidor da Dipeptidil Peptidase III
YPGLADWT	921.42	**PG**	Antiamnésica
		YP, PGL, LA, GL, PG, YPG	Inibidor da Enzima Conversora da Angiotensina
		PG	Antitrombótica
		PG	Regulador da atividade da membrana mucosa do estômago
		LA	Ativador de proteólise mediado por Ubiquitina
		LA, YP, GL, WT, AD, PG	Inibidor da Dipeptidil Peptidase IV
		YP, YPG, AD	Inibidor de alfa-glicosidase
		LA	Inibidor da Dipeptidil Peptidase III
SPGVLDAGLVMH	1194.60	**PG**	Antiamnésica
		GL, AG, DA, GV, PG, VM	Inibidor da Enzima Conversora da Angiotensina
		PG	Antitrombótica
		VL, LV	Estimulador da captação de glicose
		MH	Neuropeptídeo
		PG	Regulador da atividade da membrana mucosa do estômago
		SP, GL, AG, GV, LV,	Inibidor da Dipeptidil Peptidase IV
		MH, PG, VL, VM **DA**	Inibidor da Dipeptidil Peptidase III
LLAPLLVGQY	1085.64	**PL, LAP, AP, LA, VG, QG**	Inibidor da Enzima Conversora da Angiotensina
		LV, LL	Estimulador da captação de glicose
		GQ	Neuropeptídeo
		LA	Ativador de proteólise mediado por Ubiquitina
		LA, AP, LL, PL, LLAP, LV, QY, VG	Inibidor da Dipeptidil Peptidase IV
		LA	Inibidor da Dipeptidil Peptidase III
AKLPKW	741.45	**KW, KL, KLP, LP**	Inibidor da Enzima Conversora da Angiotensina
		LP, KW, PK	Inibidor da Dipeptidil Peptidase IV
LDNLFR	776.41	**LF, FR, LFR**	Inibidor da Enzima Conversora da Angiotensina
		DN, FR, NL	Inibidor da Dipeptidil Peptidase IV
		FR	Inibidor da Dipeptidil Peptidase III

5. DISCUSSÃO

A fauna acompanhante abrange os animais que são capturados por rede de arrasto que não fazem parte da espécie-alvo[47]. A pesca de arrasto é considerada altamente eficiente para captura da espécie-alvo, porém, não é uma prática seletiva e acaba atingindo animais que não fazem parte do alvo da pesca, animais estes que devido ao seu baixo – ou nenhuma – valor comercial são descartados mortos ou moribundos[47,79].

A captura acessória por meio de rede de arrasto é alta, frequentemente excede a captura da espécie alvo e na maioria das vezes não é registrada oficialmente[79]. Além disso, essa prática pode levar a diversos impactos nas populações e nos ecossistemas, podendo aumentar risco de extinção em espécies, gerar ampla destruição de comunidades bentônicas, afetar relações predador/presa desestabilizando todo ecossistema da região, entre outros[71,80]. Dentro das pescas por meio de arrasto, a pesca de camarão é tida como a causadora de maior impacto ambiental, visto que esta captura uma enorme quantidade de fauna acompanhante[49,81,82].

Os problemas socioeconômicos também são evidentes, no Brasil, a pesca de arrasto é considerada uma prática rudimentar e com pequena seletividade, uma vez que esta é realizada do mesmo modo que nos países com baixa diversidade marinha[83]. A maioria das comunidades pesqueiras são de cultura caiçara devido à sua origem e ao isolamento devido às áreas protegidas de preservação ao meio ambiente, os pescadores artesanais possuem renda inferior se comparado ao nível de outros setores – como agricultura e mineração – e, consequentemente, muitas vezes não garantem a renda mensal, fazendo com que as atividades secundárias sejam importantes fontes econômicas para a renda familiar anual[81–83]. A captura dessa fauna indesejada faz com que os pescadores tenham prejuízo com maior desgaste do barco e com contratação de mão-de-obra para auxiliar na triagem da espécie-alvo[70,72].

Diante desse cenário, os pescadores artesanais do litoral brasileiro não possuem condições financeiras para buscar um meio de pesca mais sustentável que cause menos impacto a esses ecossistemas. Portanto, é necessário abranger os meios de uso da fauna acompanhante visando gerar renda extra a esses pescadores, já que esta não possui valor comercial, bem como obter melhor aproveitamento à enorme biodiversidade existente na fauna acompanhante, considerando que esta oferece uma ampla gama de compostos bioativos inexplorados com grande potencial de utilização voltado à saúde humana[6,21] e à alimentação humana e animal[64,72,84], e em contra partida auxiliar na diminuição dos impactos ambientais causados pela devolução desses animais mortos ou moribundos no ambiente marinho.

Partindo desse princípio, as análises bioquímicas realizadas nas amostras de músculo de três animais mais abundantes na fauna acompanhante de Ubatuba, São Paulo, *Paralonchurus brasiliensis, Micropogonias furnieri* e *Hepatus pudibundus*, possibilitaram maior conhecimento dos compostos presentes nesses peixes e crustáceo, traçando seus perfis peptídicos e obtendo resultados válidos para melhor utilização desses animais que são comumente descartados.

As amostras foram previamente hidrolisadas, algumas com as enzimas Alcalase e outras com a enzima Protamex. Uma revisão apresentada por Tacias-Pascacio *et al*.[85], teve como objetivo abranger os usos da protease Alcalase na produção de peptídeos biologicamente ativos. A Alcalase se mostrou uma das proteases mais eficientes, sendo considerada especialmente interessante no uso dos resíduos proteicos da indústria alimentícia como matéria-prima. A hidrólise realizada com a Protamex revelou ser altamente eficiente na extração de compostos com atividade antioxidante e antimicrobianas[86–88].

Para comprovar a efetividade da digestão das hidrólises foi realizada a eletroforese SDS-PAGE. Essa técnica permite uma visualização das proteínas presentes nas amostras, considerando que os géis não acusaram nenhuma banda de proteína em ambas as porcentagens (12 e 20%), é possível afirmar que não houve proteínas intactas pós hidrólise, configurando as amostras como uma mistura de peptídeos e, portanto, comprovando a eficácia das hidrólises.

Para a determinação dos perfis cromatográficos das amostras foi utilizada a cromatografia líquida de alta eficiência com detector UV a 214nm, que é o ideal para obtenção de perfil peptídico. Tendo em vista a escassez de tais informações na literatura e a importância destas para o andamento do presente estudo, a realização dessa análise foi de suma importância. As corridas começaram com um solvente polar (A) no início (0 min) e, de acordo com os parâmetros de corrida, as bombas vão liberando o solvente apolar (B), que no caso foi utilizada a acetonitrila. Portanto, pode-se dizer que os compostos que aparecem no início da corrida são polares (hidrofílicos), enquanto os que estão no final da corrida são apolares (hidrofóbicos), já os que estão no meio da corrida são considerados com polaridade intermediária. A medida em que os compostos atingem sua polaridade ideal, saem da fase estacionaria da coluna e passam pelo refletor, gerando o pico presente no gráfico, sendo assim, cada pico pode ser indicador de uma ou várias moléculas com mesma polaridade.

Em ambos os perfis cromatográficos de *Paralonchurus brasiliensis* os picos começaram a surgir em aproximadamente 9,2 minutos de corrida e eluiram a 45% de acetonitrila, portanto, é uma amostra com picos intermediários a apolares. É possível notar que a amostra hidrolisada com Alcalase obteve quatro picos majoritários, sendo três com polaridade intermediária e um apolar, enquanto a amostra hidrolisada com Protamex apresentou apenas três picos majoritários com polaridade intermediária.

As amostras de *Micropogonias furnieri* hidrolisadas com Alcalase e Protamex apresentaram eluição em 45 a 50% aos 9,2 minutos e 9,6 minutos, respectivamente. Os picos majoritários surgiram com 50 e 60% de solvente orgânico, sendo assim uma amostra com polaridade intermediária a apolar. Na amostra de *Hepatus pudibundus* hidrolisada com Alcalase há compostos com polaridade intermediária e apolares, em contrapartida, na amostra com Protamex foram mais compostos polares do que apolares. Em uma análise geral dos perfis obtidos por cromatografia líquida de alta eficiência com detector UV (CLEA) foi registrado que a maioria dos compostos presentes nas amostras são intermediários a apolares. Os poucos compostos presentes dos 3 aos 5 minutos são polares, porém nessa faixa de tempo são encontrados sais e outras substâncias que geralmente são descartadas nas análises.

Como a amostra foi constatada como uma mistura complexa de peptídeos, a espectrometria de massas tipo MALDI-TOF foi escolhida, essa análise é muito utilizada em misturas peptídicas e auxilia na detecção de altas massas moleculares. Para sua realização é necessária a adição de uma matriz isocrática, no caso foi utilizada uma solução de ácido orgânico que cristaliza e facilita a ionização. Logo, os dados obtidos antes de 1000 Da sofrem interferência da matriz e precisam ser descartados. Acima de 3000 Da não foi obtido nenhum resultado, portanto, os dados apresentados foram de 1000 Da a 3000 Da. As análises possibilitaram notar a diferença entre as amostras hidrolisadas com Alcalase e com Protamex, confirmando que as hidrólises geraram diferentes peptídeos.

Os picos considerados mais interessantes do ponto de vista bioquímico para a prospecção de atividades biológicas voltadas à saúde humana são os que possuem massa entre 1500 Da a 2000 Da, ou seja, peptídeos que contém de 15 a 20 aminoácidos na cadeia. Tais compostos são mais versáteis e mais propensos à obtenção de maior diversidade molecular, consequentemente, diferentes efeitos biológicos, tendo em vista que os picos com massas a partir de 2000 Da, normalmente possuem maiores atividades antibióticas, antitumorais, antifúngicas, entre outras.

De acordo com esse parâmetro, as amostras de *Paralonchurus brasiliensis* hidrolisadas com Alcalase e as amostras de *Micropogonias furnieri* e *Hepatus pudibundus* hidrolisadas com Protamex foram mais assertivas, pois contaram com peptídeos maiores e mais abundantes, com potencial bioquímico e biotecnológico. Dessa maneira, com os dados obtidos através da espectrometria de massas tipo MADI-TOF foi possível ressaltar a complexibilidade e versatilidade da mistura contida nas amostras obtidas tanto pela hidrólise com Alcalase, quanto pela hidrólise com Protamex, tendo como massa média dos peptídeos obtidos das amostras de 1000 a 1800 Da, ou seja, de 10 a 18 aminoácidos em cadeia.

A hidrólise com Alcalase nas amostras de *Micropogonias furnieri* e *Hepatus pudibundus* e a hidrolise com Protamex na amostra de *Paralonchurus brasiliensis*, privilegiaram os compostos com menores massas moleculares. Tais peptídeos são mais pobres em interação nesse tipo de análise devido a supressão de sinal no início da corrida causado pela matriz. Os peptídeos menores estão mais fracionados e, por essa razão, poderiam facilmente ser utilizados em suplementos alimentares e alimentação, tanto humana, quanto animal, já que são diluídos mais facilmente.

Em resumo, os resultados obtidos pelo MALDI-TOF apontaram que, para a biotecnologia marinha voltada para a saúde humana, as amostras mais interessantes são a de *Paralonchurus brasiliensis* hidrolisada com Alcalase e as amostras de *Micropogonias furnieri* e *Hepatus pudibundus* hidrolisadas com Protamex. Já visando nutrição e suplementação as mais interessantes são e as amostras de *Micropogonias furnieri* e *Hepatus pudibundus* hidrolisadas com Alcalase e a amostra de *Paralonchurus brasiliensis* hidrolisada com Protamex. Dando destaque para as amostras do crustáceo *Hepatus pudibundus* hidrolisada com Protamex e a amostra do peixe *Paralonchurus brasiliensis* hidrolisada com Alcalase que geraram perfis com sinais mais claros e mais interessantes, contendo diversos picos de peptídeos com massa molecular entre 1500 e 2800Da, ou seja, os peptídeos encontrados possuem de 15 a 28 aminoácidos em cadeia.

Após todos esses dados obtidos por MALDI-TOF, vale ressaltar a importância da realização dessa análise para a obtenção de uma visualização geral da diversidade presente, bem como informações simultâneas de todas as amostras relacionadas à massa molecular. A possibilidade de uma utilização mais diversa das amostras também foi apontada, já que estas constataram peptídeos com massa molecular diversa.

Para melhor compreensão dos perfis peptídicos traçados por CLEA-UV foi realizado o LC/MS, um cromatógrafo líquido de fase reversa em coluna C18 acoplado a um espectrômetro de massas com detecção de troca iônica. Alguns fatores diferenciam o LC/MS da CLEA-UV, são eles: detecção por troca iônica; necessidade de uma matriz isocrática que, nos primeiros cinco minutos de corrida, auxilia na diluição e eliminação de sais e outras substâncias que não interagem com a coluna; o acoplamento a um espectrômetro de massas que possui uma tubulação mais curta e estreita, evitando a diluição da amostra. Por essas razões, o LC/MS é tido como um método mais confiável. Com o LC/MS também é possível obter resultados complementares ao MALDI-TOF, tendo em vista que o LC/MS consegue detectar baixas massas moleculares, além de possibilitar a ampliação dos picos obtidos.

Os resultados gerados por LC/MS possibilitaram concluir que, as amostras são predominantemente polares, ou seja, possuem compostos hidrofílicos os quais podem ser adicionados ou diluídos em meio líquido sem impedimento de características biofísicas. Conforme as análises representativas, a riqueza dos peptídeos predominantes nas amostras é de 4 a 6 aminoácidos na cadeia, sendo massas moleculares entre 400 e 600Da, os peptídeos com menor massa também auxiliam na diluição e adição a alimentos e suplementos nutricionais. Com relação às hidrólises, a que se mostrou mais eficiente para suplementação e alimentação foi a realizada com Protamex, já que seus resultados apresentaram maior polaridade das amostras e maior quantidade de peptídeos com menor massa molecular. Os tempos de retenção de três diferentes picos foram analisados, evidenciando que os peptídeos gerados pelas três amostras possuem baixa massa molecular e que todas as amostras geraram peptídeos complexos que variam de acordo com o número de picos, podendo assim existir mais de um composto por pico.

Diante deste cenário, foi possível observar que o LC/MS registrou diversos compostos de baixa massa que não foram detectados por MALDI-TOF devido a supressão de matriz que ocorre no início da corrida. Porém, conseguiu captar diversos compostos que podem ter sido descartados pelo LC/MS. A análise MALDI-TOF foi importante na determinação da diversidade de compostos com maior massa molecular, gerando uma informação simultânea de toda amostra, em contrapartida, o LC/MS mostrou sua importância na obtenção de maiores informações dos conteúdos dos picos em termos de aminoácidos e constatou presença de peptídeos com menores massas moleculares. Sendo assim, foram complementares e necessárias para uma observação em amplo espectro das amostras analisadas.

A análise de espectrometria de massas LC-MSMS demonstrou uma necessidade de informações de sequenciamento genético de *Paralonchurus brasiliensis, Micropogonias furnieri* e *Hepatus pudibundus*. A escassez desses registros se mostrou uma problemática, já que em razão da insuficiência de dados para distinguir as proteínas, houve a necessidade de utilização de bancos de dados que sejam próximos a eles, como o banco de dados *Teleostei* e *Arthropoda*. Por essa razão, algumas informações podem passar despercebidas pelas análises, destacando a importância dos sequenciamentos genéticos de animais presentes na fauna acompanhante para a realização de mais estudos com espécies existentes no bycatch.

Os resultados obtidos por LC/MSMS mostraram que o preparo das amostras hidrolisadas foi eficiente, havendo apenas proteínas de origem muscular, sem contaminação de outros tecidos e/ou órgãos. Essa análise evidenciou o controle positivo do preparo, armazenamento e hidrólises. Os resultados na íntegra estão em anexo.

É possível dizer que a actina encontrada pela espectrometria de massas pode estar associada aos efeitos antioxidantes obtidos em testes realizados previamente com as amostras[70–72]. As actinas são proteínas altamente conservadas e estão envolvidas em vários tipos de motilidade celular, são expressas de forma ubíqua em todas as células eucarióticas[89]. As actinas encontradas nos tecidos musculares, são as principais constituintes do aparelho contrátil. Um estudo realizado por Angelini *et al*.[90] indicou que a actina pode estar envolvida na regulação do estresse oxidativo, que é uma das principais causas de remodelação adversa durante o desenvolvimento de cardiomiopatia dilatada[90].

Vale ressaltar a importância dos peptídeos encontrados nas amostras que possuem potencial de utilização como modelo para a produção de peptídeos sintéticos devido às suas possíveis ações biológicas, sendo estes peptídeos análogos – que possuem maior permeabilidade de membrana, maior sobrevida, entre outros. Tais peptídeos são utilizados na produção de antibióticos e outros medicamentos, pois estes tornam possível a inclusão de aminoácidos sintéticos a fim de modificar sua bioatividade, como é o caso do captopril, que é um medicamento criado a partir de um peptídeo extraído de *Bothops jararaca* o qual foi sintetizado pela adição de uma prolina (aminoácido carboxiterminal do BPP_{5a}) e assim, obteve a ação necessária para se tornar um dos remédios mais utilizados para hipertensão[91].

No caso de organismos que não tenham o genoma sequenciado e, por essa razão, possuem poucas proteínas que constam nos bancos de dados, a abordagem de sequenciamento de novo é essencial. Nele os peptídeos são sequenciados por massa independente de banco de dados ou análises proteômicas. O programa de alinhamento BLAST[77] foi utilizado na busca em bancos de dados de ácidos nucléicos e proteínas por sequências homólogas, bem como para a realização do alinhamento local por pares de sequências. Com banco de dados BioPep[78] foi possível tem uma base das bioatividades já registradas pelas sequencias peptídicas existentes nas amostras.

Os resultados adquiridos pelo BLAST[77], possibilitaram a comprovação da não contaminação das amostras, ressaltando que possuem apenas proteínas musculares. Já os resultados obtidos pelo banco de dados BioPep[78] evidenciaram uma ampla gama de utilizações desses compostos. Todas as amostras demonstraram diversas bioatividades, entre elas pode-se destacar a atividade antioxidante, inibidora de enzima conversora de angiotensina, inibidora de Dipeptidil Peptidase IV e III, inibidora de alfa-glicosidase, antiamnésica, antitrombótica, inibidora de renina, reguladora da atividade de fosfoglicerato quinase, hipertensora, reguladora da atividade da membrana mucosa do estômago, ativadora de proteólise mediada por Ubiquitina, estimuladora de captação da glicose e neuropeptídica. Ressaltando assim o potencial da utilização dos compostos presentes na fauna acompanhante visando a saúde pública.

6. CONCLUSÃO

O presente estudo foi capaz de promover uma maior compreensão dos perfis bioquímicos e dos valores biológicos oriundos na fauna acompanhante presente no litoral norte de São Paulo, bem como estabelecer seus potenciais bioquímicos, terapêuticos, farmacológicos e nutricionais. Fazendo com que um possível potencial econômico seja evidenciado, gerando um novo destino a esses animais, evitando o descarte que pode causar prejuízos incalculáveis ao ecossistema marinho.

Sendo assim foi constatada uma grande abrangência de utilizações, tanto dos peptídeos de menor massa, que são diluídos com maior facilidade e podem ser utilizados para alimentação e suplementação humana e animal, bem como dos peptídeos maiores, que possuem maior potencial de prospecção de atividades biológicas e usos mais complexos, como na confecção de fármacos semissintéticos.

Como a área de bioprospecção marinha está em desenvolvimento, e são poucos os trabalhos na literatura sobre compostos da fauna marinha já descobertos e seus usos correlacionados com a saúde humana, é provável que existam adversidades como as encontradas no presente estudo. Porém, tendo como base os novos fármacos aprovados e em aprovação pelo FDA, e o impacto ambiental causado pelo *bycatch*, é de suma importância explorar mais a fundo essa área buscando a obtenção de mais compostos funcionais e bioativos provenientes da fauna acompanhante. A questão de viabilidade socioeconômica é algo a se considerar, portanto um estudo econômico baseado nos pescadores específicos que cederão a fauna acompanhante se faz necessário. Bem como a viabilidade econômica para gerar o produto final.

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ANEXOS

1. Notes

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)

Table 1. Statistics of data.

# of MS Scans	1086
# of MS/MS Scans	2771

Table 2. Result filtration parameters.

Peptide -10lgP	≥15
Protein -10lgP	≥20
Proteins unique peptides	≥0
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	86
Peptide Sequences	80
Protein Groups	26
Proteins	215
Proteins (#Unique Peptides)	57 (>2); 72 (=2); 86 (=1);
FDR (Peptide-Spectrum Matches)	14.0%
FDR (Peptide Sequences)	13.8%
FDR (Protein)	0.9%
De Novo Only Spectra	1288

Table 4. PTM profile.

Name	ΔMass	#PSM	Position

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)

Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Orbi2222	0	0	0	0	80

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS 7.0
Parent Mass Error Tolerance: 0.03 Da
Fragment Mass Error Tolerance: 0.1 Da
Precursor Mass Search Type: monoisotopic
Enzyme: None
Max Missed Cleavages: 100
Non-specific Cleavage: both
Max variable PTM per peptide: 3
Database: Teleosteo
Taxon: All
Searched Entry: 4529691
FDR Estimation: Enabled
Merge Options: 0.1 min. 0.03 Da
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB_PIMENTA_PA_20220211_03.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID/ECD
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
1	12040	tr|A0A3S2MUF9|A0A3S2MUF9_ORYJA	81.95	16	9	9	N	41945	Uncharacterized protein OS=Oryzias javanicus OX=123683 GN=OJAV_G00024300 PE=3 SV=1
1	12038	tr|F5BZL8|F5BZL8_EPIBR	81.95	16	9	9	N	41945	Alpha actin (Fragment) OS=Epinephelus bruneus OX=323802 PE=2 SV=1
1	66846	tr|A0A7J6C441|A0A7J6C441_9TELE	81.95	16	9	9	N	41959	Uncharacterized protein OS=Onychostoma macrolepis OX=369639 GN=G5714_016621 PE=3 SV=1
1	66847	tr|A0A6P7M219|A0A6P7M219_BETSP	81.95	16	9	9	N	41959	actin, alpha skeletal muscle OS=Betta splendens OX=158456 GN=acta1 PE=3 SV=1
2	66929	tr|A0A3P8SGW9|A0A3P8SGW9_AMPPE	78.71	3	9	9	N	220651	Uncharacterized protein OS=Amphiprion percula OX=161767 PE=3 SV=1
2	66812	tr|A0A6P7IKT0|A0A6P7IKT0_9TELE	78.71	3	9	9	N	221389	myosin heavy chain, fast skeletal muscle OS=Parambassis ranga OX=210632 GN=LOC114440528 PE=3 SV=1
2	66803	tr|A0A6P7IXS4|A0A6P7IXS4_9TELE	78.71	3	9	9	N	221345	myosin heavy chain, fast skeletal muscle-like OS=Parambassis ranga OX=210632 GN=LOC114440527 PE=3 SV=1
2	66811	tr|A0A3P9CRE7|A0A3P9CRE7_9CICH	78.71	3	9	9	N	219343	Myosin heavy chain, fast skeletal muscle OS=Maylandia zebra OX=106582 PE=3 SV=1
2	66915	tr|A0A3P8SE64|A0A3P8SE64_AMPPE	78.71	3	9	9	N	224259	Uncharacterized protein OS=Amphiprion percula OX=161767 PE=3 SV=1
2	71725	tr|A0A668A9K0|A0A668A9K0_9TELE	78.71	3	9	9	N	222745	Myosin heavy chain, fast skeletal muscle OS=Myripristis murdjan OX=586833 GN=LOC115363301 PE=3 SV=1
2	66813	tr|A0A3P8Q1P8|A0A3P8Q1P8_ASTCA	78.71	3	9	9	N	221800	Myosin heavy chain, fast skeletal muscle-like OS=Astatotilapia calliptera OX=8154 PE=3 SV=1
2	66814	tr|A0A3P8QMC2|A0A3P8QMC2_ASTCA	78.71	3	9	9	N	222125	Myosin heavy chain, fast skeletal muscle-like OS=Astatotilapia calliptera OX=8154 PE=3 SV=1
2	71726	tr|A0A671XUP5|A0A671XUP5_SPAAU	78.71	3	9	9	N	221269	Myosin heavy chain, fast skeletal muscle-like OS=Sparus aurata OX=8175 GN=LOC115575699 PE=3 SV=1
2	66815	tr|A0A3P8Q1G5|A0A3P8Q1G5_ASTCA	78.71	3	9	9	N	222421	Myosin heavy chain, fast skeletal muscle-like OS=Astatotilapia calliptera OX=8154 PE=3 SV=1
2	66801	tr|Q90YF6|Q90YF6_PARFO	78.71	3	9	9	N	221374	Myosin heavy chain OS=Paracirrhites forsteri OX=100206 GN=MyoHC-T54 PE=2 SV=1
14	71706	tr|A0A3Q3R2B2|A0A3Q3R2B2_MONAL	67.79	21	2	2	N	10968	Parvalbumin OS=Monopterus albus OX=43700 PE=3 SV=1

total 215 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
14	71707	tr|A0A3Q3JW30|A0A3Q3JW30_MONAL	67.79	21	2	2	N	11216	Parvalbumin OS=Monopterus albus OX=43700 PE=3 SV=1
14	71708	tr|A0A3Q3K7G4|A0A3Q3K7G4_MONAL	67.79	21	2	2	N	11274	Parvalbumin OS=Monopterus albus OX=43700 PE=3 SV=1
14	71709	tr|A0A3Q3K945|A0A3Q3K945_MONAL	67.79	21	2	2	N	11220	Parvalbumin OS=Monopterus albus OX=43700 PE=3 SV=1
14	71710	tr|H2V1I8|H2V1I8_TAKRU	67.79	20	2	2	N	11356	Parvalbumin OS=Takifugu rubripes OX=31033 GN=LOC101064450 PE=3 SV=1
14	67952	tr|A0A455R7U6|A0A455R7U6_CONMY	67.79	20	2	2	N	11823	Parvalbumin OS=Conger myriaster OX=7943 GN=PVAL_B PE=2 SV=1
14	71711	tr|A0A4W4ED54|A0A4W4ED54_ELEEL	67.79	20	2	2	N	11603	Parvalbumin OS=Electrophorus electricus OX=8005 GN=LOC113569874 PE=3 SV=1
14	71712	tr|A0A6P7N9P3|A0A6P7N9P3_BETSP	67.79	20	2	2	N	11661	Parvalbumin OS=Betta splendens OX=158456 GN=LOC114860448 PE=3 SV=1
14	71713	tr|A0A3B4CKV2|A0A3B4CKV2_PYGNA	67.79	20	2	2	N	11597	Parvalbumin OS=Pygocentrus nattereri OX=42514 PE=3 SV=1
14	71714	tr|A0A3B4TWQ8|A0A3B4TWQ8_SERDU	67.79	20	2	2	N	11752	Parvalbumin OS=Seriola dumerili OX=41447 PE=3 SV=1
14	71715	tr|A0A7N8YBR8|A0A7N8YBR8_9TELE	67.79	20	2	2	N	11613	Parvalbumin OS=Mastacembelus armatus OX=205130 PE=3 SV=1
14	67953	tr|A0A3Q3W464|A0A3Q3W464_MOLML	67.79	19	2	2	N	12300	Parvalbumin OS=Mola mola OX=94237 PE=3 SV=1
14	71716	tr|A0A3Q2WZN1|A0A3Q2WZN1_HAPBU	67.79	19	2	2	N	12192	Parvalbumin OS=Haplochromis burtoni OX=8153 PE=3 SV=1
14	71717	tr|A0A674NSY1|A0A674NSY1_TAKRU	67.79	19	2	2	N	12203	Parvalbumin OS=Takifugu rubripes OX=31033 GN=LOC101064450 PE=3 SV=1
14	71718	tr|A0A3Q3K779|A0A3Q3K779_MONAL	67.79	19	2	2	N	12568	Parvalbumin OS=Monopterus albus OX=43700 PE=3 SV=1
14	71719	tr|I3J1U3|I3J1U3_ORENI	67.79	18	2	2	N	12911	Parvalbumin OS=Oreochromis niloticus OX=8128 GN=LOC100692640 PE=3 SV=2
14	67954	tr|A0A3Q3WAG3|A0A3Q3WAG3_MOLML	67.79	18	2	2	N	13233	Parvalbumin OS=Mola mola OX=94237 PE=3 SV=1
14	71720	tr|Q804Z0|Q804Z0_ICTPU	67.79	18	2	2	N	13489	Parvalbumin (Fragment) OS=Ictalurus punctatus OX=7998 PE=2 SV=1
14	67955	tr|A0A3Q4AW30|A0A3Q4AW30_MOLML	67.79	17	2	2	N	14276	Parvalbumin OS=Mola mola OX=94237 PE=3 SV=1
14	67956	tr|A0A3Q3W3Y6|A0A3Q3W3Y6_MOLML	67.79	17	2	2	N	14526	Parvalbumin OS=Mola mola OX=94237 PE=3 SV=1
14	71721	tr|A0A3Q3K924|A0A3Q3K924_MONAL	67.79	16	2	2	N	15324	Parvalbumin OS=Monopterus albus OX=43700 PE=3 SV=1
14	67625	tr|A0A674P8J8|A0A674P8J8_TAKRU	67.79	15	2	2	N	16019	Parvalbumin OS=Takifugu rubripes OX=31033 PE=3 SV=1
14	71722	tr|A0A7N9APR6|A0A7N9APR6_9TELE	67.79	14	2	2	N	16398	Parvalbumin OS=Mastacembelus armatus OX=205130 PE=3 SV=1
14	71723	tr|A0A3Q3K937|A0A3Q3K937_MONAL	67.79	14	2	2	N	17292	Parvalbumin OS=Monopterus albus OX=43700 PE=3 SV=1
14	71724	tr|A0A3Q3JXS6|A0A3Q3JXS6_MONAL	67.79	12	2	2	N	20228	Parvalbumin OS=Monopterus albus OX=43700 PE=3 SV=1
9	71731	tr|H3CFQ5|H3CFQ5_TETNG	59.63	1	3	3	N	544663	Uncharacterized protein OS=Tetraodon nigroviridis OX=99883 PE=4 SV=1
4	71733	tr|M4AVS2|M4AVS2_XIPMA	57.11	3	4	4	N	108300	Calcium-transporting ATPase OS=Xiphophorus maculatus OX=8083 PE=3 SV=2
4	71734	tr|A0A3B3VSS0|A0A3B3VSS0_9TELE	57.11	3	4	4	N	108408	Calcium-transporting ATPase OS=Poecilia latipinna OX=48699 PE=3 SV=1
4	71735	tr|A0A0S7JRJ0|A0A0S7JRJ0_9TELE	57.11	3	4	4	N	108563	Calcium-transporting ATPase OS=Poeciliopsis prolifica OX=188132 GN=AT2A1 PE=3 SV=1
4	71736	tr|A0A0S7JR62|A0A0S7JR62_9TELE	57.11	3	4	4	N	109108	Calcium-transporting ATPase OS=Poeciliopsis prolifica OX=188132 GN=AT2A1 PE=3 SV=1

total 215 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
4	71737	tr|A0A3B5QZF8|A0A3B5QZF8_XIPMA	57.11	3	4	4	N	109027	Calcium-transporting ATPase OS=Xiphophorus maculatus OX=8083 PE=3 SV=1
4	71738	tr|G3NWV4|G3NWV4_GASAC	57.11	3	4	4	N	108017	Calcium-transporting ATPase OS=Gasterosteus aculeatus OX=69293 PE=3 SV=1
4	67754	tr|A0A6J2RNI9|A0A6J2RNI9_COTGO	57.11	3	4	4	N	108341	Calcium-transporting ATPase OS=Cottoperca gobio OX=56716 GN=LOC115024282 PE=3 SV=1
4	67755	tr|A0A6J2RKY9|A0A6J2RKY9_COTGO	57.11	3	4	4	N	108469	Calcium-transporting ATPase OS=Cottoperca gobio OX=56716 GN=LOC115024282 PE=3 SV=1
4	71739	tr|A0A3B1JPG2|A0A3B1JPG2_ASTMX	57.11	3	4	4	N	108879	Calcium-transporting ATPase OS=Astyanax mexicanus OX=7994 PE=3 SV=1
4	71740	tr|A0A667WYB6|A0A667WYB6_9TELE	57.11	3	4	4	N	108672	Calcium-transporting ATPase OS=Myripristis murdjan OX=586833 PE=3 SV=1
4	71741	tr|A0A3B4VM00|A0A3B4VM00_SERDU	57.11	3	4	4	N	109419	Calcium-transporting ATPase OS=Seriola dumerili OX=41447 PE=3 SV=1
4	71742	tr|A0A667X953|A0A667X953_9TELE	57.11	3	4	4	N	109525	Calcium-transporting ATPase OS=Myripristis murdjan OX=586833 PE=3 SV=1
4	67212	tr|A0A7N8WP58|A0A7N8WP58_9TELE	57.11	4	4	4	N	104947	Calcium-transporting ATPase OS=Mastacembelus armatus OX=205130 PE=3 SV=1
4	71743	tr|A0A7N8Y7I9|A0A7N8Y7I9_9TELE	57.11	4	4	4	N	105242	Calcium-transporting ATPase OS=Mastacembelus armatus OX=205130 PE=3 SV=1
4	71744	tr|A0A671YJD0|A0A671YJD0_SPAAU	57.11	4	4	4	N	105314	Calcium-transporting ATPase OS=Sparus aurata OX=8175 GN=LOC115570920 PE=3 SV=1
4	71745	tr|A0A7N8XW64|A0A7N8XW64_9TELE	57.11	3	4	4	N	108576	Calcium-transporting ATPase OS=Mastacembelus armatus OX=205130 PE=3 SV=1
4	71746	tr|A0A7N9AUZ7|A0A7N9AUZ7_9TELE	57.11	3	4	4	N	109022	Calcium-transporting ATPase OS=Mastacembelus armatus OX=205130 PE=3 SV=1
4	71747	tr|A0A3Q3MF18|A0A3Q3MF18_9TELE	57.11	3	4	4	N	109268	Calcium-transporting ATPase OS=Mastacembelus armatus OX=205130 PE=3 SV=2
4	71748	tr|A0A672IVR0|A0A672IVR0_SALFA	57.11	3	4	4	N	106289	Calcium-transporting ATPase OS=Salarias fasciatus OX=181472 GN=LOC115392776 PE=3 SV=1
4	71749	tr|A0A3Q1BZF5|A0A3Q1BZF5_AMPOC	57.11	3	4	4	N	108248	Calcium-transporting ATPase OS=Amphiprion ocellaris OX=80972 PE=3 SV=1
4	71750	tr|A0A3Q0SE88|A0A3Q0SE88_AMPCI	57.11	3	4	4	N	108313	Calcium-transporting ATPase OS=Amphilophus citrinellus OX=61819 PE=3 SV=1
4	67759	tr|A0A3P8SU98|A0A3P8SU98_AMPPE	57.11	3	4	4	N	108831	Calcium-transporting ATPase OS=Amphiprion percula OX=161767 PE=3 SV=1
4	71751	tr|A0A672IVP1|A0A672IVP1_SALFA	57.11	3	4	4	N	108522	Calcium-transporting ATPase OS=Salarias fasciatus OX=181472 GN=LOC115392776 PE=3 SV=1
4	71752	tr|A0A3Q1BVL9|A0A3Q1BVL9_AMPOC	57.11	3	4	4	N	108858	Calcium-transporting ATPase OS=Amphiprion ocellaris OX=80972 PE=3 SV=1
4	71753	tr|A0A672ITB5|A0A672ITB5_SALFA	57.11	3	4	4	N	109974	Calcium-transporting ATPase OS=Salarias fasciatus OX=181472 GN=LOC115392776 PE=3 SV=1
4	71754	tr|A0A672IVQ1|A0A672IVQ1_SALFA	57.11	3	4	4	N	112146	Calcium-transporting ATPase OS=Salarias fasciatus OX=181472 GN=LOC115392776 PE=3 SV=1
6	69471	tr|A0A834CTG4|A0A834CTG4_ORYME	52.57	1	3	2	N	850198	Titin OS=Oryzias melastigma OX=30732 GN=FQA47_016182 PE=4 SV=1

total 215 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
6	67005	tr|Q4RE90|Q4RE90_TETNG	52.57	1	3	2	N	863297	Chromosome undetermined SCAF15134, whole genome shotgun sequence (Fragment) OS=Tetraodon nigroviridis OX=99883 GN=GSTENG00035871001 PE=4 SV=1
3	67126	tr|A0A3P8Q9R4|A0A3P8Q9R4_ASTCA	50.61	12	5	5	N	42650	Creatine kinase OS=Astatotilapia calliptera OX=8154 GN=CKM PE=3 SV=1
3	67128	tr|A0A3Q4HL72|A0A3Q4HL72_NEOBR	50.61	12	5	5	N	42778	Creatine kinase OS=Neolamprologus brichardi OX=32507 PE=3 SV=1
3	67136	tr|A0A3B4TA77|A0A3B4TA77_SERDU	50.61	12	5	5	N	42546	Creatine kinase OS=Seriola dumerili OX=41447 GN=CKM PE=3 SV=1
3	67124	tr|A0A0F8AN20|A0A0F8AN20_LARCR	50.61	12	5	5	N	42543	Creatine kinase OS=Larimichthys crocea OX=215358 GN=EH28_08927 PE=3 SV=1
3	67115	tr|C7ASM1|C7ASM1_SINCH	50.61	12	5	5	N	42922	Creatine kinase OS=Siniperca chuatsi OX=119488 PE=2 SV=1
3	67690	tr|G3PFX6|G3PFX6_GASAC	50.61	11	5	5	N	46217	Creatine kinase OS=Gasterosteus aculeatus OX=69293 GN=CKM PE=3 SV=1
3	67691	tr|A0A6P7JDS0|A0A6P7JDS0_9TELE	50.61	10	5	5	N	51567	Creatine kinase OS=Parambassis ranga OX=210632 GN=LOC114444487 PE=3 SV=1
5	67285	tr|A0A672MA11|A0A672MA11_SINGR	47.78	17	3	3	N	16048	Myosin regulatory light chain 2, skeletal muscle isoform type 2 OS=Sinocyclocheilus grahami OX=75366 GN=LOC107571443 PE=4 SV=1
5	67157	tr|A0A4U5VU95|A0A4U5VU95_COLLU	47.78	16	3	3	N	16791	Myosin regulatory light chain 2, skeletal muscle isoform DTNB OS=Collichthys lucidus OX=240159 GN=D9C73_025504 PE=4 SV=1
5	67288	tr|A0A3B4BW75|A0A3B4BW75_PYGNA	47.78	15	3	3	N	18272	Myosin regulatory light chain 2, skeletal muscle isoform type 2 OS=Pygocentrus nattereri OX=42514 PE=4 SV=1
5	67295	tr|A0A7J6CHK6|A0A7J6CHK6_9TELE	47.78	14	3	3	N	19163	EF-hand domain-containing protein OS=Onychostoma macrolepis OX=369639 GN=G5714_012740 PE=4 SV=1
5	67158	tr|A0A6P7II88|A0A6P7II88_9TELE	47.78	14	3	3	N	18948	myosin regulatory light chain 2, skeletal muscle isoform OS=Parambassis ranga OX=210632 GN=mylpf PE=4 SV=1
5	67303	tr|A0A668VT67|A0A668VT67_OREAU	47.78	14	3	3	N	19739	Myosin light chain, phosphorylatable, fast skeletal muscle b OS=Oreochromis aureus OX=47969 PE=4 SV=1
5	67300	tr|F8U029|F8U029_EPIBR	47.78	14	3	3	N	18965	Myosin light chain 2 (Fragment) OS=Epinephelus bruneus OX=323802 PE=2 SV=1
5	67308	tr|A0A3B5RBY4|A0A3B5RBY4_XIPMA	47.78	10	3	3	N	27929	Uncharacterized protein OS=Xiphophorus maculatus OX=8083 PE=4 SV=1
16	71774	tr|A0A7J5Y2W4|A0A7J5Y2W4_DISMA	45.71	1	2	1	N	179397	Uncharacterized protein OS=Dissostichus mawsoni OX=36200 GN=F7725_002633 PE=4 SV=1
16	71780	tr|A0A4Z2HXD4|A0A4Z2HXD4_9TELE	45.71	1	2	1	N	208336	Titin OS=Liparis tanakae OX=230148 GN=TTN_5 PE=4 SV=1
11	67382	tr|A0A672HWD2|A0A672HWD2_SALFA	44.38	6	2	2	N	50618	Calsequestrin OS=Salarias fasciatus OX=181472 PE=3 SV=1
11	67383	tr|A0A672HWL2|A0A672HWL2_SALFA	44.38	6	2	2	N	51610	Calsequestrin OS=Salarias fasciatus OX=181472 PE=3 SV=1
11	67388	tr|A0A672HXF4|A0A672HXF4_SALFA	44.38	5	2	2	N	52636	Calsequestrin OS=Salarias fasciatus OX=181472 PE=3 SV=1
11	67393	tr|A0A672HXA9|A0A672HXA9_SALFA	44.38	5	2	2	N	53688	Calsequestrin OS=Salarias fasciatus OX=181472 PE=3 SV=1
15	67800	tr|A0A3Q4GK85|A0A3Q4GK85_NEOBR	41.12	7	2	2	N	21230	Adenylate kinase isoenzyme 1 OS=Neolamprologus brichardi OX=32507 GN=AK1 PE=3 SV=1

total 215 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
15	67801	tr|A0A3Q4GS43|A0A3Q4GS43_NEOBR	41.12	7	2	2	N	21240	Adenylate kinase isoenzyme 1 OS=Neolamprologus brichardi OX=32507 GN=AK1 PE=3 SV=1
15	67802	tr|A0A3P8P8S3|A0A3P8P8S3_ASTCA	41.12	7	2	2	N	21228	Adenylate kinase isoenzyme 1 OS=Astatotilapia calliptera OX=8154 GN=AK1 PE=3 SV=1
15	67795	tr|A0A3Q1HW42|A0A3Q1HW42_9TELE	41.12	7	2	2	N	21205	Adenylate kinase isoenzyme 1 OS=Acanthochromis polyacanthus OX=80966 GN=AK1 PE=3 SV=1
15	67803	tr|A0A3P9CWL7|A0A3P9CWL7_9CICH	41.12	7	2	2	N	21258	Adenylate kinase isoenzyme 1 OS=Maylandia zebra OX=106582 GN=AK1 PE=3 SV=1
15	67796	tr|A0A3B5BIY5|A0A3B5BIY5_9TELE	41.12	7	2	2	N	21206	Adenylate kinase isoenzyme 1 OS=Stegastes partitus OX=144197 GN=AK1 PE=3 SV=1
15	67804	tr|A0A3Q2VY92|A0A3Q2VY92_HAPBU	41.12	7	2	2	N	21228	Adenylate kinase isoenzyme 1 OS=Haplochromis burtoni OX=8153 GN=AK1 PE=3 SV=1
15	67805	tr|A0A3B4FMK3|A0A3B4FMK3_9CICH	41.12	7	2	2	N	21228	Adenylate kinase isoenzyme 1 OS=Pundamilia nyererei OX=303518 GN=AK1 PE=3 SV=1
15	67806	tr|A0A3Q3CWR9|A0A3Q3CWR9_HAPBU	41.12	7	2	2	N	23163	Adenylate kinase isoenzyme 1 OS=Haplochromis burtoni OX=8153 GN=AK1 PE=3 SV=1
15	67807	tr|A0A3P8P8V3|A0A3P8P8V3_ASTCA	41.12	7	2	2	N	23216	Adenylate kinase isoenzyme 1 OS=Astatotilapia calliptera OX=8154 GN=AK1 PE=3 SV=1
17	69651	tr|A0A665WT54|A0A665WT54_ECHNA	38.52	8	2	2	N	12976	LIM domain-binding protein 3-like OS=Echeneis naucrates OX=173247 GN=LOC115060026 PE=4 SV=1
17	69652	tr|A0A671N228|A0A671N228_9TELE	38.52	4	2	2	N	28684	LIM domain-binding protein 3-like OS=Sinocyclocheilus anshuiensis OX=1608454 GN=LOC107698793 PE=4 SV=1
17	69653	tr|A0A3Q3Q7K2|A0A3Q3Q7K2_MONAL	38.52	4	2	2	N	29692	Synuclein-like OS=Monopterus albus OX=43700 PE=4 SV=1
17	69654	tr|A0A671MU99|A0A671MU99_9TELE	38.52	4	2	2	N	29538	LIM domain-binding protein 3-like OS=Sinocyclocheilus anshuiensis OX=1608454 GN=LOC107698793 PE=4 SV=1
17	69655	tr|A0A672KK19|A0A672KK19_SINGR	38.52	4	2	2	N	30329	LIM domain-binding protein 3-like OS=Sinocyclocheilus grahami OX=75366 GN=LOC107552745 PE=4 SV=1
17	69656	tr|A0A673LYE6|A0A673LYE6_9TELE	38.52	4	2	2	N	30316	LIM domain-binding protein 3-like OS=Sinocyclocheilus rhinocerous OX=307959 GN=LOC107749342 PE=4 SV=1
17	69657	tr|A0A3P8VEA1|A0A3P8VEA1_CYNSE	38.52	4	2	2	N	30334	LIM domain-binding protein 3-like OS=Cynoglossus semilaevis OX=244447 PE=4 SV=1
17	69658	tr|A0A3Q1II99|A0A3Q1II99_ANATE	38.52	4	2	2	N	30310	LIM domain binding 3b OS=Anabas testudineus OX=64144 PE=4 SV=1
17	69659	tr|A0A6P7L9I7|A0A6P7L9I7_BETSP	38.52	4	2	2	N	30536	LIM domain-binding protein 3-like isoform X2 OS=Betta splendens OX=158456 GN=LOC114846412 PE=4 SV=1
17	69660	tr|A0A3P8X8T4|A0A3P8X8T4_ESOLU	38.52	4	2	2	N	30572	LIM domain-binding protein 3 OS=Esox lucius OX=8010 PE=4 SV=1
17	69661	tr|A0A3Q0R4X6|A0A3Q0R4X6_AMPCI	38.52	4	2	2	N	30403	LIM domain binding 3b OS=Amphilophus citrinellus OX=61819 PE=4 SV=1
17	69662	tr|A0A3P8VK01|A0A3P8VK01_CYNSE	38.52	4	2	2	N	30591	LIM domain-binding protein 3-like OS=Cynoglossus semilaevis OX=244447 PE=4 SV=1
17	69663	tr|A0A3P8XBI5|A0A3P8XBI5_ESOLU	38.52	4	2	2	N	30957	LIM domain-binding protein 3 OS=Esox lucius OX=8010 PE=4 SV=2
17	69664	tr|A0A3Q1H919|A0A3Q1H919_ANATE	38.52	3	2	2	N	31065	LIM domain binding 3b OS=Anabas testudineus OX=64144 PE=4 SV=1

total 215 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
17	69665	tr|A0A3Q3KN21|A0A3Q3KN21_9TELE	38.52	3	2	2	N	31352	LIM domain binding 3b OS=Mastacembelus armatus OX=205130 PE=4 SV=2
17	69666	tr|A0A6P7L9I9|A0A6P7L9I9_BETSP	38.52	3	2	2	N	31290	LIM domain-binding protein 3-like isoform X1 OS=Betta splendens OX=158456 GN=LOC114846412 PE=4 SV=1
17	69667	tr|A0A3P8VE68|A0A3P8VE68_CYNSE	38.52	3	2	2	N	31336	LIM domain-binding protein 3-like OS=Cynoglossus semilaevis OX=244447 PE=4 SV=1
17	69668	tr|A0A6G0HYN5|A0A6G0HYN5_LARCR	38.52	3	2	2	N	31123	LIM domain-binding protein 3 Protein cypher Z-band alternatively spliced PDZ-motif protein OS=Larimichthys crocea OX=215358 GN=D5F01_LYC17526 PE=4 SV=1
17	69669	tr|A0A3P8ZCR8|A0A3P8ZCR8_ESOLU	38.52	3	2	2	N	31398	LIM domain-binding protein 3 OS=Esox lucius OX=8010 PE=4 SV=1
17	69670	tr|A0A3Q3IQV7|A0A3Q3IQV7_MONAL	38.52	3	2	2	N	31456	Synuclein-like OS=Monopterus albus OX=43700 PE=4 SV=1
17	69671	tr|A0A665WTS5|A0A665WTS5_ECHNA	38.52	3	2	2	N	31290	LIM domain-binding protein 3-like OS=Echeneis naucrates OX=173247 GN=LOC115060026 PE=4 SV=1
17	69672	tr|A0A7N8Y585|A0A7N8Y585_9TELE	38.52	3	2	2	N	31804	LIM domain binding 3b OS=Mastacembelus armatus OX=205130 PE=4 SV=1
17	69673	tr|A0A6P6QFT2|A0A6P6QFT2_CARAU	38.52	3	2	2	N	31663	LIM domain-binding protein 3-like isoform X2 OS=Carassius auratus OX=7957 GN=LOC113111546 PE=4 SV=1
17	69674	tr|A0A672KNU9|A0A672KNU9_SINGR	38.52	3	2	2	N	31638	LIM domain-binding protein 3-like OS=Sinocyclocheilus grahami OX=75366 GN=LOC107552745 PE=4 SV=1
17	69675	tr|A0A673M1Q3|A0A673M1Q3_9TELE	38.52	3	2	2	N	31625	LIM domain-binding protein 3-like OS=Sinocyclocheilus rhinocerous OX=307959 GN=LOC107749342 PE=4 SV=1
17	69676	tr|A0A7J6CGV6|A0A7J6CGV6_9TELE	38.52	3	2	2	N	31765	PDZ domain-containing protein OS=Onychostoma macrolepis OX=369639 GN=G5714_012537 PE=4 SV=1
17	69677	tr|A0A6P6QIW1|A0A6P6QIW1_CARAU	38.52	3	2	2	N	34204	LIM domain-binding protein 3-like isoform X1 OS=Carassius auratus OX=7957 GN=LOC113111546 PE=4 SV=1
17	69678	tr|A0A6Q2XWF7|A0A6Q2XWF7_ESOLU	38.52	3	2	2	N	35095	LIM domain-binding protein 3 OS=Esox lucius OX=8010 PE=4 SV=1
17	69679	tr|A0A0F8AMH6|A0A0F8AMH6_LARCR	38.52	2	2	2	N	43721	LIM domain-binding protein 3 OS=Larimichthys crocea OX=215358 GN=EH28_03737 PE=4 SV=1
17	69680	tr|A0A6G0HYU6|A0A6G0HYU6_LARCR	38.52	1	2	2	N	80212	Melanopsin-A Mammalian-like melanopsin Melanopsin-M Opsin-4-A Opsin-4M OS=Larimichthys crocea OX=215358 GN=D5F01_LYC17520 PE=4 SV=1
10	67490	tr|G3N515|G3N515_GASAC	35.73	1	2	1	N	451257	Uncharacterized protein OS=Gasterosteus aculeatus OX=69293 PE=4 SV=1
20	71775	tr|A0A3P8T7F6|A0A3P8T7F6_AMPPE	34.93	8	1	1	N	20468	Myosin, light chain 1, alkali; skeletal, fast OS=Amphiprion percula OX=161767 PE=4 SV=1
20	71776	tr|A0A3Q1AWA1|A0A3Q1AWA1_AMPOC	34.93	8	1	1	N	20668	Myosin light chain 1, skeletal muscle isoform OS=Amphiprion ocellaris OX=80972 PE=4 SV=1
20	71777	tr|A0A3P8T5J7|A0A3P8T5J7_AMPPE	34.93	8	1	1	N	20668	Myosin, light chain 1, alkali; skeletal, fast OS=Amphiprion percula OX=161767 PE=4 SV=1
20	71778	tr|A0A3P8T7H6|A0A3P8T7H6_AMPPE	34.93	8	1	1	N	20912	Myosin, light chain 1, alkali; skeletal, fast OS=Amphiprion percula OX=161767 PE=4 SV=1

total 215 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
20	71779	tr|A0A3Q1B6V7|A0A3Q1B6V7_AMPOC	34.93	8	1	1	N	20912	Myosin light chain 1, skeletal muscle isoform OS=Amphiprion ocellaris OX=80972 PE=4 SV=1
18	67404	tr|A0A6F9CEX9|A0A6F9CEX9_9TELE	34.39	0	1	1	N	1022296	Uncharacterized protein OS=Coregonus sp. 'balchen' OX=861768 GN=CSTEINMANNI_LOCUS3957823 PE=4 SV=1
7	67341	tr|A0A484CUS5|A0A484CUS5_PERFV	34.12	0	2	1	N	867139	Uncharacterized protein OS=Perca flavescens OX=8167 GN=EPR50_G00113850 PE=4 SV=1
19	69536	tr|A0A834CMG6|A0A834CMG6_ORYME	32.89	1	1	1	N	157078	Myomesin-2 OS=Oryzias melastigma OX=30732 GN=FQA47_006815 PE=4 SV=1
19	69537	tr|A0A3B3BCL7|A0A3B3BCL7_ORYME	32.89	1	1	1	N	157034	Myomesin-2-like OS=Oryzias melastigma OX=30732 PE=4 SV=1
19	69541	tr|A0A3B3D3C5|A0A3B3D3C5_ORYME	32.89	1	1	1	N	157566	Myomesin-2-like OS=Oryzias melastigma OX=30732 PE=4 SV=1
19	69520	tr|A0A672ZI78|A0A672ZI78_9TELE	32.89	1	1	1	N	126360	Uncharacterized protein OS=Sphaeramia orbicularis OX=375764 GN=LOC115437523 PE=4 SV=1
19	69521	tr|A0A669ELF6|A0A669ELF6_ORENI	32.89	1	1	1	N	132152	Uncharacterized protein OS=Oreochromis niloticus OX=8128 GN=LOC100698303 PE=4 SV=1
19	71781	tr|A0A671Y3Y8|A0A671Y3Y8_SPAAU	32.89	1	1	1	N	132216	Myomesin-2-like OS=Sparus aurata OX=8175 GN=MYOM2 PE=4 SV=1
19	69522	tr|A0A4U5U6X9|A0A4U5U6X9_COLLU	32.89	1	1	1	N	136304	Myomesin-2 165 kDa connectin-associated protein 165 kDa titin-associated protein M-protein OS=Collichthys lucidus OX=240159 GN=D9C73_004091 PE=4 SV=1
19	69524	tr|A0A669CKL2|A0A669CKL2_ORENI	32.89	1	1	1	N	141158	Uncharacterized protein OS=Oreochromis niloticus OX=8128 GN=LOC100698303 PE=4 SV=1
19	69525	tr|A0A671Y401|A0A671Y401_SPAAU	32.89	1	1	1	N	145648	Myomesin-2-like OS=Sparus aurata OX=8175 GN=MYOM2 PE=4 SV=1
19	69526	tr|A0A672FNF5|A0A672FNF5_SALFA	32.89	1	1	1	N	148203	Uncharacterized protein OS=Salarias fasciatus OX=181472 GN=LOC115388674 PE=4 SV=1
19	71782	tr|A0A671Y3W3|A0A671Y3W3_SPAAU	32.89	1	1	1	N	152686	Myomesin-2-like OS=Sparus aurata OX=8175 GN=MYOM2 PE=4 SV=1
19	69527	tr|A0A6G0J0W8|A0A6G0J0W8_LARCR	32.89	1	1	1	N	152797	Myomesin-2 165 kDa connectin-associated protein OS=Larimichthys crocea OX=215358 GN=D5F01_LYC03862 PE=4 SV=1
19	69528	tr|A0A671Y575|A0A671Y575_SPAAU	32.89	1	1	1	N	154320	Myomesin-2-like OS=Sparus aurata OX=8175 GN=MYOM2 PE=4 SV=1
19	69530	tr|A0A6G1P7U8|A0A6G1P7U8_9TELE	32.89	1	1	1	N	156806	Myomesin-2 165 kDa connectin-associated protein OS=Channa argus OX=215402 GN=EXN66_Car002007 PE=4 SV=1
19	69531	tr|A0A087YFH0|A0A087YFH0_POEFO	32.89	1	1	1	N	156966	Myomesin-2-like OS=Poecilia formosa OX=48698 GN=MYOM2 PE=4 SV=2
19	69532	tr|A0A3P9PGW1|A0A3P9PGW1_POERE	32.89	1	1	1	N	156917	Myomesin-2-like OS=Poecilia reticulata OX=8081 PE=4 SV=1
19	69493	tr|A0A3P8P4C2|A0A3P8P4C2_ASTCA	32.89	1	1	1	N	157122	Myomesin-2-like OS=Astatotilapia calliptera OX=8154 GN=MYOM2 PE=4 SV=1
19	69494	tr|A0A3Q1D109|A0A3Q1D109_AMPOC	32.89	1	1	1	N	156426	Myomesin-2-like OS=Amphiprion ocellaris OX=80972 GN=MYOM2 PE=4 SV=1
19	69495	tr|A0A3Q2WWP1|A0A3Q2WWP1_HAPBU	32.89	1	1	1	N	156996	Myomesin-2-like OS=Haplochromis burtoni OX=8153 PE=4 SV=1
19	69533	tr|A0A672ZHV0|A0A672ZHV0_9TELE	32.89	1	1	1	N	156079	Uncharacterized protein OS=Sphaeramia orbicularis OX=375764 GN=LOC115437523 PE=4 SV=1
19	69534	tr|I3JDJ1|I3JDJ1_ORENI	32.89	1	1	1	N	157148	Uncharacterized protein OS=Oreochromis niloticus OX=8128 GN=LOC100698303 PE=4 SV=2

total 215 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
19	69535	tr|A0A2I4AP94|A0A2I4AP94_9TELE	32.89	1	1	1	N	156788	M-protein, striated muscle-like OS=Austrofundulus limnaeus OX=52670 GN=LOC106513170 PE=4 SV=1
19	69540	tr|A0A3P9LTE0|A0A3P9LTE0_ORYLA	32.89	1	1	1	N	157011	Uncharacterized protein OS=Oryzias latipes OX=8090 PE=4 SV=1
19	69542	tr|A0A6P7LYN0|A0A6P7LYN0_BETSP	32.89	1	1	1	N	158082	myomesin-2-like isoform X1 OS=Betta splendens OX=158456 GN=LOC114852036 PE=4 SV=1
19	69519	tr|A0A3Q4GHK3|A0A3Q4GHK3_NEOBR	32.89	2	1	1	N	99617	Myomesin-2-like OS=Neolamprologus brichardi OX=32507 GN=MYOM2 PE=4 SV=1
19	69523	tr|A0A3Q4GXU7|A0A3Q4GXU7_NEOBR	32.89	1	1	1	N	139979	Myomesin-2-like OS=Neolamprologus brichardi OX=32507 GN=MYOM2 PE=4 SV=1
19	69529	tr|A0A3B3IJA0|A0A3B3IJA0_ORYLA	32.89	1	1	1	N	155226	Uncharacterized protein OS=Oryzias latipes OX=8090 GN=LOC101163890 PE=4 SV=1
19	69538	tr|A0A3P9IT90|A0A3P9IT90_ORYLA	32.89	1	1	1	N	156872	Uncharacterized protein OS=Oryzias latipes OX=8090 PE=4 SV=1
19	69539	tr|H2M2B3|H2M2B3_ORYLA	32.89	1	1	1	N	156953	Uncharacterized protein OS=Oryzias latipes OX=8090 GN=LOC101163890 PE=4 SV=2
19	69543	tr|A0A3B3HWS2|A0A3B3HWS2_ORYLA	32.89	1	1	1	N	158285	Uncharacterized protein OS=Oryzias latipes OX=8090 GN=LOC101163890 PE=4 SV=1
12	71846	tr|A0A6G0J5U6|A0A6G0J5U6_LARCR	31.94	1	2	2	N	364928	Titin OS=Larimichthys crocea OX=215358 GN=D5F01_LYC01469 PE=4 SV=1
8	67357	tr|A0A6A5F2V4|A0A6A5F2V4_PERFL	31.73	0	2	1	N	1083091	Uncharacterized protein OS=Perca fluviatilis OX=8168 GN=PFLUV_G00150840 PE=4 SV=1
25	71784	tr|A0A7N6BJ85|A0A7N6BJ85_ANATE	29.58	2	1	1	N	83676	Uncharacterized protein OS=Anabas testudineus OX=64144 PE=4 SV=1
33	71792	tr|A0A3B3QB10|A0A3B3QB10_9TELE	28.56	1	1	1	N	135373	Uncharacterized protein OS=Paramormyrops kingsleyae OX=1676925 PE=4 SV=1
34	71847	tr|A0A668VQH5|A0A668VQH5_OREAU	26.40	4	1	1	N	33864	2-phospho-D-glycerate hydro-lyase OS=Oreochromis aureus OX=47969 PE=3 SV=1
34	71848	tr|A0A3P8Q0W3|A0A3P8Q0W3_ASTCA	26.40	3	1	1	N	42382	2-phospho-D-glycerate hydro-lyase OS=Astatotilapia calliptera OX=8154 PE=3 SV=1
34	67043	tr|F5BZS7|F5BZS7_EPIBR	26.40	3	1	1	N	43226	2-phospho-D-glycerate hydro-lyase (Fragment) OS=Epinephelus bruneus OX=323802 PE=2 SV=1
34	67478	tr|A0A4W4G2T4|A0A4W4G2T4_ELEEL	26.40	3	1	1	N	44171	2-phospho-D-glycerate hydro-lyase OS=Electrophorus electricus OX=8005 GN=eno1 PE=3 SV=1
34	67479	tr|A0A4W4G3J1|A0A4W4G3J1_ELEEL	26.40	3	1	1	N	44401	2-phospho-D-glycerate hydro-lyase OS=Electrophorus electricus OX=8005 GN=eno1 PE=3 SV=1
34	71849	tr|A0A668VQX9|A0A668VQX9_OREAU	26.40	3	1	1	N	45670	2-phospho-D-glycerate hydro-lyase OS=Oreochromis aureus OX=47969 PE=3 SV=1
34	67422	tr|A0A4W4G4V3|A0A4W4G4V3_ELEEL	26.40	3	1	1	N	45863	2-phospho-D-glycerate hydro-lyase OS=Electrophorus electricus OX=8005 GN=eno3 PE=3 SV=1
34	71850	tr|A0A668VU75|A0A668VU75_OREAU	26.40	3	1	1	N	46006	2-phospho-D-glycerate hydro-lyase OS=Oreochromis aureus OX=47969 PE=3 SV=1
34	67480	tr|A0A4W4G338|A0A4W4G338_ELEEL	26.40	3	1	1	N	46229	2-phospho-D-glycerate hydro-lyase OS=Electrophorus electricus OX=8005 GN=eno1 PE=3 SV=1
34	67481	tr|A0A3P9C6I0|A0A3P9C6I0_9CICH	26.40	3	1	1	N	46321	2-phospho-D-glycerate hydro-lyase OS=Maylandia zebra OX=106582 PE=3 SV=1
34	71851	tr|A0A668V8T6|A0A668V8T6_OREAU	26.40	3	1	1	N	47001	2-phospho-D-glycerate hydro-lyase OS=Oreochromis aureus OX=47969 PE=3 SV=1

total 215 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
34	71852	tr|A0A668VTY0|A0A668VTY0_OREAU	26.40	3	1	1	N	47197	2-phospho-D-glycerate hydro-lyase OS=Oreochromis aureus OX=47969 PE=3 SV=1
34	67891	tr|A0A6P3VUG4|A0A6P3VUG4_CLUHA	26.40	3	1	1	N	46885	2-phospho-D-glycerate hydro-lyase OS=Clupea harengus OX=7950 GN=eno1 PE=3 SV=1
34	67430	tr|A0A4W4FGS3|A0A4W4FGS3_ELEEL	26.40	3	1	1	N	47188	2-phospho-D-glycerate hydro-lyase OS=Electrophorus electricus OX=8005 GN=LOC113568057 PE=3 SV=1
34	67482	tr|A0A3P8TV75|A0A3P8TV75_AMPPE	26.40	3	1	1	N	47036	2-phospho-D-glycerate hydro-lyase OS=Amphiprion percula OX=161767 PE=3 SV=1
34	67483	tr|A0A6P7IPP6|A0A6P7IPP6_9TELE	26.40	3	1	1	N	46964	2-phospho-D-glycerate hydro-lyase OS=Parambassis ranga OX=210632 GN=eno1 PE=3 SV=1
34	67431	tr|A0A6P3W3B1|A0A6P3W3B1_CLUHA	26.40	3	1	1	N	47370	2-phospho-D-glycerate hydro-lyase OS=Clupea harengus OX=7950 GN=LOC105904565 PE=3 SV=1
34	67034	tr|A0A3B4CPC9|A0A3B4CPC9_PYGNA	26.40	3	1	1	N	47482	2-phospho-D-glycerate hydro-lyase OS=Pygocentrus nattereri OX=42514 PE=3 SV=1
34	67484	tr|A0A6P3W5E7|A0A6P3W5E7_CLUHA	26.40	3	1	1	N	47562	2-phospho-D-glycerate hydro-lyase OS=Clupea harengus OX=7950 GN=eno3 PE=3 SV=1
34	67421	tr|A0A3P8TVY9|A0A3P8TVY9_AMPPE	26.40	3	1	1	N	47574	2-phospho-D-glycerate hydro-lyase OS=Amphiprion percula OX=161767 PE=3 SV=1
34	67964	tr|A0A6P7P1U1|A0A6P7P1U1_BETSP	26.40	3	1	1	N	46869	2-phospho-D-glycerate hydro-lyase OS=Betta splendens OX=158456 GN=LOC114866120 PE=3 SV=1
34	67485	tr|A0A4W4G3C7|A0A4W4G3C7_ELEEL	26.40	3	1	1	N	47371	2-phospho-D-glycerate hydro-lyase OS=Electrophorus electricus OX=8005 GN=eno1 PE=3 SV=1
34	67486	tr|A0A4W4G3N6|A0A4W4G3N6_ELEEL	26.40	3	1	1	N	47770	2-phospho-D-glycerate hydro-lyase OS=Electrophorus electricus OX=8005 GN=eno1 PE=3 SV=1
34	67419	tr|A0A3P8NTT0|A0A3P8NTT0_ASTCA	26.40	2	1	1	N	48687	2-phospho-D-glycerate hydro-lyase OS=Astatotilapia calliptera OX=8154 PE=3 SV=1
34	67892	tr|A0A6P7MN74|A0A6P7MN74_BETSP	26.40	2	1	1	N	49625	2-phospho-D-glycerate hydro-lyase OS=Betta splendens OX=158456 GN=LOC114856168 PE=3 SV=1
34	67424	tr|A0A3B4ERE5|A0A3B4ERE5_PYGNA	26.40	2	1	1	N	49548	2-phospho-D-glycerate hydro-lyase OS=Pygocentrus nattereri OX=42514 GN=ENO3 PE=3 SV=1
34	67425	tr|A0A3B4DDR1|A0A3B4DDR1_PYGNA	26.40	2	1	1	N	51660	2-phospho-D-glycerate hydro-lyase OS=Pygocentrus nattereri OX=42514 GN=ENO3 PE=3 SV=1
34	67487	tr|A0A7J6BNX1|A0A7J6BNX1_9TELE	26.40	2	1	1	N	52093	2-phospho-D-glycerate hydro-lyase OS=Onychostoma macrolepis OX=369639 GN=G5714_022679 PE=3 SV=1
34	71853	tr|A0A6P7P064|A0A6P7P064_BETSP	26.40	2	1	1	N	53271	2-phospho-D-glycerate hydro-lyase OS=Betta splendens OX=158456 GN=LOC114866120 PE=3 SV=1
26	71889	tr|A0A5A9PD51|A0A5A9PD51_9TELE	23.02	1	1	1	N	89232	BRCA1-A complex subunit RAP80 OS=Triplophysa tibetana OX=1572043 GN=E1301_Tti012398 PE=3 SV=1
23	71815	tr|A0A6P8GQF7|A0A6P8GQF7_CLUHA	22.74	1	1	1	N	186990	kinase D-interacting substrate of 220 kDa B-like isoform X4 OS=Clupea harengus OX=7950 GN=LOC105907323 PE=4 SV=1
23	71816	tr|A0A6P8GCK4|A0A6P8GCK4_CLUHA	22.74	1	1	1	N	188190	kinase D-interacting substrate of 220 kDa B-like isoform X3 OS=Clupea harengus OX=7950 GN=LOC105907323 PE=4 SV=1
23	71817	tr|A0A6P8GCW3|A0A6P8GCW3_CLUHA	22.74	1	1	1	N	191965	kinase D-interacting substrate of 220 kDa B-like isoform X2 OS=Clupea harengus OX=7950 GN=LOC105907323 PE=4 SV=1

total 215 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
23	71818	tr|A0A6P8GNT0|A0A6P8GNT0_CLUHA	22.74	1	1	1	N	193166	kinase D-interacting substrate of 220 kDa B-like isoform X1 OS=Clupea harengus OX=7950 GN=LOC105907323 PE=4 SV=1
21	71820	tr|A0A674PAA1|A0A674PAA1_TAKRU	22.10	5	1	1	N	20437	Uncharacterized protein OS=Takifugu rubripes OX=31033 GN=tpm2 PE=3 SV=1
21	71821	tr|A0A4W5K3X5|A0A4W5K3X5_9TELE	22.10	3	1	1	N	29693	Tropomyosin 2 (beta) OS=Hucho hucho OX=62062 PE=3 SV=1
21	71822	tr|A0A4W5KNV1|A0A4W5KNV1_9TELE	22.10	3	1	1	N	32307	Tropomyosin 2 (beta) OS=Hucho hucho OX=62062 PE=3 SV=1
21	71823	tr|A0A3Q1CSK5|A0A3Q1CSK5_AMPOC	22.10	3	1	1	N	32534	Tropomyosin beta chain OS=Amphiprion ocellaris OX=80972 PE=3 SV=1
21	71824	tr|A0A4W5KNI2|A0A4W5KNI2_9TELE	22.10	3	1	1	N	32801	Tropomyosin 2 (beta) OS=Hucho hucho OX=62062 PE=3 SV=1
21	71825	tr|A0A6G0HZW7|A0A6G0HZW7_LARCR	22.10	3	1	1	N	32504	Uncharacterized protein OS=Larimichthys crocea OX=215358 GN=D5F01_LYC16153 PE=3 SV=1
21	71875	tr|A0A6J2PEZ1|A0A6J2PEZ1_COTGO	22.10	3	1	1	N	32878	tropomyosin alpha-1 chain-like isoform X3 OS=Cottoperca gobio OX=56716 GN=LOC115005840 PE=3 SV=1
35	67518	tr|D2KQG3|D2KQG3_SINCH	20.02	11	1	1	N	11617	Parvalbumin OS=Siniperca chuatsi OX=119488 PE=2 SV=1
35	67519	tr|B9VJM3|B9VJM3_SINCH	20.02	11	1	1	N	11589	Parvalbumin OS=Siniperca chuatsi OX=119488 PE=2 SV=1

total 215 proteins

tr|A0A3S2MUF9|A0A3S2MUF9_ORYJA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AGFAGDDAPRAVFPS.I	Y	32.99	1476.6997	-0.9	739.3564	2	12.29	1805	1	21	35	
R.VAPEEHPTLL.T	Y	29.42	1104.5815	-0.1	553.2980	2	11.68	1691	1	98	107	
G.FAGDDAPRAVFPS.I	Y	29.26	1348.6411	-0.7	675.3274	2	12.03	1756	1	23	35	
A.GDDAPRAVFPS.I	Y	28.88	1130.5356	-1.2	566.2744	2	11.46	1652	1	25	35	
K.AGFAGDDAPRA.V	Y	26.29	1046.4780	-0.6	524.2460	2	10.36	1456	1	21	31	
L.TEAPLNPK.A	Y	22.76	868.4654	0.1	435.2400	2	22.88	3566	17	108	115	
L.DAGDGVTH.N	Y	22.53	770.3195	-0.2	386.1669	2	8.67	1162	3	156	163	
F.AGDDAPRAVFPS.I	Y	22.15	1201.5728	0.4	601.7939	2	17.84	2753	1	24	35	
K.IIAPPERKYSVWIGGSIL.A	Y	20.07	1998.1301	-2.6	1000.0698	2	13.65	2050	1	331	348	

total 9 peptides

tr|F5BZL8|F5BZL8_EPIBR
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AGFAGDDAPRAVFPS.I	Y	32.99	1476.6997	-0.9	739.3564	2	12.29	1805	1	21	35	
R.VAPEEHPTLL.T	Y	29.42	1104.5815	-0.1	553.2980	2	11.68	1691	1	98	107	
G.FAGDDAPRAVFPS.I	Y	29.26	1348.6411	-0.7	675.3274	2	12.03	1756	1	23	35	
A.GDDAPRAVFPS.I	Y	28.88	1130.5356	-1.2	566.2744	2	11.46	1652	1	25	35	
K.AGFAGDDAPRA.V	Y	26.29	1046.4780	-0.6	524.2460	2	10.36	1456	1	21	31	
L.TEAPLNPK.A	Y	22.76	868.4654	0.1	435.2400	2	22.88	3566	17	108	115	
L.DAGDGVTH.N	Y	22.53	770.3195	-0.2	386.1669	2	8.67	1162	3	156	163	
F.AGDDAPRAVFPS.I	Y	22.15	1201.5728	0.4	601.7939	2	17.84	2753	1	24	35	
K.IIAPPERKYSVWIGGSIL.A	Y	20.07	1998.1301	-2.6	1000.0698	2	13.65	2050	1	331	348	

total 9 peptides

tr|A0A7J6C441|A0A7J6C441_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AGFAGDDAPRAVFPS.I	Y	32.99	1476.6997	-0.9	739.3564	2	12.29	1805	1	21	35	
R.VAPEEHPTLL.T	Y	29.42	1104.5815	-0.1	553.2980	2	11.68	1691	1	98	107	
G.FAGDDAPRAVFPS.I	Y	29.26	1348.6411	-0.7	675.3274	2	12.03	1756	1	23	35	
A.GDDAPRAVFPS.I	Y	28.88	1130.5356	-1.2	566.2744	2	11.46	1652	1	25	35	
K.AGFAGDDAPRA.V	Y	26.29	1046.4780	-0.6	524.2460	2	10.36	1456	1	21	31	
L.TEAPLNPK.A	Y	22.76	868.4654	0.1	435.2400	2	22.88	3566	17	108	115	
L.DAGDGVTH.N	Y	22.53	770.3195	-0.2	386.1669	2	8.67	1162	3	156	163	
F.AGDDAPRAVFPS.I	Y	22.15	1201.5728	0.4	601.7939	2	17.84	2753	1	24	35	
K.IIAPPERKYSVWIGGSIL.A	Y	20.07	1998.1301	-2.6	1000.0698	2	13.65	2050	1	331	348	

total 9 peptides

tr|A0A6P7M219|A0A6P7M219_BETSP
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AGFAGDDAPRAVFPS.I	Y	32.99	1476.6997	-0.9	739.3564	2	12.29	1805	1	21	35	
R.VAPEEHPTLL.T	Y	29.42	1104.5815	-0.1	553.2980	2	11.68	1691	1	98	107	
G.FAGDDAPRAVFPS.I	Y	29.26	1348.6411	-0.7	675.3274	2	12.03	1756	1	23	35	
A.GDDAPRAVFPS.I	Y	28.88	1130.5356	-1.2	566.2744	2	11.46	1652	1	25	35	
K.AGFAGDDAPRA.V	Y	26.29	1046.4780	-0.6	524.2460	2	10.36	1456	1	21	31	
L.TEAPLNPK.A	Y	22.76	868.4654	0.1	435.2400	2	22.88	3566	17	108	115	
L.DAGDGVTH.N	Y	22.53	770.3195	-0.2	386.1669	2	8.67	1162	3	156	163	
F.AGDDAPRAVFPS.I	Y	22.15	1201.5728	0.4	601.7939	2	17.84	2753	1	24	35	
K.IIAPPERKYSVWIGGSIL.A	Y	20.07	1998.1301	-2.6	1000.0698	2	13.65	2050	1	331	348	

total 9 peptides

tr|A0A3P8SGW9|A0A3P8SGW9_AMPPE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.LDKNKDPLNDSVVQ.L	Y	41.85	1583.8154	-0.2	792.9148	2	10.85	1542	1	596	609	
K.KRIEAPPHIF.S	Y	24.65	1206.6873	-0.7	604.3505	2	11.08	1582	2	147	156	
A.SERVGLL.H	Y	20.45	772.4443	-0.4	387.2292	2	11.54	1667	1	1709	1715	
W.LDKNKDPLNDS.V	Y	19.64	1257.6201	-1.1	629.8167	2	9.75	1352	1	596	606	
L.HLDDAVR.G	Y	19.12	824.4141	-1.0	413.2139	2	9.20	1258	1	1655	1661	
V.GWLDKNKDPLNDS.V	Y	17.14	1500.7208	-0.5	751.3673	2	11.84	1721	1	594	606	
K.RIEAPPHIF.S	Y	17.08	1078.5923	-0.7	540.3030	2	11.77	1708	1	148	156	
L.SKIEDEQSL.G	Y	16.08	1047.5084	-0.7	524.7611	2	10.21	1432	1	1091	1099	
F.EKPKPGKGKAE.A	Y	15.04	1167.6611	0.4	584.8381	2	5.03	627	1	566	576	

total 9 peptides

tr|A0A6P7IKT0|A0A6P7IKT0_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.LDKNKDPLNDSVVQ.L	Y	41.85	1583.8154	-0.2	792.9148	2	10.85	1542	1	596	609	
K.KRIEAPPHIF.S	Y	24.65	1206.6873	-0.7	604.3505	2	11.08	1582	2	147	156	
A.SERVGLL.H	Y	20.45	772.4443	-0.4	387.2292	2	11.54	1667	1	1714	1720	
W.LDKNKDPLNDS.V	Y	19.64	1257.6201	-1.1	629.8167	2	9.75	1352	1	596	606	
L.HLDDAVR.G	Y	19.12	824.4141	-1.0	413.2139	2	9.20	1258	1	1660	1666	
S.GWLDKNKDPLNDS.V	Y	17.14	1500.7208	-0.5	751.3673	2	11.84	1721	1	594	606	
K.RIEAPPHIF.S	Y	17.08	1078.5923	-0.7	540.3030	2	11.77	1708	1	148	156	
L.SKIEDEQSL.G	Y	16.08	1047.5084	-0.7	524.7611	2	10.21	1432	1	1096	1104	
F.EKPKPGKGKAE.A	Y	15.04	1167.6611	0.4	584.8381	2	5.03	627	1	566	576	

total 9 peptides

tr|A0A6P7IXS4|A0A6P7IXS4_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.LDKNKDPLNDSVVQ.L	Y	41.85	1583.8154	-0.2	792.9148	2	10.85	1542	1	596	609	
K.KRIEAPPHIF.S	Y	24.65	1206.6873	-0.7	604.3505	2	11.08	1582	2	147	156	
A.SERVGLL.H	Y	20.45	772.4443	-0.4	387.2292	2	11.54	1667	1	1715	1721	
W.LDKNKDPLNDS.V	Y	19.64	1257.6201	-1.1	629.8167	2	9.75	1352	1	596	606	
L.HLDDAVR.G	Y	19.12	824.4141	-1.0	413.2139	2	9.20	1258	1	1661	1667	
S.GWLDKNKDPLNDS.V	Y	17.14	1500.7208	-0.5	751.3673	2	11.84	1721	1	594	606	
K.RIEAPPHIF.S	Y	17.08	1078.5923	-0.7	540.3030	2	11.77	1708	1	148	156	
L.SKIEDEQSL.G	Y	16.08	1047.5084	-0.7	524.7611	2	10.21	1432	1	1097	1105	
F.EKPKPGKGKAE.A	Y	15.04	1167.6611	0.4	584.8381	2	5.03	627	1	566	576	

total 9 peptides

tr|A0A3P9CRE7|A0A3P9CRE7_9CICH

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.LDKNKDPLNDSVVQ.L	Y	41.85	1583.8154	-0.2	792.9148	2	10.85	1542	1	571	584	
K.KRIEAPPHIF.S	Y	24.65	1206.6873	-0.7	604.3505	2	11.08	1582	2	140	149	
A.SERVGLL.H	Y	20.45	772.4443	-0.4	387.2292	2	11.54	1667	1	1682	1688	
W.LDKNKDPLNDS.V	Y	19.64	1257.6201	-1.1	629.8167	2	9.75	1352	1	571	581	
L.HLDDAVR.G	Y	19.12	824.4141	-1.0	413.2139	2	9.20	1258	1	1628	1634	
T.GWLDKNKDPLNDS.V	Y	17.14	1500.7208	-0.5	751.3673	2	11.84	1721	1	569	581	
K.RIEAPPHIF.S	Y	17.08	1078.5923	-0.7	540.3030	2	11.77	1708	1	141	149	
L.SKIEDEQSL.G	Y	16.08	1047.5084	-0.7	524.7611	2	10.21	1432	1	1064	1072	
F.EKPKPGKGKAE.A	Y	15.04	1167.6611	0.4	584.8381	2	5.03	627	1	541	551	

total 9 peptides

tr|A0A3P8SE64|A0A3P8SE64_AMPPE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.LDKNKDPLNDSVVQ.L	Y	41.85	1583.8154	-0.2	792.9148	2	10.85	1542	1	597	610	
K.KRIEAPPHIF.S	Y	24.65	1206.6873	-0.7	604.3505	2	11.08	1582	2	147	156	
A.SERVGLL.H	Y	20.45	772.4443	-0.4	387.2292	2	11.54	1667	1	1709	1715	
W.LDKNKDPLNDS.V	Y	19.64	1257.6201	-1.1	629.8167	2	9.75	1352	1	597	607	
L.HLDDAVR.G	Y	19.12	824.4141	-1.0	413.2139	2	9.20	1258	1	1655	1661	
T.GWLDKNKDPLNDS.V	Y	17.14	1500.7208	-0.5	751.3673	2	11.84	1721	1	595	607	
K.RIEAPPHIF.S	Y	17.08	1078.5923	-0.7	540.3030	2	11.77	1708	1	148	156	
L.SKIEDEQSL.G	Y	16.08	1047.5084	-0.7	524.7611	2	10.21	1432	1	1092	1100	
F.EKPKPGKGKAE.A	Y	15.04	1167.6611	0.4	584.8381	2	5.03	627	1	567	577	

total 9 peptides

tr|A0A668A9K0|A0A668A9K0_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.LDKNKDPLNDSVVQ.L	Y	41.85	1583.8154	-0.2	792.9148	2	10.85	1542	1	597	610	
K.KRIEAPPHIF.S	Y	24.65	1206.6873	-0.7	604.3505	2	11.08	1582	2	147	156	
A.SERVGLL.H	Y	20.45	772.4443	-0.4	387.2292	2	11.54	1667	1	1712	1718	
W.LDKNKDPLNDS.V	Y	19.64	1257.6201	-1.1	629.8167	2	9.75	1352	1	597	607	
L.HLDDAVR.G	Y	19.12	824.4141	-1.0	413.2139	2	9.20	1258	1	1658	1664	
A.GWLDKNKDPLNDS.V	Y	17.14	1500.7208	-0.5	751.3673	2	11.84	1721	1	595	607	
K.RIEAPPHIF.S	Y	17.08	1078.5923	-0.7	540.3030	2	11.77	1708	1	148	156	
L.SKIEDEQSL.G	Y	16.08	1047.5084	-0.7	524.7611	2	10.21	1432	1	1094	1102	
F.EKPKPGKGKAE.A	Y	15.04	1167.6611	0.4	584.8381	2	5.03	627	1	567	577	

total 9 peptides

tr|A0A3P8Q1P8|A0A3P8Q1P8_ASTCA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.LDKNKDPLNDSVVQ.L	Y	41.85	1583.8154	-0.2	792.9148	2	10.85	1542	1	596	609	
K.KRIEAPPHIF.S	Y	24.65	1206.6873	-0.7	604.3505	2	11.08	1582	2	147	156	
A.SERVGLL.H	Y	20.45	772.4443	-0.4	387.2292	2	11.54	1667	1	1711	1717	
W.LDKNKDPLNDS.V	Y	19.64	1257.6201	-1.1	629.8167	2	9.75	1352	1	596	606	
L.HLDDAVR.G	Y	19.12	824.4141	-1.0	413.2139	2	9.20	1258	1	1657	1663	
T.GWLDKNKDPLNDS.V	Y	17.14	1500.7208	-0.5	751.3673	2	11.84	1721	1	594	606	
K.RIEAPPHIF.S	Y	17.08	1078.5923	-0.7	540.3030	2	11.77	1708	1	148	156	
L.SKIEDEQSL.G	Y	16.08	1047.5084	-0.7	524.7611	2	10.21	1432	1	1093	1101	
F.EKPKPGKGKAE.A	Y	15.04	1167.6611	0.4	584.8381	2	5.03	627	1	566	576	

total 9 peptides

tr|A0A3P8QMC2|A0A3P8QMC2_ASTCA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.LDKNKDPLNDSVVQ.L	Y	41.85	1583.8154	-0.2	792.9148	2	10.85	1542	1	596	609	
K.KRIEAPPHIF.S	Y	24.65	1206.6873	-0.7	604.3505	2	11.08	1582	2	147	156	
A.SERVGLL.H	Y	20.45	772.4443	-0.4	387.2292	2	11.54	1667	1	1708	1714	
W.LDKNKDPLNDS.V	Y	19.64	1257.6201	-1.1	629.8167	2	9.75	1352	1	596	606	
L.HLDDAVR.G	Y	19.12	824.4141	-1.0	413.2139	2	9.20	1258	1	1654	1660	
T.GWLDKNKDPLNDS.V	Y	17.14	1500.7208	-0.5	751.3673	2	11.84	1721	1	594	606	
K.RIEAPPHIF.S	Y	17.08	1078.5923	-0.7	540.3030	2	11.77	1708	1	148	156	
L.SKIEDEQSL.G	Y	16.08	1047.5084	-0.7	524.7611	2	10.21	1432	1	1090	1098	
F.EKPKPGKGKAE.A	Y	15.04	1167.6611	0.4	584.8381	2	5.03	627	1	566	576	

total 9 peptides

tr|A0A671XUP5|A0A671XUP5_SPAAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.LDKNKDPLNDSVVQ.L	Y	41.85	1583.8154	-0.2	792.9148	2	10.85	1542	1	589	602	
K.KRIEAPPHIF.S	Y	24.65	1206.6873	-0.7	604.3505	2	11.08	1582	2	147	156	
A.SERVGLL.H	Y	20.45	772.4443	-0.4	387.2292	2	11.54	1667	1	1705	1711	
W.LDKNKDPLNDS.V	Y	19.64	1257.6201	-1.1	629.8167	2	9.75	1352	1	589	599	
L.HLDDAVR.G	Y	19.12	824.4141	-1.0	413.2139	2	9.20	1258	1	1651	1657	
N.GWLDKNKDPLNDS.V	Y	17.14	1500.7208	-0.5	751.3673	2	11.84	1721	1	587	599	
K.RIEAPPHIF.S	Y	17.08	1078.5923	-0.7	540.3030	2	11.77	1708	1	148	156	
L.SKIEDEQSL.G	Y	16.08	1047.5084	-0.7	524.7611	2	10.21	1432	1	1087	1095	
F.EKPKPGKGKAE.A	Y	15.04	1167.6611	0.4	584.8381	2	5.03	627	1	559	569	

total 9 peptides

tr|A0A3P8Q1G5|A0A3P8Q1G5_ASTCA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.LDKNKDPLNDSVVQ.L	Y	41.85	1583.8154	-0.2	792.9148	2	10.85	1542	1	596	609	
K.KRIEAPPHIF.S	Y	24.65	1206.6873	-0.7	604.3505	2	11.08	1582	2	147	156	
A.SERVGLL.H	Y	20.45	772.4443	-0.4	387.2292	2	11.54	1667	1	1709	1715	
W.LDKNKDPLNDS.V	Y	19.64	1257.6201	-1.1	629.8167	2	9.75	1352	1	596	606	
L.HLDDAVR.G	Y	19.12	824.4141	-1.0	413.2139	2	9.20	1258	1	1655	1661	
T.GWLDKNKDPLNDS.V	Y	17.14	1500.7208	-0.5	751.3673	2	11.84	1721	1	594	606	
K.RIEAPPHIF.S	Y	17.08	1078.5923	-0.7	540.3030	2	11.77	1708	1	148	156	
L.SKIEDEQSL.G	Y	16.08	1047.5084	-0.7	524.7611	2	10.21	1432	1	1091	1099	
F.EKPKPGKGKAE.A	Y	15.04	1167.6611	0.4	584.8381	2	5.03	627	1	566	576	

total 9 peptides

tr|Q90YF6|Q90YF6_PARFO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.LDKNKDPLNDSVVQ.L	Y	41.85	1583.8154	-0.2	792.9148	2	10.85	1542	[illegible]	596	609	
K.KRIEAPPHIF.S	Y	24.65	1206.6873	-0.7	604.3505	2	11.08	1582	2	147	156	
A.SERVGLL.H	Y	20.45	772.4443	-0.4	387.2292	2	11.54	1667	1	1712	1718	
W.LDKNKDPLNDS.V	Y	19.64	1257.6201	-1.1	629.8167	2	9.75	1352	1	596	606	
L.HLDDAVR.G	Y	19.12	824.4141	-1.0	413.2139	2	9.20	1258	1	1658	1664	
S.GWLDKNKDPLNDS.V	Y	17.14	1500.7208	-0.5	751.3673	2	11.84	1721	1	594	606	
K.RIEAPPHIF.S	Y	17.08	1078.5923	-0.7	540.3030	2	11.77	1708	1	148	156	
L.SKIEDEQSL.G	Y	16.08	1047.5084	-0.7	524.7611	2	10.21	1432	1	1094	1102	
F.EKPKPGKGKAE.A	Y	15.04	1167.6611	0.4	584.8381	2	5.03	627	1	566	576	

total 9 peptides

tr|A0A3Q3R2B2|A0A3Q3R2B2_MONAL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDKSGFIE.E	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	50	60	
K.AGDTDGDGKIG.F	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	89	99	

total 2 peptides

tr|A0A3Q3JW30|A0A3Q3JW30_MONAL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDKSGFIE.E	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	50	60	
K.AGDTDGDGKIG.V	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	89	99	

total 2 peptides

tr|A0A3Q3K7G4|A0A3Q3K7G4_MONAL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDKSGFIE.E	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	49	59	
K.AGDTDGDGKIG.V	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	87	97	

total 2 peptides

tr|A0A3Q3K945|A0A3Q3K945_MONAL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDKSGFIE.E	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	50	60	
K.AGDTDGDGKIG.G	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	89	99	

total 2 peptides

tr|H2V1I8|H2V1I8_TAKRU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.IIDQDKSGFIE.E	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	50	60	
K.AGDTDGDGKIG.V	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	89	99	

total 2 peptides

tr|A0A455R7U6|A0A455R7U6_CONMY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.IIDQDKSGFIE.E	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	48	58	

total 2 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AGDTDGDGKIG.V	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	87	97	

total 2 peptides

tr|A0A4W4ED54|A0A4W4ED54_ELEEL
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDKSGFIE.E	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	50	60	
K.AGDTDGDGKIG.A	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	89	99	

total 2 peptides

tr|A0A6P7N9P3|A0A6P7N9P3_BETSP
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDKSGFIE.E	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	50	60	
Q.AGDTDGDGKIG.A	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	89	99	

total 2 peptides

tr|A0A3B4CKV2|A0A3B4CKV2_PYGNA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDKSGFIE.E	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	50	60	
K.AGDTDGDGKIG.A	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	89	99	

total 2 peptides

tr|A0A3B4TWQ8|A0A3B4TWQ8_SERDU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDKSGFIE.E	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	50	60	
K.AGDTDGDGKIG.V	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	89	99	

total 2 peptides

tr|A0A7N8YBR8|A0A7N8YBR8_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDKSGFIE.E	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	50	60	
K.AGDTDGDGKIG.V	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	89	99	

total 2 peptides

tr|A0A3Q3W464|A0A3Q3W464_MOLML
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.IIDQDKSGFIE.K	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	50	60	
R.AGDTDGDGKIG.A	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	89	99	

total 2 peptides

tr|A0A3Q2WZN1|A0A3Q2WZN1_HAPBU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM

total 2 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDKSGFIE.E	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	50	60	
G.AGDTDGDGKIG.A	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	89	99	

total 2 peptides

tr|A0A674NSY1|A0A674NSY1_TAKRU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.IIDQDKSGFIE.E	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	58	68	
K.AGDTDGDGKIG.V	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	97	107	

total 2 peptides

tr|A0A3Q3K779|A0A3Q3K779_MONAL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDKSGFIE.E	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	50	60	
K.AGDTDGDGKIG.V	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	89	99	

total 2 peptides

tr|I3J1U3|I3J1U3_ORENI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDKSGFIE.E	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	61	71	
G.AGDTDGDGKIG.A	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	100	110	

total 2 peptides

tr|A0A3Q3WAG3|A0A3Q3WAG3_MOLML
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.IIDQDKSGFIE.K	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	50	60	
R.AGDTDGDGKIG.A	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	89	99	

total 2 peptides

tr|Q804Z0|Q804Z0_ICTPU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDKSGFIE.E	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	66	76	
K.AGDTDGDGKIG.V	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	105	115	

total 2 peptides

tr|A0A3Q4AW30|A0A3Q4AW30_MOLML
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.IIDQDKSGFIE.K	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	50	60	
R.AGDTDGDGKIG.A	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	89	99	

total 2 peptides

tr|A0A3Q3W3Y6|A0A3Q3W3Y6_MOLML
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.IIDQDKSGFIE.K	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	50	60	
R.AGDTDGDGKIG.A	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	89	99	

total 2 peptides

tr|A0A3Q3K924|A0A3Q3K924_MONAL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDKSGFIE.E	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	50	60	
K.AGDTDGDGKIG.V	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	89	99	

total 2 peptides

tr|A0A674P8J8|A0A674P8J8_TAKRU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.IIDQDKSGFIE.E	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	90	100	
K.AGDTDGDGKIG.A	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	129	139	

total 2 peptides

tr|A0A7N9APR6|A0A7N9APR6_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDKSGFIE.E	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	50	60	
K.AGDTDGDGKIG.V	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	89	99	

total 2 peptides

tr|A0A3Q3K937|A0A3Q3K937_MONAL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDKSGFIE.E	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	50	60	
K.AGDTDGDGKIG.T	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	89	99	

total 2 peptides

tr|A0A3Q3JXS6|A0A3Q3JXS6_MONAL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDKSGFIE.E	Y	52.71	1263.6346	5.1	632.8278	2	11.60	1678	1	50	60	
K.AGDTDGDGKIG.H	Y	30.16	1004.4410	-0.1	503.2278	2	9.19	1256	1	89	99	

total 2 peptides

tr|H3CFQ5|H3CFQ5_TETNG

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.TIPGPPSTPWLGF.V	Y	45.63	1368.7078	-0.6	685.3608	2	15.15	2310	1	619	631	
Q.GEFVAIGPI.K	Y	17.46	901.4908	-1.9	451.7519	2	19.18	2965	2	1496	1504	
A.IGPIKVI.D	Y	15.80	738.5003	-0.1	370.2574	2	12.15	1780	1	1501	1507	

total 3 peptides

tr|M4AVS2|M4AVS2_XIPMA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLLRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	912	926	
Q.SLLRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	916	926	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	151	159	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	803	812	

total 4 peptides

tr|A0A3B3VSS0|A0A3B3VSS0_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLLRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	912	926	
Q.SLLRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	916	926	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	151	159	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	803	812	

total 4 peptides

tr|A0A0S7JRJ0|A0A0S7JRJ0_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLLRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	914	928	
Q.SLLRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	918	928	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	153	161	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	805	814	

total 4 peptides

tr|A0A0S7JR62|A0A0S7JR62_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLLRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	914	928	
Q.SLLRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	918	928	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	153	161	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	805	814	

total 4 peptides

tr|A0A3B5QZF8|A0A3B5QZF8_XIPMA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLLRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	914	928	
Q.SLLRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	918	928	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	153	161	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	805	814	

total 4 peptides

tr|G3NWV4|G3NWV4_GASAC
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLIRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	906	920	
Q.SLIRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	910	920	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	153	161	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	804	813	

total 4 peptides

tr|A0A6J2RNI9|A0A6J2RNI9_COTGO
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLIRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	914	928	
Q.SLIRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	918	928	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	153	161	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	805	814	

total 4 peptides

tr|A0A6J2RKY9|A0A6J2RKY9_COTGO
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLIRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	914	928	
Q.SLIRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	918	928	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	153	161	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	805	814	

total 4 peptides

tr|A0A3B1JPG2|A0A3B1JPG2_ASTMX
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLIRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	914	928	
Q.SLIRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	918	928	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	153	161	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	805	814	

total 4 peptides

tr|A0A667WYB6|A0A667WYB6_9TELE
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLLRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	906	920	
Q.SLLRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	910	920	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	151	159	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	797	806	

total 4 peptides

tr|A0A3B4VM00|A0A3B4VM00_SERDU
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLIRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	912	926	
Q.SLIRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	916	926	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	151	159	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	803	812	

total 4 peptides

tr|A0A667X953|A0A667X953_9TELE
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLLRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	914	928	
Q.SLLRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	918	928	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	153	161	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	805	814	

total 4 peptides

tr|A0A7N8WP58|A0A7N8WP58_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLLRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	880	894	
Q.SLLRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	884	894	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	119	127	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	771	780	

total 4 peptides

tr|A0A7N8Y7I9|A0A7N8Y7I9_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLLRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	884	898	
Q.SLLRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	888	898	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	153	161	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	775	784	

total 4 peptides

tr|A0A671YJD0|A0A671YJD0_SPAAU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLIRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	914	928	
Q.SLIRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	918	928	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	153	161	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	805	814	

total 4 peptides

tr|A0A7N8XW64|A0A7N8XW64_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLLRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	914	928	
Q.SLLRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	918	928	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	153	161	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	805	814	

total 4 peptides

tr|A0A7N9AUZ7|A0A7N9AUZ7_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLLRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	901	915	
Q.SLLRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	905	915	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	147	155	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	792	801	

total 4 peptides

tr|A0A3Q3MF18|A0A3Q3MF18_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLLRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	919	933	
Q.SLLRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	923	933	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	153	161	

total 4 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	810	819	

total 4 peptides

tr|A0A672IVR0|A0A672IVR0_SALFA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLLRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	879	893	
Q.SLLRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	883	893	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	118	126	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	770	779	

total 4 peptides

tr|A0A3Q1BZF5|A0A3Q1BZF5_AMPOC
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLLRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	912	926	
Q.SLLRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	916	926	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	151	159	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	803	812	

total 4 peptides

tr|A0A3Q0SE88|A0A3Q0SE88_AMPCI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLLRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	912	926	
Q.SLLRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	916	926	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	151	159	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	803	812	

total 4 peptides

tr|A0A3P8SU98|A0A3P8SU98_AMPPE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLLRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	914	928	
Q.SLLRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	918	928	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	153	161	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	805	814	

total 4 peptides

tr|A0A672IVP1|A0A672IVP1_SALFA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLLRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	914	928	
Q.SLLRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	918	928	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	153	161	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	805	814	

total 4 peptides

tr|A0A3Q1BVL9|A0A3Q1BVL9_AMPOC
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLLRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	914	928	
Q.SLLRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	918	928	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	153	161	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	805	814	

total 4 peptides

tr|A0A672ITB5|A0A672ITB5_SALFA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLLRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	914	928	
Q.SLLRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	918	928	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	153	161	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	805	814	

total 4 peptides

tr|A0A672IVQ1|A0A672IVQ1_SALFA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SENQSLLRMPPWSNF.W	Y	34.74	1804.8567	3.7	903.4390	2	15.03	2289	1	914	928	
Q.SLLRMPPWSNF.W	Y	25.24	1346.6805	-0.7	674.3471	2	15.17	2314	1	918	928	
E.VSVGDKVPA.D	Y	16.99	870.4811	-1.5	436.2472	2	10.13	1418	1	153	161	
L.GFNPPDLDIM.G	Y	16.33	1117.5114	0.4	559.7632	2	14.27	2156	1	805	814	

total 4 peptides

tr|A0A834CTG4|A0A834CTG4_ORYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.AVDPVYPPGPPAFPK.V	N	36.21	1550.8132	-1.1	776.4130	2	12.35	1817	1	3990	4004	
T.VVDRPQPPEGPVVF.N	Y	21.55	1534.8143	-0.9	768.4138	2	12.52	1847	1	1315	1328	
A.MNPLFPPGPPKDL.H	Y	16.76	1421.7377	-1.0	711.8754	2	13.15	1962	1	1811	1823	

total 3 peptides

tr|Q4RE90|Q4RE90_TETNG

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.AVDPVYPPGPPAFPK.V	N	36.21	1550.8132	-1.1	776.4130	2	12.35	1817	1	7117	7131	
T.VVDRPQPPEGPVVF.N	Y	21.55	1534.8143	-0.9	768.4138	2	12.52	1847	1	4491	4504	
A.MNPLFPPGPPKDL.H	Y	16.76	1421.7377	-1.0	711.8754	2	13.15	1962	1	4987	4999	

total 3 peptides

tr|A0A3P8Q9R4|A0A3P8Q9R4_ASTCA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.KDLLDPIISDR.H	Y	24.21	1283.7085	-1.3	642.8607	2	12.39	1822	1	85	95	
L.FDKPVSPL.L	Y	23.03	901.4908	-0.8	451.7523	2	23.12	3597	6	193	200	
T.GVDNPGHPF.I	Y	22.06	938.4246	-0.3	470.2195	2	10.75	1523	2	59	67	
R.HGGYKPT.D	Y	17.16	758.3711	0.2	380.1929	2	8.46	1123	1	96	102	
W.VNEEDHLRVI.S	Y	16.15	1222.6306	-0.9	612.3220	2	11.23	1610	1	228	237	

total 5 peptides

tr|A0A3Q4HL72|A0A3Q4HL72_NEOBR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.KDLLDPIISDR.H	Y	24.21	1283.7085	-1.3	642.8607	2	12.39	1822	1	85	95	
L.FDKPVSPL.L	Y	23.03	901.4908	-0.8	451.7523	2	23.12	3597	6	193	200	
T.GVDNPGHPF.I	Y	22.06	938.4246	-0.3	470.2195	2	10.75	1523	2	59	67	
R.HGGYKPT.D	Y	17.16	758.3711	0.2	380.1929	2	8.46	1123	1	96	102	
W.VNEEDHLRVI.S	Y	16.15	1222.6306	-0.9	612.3220	2	11.23	1610	1	228	237	

total 5 peptides

tr|A0A3B4TA77|A0A3B4TA77_SERDU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.KDLLDPIISDR.H	Y	24.21	1283.7085	-1.3	642.8607	2	12.39	1822	1	85	95	
L.FDKPVSPL.L	Y	23.03	901.4908	-0.8	451.7523	2	23.12	3597	6	193	200	
T.GVDNPGHPF.I	Y	22.06	938.4246	-0.3	470.2195	2	10.75	1523	2	59	67	
R.HGGYKPT.D	Y	17.16	758.3711	0.2	380.1929	2	8.46	1123	1	96	102	
W.VNEEDHLRVI.S	Y	16.15	1222.6306	-0.9	612.3220	2	11.23	1610	1	228	237	

total 5 peptides

tr|A0A0F8AN20|A0A0F8AN20_LARCR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.KDLLDPIISDR.H	Y	24.21	1283.7085	-1.3	642.8607	2	12.39	1822	1	85	95	
L.FDKPVSPL.L	Y	23.03	901.4908	-0.8	451.7523	2	23.12	3597	6	193	200	
T.GVDNPGHPF.I	Y	22.06	938.4246	-0.3	470.2195	2	10.75	1523	2	59	67	
R.HGGYKPT.D	Y	17.16	758.3711	0.2	380.1929	2	8.46	1123	1	96	102	
W.VNEEDHLRVI.S	Y	16.15	1222.6306	-0.9	612.3220	2	11.23	1610	1	228	237	

total 5 peptides

tr|C7ASM1|C7ASM1_SINCH
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.KDLLDPIISDR.H	Y	24.21	1283.7085	-1.3	642.8607	2	12.39	1822	1	86	96	
L.FDKPVSPL.L	Y	23.03	901.4908	-0.8	451.7523	2	23.12	3597	6	194	201	
T.GVDNPGHPF.I	Y	22.06	938.4246	-0.3	470.2195	2	10.75	1523	2	60	68	
R.HGGYKPT.D	Y	17.16	758.3711	0.2	380.1929	2	8.46	1123	1	97	103	
W.VNEEDHLRVI.S	Y	16.15	1222.6306	-0.9	612.3220	2	11.23	1610	1	229	238	

total 5 peptides

tr|G3PFX6|G3PFX6_GASAC
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.KDLLDPIISDR.H	Y	24.21	1283.7085	-1.3	642.8607	2	12.39	1822	1	119	129	
L.FDKPVSPL.L	Y	23.03	901.4908	-0.8	451.7523	2	23.12	3597	6	227	234	
T.GVDNPGHPF.I	Y	22.06	938.4246	-0.3	470.2195	2	10.75	1523	2	93	101	
R.HGGYKPT.D	Y	17.16	758.3711	0.2	380.1929	2	8.46	1123	1	130	136	
W.VNEEDHLRVI.S	Y	16.15	1222.6306	-0.9	612.3220	2	11.23	1610	1	262	271	

total 5 peptides

tr|A0A6P7JDS0|A0A6P7JDS0_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.KDLLDPIISDR.H	Y	24.21	1283.7085	-1.3	642.8607	2	12.39	1822	1	167	177	
L.FDKPVSPL.L	Y	23.03	901.4908	-0.8	451.7523	2	23.12	3597	6	275	282	

total 5 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.GVDNPGHPF.I	Y	22.06	938.4246	-0.3	470.2195	2	10.75	1523	2	141	149	
R.HGGYKPT.D	Y	17.16	758.3711	0.2	380.1929	2	8.46	1123	1	178	184	
W.VNEEDHLRVI.S	Y	16.15	1222.6306	-0.9	612.3220	2	11.23	1610	1	310	319	

total 5 peptides

tr|A0A672MA11|A0A672MA11_SINGR
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.GEKLKGADPEDVILS.A	Y	28.44	1569.8250	-0.2	785.9196	2	11.67	1690	1	62	76	
F.GEKLKGADPEDVIL.S	Y	24.67	1482.7930	-0.8	742.4032	2	11.90	1732	1	62	75	
L.WAAFPPDVA.G	Y	20.98	972.4705	-0.5	487.2423	2	13.51	2026	4	114	122	

total 3 peptides

tr|A0A4U5VU95|A0A4U5VU95_COLLU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.GEKLKGADPEDVILS.A	Y	28.44	1569.8250	-0.2	785.9196	2	11.67	1690	1	68	82	
F.GEKLKGADPEDVIL.S	Y	24.67	1482.7930	-0.8	742.4032	2	11.90	1732	1	68	81	
M.WAAFPPDVA.G	Y	20.98	972.4705	-0.5	487.2423	2	13.51	2026	4	120	128	

total 3 peptides

tr|A0A3B4BW75|A0A3B4BW75_PYGNA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.GEKLKGADPEDVILS.G	Y	28.44	1569.8250	-0.2	785.9196	2	11.67	1690	1	82	96	
F.GEKLKGADPEDVIL.S	Y	24.67	1482.7930	-0.8	742.4032	2	11.90	1732	1	82	95	
L.WAAFPPDVA.G	Y	20.98	972.4705	-0.5	487.2423	2	13.51	2026	4	134	142	

total 3 peptides

tr|A0A7J6CHK6|A0A7J6CHK6_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.GEKLKGADPEDVILS.A	Y	28.44	1569.8250	-0.2	785.9196	2	11.67	1690	1	89	103	
F.GEKLKGADPEDVIL.S	Y	24.67	1482.7930	-0.8	742.4032	2	11.90	1732	1	89	102	
L.WAAFPPDVA.G	Y	20.98	972.4705	-0.5	487.2423	2	13.51	2026	4	141	149	

total 3 peptides

tr|A0A6P7II88|A0A6P7II88_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.GEKLKGADPEDVILS.A	Y	28.44	1569.8250	-0.2	785.9196	2	11.67	1690	1	90	104	
F.GEKLKGADPEDVIL.S	Y	24.67	1482.7930	-0.8	742.4032	2	11.90	1732	1	90	103	
M.WAAFPPDVA.G	Y	20.98	972.4705	-0.5	487.2423	2	13.51	2026	4	142	150	

total 3 peptides

tr|A0A668VT67|A0A668VT67_OREAU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.GEKLKGADPEDVILS.A	Y	28.44	1569.8250	-0.2	785.9196	2	11.67	1690	1	97	111	

total 3 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.GEKLKGADPEDVIL.S	Y	24.67	1482.7930	-0.8	742.4032	2	11.90	1732	1	97	110	
L.WAAFPPDVA.G	Y	20.98	972.4705	-0.5	487.2423	2	13.51	2026	4	149	157	

total 3 peptides

tr|F8U029|F8U029_EPIBR
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.GEKLKGADPEDVILS.S	Y	28.44	1569.8250	-0.2	785.9196	2	11.67	1690	1	90	104	
F.GEKLKGADPEDVIL.S	Y	24.67	1482.7930	-0.8	742.4032	2	11.90	1732	1	90	103	
M.WAAFPPDVA.G	Y	20.98	972.4705	-0.5	487.2423	2	13.51	2026	4	142	150	

total 3 peptides

tr|A0A3B5RBY4|A0A3B5RBY4_XIPMA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.GEKLKGADPEDVILS.A	Y	28.44	1569.8250	-0.2	785.9196	2	11.67	1690	1	169	183	
F.GEKLKGADPEDVIL.S	Y	24.67	1482.7930	-0.8	742.4032	2	11.90	1732	1	169	182	
M.WAAFPPDVA.G	Y	20.98	972.4705	-0.5	487.2423	2	13.51	2026	4	221	229	

total 3 peptides

tr|A0A7J5Y2W4|A0A7J5Y2W4_DISMA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.AVDPVYPPGPPAFPK.V	N	36.21	1550.8132	-1.1	776.4130	2	12.35	1817	1	79	93	
C.TGPIKF.D	Y	19.01	661.3799	-0.8	331.6970	2	11.39	1639	1	564	569	

total 2 peptides

tr|A0A4Z2HXD4|A0A4Z2HXD4_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.AVDPVYPPGPPAFPK.V	N	36.21	1550.8132	-1.1	776.4130	2	12.35	1817	1	60	74	
C.TGPIKF.D	Y	19.01	661.3799	-0.8	331.6970	2	11.39	1639	1	558	563	

total 2 peptides

tr|A0A672HWD2|A0A672HWD2_SALFA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.WIDPDDFPLLLPH.W	Y	32.22	1576.7925	0.6	789.4040	2	15.34	2344	1	295	307	
F.MDDPVVIPGKPY.T	Y	24.31	1329.6638	-1.0	665.8385	2	12.25	1798	1	211	222	

total 2 peptides

tr|A0A672HWL2|A0A672HWL2_SALFA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.WIDPDDFPLLLPH.W	Y	32.22	1576.7925	0.6	789.4040	2	15.34	2344	1	302	314	
F.MDDPVVIPGKPY.T	Y	24.31	1329.6638	-1.0	665.8385	2	12.25	1798	1	218	229	

total 2 peptides

tr|A0A672HXF4|A0A672HXF4_SALFA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.WIDPDDFPLLLPH.W	Y	32.22	1576.7925	0.6	789.4040	2	15.34	2344	1	313	325	
F.MDDPVVIPGKPY.T	Y	24.31	1329.6638	-1.0	665.8385	2	12.25	1798	1	229	240	

total 2 peptides

tr|A0A672HXA9|A0A672HXA9_SALFA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.WIDPDDFPLLLPH.W	Y	32.22	1576.7925	0.6	789.4040	2	15.34	2344	1	322	334	
F.MDDPVVIPGKPY.T	Y	24.31	1329.6638	-1.0	665.8385	2	12.25	1798	1	238	249	

total 2 peptides

tr|A0A3Q4GK85|A0A3Q4GK85_NEOBR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.KVDSELPVDDVFGQ.V	Y	31.17	1546.7515	-1.0	774.3822	2	13.13	1957	1	171	184	
K.VDSELPVDDVFGQ.V	Y	19.90	1418.6565	-0.8	710.3350	2	13.87	2087	1	172	184	

total 2 peptides

tr|A0A3Q4GS43|A0A3Q4GS43_NEOBR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.KVDSELPVDDVFGQ.V	Y	31.17	1546.7515	-1.0	774.3822	2	13.13	1957	1	172	185	
K.VDSELPVDDVFGQ.V	Y	19.90	1418.6565	-0.8	710.3350	2	13.87	2087	1	173	185	

total 2 peptides

tr|A0A3P8P8S3|A0A3P8P8S3_ASTCA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.KVDSELPVDDVFGQ.V	Y	31.17	1546.7515	-1.0	774.3822	2	13.13	1957	1	172	185	
K.VDSELPVDDVFGQ.V	Y	19.90	1418.6565	-0.8	710.3350	2	13.87	2087	1	173	185	

total 2 peptides

tr|A0A3Q1HW42|A0A3Q1HW42_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.KVDSELPVDDVFGQ.V	Y	31.17	1546.7515	-1.0	774.3822	2	13.13	1957	1	172	185	
K.VDSELPVDDVFGQ.V	Y	19.90	1418.6565	-0.8	710.3350	2	13.87	2087	1	173	185	

total 2 peptides

tr|A0A3P9CWL7|A0A3P9CWL7_9CICH

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.KVDSELPVDDVFGQ.V	Y	31.17	1546.7515	-1.0	774.3822	2	13.13	1957	1	172	185	
K.VDSELPVDDVFGQ.V	Y	19.90	1418.6565	-0.8	710.3350	2	13.87	2087	1	173	185	

total 2 peptides

tr|A0A3B5BIY5|A0A3B5BIY5_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.KVDSELPVDDVFGQ.V	Y	31.17	1546.7515	-1.0	774.3822	2	13.13	1957	1	172	185	
K.VDSELPVDDVFGQ.V	Y	19.90	1418.6565	-0.8	710.3350	2	13.87	2087	1	173	185	

total 2 peptides

tr|A0A3Q2VY92|A0A3Q2VY92_HAPBU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.KVDSELPVDDVFGQ.V	Y	31.17	1546.7515	-1.0	774.3822	2	13.13	1957	1	172	185	
K.VDSELPVDDVFGQ.V	Y	19.90	1418.6565	-0.8	710.3350	2	13.87	2087	1	173	185	

total 2 peptides

tr|A0A3B4FMK3|A0A3B4FMK3_9CICH
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.KVDSELPVDDVFGQ.V	Y	31.17	1546.7515	-1.0	774.3822	2	13.13	1957	1	172	185	
K.VDSELPVDDVFGQ.V	Y	19.90	1418.6565	-0.8	710.3350	2	13.87	2087	1	173	185	

total 2 peptides

tr|A0A3Q3CWR9|A0A3Q3CWR9_HAPBU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.KVDSELPVDDVFGQ.V	Y	31.17	1546.7515	-1.0	774.3822	2	13.13	1957	1	190	203	
K.VDSELPVDDVFGQ.V	Y	19.90	1418.6565	-0.8	710.3350	2	13.87	2087	1	191	203	

total 2 peptides

tr|A0A3P8P8V3|A0A3P8P8V3_ASTCA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.KVDSELPVDDVFGQ.V	Y	31.17	1546.7515	-1.0	774.3822	2	13.13	1957	1	190	203	
K.VDSELPVDDVFGQ.V	Y	19.90	1418.6565	-0.8	710.3350	2	13.87	2087	1	191	203	

total 2 peptides

tr|A0A665WT54|A0A665WT54_ECHNA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A671N228|A0A671N228_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A3Q3Q7K2|A0A3Q3Q7K2_MONAL
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A671MU99|A0A671MU99_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A672KK19|A0A672KK19_SINGR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A673LYE6|A0A673LYE6_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A3P8VEA1|A0A3P8VEA1_CYNSE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A3Q1II99|A0A3Q1II99_ANATE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A6P7L9I7|A0A6P7L9I7_BETSP

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A3P8X8T4|A0A3P8X8T4_ESOLU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	96	105	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	97	105	

total 2 peptides

tr|A0A3Q0R4X6|A0A3Q0R4X6_AMPCI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A3P8VK01|A0A3P8VK01_CYNSE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A3P8XBI5|A0A3P8XBI5_ESOLU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	96	105	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	97	105	

total 2 peptides

tr|A0A3Q1H919|A0A3Q1H919_ANATE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A3Q3KN21|A0A3Q3KN21_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A6P7L9I9|A0A6P7L9I9_BETSP

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A3P8VE68|A0A3P8VE68_CYNSE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A6G0HYN5|A0A6G0HYN5_LARCR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A3P8ZCR8|A0A3P8ZCR8_ESOLU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	96	105	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	97	105	

total 2 peptides

tr|A0A3Q3IQV7|A0A3Q3IQV7_MONAL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A665WTS5|A0A665WTS5_ECHNA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A7N8Y585|A0A7N8Y585_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	100	109	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	101	109	

total 2 peptides

tr|A0A6P6QFT2|A0A6P6QFT2_CARAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A672KNU9|A0A672KNU9_SINGR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A673M1Q3|A0A673M1Q3_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A7J6CGV6|A0A7J6CGV6_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A6P6QIW1|A0A6P6QIW1_CARAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A6Q2XWF7|A0A6Q2XWF7_ESOLU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	96	105	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	97	105	

total 2 peptides

tr|A0A0F8AMH6|A0A0F8AMH6_LARCR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	97	106	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	98	106	

total 2 peptides

tr|A0A6G0HYU6|A0A6G0HYU6_LARCR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MDSPMPIIPH.Q	Y	28.61	1136.5359	-2.5	569.2738	2	12.55	1852	1	544	553	
M.DSPMPIIPH.Q	Y	19.82	1005.4954	-1.1	503.7544	2	12.29	1806	1	545	553	

total 2 peptides

tr|G3N515|G3N515_GASAC
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.LDVIDVPAPVKNL.R	Y	24.20	1391.8024	-0.5	696.9081	2	13.83	2080	1	1994	2006	
E.TDPVLIKDPIDPPWAPGKPVIR.D	N	23.05	2423.3577	-1.0	808.7924	3	12.93	1921	2	2882	2903	

total 2 peptides

tr|A0A3P8T7F6|A0A3P8T7F6_AMPPE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.KKAEPAPAPAPAAPEP.A	Y	34.93	1540.8248	-1.0	771.4189	2	9.56	1321	1	12	27	

total 1 peptides

tr|A0A3Q1AWA1|A0A3Q1AWA1_AMPOC
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.KKAEPAPAPAPAAPEP.A	Y	34.93	1540.8248	-1.0	771.4189	2	9.56	1321	1	12	27	

total 1 peptides

tr|A0A3P8T5J7|A0A3P8T5J7_AMPPE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.KKAEPAPAPAPAAPEP.A	Y	34.93	1540.8248	-1.0	771.4189	2	9.56	1321	1	12	27	

total 1 peptides

tr|A0A3P8T7H6|A0A3P8T7H6_AMPPE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.KKAEPAPAPAPAAPEP.A	Y	34.93	1540.8248	-1.0	771.4189	2	9.56	1321	1	12	27	

total 1 peptides

tr|A0A3Q1B6V7|A0A3Q1B6V7_AMPOC
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.KKAEPAPAPAPAAPEP.A	Y	34.93	1540.8248	-1.0	771.4189	2	9.56	1321	1	12	27	

total 1 peptides

tr|A0A6F9CEX9|A0A6F9CEX9_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.LDPIDAPGKPDVISIT.R	Y	34.39	1649.8876	-1.2	825.9501	2	12.86	1909	1	8748	8763	

total 1 peptides

tr|A0A484CUS5|A0A484CUS5_PERFV
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TDPVLIKDPIDPPWAPGKPVIR.D	N	23.05	2423.3577	-1.0	808.7924	3	12.93	1921	2	710	731	
T.VVDRPTPPVGPV.V	Y	22.13	1231.6924	-0.6	616.8531	2	11.28	1619	1	3654	3665	

total 2 peptides

tr|A0A834CMG6|A0A834CMG6_ORYME
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1366	1380	

total 1 peptides

tr|A0A3B3BCL7|A0A3B3BCL7_ORYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1366	1380	

total 1 peptides

tr|A0A3B3D3C5|A0A3B3D3C5_ORYME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1371	1385	

total 1 peptides

tr|A0A672ZI78|A0A672ZI78_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1101	1115	

total 1 peptides

tr|A0A669ELF6|A0A669ELF6_ORENI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1146	1160	

total 1 peptides

tr|A0A671Y3Y8|A0A671Y3Y8_SPAAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1151	1165	

total 1 peptides

tr|A0A4U5U6X9|A0A4U5U6X9_COLLU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1190	1204	

total 1 peptides

tr|A0A669CKL2|A0A669CKL2_ORENI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1224	1238	

total 1 peptides

tr|A0A671Y401|A0A671Y401_SPAAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1268	1282	

total 1 peptides

tr|A0A672FNF5|A0A672FNF5_SALFA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1294	1308	

total 1 peptides

tr|A0A671Y3W3|A0A671Y3W3_SPAAU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1334	1348	

total 1 peptides

tr|A0A6G0J0W8|A0A6G0J0W8_LARCR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1335	1349	

total 1 peptides

tr|A0A671Y575|A0A671Y575_SPAAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1349	1363	

total 1 peptides

tr|A0A6G1P7U8|A0A6G1P7U8_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1366	1380	

total 1 peptides

tr|A0A087YFH0|A0A087YFH0_POEFO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1365	1379	

total 1 peptides

tr|A0A3P9PGW1|A0A3P9PGW1_POERE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1365	1379	

total 1 peptides

tr|A0A3P8P4C2|A0A3P8P4C2_ASTCA

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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1366	1380	

total 1 peptides

tr|A0A3Q1D109|A0A3Q1D109_AMPOC
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1366	1380	

total 1 peptides

tr|A0A3Q2WWP1|A0A3Q2WWP1_HAPBU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1366	1380	

total 1 peptides

tr|A0A672ZHV0|A0A672ZHV0_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1366	1380	

total 1 peptides

tr|I3JDJ1|I3JDJ1_ORENI
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1366	1380	

total 1 peptides

tr|A0A2I4AP94|A0A2I4AP94_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1366	1380	

total 1 peptides

tr|A0A3P9LTE0|A0A3P9LTE0_ORYLA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1366	1380	

total 1 peptides

tr|A0A6P7LYN0|A0A6P7LYN0_BETSP
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIELPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1382	1396	

total 1 peptides

tr|A0A3Q4GHK3|A0A3Q4GHK3_NEOBR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.P	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	858	872	

total 1 peptides

tr|A0A3Q4GXU7|A0A3Q4GXU7_NEOBR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.P	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1184	1198	

total 1 peptides

tr|A0A3B3IJA0|A0A3B3IJA0_ORYLA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1351	1365	

total 1 peptides

tr|A0A3P9IT90|A0A3P9IT90_ORYLA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1366	1380	

total 1 peptides

tr|H2M2B3|H2M2B3_ORYLA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1366	1380	

total 1 peptides

tr|A0A3B3HWS2|A0A3B3HWS2_ORYLA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	32.89	1683.0334	-1.7	842.5226	2	13.09	1951	2	1378	1392	

total 1 peptides

tr|A0A6G0J5U6|A0A6G0J5U6_LARCR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.IVRPPQDMFEPPGSDIVF.E	Y	21.70	2043.0134	2.4	1022.5165	2	14.33	2166	1	119	136	
E.IVRPPQDMFEPPGSDIVFE.V	Y	20.48	2172.0562	-0.7	1087.0345	2	13.99	2108	1	119	137	

total 2 peptides

tr|A0A6A5F2V4|A0A6A5F2V4_PERFL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM

total 2 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TDPVLIKDPIDPPWAPGKPVIR.D	N	23.05	2423.3577	-1.0	808.7924	3	12.93	1921	2	6913	6934	
K.AIGNPLPDIVWL.K	Y	17.35	1306.7285	0.2	654.3716	2	16.02	2459	1	622	633	

total 2 peptides

tr|A0A7N6BJ85|A0A7N6BJ85_ANATE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.LDPVDPPGQPVPIF.V	Y	29.58	1489.7816	-0.1	745.8980	2	14.35	2169	1	17	30	

total 1 peptides

tr|A0A3B3QB10|A0A3B3QB10_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.DRPGPPEGPISIY.G	Y	28.56	1396.6986	-1.1	699.3558	2	12.64	1868	1	760	772	

total 1 peptides

tr|A0A668VQH5|A0A668VQH5_OREAU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.A	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	165	175	

total 1 peptides

tr|A0A3P8Q0W3|A0A3P8Q0W3_ASTCA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.A	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	249	259	

total 1 peptides

tr|F5BZS7|F5BZS7_EPIBR
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.N	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	292	302	

total 1 peptides

tr|A0A4W4G2T4|A0A4W4G2T4_ELEEL
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.A	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	265	275	

total 1 peptides

tr|A0A4W4G3J1|A0A4W4G3J1_ELEEL
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.A	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	267	277	

total 1 peptides

tr|A0A668VQX9|A0A668VQX9_OREAU
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.A	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	292	302	

total 1 peptides

tr|A0A4W4G4V3|A0A4W4G4V3_ELEEL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.N	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	292	302	

total 1 peptides

tr|A0A668VU75|A0A668VU75_OREAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.A	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	281	291	

total 1 peptides

tr|A0A4W4G338|A0A4W4G338_ELEEL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.A	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	282	292	

total 1 peptides

tr|A0A3P9C6I0|A0A3P9C6I0_9CICH

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.A	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	283	293	

total 1 peptides

tr|A0A668V8T6|A0A668V8T6_OREAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.H	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	292	302	

total 1 peptides

tr|A0A668VTY0|A0A668VTY0_OREAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.A	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	292	302	

total 1 peptides

tr|A0A6P3VUG4|A0A6P3VUG4_CLUHA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.A	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	292	302	

total 1 peptides

tr|A0A4W4FGS3|A0A4W4FGS3_ELEEL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.N	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	290	300	

total 1 peptides

tr|A0A3P8TV75|A0A3P8TV75_AMPPE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.A	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	292	302	

total 1 peptides

tr|A0A6P7IPP6|A0A6P7IPP6_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.A	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	292	302	

total 1 peptides

tr|A0A6P3W3B1|A0A6P3W3B1_CLUHA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.N	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	292	302	

total 1 peptides

tr|A0A3B4CPC9|A0A3B4CPC9_PYGNA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.N	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	292	302	

total 1 peptides

tr|A0A6P3W5E7|A0A6P3W5E7_CLUHA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.N	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	292	302	

total 1 peptides

tr|A0A3P8TVY9|A0A3P8TVY9_AMPPE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.N	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	292	302	

total 1 peptides

tr|A0A6P7P1U1|A0A6P7P1U1_BETSP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.A	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	292	302	

total 1 peptides

tr|A0A4W4G3C7|A0A4W4G3C7_ELEEL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.A	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	322	332	

total 1 peptides

tr|A0A4W4G3N6|A0A4W4G3N6_ELEEL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.A	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	298	308	

total 1 peptides

tr|A0A3P8NTT0|A0A3P8NTT0_ASTCA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.Q	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	303	313	

total 1 peptides

tr|A0A6P7MN74|A0A6P7MN74_BETSP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.A	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	311	321	

total 1 peptides

tr|A0A3B4ERE5|A0A3B4ERE5_PYGNA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.N	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	312	322	

total 1 peptides

tr|A0A3B4DDR1|A0A3B4DDR1_PYGNA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.N	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	328	338	

total 1 peptides

tr|A0A7J6BNX1|A0A7J6BNX1_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.A	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	337	347	

total 1 peptides

tr|A0A6P7P064|A0A6P7P064_BETSP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IEDPFDQDDWE.A	Y	26.40	1407.5466	-0.3	704.7804	2	14.04	2116	1	349	359	

total 1 peptides

tr|A0A5A9PD51|A0A5A9PD51_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.KEDKAGSQ.G	Y	23.02	861.4192	-0.4	431.7167	2	2.00	253	2	587	594	

total 1 peptides

tr|A0A6P8GQF7|A0A6P8GQF7_CLUHA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.GADDKLKDK.I	Y	22.74	988.5189	-0.5	495.2665	2	8.10	1053	1	1371	1379	

total 1 peptides

tr|A0A6P8GCK4|A0A6P8GCK4_CLUHA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.GADDKLKDK.I	Y	22.74	988.5189	-0.5	495.2665	2	8.10	1053	1	1381	1389	

total 1 peptides

tr|A0A6P8GCW3|A0A6P8GCW3_CLUHA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.GADDKLKDK.I	Y	22.74	988.5189	-0.5	495.2665	2	8.10	1053	1	1414	1422	

total 1 peptides

tr|A0A6P8GNT0|A0A6P8GNT0_CLUHA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.GADDKLKDK.I	Y	22.74	988.5189	-0.5	495.2665	2	8.10	1053	1	1424	1432	

total 1 peptides

tr|A0A674PAA1|A0A674PAA1_TAKRU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.KTIDDLEDE.V	Y	22.10	1076.4873	-0.3	539.2508	2	10.91	1552	1	145	153	

total 1 peptides

tr|A0A4W5K3X5|A0A4W5K3X5_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.KTIDDLEDE.V	Y	22.10	1076.4873	-0.3	539.2508	2	10.91	1552	1	225	233	

total 1 peptides

tr|A0A4W5KNV1|A0A4W5KNV1_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.KTIDDLEDE.V	Y	22.10	1076.4873	-0.3	539.2508	2	10.91	1552	1	246	254	

total 1 peptides

tr|A0A3Q1CSK5|A0A3Q1CSK5_AMPOC

back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.KTIDDLEDE.V	Y	22.10	1076.4873	-0.3	539.2508	2	10.91	1552	1	251	259	

total 1 peptides

tr|A0A4W5KNI2|A0A4W5KNI2_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.KTIDDLEDE.V	Y	22.10	1076.4873	-0.3	539.2508	2	10.91	1552	1	251	259	

total 1 peptides

tr|A0A6G0HZW7|A0A6G0HZW7_LARCR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.KTIDDLEDE.V	Y	22.10	1076.4873	-0.3	539.2508	2	10.91	1552	1	251	259	

total 1 peptides

tr|A0A6J2PEZ1|A0A6J2PEZ1_COTGO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.KTIDDLEDE.L	Y	22.10	1076.4873	-0.3	539.2508	2	10.91	1552	1	251	259	

total 1 peptides

tr|D2KQG3|D2KQG3_SINCH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.EVIDQDKSGFIE.E	Y	20.02	1378.6616	-1.6	690.3370	2	12.51	1846	1	49	60	

total 1 peptides

tr|B9VJM3|B9VJM3_SINCH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.EVIDQDKSGFIE.E	Y	20.02	1378.6616	-1.6	690.3370	2	12.51	1846	1	49	60	

total 1 peptides

Protein List

1. Notes

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)

Table 1. Statistics of data.

# of MS Scans	1037
# of MS/MS Scans	2829

Table 2. Result filtration parameters.

Peptide -10lgP	≥15
Protein -10lgP	≥20
Proteins unique peptides	≥0
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	131
Peptide Sequences	123
Protein Groups	43
Proteins	256
Proteins (#Unique Peptides)	43 (>2); 47 (=2); 137 (=1);
FDR (Peptide-Spectrum Matches)	10.7%
FDR (Peptide Sequences)	11.4%
FDR (Protein)	0.4%
De Novo Only Spectra	1244

Table 4. PTM profile.

Name	ΔMass	#PSM	Position

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)

Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Orbi2222	0	0	0	0	123

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS 7.0
Parent Mass Error Tolerance: 0.03 Da
Fragment Mass Error Tolerance: 0.1 Da
Precursor Mass Search Type: monoisotopic
Enzyme: None
Max Missed Cleavages: 100
Non-specific Cleavage: both
Max variable PTM per peptide: 3
Database: Teleosteo
Taxon: All
Searched Entry: 4529691
FDR Estimation: Enabled
Merge Options: 0.1 min. 0.03 Da
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB_PIMENTA_PP_20220211_06.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID/ECD
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
1	12040	tr|A0A3S2MUF9|A0A3S2MUF9_ORYJA	138.72	20	23	23	N	41945	Uncharacterized protein OS=Oryzias javanicus OX=123683 GN=OJAV_G00024300 PE=3 SV=1
1	66846	tr|A0A7J6C441|A0A7J6C441_9TELE	138.72	20	23	23	N	41959	Uncharacterized protein OS=Onychostoma macrolepis OX=369639 GN=G5714_016621 PE=3 SV=1
10	73802	tr|A0A5C6NQR5|A0A5C6NQR5_9TELE	131.22	7	8	0	N	52820	Parvalbumin OS=Takifugu flavidus OX=433684 GN=D4764_18G0006780 PE=3 SV=1
2	73777	tr|A0A6P6N9Z4|A0A6P6N9Z4_CARAU	126.95	6	14	0	N	221582	myosin heavy chain, fast skeletal muscle-like OS=Carassius auratus OX=7957 GN=LOC113076612 PE=3 SV=1
3	66917	tr|A0A3B4CZR3|A0A3B4CZR3_PYGNA	126.54	6	14	0	N	213482	Uncharacterized protein OS=Pygocentrus nattereri OX=42514 PE=3 SV=1
4	66800	tr|A0A674NSP7|A0A674NSP7_TAKRU	125.65	6	13	0	N	223905	Uncharacterized protein OS=Takifugu rubripes OX=31033 GN=myhm86-1 PE=3 SV=1
14	67489	tr|A0A6A4SNF9|A0A6A4SNF9_SCOMX	124.92	4	6	0	N	77468	Parvalbumin OS=Scophthalmus maximus OX=52904 GN=F2P81_014924 PE=3 SV=1
5	66801	tr|Q90YF6|Q90YF6_PARFO	124.71	5	12	0	N	221374	Myosin heavy chain OS=Paracirrhites forsteri OX=100206 GN=MyoHC-T54 PE=2 SV=1
12	73788	tr|W5LNC0|W5LNC0_ASTMX	115.33	33	7	0	N	11525	Parvalbumin OS=Astyanax mexicanus OX=7994 PE=3 SV=2
12	73789	tr|A0A2I4BRJ5|A0A2I4BRJ5_9TELE	115.33	33	7	0	N	11457	Parvalbumin OS=Austrofundulus limnaeus OX=52670 GN=LOC106522062 PE=3 SV=1
12	73790	tr|A0A3B4TWT0|A0A3B4TWT0_SERDU	115.33	33	7	0	N	11497	Parvalbumin OS=Seriola dumerili OX=41447 PE=3 SV=1
12	73791	tr|A0A1A8L493|A0A1A8L493_9TELE	115.33	33	7	0	N	11514	Parvalbumin OS=Nothobranchius pienaari OX=704102 GN=PVALB1 PE=3 SV=1
12	73792	tr|A0A672FI61|A0A672FI61_SALFA	115.33	33	7	0	N	11436	Parvalbumin OS=Salarias fasciatus OX=181472 GN=LOC115387769 PE=3 SV=1
12	73793	tr|A0A1A8G5F7|A0A1A8G5F7_9TELE	115.33	33	7	0	N	11544	Parvalbumin OS=Nothobranchius korthausae OX=1143690 GN=PVALB1 PE=3 SV=1
12	73794	tr|A0A4W6DV48|A0A4W6DV48_LATCA	115.33	33	7	0	N	11469	Parvalbumin OS=Lates calcarifer OX=8187 GN=LOC108880037 PE=3 SV=1
12	67611	tr|F8U037|F8U037_EPIBR	115.33	33	7	0	N	11432	Parvalbumin (Fragment) OS=Epinephelus bruneus OX=323802 PE=2 SV=1
12	67613	tr|A0A1A7WW39|A0A1A7WW39_9TELE	115.33	33	7	0	N	11532	Parvalbumin OS=Iconisemion striatum OX=60296 GN=PVALB1 PE=3 SV=1

total 256 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
12	73795	tr|A0A1A8C322|A0A1A8C322_9TELE	115.33	33	7	0	N	11498	Parvalbumin OS=Nothobranchius kadleci OX=1051664 GN=PVALB1 PE=3 SV=1
12	73796	tr|A0A3Q3GY11|A0A3Q3GY11_9LABR	115.33	33	7	0	N	11308	Parvalbumin OS=Labrus bergylta OX=56723 PE=3 SV=1
12	73797	tr|A0A1A8J4D2|A0A1A8J4D2_NOTKU	115.33	33	7	0	N	11498	Parvalbumin OS=Nothobranchius kuhntae OX=321403 GN=PVALB1 PE=3 SV=1
13	67241	tr|A0A672Y4P6|A0A672Y4P6_9TELE	102.98	23	6	6	N	17050	Nucleoside diphosphate kinase B OS=Sphaeramia orbicularis OX=375764 GN=LOC115423821 PE=3 SV=1
13	67242	tr|A0A2I4CF45|A0A2I4CF45_9TELE	102.98	23	6	6	N	16890	Nucleoside diphosphate kinase B OS=Austrofundulus limnaeus OX=52670 GN=LOC106528082 PE=3 SV=1
13	67245	tr|A0A6P7ISB4|A0A6P7ISB4_9TELE	102.98	23	6	6	N	16935	Nucleoside diphosphate kinase B OS=Parambassis ranga OX=210632 GN=LOC114440125 PE=3 SV=1
13	67246	tr|A0A3Q4I698|A0A3Q4I698_NEOBR	102.98	23	6	6	N	16950	Nucleoside diphosphate kinase B OS=Neolamprologus brichardi OX=32507 PE=3 SV=1
13	73835	tr|A0A3B3Z6H5|A0A3B3Z6H5_9TELE	102.98	23	6	6	N	16834	Nucleoside diphosphate kinase B OS=Poecilia mexicana OX=48701 PE=3 SV=1
13	67249	tr|A0A3Q3A341|A0A3Q3A341_KRYMA	102.98	23	6	6	N	16887	Nucleoside diphosphate kinase B OS=Kryptolebias marmoratus OX=37003 PE=3 SV=1
13	67251	tr|A0A3P8Q104|A0A3P8Q104_ASTCA	102.98	23	6	6	N	17195	Nucleoside diphosphate kinase B OS=Astatotilapia calliptera OX=8154 PE=3 SV=1
13	67252	tr|A0A3Q3CUD8|A0A3Q3CUD8_HAPBU	102.98	23	6	6	N	17195	Nucleoside diphosphate kinase B OS=Haplochromis burtoni OX=8153 PE=3 SV=1
13	67253	tr|A0A3Q4I6B8|A0A3Q4I6B8_NEOBR	102.98	23	6	6	N	17195	Nucleoside diphosphate kinase B OS=Neolamprologus brichardi OX=32507 PE=3 SV=1
13	67258	tr|M4ADR4|M4ADR4_XIPMA	102.98	22	6	6	N	18277	Nucleoside diphosphate kinase B OS=Xiphophorus maculatus OX=8083 PE=3 SV=2
13	73836	tr|A0A3B3Z5H2|A0A3B3Z5H2_9TELE	102.98	21	6	6	N	18371	Nucleoside diphosphate kinase B OS=Poecilia mexicana OX=48701 PE=3 SV=1
13	73837	tr|A0A087YID2|A0A087YID2_POEFO	102.98	21	6	6	N	18371	Nucleoside diphosphate kinase B OS=Poecilia formosa OX=48698 PE=3 SV=2
13	73838	tr|A0A3Q2PNK7|A0A3Q2PNK7_FUNHE	102.98	14	6	6	N	26728	Nucleoside diphosphate kinase B OS=Fundulus heteroclitus OX=8078 PE=3 SV=1
9	67400	tr|A0A4W4EA72|A0A4W4EA72_ELEEL	102.77	16	7	5	N	11756	Parvalbumin OS=Electrophorus electricus OX=8005 GN=LOC113569881 PE=3 SV=1
15	73844	tr|A0A3B4TLJ3|A0A3B4TLJ3_SERDU	96.43	29	5	0	N	11348	Parvalbumin OS=Seriola dumerili OX=41447 PE=3 SV=1
15	73845	tr|A9ZTF1|A9ZTF1_KATPE	96.43	28	5	0	N	11442	Parvalbumin OS=Katsuwonus pelamis OX=8226 GN=Kat p 1 PE=2 SV=1
15	73846	tr|G8GWA1|G8GWA1_CARAU	96.43	28	5	0	N	11655	Parvalbumin OS=Carassius auratus OX=7957 PE=2 SV=2
15	73847	tr|A0A3B4TM81|A0A3B4TM81_SERDU	96.43	28	5	0	N	11521	Parvalbumin OS=Seriola dumerili OX=41447 PE=3 SV=1
15	73848	tr|A0A6P6KMF1|A0A6P6KMF1_CARAU	96.43	28	5	0	N	11567	Parvalbumin OS=Carassius auratus OX=7957 GN=LOC113052464 PE=3 SV=1
6	73779	tr|A0A6G0IXD3|A0A6G0IXD3_LARCR	90.98	5	12	1	N	217948	Myosin heavy chain, fast skeletal muscle OS=Larimichthys crocea OX=215358 GN=D5F01_LYC04733 PE=3 SV=1
6	73780	tr|A0A6G0IXM2|A0A6G0IXM2_LARCR	90.98	5	12	1	N	219009	Myosin heavy chain, fast skeletal muscle OS=Larimichthys crocea OX=215358 GN=D5F01_LYC04735 PE=3 SV=1

total 256 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
6	73781	tr|A0A6G0IXG4|A0A6G0IXG4_LARCR	90.98	5	12	1	N	220119	Myosin heavy chain, fast skeletal muscle OS=Larimichthys crocea OX=215358 GN=D5F01_LYC04732 PE=3 SV=1
7	73782	tr|G3NEV3|G3NEV3_GASAC	87.61	5	10	0	N	220538	Uncharacterized protein OS=Gasterosteus aculeatus OX=69293 PE=3 SV=1
7	73783	tr|A0A6P8W5C3|A0A6P8W5C3_GYMAC	87.61	5	10	0	N	221042	myosin heavy chain, fast skeletal muscle-like OS=Gymnodraco acuticeps OX=8218 GN=LOC117560824 PE=3 SV=1
7	73784	tr|A0A6P8VS48|A0A6P8VS48_GYMAC	87.61	5	10	0	N	221057	myosin heavy chain, fast skeletal muscle-like OS=Gymnodraco acuticeps OX=8218 GN=LOC117560783 PE=3 SV=1
24	67953	tr|A0A3Q3W464|A0A3Q3W464_MOLML	85.00	17	3	1	N	12300	Parvalbumin OS=Mola mola OX=94237 PE=3 SV=1
24	67954	tr|A0A3Q3WAG3|A0A3Q3WAG3_MOLML	85.00	15	3	1	N	13233	Parvalbumin OS=Mola mola OX=94237 PE=3 SV=1
24	67955	tr|A0A3Q4AW30|A0A3Q4AW30_MOLML	85.00	15	3	1	N	14276	Parvalbumin OS=Mola mola OX=94237 PE=3 SV=1
24	67956	tr|A0A3Q3W3Y6|A0A3Q3W3Y6_MOLML	85.00	14	3	1	N	14526	Parvalbumin OS=Mola mola OX=94237 PE=3 SV=1
8	66953	tr|A0A6P8GNA2|A0A6P8GNA2_CLUHA	83.39	4	9	1	N	221189	myosin heavy chain, fast skeletal muscle-like isoform X1 OS=Clupea harengus OX=7950 GN=LOC105899558 PE=3 SV=1
17	67795	tr|A0A3Q1HW42|A0A3Q1HW42_9TELE	73.03	12	5	1	N	21205	Adenylate kinase isoenzyme 1 OS=Acanthochromis polyacanthus OX=80966 GN=AK1 PE=3 SV=1
17	67796	tr|A0A3B5BIY5|A0A3B5BIY5_9TELE	73.03	12	5	1	N	21206	Adenylate kinase isoenzyme 1 OS=Stegastes partitus OX=144197 GN=AK1 PE=3 SV=1
25	67396	tr|A0A4U5UZN8|A0A4U5UZN8_COLLU	67.80	3	3	3	N	98899	Calsequestrin OS=Collichthys lucidus OX=240159 GN=D9C73_013496 PE=3 SV=1
25	67200	tr|A0A7N8YD85|A0A7N8YD85_9TELE	67.80	6	3	3	N	50163	Calsequestrin OS=Mastacembelus armatus OX=205130 PE=3 SV=1
25	67202	tr|A0A7N8Y4P6|A0A7N8Y4P6_9TELE	67.80	6	3	3	N	50544	Calsequestrin OS=Mastacembelus armatus OX=205130 PE=3 SV=1
25	67204	tr|A0A7N8XJX7|A0A7N8XJX7_9TELE	67.80	6	3	3	N	52431	Calsequestrin OS=Mastacembelus armatus OX=205130 PE=3 SV=1
25	67205	tr|A0A3Q3SHA7|A0A3Q3SHA7_9TELE	67.80	6	3	3	N	52425	Calsequestrin OS=Mastacembelus armatus OX=205130 PE=3 SV=2
25	67206	tr|A0A7N8XSZ9|A0A7N8XSZ9_9TELE	67.80	6	3	3	N	52256	Calsequestrin OS=Mastacembelus armatus OX=205130 PE=3 SV=1
25	67207	tr|A0A7N8XRW1|A0A7N8XRW1_9TELE	67.80	6	3	3	N	52191	Calsequestrin OS=Mastacembelus armatus OX=205130 PE=3 SV=1
25	67208	tr|A0A7N8Y2R6|A0A7N8Y2R6_9TELE	67.80	6	3	3	N	52373	Calsequestrin OS=Mastacembelus armatus OX=205130 PE=3 SV=1
25	67209	tr|A0A7N8Y336|A0A7N8Y336_9TELE	67.80	6	3	3	N	52793	Calsequestrin OS=Mastacembelus armatus OX=205130 PE=3 SV=1
22	67099	tr|A0A1A8GBU0|A0A1A8GBU0_9TELE	67.52	28	4	1	N	11460	Parvalbumin OS=Nothobranchius korthausae OX=1143690 GN=PVALB4 PE=3 SV=1
31	67449	tr|A0A3B3ZS88|A0A3B3ZS88_9GOBI	66.66	9	2	2	N	25528	Uncharacterized protein OS=Periophthalmus magnuspinnatus OX=409849 PE=3 SV=1
31	67450	tr|A0A3Q1CJW7|A0A3Q1CJW7_AMPOC	66.66	9	2	2	N	26282	Troponin T, fast skeletal muscle isoforms-like OS=Amphiprion ocellaris OX=80972 PE=3 SV=1
31	67451	tr|A0A3Q3EFK1|A0A3Q3EFK1_9LABR	66.66	9	2	2	N	26666	Troponin T, fast skeletal muscle isoforms-like OS=Labrus bergylta OX=56723 PE=3 SV=1
31	67452	tr|A0A3Q3AF19|A0A3Q3AF19_KRYMA	66.66	9	2	2	N	26771	Troponin T, fast skeletal muscle isoforms-like OS=Kryptolebias marmoratus OX=37003 PE=3 SV=1
31	67453	tr|A0A3Q3AF32|A0A3Q3AF32_KRYMA	66.66	9	2	2	N	26884	Troponin T, fast skeletal muscle isoforms-like OS=Kryptolebias marmoratus OX=37003 PE=3 SV=1

total 256 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
31	67454	tr|A0A3P8UNE3|A0A3P8UNE3_CYNSE	66.66	9	2	2	N	27351	Troponin T, fast skeletal muscle isoforms-like OS=Cynoglossus semilaevis OX=244447 PE=3 SV=1
31	67456	tr|A0A672Y3T4|A0A672Y3T4_9TELE	66.66	9	2	2	N	27423	Uncharacterized protein OS=Sphaeramia orbicularis OX=375764 GN=LOC115421585 PE=3 SV=1
31	67458	tr|A0A3P8UNF6|A0A3P8UNF6_CYNSE	66.66	8	2	2	N	28353	Troponin T, fast skeletal muscle isoforms-like OS=Cynoglossus semilaevis OX=244447 PE=3 SV=1
31	67459	tr|A0A3B4UYC0|A0A3B4UYC0_SERDU	66.66	8	2	2	N	29388	Troponin T type 3a (skeletal, fast) OS=Seriola dumerili OX=41447 PE=3 SV=1
31	67460	tr|A0A3P8URR7|A0A3P8URR7_CYNSE	66.66	8	2	2	N	29425	Troponin T, fast skeletal muscle isoforms-like OS=Cynoglossus semilaevis OX=244447 PE=3 SV=1
31	67461	tr|A0A3P8URM3|A0A3P8URM3_CYNSE	66.66	8	2	2	N	30206	Troponin T, fast skeletal muscle isoforms-like OS=Cynoglossus semilaevis OX=244447 PE=3 SV=1
31	67462	tr|A0A3Q3XL97|A0A3Q3XL97_MOLML	66.66	8	2	2	N	30493	Troponin T type 3a (skeletal, fast) OS=Mola mola OX=94237 PE=3 SV=1
31	67463	tr|A0A3P8ULW6|A0A3P8ULW6_CYNSE	66.66	7	2	2	N	31797	Troponin T, fast skeletal muscle isoforms-like OS=Cynoglossus semilaevis OX=244447 PE=3 SV=1
31	67464	tr|A0A5C6P7G2|A0A5C6P7G2_9TELE	66.66	7	2	2	N	32128	Troponin T, fast skeletal muscle isoforms OS=Takifugu flavidus OX=433684 GN=D4764_13G0000270 PE=3 SV=1
31	67465	tr|A0A3Q1CRB3|A0A3Q1CRB3_AMPOC	66.66	7	2	2	N	32379	Troponin T, fast skeletal muscle isoforms-like OS=Amphiprion ocellaris OX=80972 PE=3 SV=1
31	67466	tr|A0A665T7Y2|A0A665T7Y2_ECHNA	66.66	7	2	2	N	33067	Troponin T type 3a (skeletal, fast) OS=Echeneis naucrates OX=173247 PE=3 SV=1
31	67467	tr|A0A3Q1BEW8|A0A3Q1BEW8_AMPOC	66.66	7	2	2	N	33080	Troponin T, fast skeletal muscle isoforms-like OS=Amphiprion ocellaris OX=80972 PE=3 SV=1
31	67468	tr|A0A3P8THB6|A0A3P8THB6_AMPPE	66.66	7	2	2	N	33365	Troponin T type 3a (skeletal, fast) OS=Amphiprion percula OX=161767 PE=3 SV=1
31	67470	tr|A0A672YCL7|A0A672YCL7_9TELE	66.66	7	2	2	N	33478	Uncharacterized protein OS=Sphaeramia orbicularis OX=375764 GN=LOC115421585 PE=3 SV=1
31	67471	tr|A0A672YCL2|A0A672YCL2_9TELE	66.66	7	2	2	N	34165	Uncharacterized protein OS=Sphaeramia orbicularis OX=375764 GN=LOC115421585 PE=3 SV=1
31	67472	tr|A0A6P7KCL6|A0A6P7KCL6_9TELE	66.66	7	2	2	N	34619	troponin T, fast skeletal muscle isoforms-like isoform X3 OS=Parambassis ranga OX=210632 GN=LOC114452235 PE=3 SV=1
31	67473	tr|A0A6P7KCQ1|A0A6P7KCQ1_9TELE	66.66	7	2	2	N	35105	troponin T, fast skeletal muscle isoforms-like isoform X2 OS=Parambassis ranga OX=210632 GN=LOC114452235 PE=3 SV=1
16	67269	tr|A0A6P7KDL5|A0A6P7KDL5_9TELE	65.64	15	5	5	N	32714	tropomyosin alpha-1 chain isoform X1 OS=Parambassis ranga OX=210632 GN=LOC114452528 PE=3 SV=1
16	67270	tr|A0A6P7MR93|A0A6P7MR93_BETSP	65.64	15	5	5	N	32714	tropomyosin alpha-1 chain isoform X1 OS=Betta splendens OX=158456 GN=tpm1 PE=3 SV=1
16	67282	tr|X2J4M2|X2J4M2_PAROL	65.64	15	5	5	N	32670	Tropomyosin alpha-1 OS=Paralichthys olivaceus OX=8255 PE=2 SV=1
16	67271	tr|A0A3P9D7I0|A0A3P9D7I0_9CICH	65.64	15	5	5	N	32822	Tropomyosin 1 OS=Maylandia zebra OX=106582 GN=TPM1 PE=3 SV=1
16	67272	tr|A0A665VR95|A0A665VR95_ECHNA	65.64	15	5	5	N	32714	Tropomyosin 1 OS=Echeneis naucrates OX=173247 GN=tpm1 PE=3 SV=1

total 256 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
20	73841	tr|A0A3P9LRU7|A0A3P9LRU7_ORYLA	65.15	8	4	2	N	42871	Creatine kinase OS=Oryzias latipes OX=8090 PE=3 SV=1
20	67264	tr|A0A2I4BW49|A0A2I4BW49_9TELE	65.15	8	4	2	N	43000	Creatine kinase OS=Austrofundulus limnaeus OX=52670 GN=LOC106523169 PE=3 SV=1
20	73842	tr|A0A3B3I369|A0A3B3I369_ORYLA	65.15	8	4	2	N	42871	Creatine kinase OS=Oryzias latipes OX=8090 GN=LOC101166239 PE=3 SV=1
20	73843	tr|A0A3P9HLZ1|A0A3P9HLZ1_ORYLA	65.15	8	4	2	N	42898	Creatine kinase OS=Oryzias latipes OX=8090 PE=3 SV=1
20	67263	tr|A0A3P8WTN2|A0A3P8WTN2_CYNSE	65.15	8	4	2	N	42864	Creatine kinase OS=Cynoglossus semilaevis OX=244447 PE=3 SV=1
19	67126	tr|A0A3P8Q9R4|A0A3P8Q9R4_ASTCA	61.93	8	4	2	N	42650	Creatine kinase OS=Astatotilapia calliptera OX=8154 GN=CKM PE=3 SV=1
19	67691	tr|A0A6P7JDS0|A0A6P7JDS0_9TELE	61.93	6	4	2	N	51567	Creatine kinase OS=Parambassis ranga OX=210632 GN=LOC114444487 PE=3 SV=1
19	67717	tr|A0A3Q2Q7Q3|A0A3Q2Q7Q3_FUNHE	61.93	9	4	2	N	38158	Creatine kinase OS=Fundulus heteroclitus OX=8078 GN=CKM PE=3 SV=1
19	67705	tr|A0A3B4BZV1|A0A3B4BZV1_PYGNA	61.93	8	4	2	N	42761	Creatine kinase OS=Pygocentrus nattereri OX=42514 PE=3 SV=1
19	67706	tr|A0A6P7PB38|A0A6P7PB38_BETSP	61.93	8	4	2	N	42709	Creatine kinase OS=Betta splendens OX=158456 GN=LOC114867752 PE=3 SV=1
19	67693	tr|A0A3P8NKE2|A0A3P8NKE2_ASTCA	61.93	8	4	2	N	43092	Creatine kinase OS=Astatotilapia calliptera OX=8154 PE=3 SV=1
19	67134	tr|A0A6P7JIX2|A0A6P7JIX2_9TELE	61.93	8	4	2	N	43056	Creatine kinase OS=Parambassis ranga OX=210632 GN=LOC114445771 PE=3 SV=1
19	67716	tr|A0A6P7PLI8|A0A6P7PLI8_BETSP	61.93	8	4	2	N	42883	Creatine kinase OS=Betta splendens OX=158456 GN=LOC114869114 PE=3 SV=1
19	67711	tr|A0A674PS54|A0A674PS54_TAKRU	61.93	8	4	2	N	40422	Creatine kinase OS=Takifugu rubripes OX=31033 GN=LOC101077669 PE=3 SV=1
19	67401	tr|A0A437CN94|A0A437CN94_ORYJA	61.93	8	4	2	N	42979	Creatine kinase OS=Oryzias javanicus OX=123683 GN=OJAV_G00145090 PE=3 SV=1
19	67715	tr|A0A6J2R235|A0A6J2R235_COTGO	61.93	8	4	2	N	42867	Creatine kinase OS=Cottoperca gobio OX=56716 GN=LOC115019392 PE=3 SV=1
11	67157	tr|A0A4U5VU95|A0A4U5VU95_COLLU	60.50	30	6	6	N	16791	Myosin regulatory light chain 2, skeletal muscle isoform DTNB OS=Collichthys lucidus OX=240159 GN=D9C73_025504 PE=4 SV=1
11	67158	tr|A0A6P7II88|A0A6P7II88_9TELE	60.50	26	6	6	N	18948	myosin regulatory light chain 2, skeletal muscle isoform OS=Parambassis ranga OX=210632 GN=mylpf PE=4 SV=1
11	67285	tr|A0A672MA11|A0A672MA11_SINGR	60.50	31	6	6	N	16048	Myosin regulatory light chain 2, skeletal muscle isoform type 2 OS=Sinocyclocheilus grahami OX=75366 GN=LOC107571443 PE=4 SV=1
11	67287	tr|A0A669DZW9|A0A669DZW9_ORENI	60.50	28	6	6	N	18203	Myosin light chain, phosphorylatable, fast skeletal muscle a OS=Oreochromis niloticus OX=8128 PE=4 SV=1
11	67288	tr|A0A3B4BW75|A0A3B4BW75_PYGNA	60.50	28	6	6	N	18272	Myosin regulatory light chain 2, skeletal muscle isoform type 2 OS=Pygocentrus nattereri OX=42514 PE=4 SV=1
11	67289	tr|I3JU24|I3JU24_ORENI	60.50	28	6	6	N	18257	Myosin light chain, phosphorylatable, fast skeletal muscle a OS=Oreochromis niloticus OX=8128 PE=4 SV=2
11	67295	tr|A0A7J6CHK6|A0A7J6CHK6_9TELE	60.50	26	6	6	N	19163	EF-hand domain-containing protein OS=Onychostoma macrolepis OX=369639 GN=G5714_012740 PE=4 SV=1

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Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
11	67298	tr|A0A0F8CBC9|A0A0F8CBC9_LARCR	60.50	26	6	6	N	19051	Myosin regulatory light chain 2, skeletal muscle isoform type 2 OS=Larimichthys crocea OX=215358 GN=D5F01_LYC18898 PE=4 SV=1
11	67305	tr|A0A7N8XBQ9|A0A7N8XBQ9_9TELE	60.50	23	6	6	N	21687	Myosin light chain, phosphorylatable, fast skeletal muscle a OS=Mastacembelus armatus OX=205130 PE=4 SV=1
11	67300	tr|F8U029|F8U029_EPIBR	60.50	26	6	6	N	18965	Myosin light chain 2 (Fragment) OS=Epinephelus bruneus OX=323802 PE=2 SV=1
11	67308	tr|A0A3B5RBY4|A0A3B5RBY4_XIPMA	60.50	18	6	6	N	27929	Uncharacterized protein OS=Xiphophorus maculatus OX=8083 PE=4 SV=1
28	67490	tr|G3N515|G3N515_GASAC	57.97	1	3	1	N	451257	Uncharacterized protein OS=Gasterosteus aculeatus OX=69293 PE=4 SV=1
27	67497	tr|Q4T444|Q4T444_TETNG	57.72	0	3	1	N	1041680	Chromosome undetermined SCAF9829, whole genome shotgun sequence (Fragment) OS=Tetraodon nigroviridis OX=99883 GN=GSTENG00007498001 PE=4 SV=1
21	67518	tr|D2KQG3|D2KQG3_SINCH	56.80	12	2	2	N	11617	Parvalbumin OS=Siniperca chuatsi OX=119488 PE=2 SV=1
21	67519	tr|B9VJM3|B9VJM3_SINCH	56.80	12	2	2	N	11589	Parvalbumin OS=Siniperca chuatsi OX=119488 PE=2 SV=1
18	67896	tr|A0A3P8TDG8|A0A3P8TDG8_AMPPE	54.14	13	5	1	N	21234	Adenylate kinase isoenzyme 1 OS=Amphiprion percula OX=161767 GN=AK1 PE=3 SV=1
26	67111	tr|A0A556TIT9|A0A556TIT9_BAGYA	52.70	13	3	0	N	21698	Parvalbumin OS=Bagarius yarrelli OX=175774 GN=Baya_0626 PE=3 SV=1
35	67341	tr|A0A484CUS5|A0A484CUS5_PERFV	51.89	0	2	1	N	867139	Uncharacterized protein OS=Perca flavescens OX=8167 GN=EPR50_G00113850 PE=4 SV=1
23	69598	tr|A0A2I4CWS8|A0A2I4CWS8_9TELE	46.95	2	3	3	N	108703	Calcium-transporting ATPase OS=Austrofundulus limnaeus OX=52670 GN=LOC106532815 PE=3 SV=1
23	67219	tr|A0A3P9C9M1|A0A3P9C9M1_9CICH	46.95	2	3	3	N	109087	Calcium-transporting ATPase OS=Maylandia zebra OX=106582 PE=3 SV=1
42	68221	tr|A0A7J6CZM2|A0A7J6CZM2_9TELE	43.01	2	1	1	N	53517	2-phospho-D-glycerate hydro-lyase OS=Onychostoma macrolepis OX=369639 GN=G5714_007188 PE=3 SV=1
32	69517	tr|A0A0F8AZU0|A0A0F8AZU0_LARCR	39.53	1	2	0	N	246883	Vacuolar fusion protein CCZ1 OS=Larimichthys crocea OX=215358 GN=EH28_05173 PE=3 SV=1
36	73896	tr|A0A4W4GVK8|A0A4W4GVK8_ELEEL	37.84	7	1	1	N	16665	EF-hand domain-containing protein OS=Electrophorus electricus OX=8005 GN=LOC113579190 PE=4 SV=1
36	73897	tr|A0A4W4GPW6|A0A4W4GPW6_ELEEL	37.84	7	1	1	N	16847	Uncharacterized protein OS=Electrophorus electricus OX=8005 GN=LOC113579190 PE=4 SV=1
36	73898	tr|A0A4W4GW96|A0A4W4GW96_ELEEL	37.84	7	1	1	N	16889	EF-hand domain-containing protein OS=Electrophorus electricus OX=8005 GN=LOC113579190 PE=4 SV=1
36	73926	tr|A0A665WHZ7|A0A665WHZ7_ECHNA	37.84	8	1	1	N	16102	Myosin light chain 3, skeletal muscle isoform OS=Echeneis naucrates OX=173247 GN=LOC115051647 PE=4 SV=1
36	73927	tr|A0A3B4FQL1|A0A3B4FQL1_9CICH	37.84	7	1	1	N	16666	Myosin light chain 1 OS=Pundamilia nyererei OX=303518 PE=4 SV=1
36	73928	tr|A0A3P8PB88|A0A3P8PB88_ASTCA	37.84	7	1	1	N	16666	Myosin light chain 1 OS=Astatotilapia calliptera OX=8154 PE=4 SV=1

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Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
36	73929	tr|A0A665WHJ1|A0A665WHJ1_ECHNA	37.84	7	1	1	N	16702	Myosin light chain 3, skeletal muscle isoform OS=Echeneis naucrates OX=173247 GN=LOC115051647 PE=4 SV=1
36	73930	tr|F2WR27|F2WR27_EPICO	37.84	7	1	1	N	16657	Myosin light chain 3 OS=Epinephelus coioides OX=94232 PE=2 SV=1
36	73931	tr|A0A4W6FFD1|A0A4W6FFD1_LATCA	37.84	7	1	1	N	16686	Myosin light chain 3, skeletal muscle isoform OS=Lates calcarifer OX=8187 GN=LOC108873036 PE=4 SV=1
36	73932	tr|A0A3B3C1H6|A0A3B3C1H6_ORYME	37.84	7	1	1	N	16638	Myosin light chain 3, skeletal muscle isoform OS=Oryzias melastigma OX=30732 PE=4 SV=1
36	73933	tr|A0A3Q1B309|A0A3Q1B309_AMPOC	37.84	7	1	1	N	16588	Myosin light chain 3, skeletal muscle isoform OS=Amphiprion ocellaris OX=80972 PE=4 SV=1
36	73934	tr|A0A3B4VIP0|A0A3B4VIP0_SERDU	37.84	7	1	1	N	17424	Myosin light chain 3, skeletal muscle isoform OS=Seriola dumerili OX=41447 PE=4 SV=1
36	73935	tr|A0A3B5RBB9|A0A3B5RBB9_XIPMA	37.84	7	1	1	N	17895	Uncharacterized protein OS=Xiphophorus maculatus OX=8083 PE=4 SV=1
36	73936	tr|A0A3B5R1L0|A0A3B5R1L0_XIPMA	37.84	7	1	1	N	17816	EF-hand domain-containing protein OS=Xiphophorus maculatus OX=8083 PE=4 SV=1
36	73937	tr|A0A3P9CCX0|A0A3P9CCX0_9CICH	37.84	7	1	1	N	17897	Myosin light chain 1 OS=Maylandia zebra OX=106582 PE=4 SV=1
36	73938	tr|A0A665WHZ4|A0A665WHZ4_ECHNA	37.84	7	1	1	N	18047	Myosin light chain 3, skeletal muscle isoform OS=Echeneis naucrates OX=173247 GN=LOC115051647 PE=4 SV=1
36	73939	tr|A0A4W6FCG2|A0A4W6FCG2_LATCA	37.84	7	1	1	N	18787	Myosin light chain 3, skeletal muscle isoform OS=Lates calcarifer OX=8187 GN=LOC108873036 PE=4 SV=1
36	73940	tr|A0A4W6FFD6|A0A4W6FFD6_LATCA	37.84	6	1	1	N	18836	Myosin light chain 3, skeletal muscle isoform OS=Lates calcarifer OX=8187 GN=LOC108873036 PE=4 SV=1
36	73941	tr|A0A665WI19|A0A665WI19_ECHNA	37.84	6	1	1	N	18811	Myosin light chain 3, skeletal muscle isoform OS=Echeneis naucrates OX=173247 GN=LOC115051647 PE=4 SV=1
36	73942	tr|B9V2Y1|B9V2Y1_EPICO	37.84	6	1	1	N	19048	Myosin light chain 3 (Fragment) OS=Epinephelus coioides OX=94232 PE=2 SV=1
36	73943	tr|A0A4W6FDH6|A0A4W6FDH6_LATCA	37.84	6	1	1	N	20136	Myosin light chain 3, skeletal muscle isoform OS=Lates calcarifer OX=8187 GN=LOC108873036 PE=4 SV=1
36	73944	tr|A0A669EYH8|A0A669EYH8_ORENI	37.84	5	1	1	N	23743	Uncharacterized protein OS=Oreochromis niloticus OX=8128 GN=LOC100698429 PE=4 SV=1
36	73945	tr|A0A3B4VK07|A0A3B4VK07_SERDU	37.84	5	1	1	N	24449	Myosin light chain 3, skeletal muscle isoform OS=Seriola dumerili OX=41447 PE=4 SV=1
36	73946	tr|A0A3B4VK38|A0A3B4VK38_SERDU	37.84	5	1	1	N	25360	Myosin light chain 3, skeletal muscle isoform OS=Seriola dumerili OX=41447 PE=4 SV=1
36	73947	tr|A0A834C4M6|A0A834C4M6_ORYME	37.84	5	1	1	N	26998	Myosin light chain 3, skeletal muscle isoform OS=Oryzias melastigma OX=30732 GN=FQA47_014212 PE=4 SV=1
36	73948	tr|A0A315W7Q8|A0A315W7Q8_GAMAF	37.84	5	1	1	N	26671	Uncharacterized protein OS=Gambusia affinis OX=33528 GN=CCH79_00013367 PE=4 SV=1
36	73958	tr|A0A672K127|A0A672K127_SINGR	37.84	9	1	1	N	12988	Myosin light chain 3, skeletal muscle isoform-like OS=Sinocyclocheilus grahami OX=75366 GN=LOC107579269 PE=4 SV=1
36	73959	tr|A0A7J6DIX6|A0A7J6DIX6_9TELE	37.84	7	1	1	N	16756	Uncharacterized protein OS=Onychostoma macrolepis OX=369639 GN=G5714_001122 PE=4 SV=1

total 256 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
36	73960	tr|A0A4W5MNE5|A0A4W5MNE5_9TELE	37.84	7	1	1	N	17699	Myosin, light chain 1, alkali; skeletal, fast OS=Hucho hucho OX=62062 PE=4 SV=1
36	73961	tr|A0A4W5MRK6|A0A4W5MRK6_9TELE	37.84	7	1	1	N	18798	Myosin, light chain 1, alkali; skeletal, fast OS=Hucho hucho OX=62062 PE=4 SV=1
36	73962	tr|A0A4W5MMD2|A0A4W5MMD2_9TELE	37.84	6	1	1	N	20159	Myosin, light chain 1, alkali; skeletal, fast OS=Hucho hucho OX=62062 PE=4 SV=1
36	73963	tr|A0A3Q3JIG8|A0A3Q3JIG8_MONAL	37.84	6	1	1	N	20937	Myosin light chain 1, skeletal muscle isoform-like OS=Monopterus albus OX=43700 PE=4 SV=1
36	73964	tr|Q90332|Q90332_CYPCA	37.84	6	1	1	N	21134	Fast skeletal myosin light chain 1b OS=Cyprinus carpio OX=7962 PE=2 SV=1
36	73965	tr|Q90WC7|Q90WC7_ONCMY	37.84	6	1	1	N	21057	Myosin light chain 1 OS=Oncorhynchus mykiss OX=8022 PE=2 SV=1
36	72069	tr|A0A7J6CQG1|A0A7J6CQG1_9TELE	37.84	6	1	1	N	21007	Uncharacterized protein OS=Onychostoma macrolepis OX=369639 GN=G5714_009908 PE=4 SV=1
36	72070	tr|Q90W52|Q90W52_PSEDN	37.84	6	1	1	N	20741	Myosin light chain 1 OS=Pseudocaranx dentex OX=349646 GN=mlc1 PE=2 SV=1
36	73966	tr|Q90W46|Q90W46_DECMR	37.84	6	1	1	N	21098	Myosin light chain 1 OS=Decapterus macrosoma OX=166264 GN=mlc1 PE=2 SV=1
36	73967	tr|A0A4W5MQC0|A0A4W5MQC0_9TELE	37.84	5	1	1	N	22406	Myosin, light chain 1, alkali; skeletal, fast OS=Hucho hucho OX=62062 PE=4 SV=1
36	73970	tr|A0A0P7TY12|A0A0P7TY12_SCLFO	37.84	7	1	1	N	19172	Myosin light chain 3 skeletal muscle-like (Fragment) OS=Scleropages formosus OX=113540 GN=Z043_115197 PE=4 SV=1
36	73979	tr|A0A672GTD6|A0A672GTD6_SALFA	37.84	7	1	1	N	16528	Myosin, light polypeptide 3, skeletal muscle OS=Salarias fasciatus OX=181472 PE=4 SV=1
36	73980	tr|A0A3P8V7S6|A0A3P8V7S6_CYNSE	37.84	7	1	1	N	16686	Myosin light chain 3, skeletal muscle isoform OS=Cynoglossus semilaevis OX=244447 PE=4 SV=1
36	73981	tr|A0A671WWZ3|A0A671WWZ3_SPAAU	37.84	7	1	1	N	16973	Myosin light chain 3, skeletal muscle isoform OS=Sparus aurata OX=8175 GN=LOC115577181 PE=4 SV=1
36	73982	tr|A0A672GWW2|A0A672GWW2_SALFA	37.84	7	1	1	N	17237	Myosin, light polypeptide 3, skeletal muscle OS=Salarias fasciatus OX=181472 PE=4 SV=1
36	73983	tr|A0A671X3G3|A0A671X3G3_SPAAU	37.84	7	1	1	N	17479	Myosin light chain 3, skeletal muscle isoform OS=Sparus aurata OX=8175 GN=LOC115577181 PE=4 SV=1
36	73984	tr|A0A672H327|A0A672H327_SALFA	37.84	7	1	1	N	17490	Myosin, light polypeptide 3, skeletal muscle OS=Salarias fasciatus OX=181472 PE=4 SV=1
36	73985	tr|A0A7N8Y8C7|A0A7N8Y8C7_9TELE	37.84	7	1	1	N	17841	Myosin, light polypeptide 3, skeletal muscle OS=Mastacembelus armatus OX=205130 PE=4 SV=1
36	73986	tr|A0A672GRY1|A0A672GRY1_SALFA	37.84	7	1	1	N	17938	Myosin, light polypeptide 3, skeletal muscle OS=Salarias fasciatus OX=181472 PE=4 SV=1
36	73987	tr|A0A3Q2XPR8|A0A3Q2XPR8_HIPCM	37.84	6	1	1	N	19433	Myosin light chain 1, skeletal muscle isoform OS=Hippocampus comes OX=109280 PE=4 SV=1
36	73988	tr|A0A6J2QQE0|A0A6J2QQE0_COTGO	37.84	6	1	1	N	20126	LOW QUALITY PROTEIN: myosin light chain 3, skeletal muscle isoform-like OS=Cottoperca gobio OX=56716 GN=LOC115016756 PE=4 SV=1
36	73989	tr|A0A3Q3D9S9|A0A3Q3D9S9_HIPCM	37.84	5	1	1	N	22021	Myosin light chain 1, skeletal muscle isoform OS=Hippocampus comes OX=109280 PE=4 SV=1
29	67640	tr|A0A4Z2CI05|A0A4Z2CI05_9TELE	35.86	0	2	0	N	507153	Uncharacterized protein OS=Takifugu bimaculatus OX=433685 GN=fugu_000743 PE=4 SV=1

total 256 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
30	67005	tr|Q4RE90|Q4RE90_TETNG	35.57	0	2	1	N	863297	Chromosome undetermined SCAF15134, whole genome shotgun sequence (Fragment) OS=Tetraodon nigroviridis OX=99883 GN=GSTENG00035871001 PE=4 SV=1
33	67404	tr|A0A6F9CEX9|A0A6F9CEX9_9TELE	35.33	0	2	1	N	1022296	Uncharacterized protein OS=Coregonus sp. 'balchen' OX=861768 GN=CSTEINMANNI_LOCUS3957823 PE=4 SV=1
33	67667	tr|A0A060W3X5|A0A060W3X5_ONCMY	35.33	1	2	1	N	453353	Uncharacterized protein OS=Oncorhynchus mykiss OX=8022 GN=GSONMT00066266001 PE=4 SV=1
34	67431	tr|A0A6P3W3B1|A0A6P3W3B1_CLUHA	31.61	3	2	2	N	47370	2-phospho-D-glycerate hydro-lyase OS=Clupea harengus OX=7950 GN=LOC105904565 PE=3 SV=1
34	67043	tr|F5BZS7|F5BZS7_EPIBR	31.61	3	2	2	N	43226	2-phospho-D-glycerate hydro-lyase (Fragment) OS=Epinephelus bruneus OX=323802 PE=2 SV=1
34	71851	tr|A0A668V8T6|A0A668V8T6_OREAU	31.61	3	2	2	N	47001	2-phospho-D-glycerate hydro-lyase OS=Oreochromis aureus OX=47969 PE=3 SV=1
34	67430	tr|A0A4W4FGS3|A0A4W4FGS3_ELEEL	31.61	3	2	2	N	47188	2-phospho-D-glycerate hydro-lyase OS=Electrophorus electricus OX=8005 GN=LOC113568057 PE=3 SV=1
34	67034	tr|A0A3B4CPC9|A0A3B4CPC9_PYGNA	31.61	3	2	2	N	47482	2-phospho-D-glycerate hydro-lyase OS=Pygocentrus nattereri OX=42514 PE=3 SV=1
34	67421	tr|A0A3P8TVY9|A0A3P8TVY9_AMPPE	31.61	3	2	2	N	47574	2-phospho-D-glycerate hydro-lyase OS=Amphiprion percula OX=161767 PE=3 SV=1
34	67419	tr|A0A3P8NTT0|A0A3P8NTT0_ASTCA	31.61	2	2	2	N	48687	2-phospho-D-glycerate hydro-lyase OS=Astatotilapia calliptera OX=8154 PE=3 SV=1
43	67539	tr|A0A7J6BP23|A0A7J6BP23_9TELE	29.88	12	1	1	N	13461	Uncharacterized protein OS=Onychostoma macrolepis OX=369639 GN=G5714_022729 PE=4 SV=1
43	67166	tr|A0A4Z2FMJ8|A0A4Z2FMJ8_9TELE	29.88	11	1	1	N	14750	Troponin C, skeletal muscle OS=Liparis tanakae OX=230148 GN=TNNC2 PE=4 SV=1
43	67020	tr|A0A1A8D9W7|A0A1A8D9W7_9TELE	29.88	10	1	1	N	15353	Troponin C type 2 (Fast) OS=Nothobranchius kadleci OX=1051664 GN=TNNC2 PE=4 SV=1
43	67540	tr|A0A6P3VH61|A0A6P3VH61_CLUHA	29.88	10	1	1	N	16370	troponin C, skeletal muscle OS=Clupea harengus OX=7950 GN=LOC105890625 PE=4 SV=1
43	67167	tr|A0A3B4CI86|A0A3B4CI86_PYGNA	29.88	10	1	1	N	16455	Troponin C type 2 (fast) OS=Pygocentrus nattereri OX=42514 PE=4 SV=1
43	67168	tr|A0A3B4E1V9|A0A3B4E1V9_PYGNA	29.88	9	1	1	N	17769	Troponin C type 2 (fast) OS=Pygocentrus nattereri OX=42514 PE=4 SV=1
43	67170	tr|A0A6J2Q142|A0A6J2Q142_COTGO	29.88	9	1	1	N	18257	troponin C, skeletal muscle OS=Cottoperca gobio OX=56716 GN=LOC115011252 PE=4 SV=1
43	67171	tr|A0A3B4E4D7|A0A3B4E4D7_PYGNA	29.88	9	1	1	N	18081	Troponin C, skeletal muscle OS=Pygocentrus nattereri OX=42514 PE=4 SV=1
43	67172	tr|H2SBN2|H2SBN2_TAKRU	29.88	9	1	1	N	18200	Uncharacterized protein OS=Takifugu rubripes OX=31033 GN=LOC101074449 PE=4 SV=2
43	67174	tr|A0A2R8QMW7|A0A2R8QMW7_DANRE	29.88	9	1	1	N	18043	Si:rp71-17i16.4 OS=Danio rerio OX=7955 GN=si:rp71-17i16.4 PE=4 SV=1
43	67175	tr|A0A4W4EUJ0|A0A4W4EUJ0_ELEEL	29.88	9	1	1	N	18156	Uncharacterized protein OS=Electrophorus electricus OX=8005 GN=LOC113569977 PE=4 SV=1

total 256 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
43	67176	tr|A0A3Q3G540|A0A3Q3G540_9LABR	29.88	9	1	1	N	18223	Troponin C, skeletal muscle-like OS=Labrus bergylta OX=56723 PE=4 SV=1
43	67030	tr|G3NJM6|G3NJM6_GASAC	29.88	9	1	1	N	18300	Troponin C type 2 (fast) OS=Gasterosteus aculeatus OX=69293 PE=4 SV=1
43	66968	tr|W5UMX1|W5UMX1_ICTPU	29.88	9	1	1	N	18231	Troponin C, skeletal muscle OS=Ictalurus punctatus OX=7998 GN=TNNC2 PE=2 SV=1
43	67178	tr|A0A3P8P1R5|A0A3P8P1R5_ASTCA	29.88	9	1	1	N	18230	Troponin C, skeletal muscle OS=Astatotilapia calliptera OX=8154 PE=4 SV=1
43	67179	tr|A0A4W4EW29|A0A4W4EW29_ELEEL	29.88	9	1	1	N	18171	Uncharacterized protein OS=Electrophorus electricus OX=8005 GN=LOC113569977 PE=4 SV=1
43	67180	tr|A0A6P7IM54|A0A6P7IM54_9TELE	29.88	9	1	1	N	18225	troponin C, skeletal muscle OS=Parambassis ranga OX=210632 GN=LOC114439031 PE=4 SV=1
43	67181	tr|A0A4W4EVB1|A0A4W4EVB1_ELEEL	29.88	9	1	1	N	18179	Uncharacterized protein OS=Electrophorus electricus OX=8005 GN=LOC113569977 PE=4 SV=1
43	67182	tr|I3IZI3|I3IZI3_ORENI	29.88	9	1	1	N	18271	Uncharacterized protein OS=Oreochromis niloticus OX=8128 GN=LOC100703845 PE=4 SV=2
43	67183	tr|A0A3Q1CAA4|A0A3Q1CAA4_AMPOC	29.88	9	1	1	N	18190	Troponin C, skeletal muscle OS=Amphiprion ocellaris OX=80972 PE=4 SV=1
43	67184	tr|A0A3Q3G8Q9|A0A3Q3G8Q9_9LABR	29.88	9	1	1	N	18220	Troponin C, skeletal muscle-like OS=Labrus bergylta OX=56723 PE=4 SV=1
43	67541	tr|A0A4W5NYP8|A0A4W5NYP8_9TELE	29.88	9	1	1	N	18187	Troponin C type 2 (fast) OS=Hucho hucho OX=62062 PE=4 SV=1
43	67185	tr|A0A672J300|A0A672J300_SALFA	29.88	9	1	1	N	18135	Troponin C type 2 (fast) OS=Salarias fasciatus OX=181472 PE=4 SV=1
43	67187	tr|A0A3Q2W3W0|A0A3Q2W3W0_HAPBU	29.88	9	1	1	N	18305	Troponin C, skeletal muscle OS=Haplochromis burtoni OX=8153 PE=4 SV=1
43	67542	tr|A0A3Q2WC94|A0A3Q2WC94_HAPBU	29.88	8	1	1	N	19498	Troponin C, skeletal muscle-like OS=Haplochromis burtoni OX=8153 PE=4 SV=1
43	67188	tr|A0A669E7L6|A0A669E7L6_ORENI	29.88	8	1	1	N	19478	Uncharacterized protein OS=Oreochromis niloticus OX=8128 GN=LOC100703845 PE=4 SV=1
43	67189	tr|A0A3B3TEJ6|A0A3B3TEJ6_9TELE	29.88	8	1	1	N	19607	Troponin C, skeletal muscle OS=Paramormyrops kingsleyae OX=1676925 PE=4 SV=1
43	67192	tr|A0A3P8P1N2|A0A3P8P1N2_ASTCA	29.88	8	1	1	N	20987	Troponin C, skeletal muscle OS=Astatotilapia calliptera OX=8154 PE=4 SV=1
43	67194	tr|A0A3P9N7Z1|A0A3P9N7Z1_POERE	29.88	6	1	1	N	24749	Troponin C, skeletal muscle OS=Poecilia reticulata OX=8081 PE=4 SV=1
43	67195	tr|A0A6F9C7M8|A0A6F9C7M8_9TELE	29.88	4	1	1	N	42179	Uncharacterized protein OS=Coregonus sp. 'balchen' OX=861768 GN=CSTEINMANNI_LOCUS3751028 PE=4 SV=1
44	74035	tr|A0A315VUM5|A0A315VUM5_GAMAF	24.10	1	1	1	N	199740	Uncharacterized protein OS=Gambusia affinis OX=33528 GN=CCH79_00015210 PE=4 SV=1
45	74042	tr|A0A3Q0S4A7|A0A3Q0S4A7_AMPCI	23.39	1	1	1	N	104043	Ankyrin repeat and FYVE domain containing 1 OS=Amphilophus citrinellus OX=61819 PE=4 SV=1
45	74043	tr|A0A3B4V2S1|A0A3B4V2S1_SERDU	23.39	1	1	1	N	104725	Ankyrin repeat and FYVE domain containing 1 OS=Seriola dumerili OX=41447 PE=4 SV=1
45	74044	tr|A0A4W4FZE0|A0A4W4FZE0_ELEEL	23.39	1	1	1	N	114557	FYVE-type domain-containing protein OS=Electrophorus electricus OX=8005 GN=ankfy1 PE=4 SV=1

total 256 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
45	74045	tr|A0A1A8RP46|A0A1A8RP46_9TELE	23.39	1	1	1	N	115767	Ankyrin repeat and FYVE domain containing 1 OS=Nothobranchius rachovii OX=451742 GN=ANKFY1 PE=4 SV=1
45	74046	tr|A0A6Q2ZPR8|A0A6Q2ZPR8_ESOLU	23.39	1	1	1	N	118078	Ankyrin repeat and FYVE domain containing 1 OS=Esox lucius OX=8010 PE=4 SV=1
45	74047	tr|A0A674AQG9|A0A674AQG9_SALTR	23.39	1	1	1	N	121601	Rabankyrin-5-like OS=Salmo trutta OX=8032 GN=LOC115153911 PE=4 SV=1
45	74048	tr|A0A3P8T5S7|A0A3P8T5S7_AMPPE	23.39	1	1	1	N	125156	Ankyrin repeat and FYVE domain containing 1 OS=Amphiprion percula OX=161767 PE=4 SV=1
45	74049	tr|A0A4W4FZ81|A0A4W4FZ81_ELEEL	23.39	1	1	1	N	126038	Uncharacterized protein OS=Electrophorus electricus OX=8005 GN=ankfy1 PE=4 SV=1
45	74050	tr|A0A4W5QGX5|A0A4W5QGX5_9TELE	23.39	1	1	1	N	125662	Ankyrin repeat and FYVE domain containing 1 OS=Hucho hucho OX=62062 PE=4 SV=1
45	74051	tr|A0A3B3DDJ3|A0A3B3DDJ3_ORYME	23.39	1	1	1	N	126170	Ankyrin repeat and FYVE domain containing 1 OS=Oryzias melastigma OX=30732 PE=4 SV=1
45	74052	tr|A0A4W4FW94|A0A4W4FW94_ELEEL	23.39	1	1	1	N	126337	Uncharacterized protein OS=Electrophorus electricus OX=8005 GN=ankfy1 PE=4 SV=1
45	74053	tr|A0A674AP52|A0A674AP52_SALTR	23.39	1	1	1	N	126358	Rabankyrin-5-like OS=Salmo trutta OX=8032 GN=LOC115153911 PE=4 SV=1
45	74054	tr|A0A834KWF7|A0A834KWF7_ORYME	23.39	1	1	1	N	127178	Rabankyrin-5 OS=Oryzias melastigma OX=30732 GN=FQA47_010782 PE=4 SV=1
45	74055	tr|A0A667ZHJ6|A0A667ZHJ6_9TELE	23.39	1	1	1	N	127368	Ankyrin repeat and FYVE domain containing 1 OS=Myripristis murdjan OX=586833 GN=ankfy1 PE=4 SV=1
45	74056	tr|A0A3B4DWJ2|A0A3B4DWJ2_PYGNA	23.39	1	1	1	N	127828	Ankyrin repeat and FYVE domain containing 1 OS=Pygocentrus nattereri OX=42514 PE=4 SV=1
45	74057	tr|A0A3Q2XWS4|A0A3Q2XWS4_HIPCM	23.39	1	1	1	N	127881	Ankyrin repeat and FYVE domain containing 1 OS=Hippocampus comes OX=109280 PE=4 SV=1
45	74058	tr|A0A667ZHH4|A0A667ZHH4_9TELE	23.39	1	1	1	N	127517	Ankyrin repeat and FYVE domain containing 1 OS=Myripristis murdjan OX=586833 GN=ankfy1 PE=4 SV=1
45	74059	tr|A0A3Q3G3V8|A0A3Q3G3V8_KRYMA	23.39	1	1	1	N	127886	Ankyrin repeat and FYVE domain containing 1 OS=Kryptolebias marmoratus OX=37003 PE=4 SV=1
45	74060	tr|A0A3P8R774|A0A3P8R774_ASTCA	23.39	1	1	1	N	128068	Ankyrin repeat and FYVE domain containing 1 OS=Astatotilapia calliptera OX=8154 PE=4 SV=1
45	74061	tr|A0A484CLN2|A0A484CLN2_PERFV	23.39	1	1	1	N	127679	Uncharacterized protein OS=Perca flavescens OX=8167 GN=EPR50_G00135050 PE=4 SV=1
45	74062	tr|A0A4W4FZM1|A0A4W4FZM1_ELEEL	23.39	1	1	1	N	128150	Uncharacterized protein OS=Electrophorus electricus OX=8005 GN=ankfy1 PE=4 SV=1
45	74063	tr|A0A4W5M1U7|A0A4W5M1U7_9TELE	23.39	1	1	1	N	127954	Ankyrin repeat and FYVE domain containing 1 OS=Hucho hucho OX=62062 PE=4 SV=1
45	74064	tr|A0A674ARJ6|A0A674ARJ6_SALTR	23.39	1	1	1	N	128040	Rabankyrin-5-like OS=Salmo trutta OX=8032 GN=LOC115153911 PE=4 SV=1
45	74065	tr|A0A4W4FZR2|A0A4W4FZR2_ELEEL	23.39	1	1	1	N	128360	Uncharacterized protein OS=Electrophorus electricus OX=8005 GN=ankfy1 PE=4 SV=1
45	74066	tr|A0A4W5M1X7|A0A4W5M1X7_9TELE	23.39	1	1	1	N	128147	Ankyrin repeat and FYVE domain containing 1 OS=Hucho hucho OX=62062 PE=4 SV=1
45	74067	tr|A0A3Q3Q182|A0A3Q3Q182_MONAL	23.39	1	1	1	N	128884	Ankyrin repeat and FYVE domain containing 1 OS=Monopterus albus OX=43700 PE=4 SV=1

total 256 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
45	74068	tr|A0A4W5QMX9|A0A4W5QMX9_9TELE	23.39	1	1	1	N	128910	Ankyrin repeat and FYVE domain containing 1 OS=Hucho hucho OX=62062 PE=4 SV=1
45	74069	tr|A0A673Z592|A0A673Z592_SALTR	23.39	1	1	1	N	129266	Rabankyrin-5-like OS=Salmo trutta OX=8032 GN=LOC115148449 PE=4 SV=1
45	74070	tr|A0A5N5JWC6|A0A5N5JWC6_PANHP	23.39	1	1	1	N	131933	Uncharacterized protein OS=Pangasianodon hypophthalmus OX=310915 GN=PHYPO_G00159810 PE=4 SV=1
45	74071	tr|A0A4W4FWH2|A0A4W4FWH2_ELEEL	23.39	1	1	1	N	132613	Uncharacterized protein OS=Electrophorus electricus OX=8005 GN=ankfy1 PE=4 SV=1
46	74072	tr|A0A2D0QGH0|A0A2D0QGH0_ICTPU	22.34	0	1	1	N	391648	lysosomal-trafficking regulator isoform X5 OS=Ictalurus punctatus OX=7998 GN=lyst PE=4 SV=1
46	74073	tr|A0A2D0QIP4|A0A2D0QIP4_ICTPU	22.34	0	1	1	N	425932	lysosomal-trafficking regulator isoform X3 OS=Ictalurus punctatus OX=7998 GN=lyst PE=4 SV=1
46	74074	tr|A0A2D0QFG9|A0A2D0QFG9_ICTPU	22.34	0	1	1	N	428327	lysosomal-trafficking regulator isoform X1 OS=Ictalurus punctatus OX=7998 GN=lyst PE=4 SV=1
47	74075	tr|A0EXC6|A0EXC6_DANRE	21.77	3	1	1	N	33478	Sulfotransferase OS=Danio rerio OX=7955 GN=sult2st3 PE=2 SV=1
47	74076	tr|A4FUP0|A4FUP0_DANRE	21.77	3	1	1	N	33460	Sulfotransferase OS=Danio rerio OX=7955 GN=sult2st3 PE=1 SV=1
37	68305	tr|A0A4V6ASI9|A0A4V6ASI9_COLLU	20.00	1	1	1	N	126874	Collagen alpha-2(I) chain OS=Collichthys lucidus OX=240159 GN=D9C73_023018 PE=4 SV=1
37	71897	tr|A0A5J6XX13|A0A5J6XX13_NIBCO	20.00	1	1	1	N	126736	Collagen type I alpha 2 chain OS=Nibea coibor OX=396775 GN=COL1A2 PE=2 SV=1

total 256 proteins

tr|A0A3S2MUF9|A0A3S2MUF9_ORYJA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.KSYELPDGQVITIGNE.R	Y	52.22	1761.8784	-0.6	881.9460	2	13.41	1921	1	240	255	
S.LEKSYELPDGQVITI.G	Y	50.90	1703.8981	0.2	852.9565	2	13.97	2015	1	238	252	
E.KSYELPDGQVITIG.N	Y	37.16	1518.7930	-0.3	760.4035	2	13.49	1935	2	240	253	
L.EKSYELPDGQVIT.I	Y	35.16	1477.7300	-4.0	739.8693	2	12.16	1702	1	239	251	
A.GFAGDDAPRA.V	Y	33.15	975.4410	2.2	488.7289	2	10.28	1386	1	22	31	
K.SYELPDGQVITIG.N	Y	31.23	1390.6980	0.0	696.3563	2	14.16	2047	1	241	253	
K.ANREKMTQ.I	Y	28.79	976.4760	0.2	489.2454	2	8.23	1140	1	116	123	
S.LEKSYELPDGQVITIG.N	Y	27.54	1760.9196	-0.4	881.4667	2	13.69	1969	1	238	253	
L.DAGDGVTH.N	Y	25.64	770.3195	-0.1	386.1670	2	8.68	1226	7	156	163	
G.IITNWDDMEK.I	Y	23.28	1263.5806	5.9	632.8013	2	12.12	1695	1	77	86	
E.KSYELPDGQ.V	Y	22.22	1035.4873	2.3	518.7521	2	10.74	1457	1	240	248	
S.LEKSYELPDGQ.V	Y	21.06	1277.6139	-0.6	639.8138	2	11.19	1533	1	238	248	
S.LEKSYELPDGQVI.T	Y	20.25	1489.7664	-0.7	745.8900	2	12.83	1820	1	238	250	
K.SYELPDGQVIT.I	Y	19.84	1220.5924	-1.2	611.3027	2	13.08	1863	1	241	251	
K.SYELPDGQVITI.G	Y	19.30	1333.6765	-1.6	667.8445	2	14.45	2096	1	241	252	
G.FAGDDAPRA.V	Y	18.98	918.4195	1.4	460.2177	2	15.22	2229	11	23	31	
E.KSYELPDGQV.I	Y	18.67	1134.5557	0.0	568.2851	2	11.34	1560	1	240	249	
S.LEKSYELPDGQVIT.I	Y	18.03	1590.8141	-0.8	796.4137	2	12.31	1729	1	238	251	
D.LAGRDLTDY.L	Y	17.35	1022.5032	-0.4	512.2587	2	11.31	1553	1	182	190	
T.MYPGIADRM.Q	Y	17.18	1052.4783	-0.5	527.2462	2	11.87	1654	1	307	315	
D.LAGRDLTDYLMK.I	Y	17.06	1394.7228	-1.0	698.3680	2	12.55	1772	1	182	193	
E.KSYELPDGQVITI.G	Y	15.81	1461.7715	-1.4	731.8920	2	13.59	1952	1	240	252	
E.KSYELPDGQVIT.I	Y	15.38	1348.6874	-0.7	675.3505	2	12.00	1676	1	240	251	

total 23 peptides

tr|A0A7J6C441|A0A7J6C441_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.KSYELPDGQVITIGNE.R	Y	52.22	1761.8784	-0.6	881.9460	2	13.41	1921	1	240	255	
S.LEKSYELPDGQVITI.G	Y	50.90	1703.8981	0.2	852.9565	2	13.97	2015	1	238	252	
E.KSYELPDGQVITIG.N	Y	37.16	1518.7930	-0.3	760.4035	2	13.49	1935	2	240	253	
L.EKSYELPDGQVIT.I	Y	35.16	1477.7300	-4.0	739.8693	2	12.16	1702	1	239	251	
A.GFAGDDAPRA.V	Y	33.15	975.4410	2.2	488.7289	2	10.28	1386	1	22	31	
K.SYELPDGQVITIG.N	Y	31.23	1390.6980	0.0	696.3563	2	14.16	2047	1	241	253	
K.ANREKMTQ.I	Y	28.79	976.4760	0.2	489.2454	2	8.23	1140	1	116	123	
S.LEKSYELPDGQVITIG.N	Y	27.54	1760.9196	-0.4	881.4667	2	13.69	1969	1	238	253	
L.DAGDGVTH.N	Y	25.64	770.3195	-0.1	386.1670	2	8.68	1226	7	156	163	
G.IITNWDDMEK.I	Y	23.28	1263.5806	5.9	632.8013	2	12.12	1695	1	77	86	
E.KSYELPDGQ.V	Y	22.22	1035.4873	2.3	518.7521	2	10.74	1457	1	240	248	
S.LEKSYELPDGQ.V	Y	21.06	1277.6139	-0.6	639.8138	2	11.19	1533	1	238	248	
S.LEKSYELPDGQVI.T	Y	20.25	1489.7664	-0.7	745.8900	2	12.83	1820	1	238	250	
K.SYELPDGQVIT.I	Y	19.84	1220.5924	-1.2	611.3027	2	13.08	1863	1	241	251	
K.SYELPDGQVITI.G	Y	19.30	1333.6765	-1.6	667.8445	2	14.45	2096	1	241	252	
G.FAGDDAPRA.V	Y	18.98	918.4195	1.4	460.2177	2	15.22	2229	11	23	31	
E.KSYELPDGQV.I	Y	18.67	1134.5557	0.0	568.2851	2	11.34	1560	1	240	249	
S.LEKSYELPDGQVIT.I	Y	18.03	1590.8141	-0.8	796.4137	2	12.31	1729	1	238	251	
D.LAGRDLTDY.L	Y	17.35	1022.5032	-0.4	512.2587	2	11.31	1553	1	182	190	
T.MYPGIADRM.Q	Y	17.18	1052.4783	-0.5	527.2462	2	11.87	1654	1	307	315	
D.LAGRDLTDYLMK.I	Y	17.06	1394.7228	-1.0	698.3680	2	12.55	1772	1	182	193	
E.KSYELPDGQVITI.G	Y	15.81	1461.7715	-1.4	731.8920	2	13.59	1952	1	240	252	
E.KSYELPDGQVIT.I	Y	15.38	1348.6874	-0.7	675.3505	2	12.00	1676	1	240	251	

total 23 peptides

tr|A0A5C6NQR5|A0A5C6NQR5_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDNSGFIEEEELK.L	N	67.46	1877.8894	-1.0	939.9510	2	12.28	1724	1	207	222	
E.IIDQDKSGFIEEEELK.L	N	49.57	1891.9414	-0.6	946.9774	2	11.72	1627	1	304	319	
E.IIDQDKSGFIE.E	N	44.01	1263.6346	-0.5	632.8243	2	11.60	1605	1	304	314	
S.GFIEEEELK.L	N	31.42	1092.5338	-0.1	547.2741	2	11.80	1641	1	214	222	
A.IIDQDNSGFIEEEELKLF.L	N	30.80	2138.0417	0.6	1070.0288	2	14.58	2119	1	207	224	
F.AIIDQDNSGFIE.E	N	26.76	1320.6198	-0.6	661.3168	2	12.86	1825	1	206	217	
Q.DKSGFIEEEELK.L	N	25.85	1422.6877	-0.4	712.3508	2	11.40	1570	1	308	319	
A.IIDQDNSGFIEEEE.L	N	16.99	1636.7103	0.3	819.3627	2	12.36	1738	1	207	220	

total 8 peptides

tr|A0A6P6N9Z4|A0A6P6N9Z4_CARAU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.LDKNKDPLNDSVVQL.Y	N	55.11	1696.8995	-0.3	849.4568	2	12.23	1715	1	596	610	
W.LDKNKDPLNDSVVQ.L	N	49.71	1583.8154	-0.7	792.9144	2	10.89	1481	5	596	609	
L.SKIEDEQSLGAQ.L	N	35.68	1303.6255	4.7	652.8231	2	10.20	1374	1	1095	1106	
K.LEQQVDDLEGSLE.Q	N	32.76	1473.6835	-0.5	737.8486	2	12.65	1789	1	1030	1042	
K.NDENVRQ.L	N	29.03	873.3940	-0.4	437.7041	2	8.49	1190	1	1266	1272	
Q.GEVDDTVQEAR.N	N	25.82	1217.5524	4.7	609.7863	2	10.04	1355	1	1742	1752	
K.KMEGDLNEM.E	N	25.67	1065.4470	-0.7	533.7304	2	11.02	1504	1	1620	1628	
K.FDKIEDM.A	N	23.34	896.3950	-0.6	449.2045	2	11.46	1581	2	84	90	
E.LKKEQDTSAH.L	N	22.49	1155.5884	-0.2	578.8013	2	7.77	1050	1	1772	1781	
Q.GEVDDTVQEA.R	N	20.03	1061.4513	-0.3	531.7328	2	10.64	1439	1	1742	1751	
Q.TALEEAEGTL.E	N	19.11	1032.4974	-0.7	517.2556	2	12.43	1750	1	1545	1554	
M.AEELKKE.Q	N	18.25	845.4494	-0.4	423.7318	2	8.54	1200	1	1769	1775	
M.NPPKFDKIEDM.A	N	17.32	1332.6383	-0.5	667.3261	2	11.50	1587	1	80	90	
K.SINDVEEF.I	N	15.40	951.4185	-0.3	476.7164	2	12.52	1766	1	324	331	

total 14 peptides

tr|A0A3B4CZR3|A0A3B4CZR3_PYGNA
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.LDKNKDPLNDSVVQL.Y	N	55.11	1696.8995	-0.3	849.4568	2	12.23	1715	1	558	572	
W.LDKNKDPLNDSVVQ.L	N	49.71	1583.8154	-0.7	792.9144	2	10.89	1481	5	558	571	
L.SKIEDEQSLGAQ.L	N	35.68	1303.6255	4.7	652.8231	2	10.20	1374	1	1055	1066	
K.LEQQVDDLEGSLE.Q	N	32.76	1473.6835	-0.5	737.8486	2	12.65	1789	1	990	1002	
A.EWKQKYEEGQAELE.G	N	26.99	1765.8158	-0.6	883.9147	2	11.00	1500	1	1418	1431	
Q.GEVDDTVQEAR.N	N	25.82	1217.5524	4.7	609.7863	2	10.04	1355	1	1702	1712	
K.KMEGDLNEM.E	N	25.67	1065.4470	-0.7	533.7304	2	11.02	1504	1	1580	1588	
K.FDKIEDM.A	N	23.34	896.3950	-0.6	449.2045	2	11.46	1581	2	84	90	
E.LKKEQDTSAH.L	N	22.49	1155.5884	-0.2	578.8013	2	7.77	1050	1	1732	1741	
Q.GEVDDTVQEA.R	N	20.03	1061.4513	-0.3	531.7328	2	10.64	1439	1	1702	1711	
Q.TALEEAEGTL.E	N	19.11	1032.4974	-0.7	517.2556	2	12.43	1750	1	1505	1514	
M.AEELKKE.Q	N	18.25	845.4494	-0.4	423.7318	2	8.54	1200	1	1729	1735	
M.NPPKFDKIEDM.A	N	17.32	1332.6383	-0.5	667.3261	2	11.50	1587	1	80	90	
K.SINDVEEF.I	N	15.40	951.4185	-0.3	476.7164	2	12.52	1766	1	316	323	

total 14 peptides

tr|A0A674NSP7|A0A674NSP7_TAKRU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.LDKNKDPLNDSVVQL.Y	N	55.11	1696.8995	-0.3	849.4568	2	12.23	1715	1	597	611	
W.LDKNKDPLNDSVVQ.L	N	49.71	1583.8154	-0.7	792.9144	2	10.89	1481	5	597	610	
L.SKIEDEQSLGAQ.L	N	35.68	1303.6255	4.7	652.8231	2	10.20	1374	1	1097	1108	
K.LEQQVDDLEGSLE.Q	N	32.76	1473.6835	-0.5	737.8486	2	12.65	1789	1	1032	1044	
K.NDENVRQ.L	N	29.03	873.3940	-0.4	437.7041	2	8.49	1190	1	1268	1274	
A.EWKQKYEEGQAELE.G	N	26.99	1765.8158	-0.6	883.9147	2	11.00	1500	1	1460	1473	
K.KMEGDLNEM.E	N	25.67	1065.4470	-0.7	533.7304	2	11.02	1504	1	1622	1630	
K.FDKIEDM.A	N	23.34	896.3950	-0.6	449.2045	2	11.46	1581	2	85	91	
E.LKKEQDTSAH.L	N	22.49	1155.5884	-0.2	578.8013	2	7.77	1050	1	1774	1783	
Q.TALEEAEGTL.E	N	19.11	1032.4974	-0.7	517.2556	2	12.43	1750	1	1547	1556	
M.AEELKKE.Q	N	18.25	845.4494	-0.4	423.7318	2	8.54	1200	1	1771	1777	
M.NPPKFDKIEDM.A	N	17.32	1332.6383	-0.5	667.3261	2	11.50	1587	1	81	91	
K.SINDVEEF.I	N	15.40	951.4185	-0.3	476.7164	2	12.52	1766	1	325	332	

total 13 peptides

tr|A0A6A4SNF9|A0A6A4SNF9_SCOMX

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.IIDQDNSGFIEEEELK.L	N	67.46	1877.8894	-1.0	939.9510	2	12.28	1724	1	147	162	
A.FDIIDQDKSGFIE.E	N	51.87	1525.7300	-1.4	763.8712	2	13.28	1898	1	226	238	
D.IIDQDKSGFIE.E	N	44.01	1263.6346	-0.5	632.8243	2	11.60	1605	1	228	238	
S.GFIEEEELK.L	N	31.42	1092.5338	-0.1	547.2741	2	11.80	1641	1	154	162	
Q.IIDQDNSGFIEEEELKLF.L	N	30.80	2138.0417	0.6	1070.0288	2	14.58	2119	1	147	164	
Q.IIDQDNSGFIEEEE.L	N	16.99	1636.7103	0.3	819.3627	2	12.36	1738	1	147	160	

total 6 peptides

tr|Q90YF6|Q90YF6_PARFO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.LDKNKDPLNDSVVQL.Y	N	55.11	1696.8995	-0.3	849.4568	2	12.23	1715	1	596	610	
W.LDKNKDPLNDSVVQ.L	N	49.71	1583.8154	-0.7	792.9144	2	10.89	1481	5	596	609	
L.SKIEDEQSLGAQ.L	N	35.68	1303.6255	4.7	652.8231	2	10.20	1374	1	1094	1105	
K.LEQQVDDLEGSLE.Q	N	32.76	1473.6835	-0.5	737.8486	2	12.65	1789	1	1029	1041	
K.NDENVRQ.L	N	29.03	873.3940	-0.4	437.7041	2	8.49	1190	1	1265	1271	
A.EWKQKYEEGQAELE.G	N	26.99	1765.8158	-0.6	883.9147	2	11.00	1500	1	1457	1470	
Q.GEVDDTVQEAR.N	N	25.82	1217.5524	4.7	609.7863	2	10.04	1355	1	1741	1751	

total 12 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.KMEGDLNEM.E	N	25.67	1065.4470	-0.7	533.7304	2	11.02	1504	1	1619	1627	
E.LKKEQDTSAH.L	N	22.49	1155.5884	-0.2	578.8013	2	7.77	1050	1	1771	1780	
Q.GEVDDTVQEA.R	N	20.03	1061.4513	-0.3	531.7328	2	10.64	1439	1	1741	1750	
M.AEELKKE.Q	N	18.25	845.4494	-0.4	423.7318	2	8.54	1200	1	1768	1774	
K.SINDVEEF.I	N	15.40	951.4185	-0.3	476.7164	2	12.52	1766	1	324	331	

total 12 peptides

tr|W5LNC0|W5LNC0_ASTMX

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDNSGFIEEEELK.L	N	67.46	1877.8894	-1.0	939.9510	2	12.28	1724	1	50	65	
A.GDSDGDGKIGVDEF.A	N	35.47	1409.5946	-1.1	705.8038	2	11.99	1675	1	90	103	
S.GFIEEEELK.L	N	31.42	1092.5338	-0.1	547.2741	2	11.80	1641	1	57	65	
A.IIDQDNSGFIEEEELKLF.L	N	30.80	2138.0417	0.6	1070.0288	2	14.58	2119	1	50	67	
F.AIIDQDNSGFIE.E	N	26.76	1320.6198	-0.6	661.3168	2	12.86	1825	1	49	60	
F.LAAGDSDGDGKIGVD.E	N	25.04	1388.6418	-0.5	695.3278	2	10.74	1456	1	87	101	
A.IIDQDNSGFIEEEE.L	N	16.99	1636.7103	0.3	819.3627	2	12.36	1738	1	50	63	

total 7 peptides

tr|A0A2I4BRJ5|A0A2I4BRJ5_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDNSGFIEEEELK.L	N	67.46	1877.8894	-1.0	939.9510	2	12.28	1724	1	50	65	
A.GDSDGDGKIGVDEF.A	N	35.47	1409.5946	-1.1	705.8038	2	11.99	1675	1	90	103	
S.GFIEEEELK.L	N	31.42	1092.5338	-0.1	547.2741	2	11.80	1641	1	57	65	
A.IIDQDNSGFIEEEELKLF.L	N	30.80	2138.0417	0.6	1070.0288	2	14.58	2119	1	50	67	
F.AIIDQDNSGFIE.E	N	26.76	1320.6198	-0.6	661.3168	2	12.86	1825	1	49	60	
F.LAAGDSDGDGKIGVD.E	N	25.04	1388.6418	-0.5	695.3278	2	10.74	1456	1	87	101	
A.IIDQDNSGFIEEEE.L	N	16.99	1636.7103	0.3	819.3627	2	12.36	1738	1	50	63	

total 7 peptides

tr|A0A3B4TWT0|A0A3B4TWT0_SERDU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDNSGFIEEEELK.L	N	67.46	1877.8894	-1.0	939.9510	2	12.28	1724	1	50	65	
A.GDSDGDGKIGVDEF.A	N	35.47	1409.5946	-1.1	705.8038	2	11.99	1675	1	90	103	
S.GFIEEEELK.L	N	31.42	1092.5338	-0.1	547.2741	2	11.80	1641	1	57	65	
A.IIDQDNSGFIEEEELKLF.L	N	30.80	2138.0417	0.6	1070.0288	2	14.58	2119	1	50	67	
F.AIIDQDNSGFIE.E	N	26.76	1320.6198	-0.6	661.3168	2	12.86	1825	1	49	60	
F.LAAGDSDGDGKIGVD.E	N	25.04	1388.6418	-0.5	695.3278	2	10.74	1456	1	87	101	
A.IIDQDNSGFIEEEE.L	N	16.99	1636.7103	0.3	819.3627	2	12.36	1738	1	50	63	

total 7 peptides

tr|A0A1A8L493|A0A1A8L493_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDNSGFIEEEELK.L	N	67.46	1877.8894	-1.0	939.9510	2	12.28	1724	1	50	65	
A.GDSDGDGKIGVDEF.A	N	35.47	1409.5946	-1.1	705.8038	2	11.99	1675	1	90	103	
S.GFIEEEELK.L	N	31.42	1092.5338	-0.1	547.2741	2	11.80	1641	1	57	65	
A.IIDQDNSGFIEEEELKLF.L	N	30.80	2138.0417	0.6	1070.0288	2	14.58	2119	1	50	67	
F.AIIDQDNSGFIE.E	N	26.76	1320.6198	-0.6	661.3168	2	12.86	1825	1	49	60	
F.LAAGDSDGDGKIGVD.E	N	25.04	1388.6418	-0.5	695.3278	2	10.74	1456	1	87	101	
A.IIDQDNSGFIEEEE.L	N	16.99	1636.7103	0.3	819.3627	2	12.36	1738	1	50	63	

total 7 peptides

tr|A0A672FI61|A0A672FI61_SALFA

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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDNSGFIEEEELK.L	N	67.46	1877.8894	-1.0	939.9510	2	12.28	1724	1	50	65	
A.GDSDGDGKIGVDEF.A	N	35.47	1409.5946	-1.1	705.8038	2	11.99	1675	1	90	103	
S.GFIEEEELK.L	N	31.42	1092.5338	-0.1	547.2741	2	11.80	1641	1	57	65	
A.IIDQDNSGFIEEEELKLF.L	N	30.80	2138.0417	0.6	1070.0288	2	14.58	2119	1	50	67	
F.AIIDQDNSGFIE.E	N	26.76	1320.6198	-0.6	661.3168	2	12.86	1825	1	49	60	
F.LAAGDSDGDGKIGVD.E	N	25.04	1388.6418	-0.5	695.3278	2	10.74	1456	1	87	101	
A.IIDQDNSGFIEEEE.L	N	16.99	1636.7103	0.3	819.3627	2	12.36	1738	1	50	63	

total 7 peptides

tr|A0A1A8G5F7|A0A1A8G5F7_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDNSGFIEEEELK.L	N	67.46	1877.8894	-1.0	939.9510	2	12.28	1724	1	50	65	
A.GDSDGDGKIGVDEF.A	N	35.47	1409.5946	-1.1	705.8038	2	11.99	1675	1	90	103	
S.GFIEEEELK.L	N	31.42	1092.5338	-0.1	547.2741	2	11.80	1641	1	57	65	
A.IIDQDNSGFIEEEELKLF.L	N	30.80	2138.0417	0.6	1070.0288	2	14.58	2119	1	50	67	
F.AIIDQDNSGFIE.E	N	26.76	1320.6198	-0.6	661.3168	2	12.86	1825	1	49	60	
F.LAAGDSDGDGKIGVD.E	N	25.04	1388.6418	-0.5	695.3278	2	10.74	1456	1	87	101	
A.IIDQDNSGFIEEEE.L	N	16.99	1636.7103	0.3	819.3627	2	12.36	1738	1	50	63	

total 7 peptides

tr|A0A4W6DV48|A0A4W6DV48_LATCA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDNSGFIEEEELK.L	N	67.46	1877.8894	-1.0	939.9510	2	12.28	1724	1	50	65	
A.GDSDGDGKIGVDEF.A	N	35.47	1409.5946	-1.1	705.8038	2	11.99	1675	1	90	103	
S.GFIEEEELK.L	N	31.42	1092.5338	-0.1	547.2741	2	11.80	1641	1	57	65	
A.IIDQDNSGFIEEEELKLF.L	N	30.80	2138.0417	0.6	1070.0288	2	14.58	2119	1	50	67	
F.AIIDQDNSGFIE.E	N	26.76	1320.6198	-0.6	661.3168	2	12.86	1825	1	49	60	
F.LAAGDSDGDGKIGVD.E	N	25.04	1388.6418	-0.5	695.3278	2	10.74	1456	1	87	101	
A.IIDQDNSGFIEEEE.L	N	16.99	1636.7103	0.3	819.3627	2	12.36	1738	1	50	63	

total 7 peptides

tr|F8U037|F8U037_EPIBR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDNSGFIEEEELK.L	N	67.46	1877.8894	-1.0	939.9510	2	12.28	1724	1	50	65	
A.GDSDGDGKIGVDEF.A	N	35.47	1409.5946	-1.1	705.8038	2	11.99	1675	1	90	103	
S.GFIEEEELK.L	N	31.42	1092.5338	-0.1	547.2741	2	11.80	1641	1	57	65	
A.IIDQDNSGFIEEEELKLF.L	N	30.80	2138.0417	0.6	1070.0288	2	14.58	2119	1	50	67	
F.AIIDQDNSGFIE.E	N	26.76	1320.6198	-0.6	661.3168	2	12.86	1825	1	49	60	
F.LAAGDSDGDGKIGVD.E	N	25.04	1388.6418	-0.5	695.3278	2	10.74	1456	1	87	101	
A.IIDQDNSGFIEEEE.L	N	16.99	1636.7103	0.3	819.3627	2	12.36	1738	1	50	63	

total 7 peptides

tr|A0A1A7WW39|A0A1A7WW39_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDNSGFIEEEELK.L	N	67.46	1877.8894	-1.0	939.9510	2	12.28	1724	1	50	65	
A.GDSDGDGKIGVDEF.A	N	35.47	1409.5946	-1.1	705.8038	2	11.99	1675	1	90	103	
S.GFIEEEELK.L	N	31.42	1092.5338	-0.1	547.2741	2	11.80	1641	1	57	65	
A.IIDQDNSGFIEEEELKLF.L	N	30.80	2138.0417	0.6	1070.0288	2	14.58	2119	1	50	67	

total 7 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.AIIDQDNSGFIE.E	N	26.76	1320.6198	-0.6	661.3168	2	12.86	1825	1	49	60	
F.LAAGDSDGDGKIGVD.E	N	25.04	1388.6418	-0.5	695.3278	2	10.74	1456	1	87	101	
A.IIDQDNSGFIEEEE.L	N	16.99	1636.7103	0.3	819.3627	2	12.36	1738	1	50	63	

total 7 peptides

tr|A0A1A8C322|A0A1A8C322_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDNSGFIEEEELK.L	N	67.46	1877.8894	-1.0	939.9510	2	12.28	1724	1	50	65	
A.GDSDGDGKIGVDEF.A	N	35.47	1409.5946	-1.1	705.8038	2	11.99	1675	1	90	103	
S.GFIEEEELK.L	N	31.42	1092.5338	-0.1	547.2741	2	11.80	1641	1	57	65	
A.IIDQDNSGFIEEEELKLF.L	N	30.80	2138.0417	0.6	1070.0288	2	14.58	2119	1	50	67	
F.AIIDQDNSGFIE.E	N	26.76	1320.6198	-0.6	661.3168	2	12.86	1825	1	49	60	
F.LAAGDSDGDGKIGVD.E	N	25.04	1388.6418	-0.5	695.3278	2	10.74	1456	1	87	101	
A.IIDQDNSGFIEEEE.L	N	16.99	1636.7103	0.3	819.3627	2	12.36	1738	1	50	63	

total 7 peptides

tr|A0A3Q3GY11|A0A3Q3GY11_9LABR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDNSGFIEEEELK.L	N	67.46	1877.8894	-1.0	939.9510	2	12.28	1724	1	50	65	
A.GDSDGDGKIGVDEF.A	N	35.47	1409.5946	-1.1	705.8038	2	11.99	1675	1	90	103	
S.GFIEEEELK.L	N	31.42	1092.5338	-0.1	547.2741	2	11.80	1641	1	57	65	
A.IIDQDNSGFIEEEELKLF.L	N	30.80	2138.0417	0.6	1070.0288	2	14.58	2119	1	50	67	
F.AIIDQDNSGFIE.E	N	26.76	1320.6198	-0.6	661.3168	2	12.86	1825	1	49	60	
F.LAAGDSDGDGKIGVD.E	N	25.04	1388.6418	-0.5	695.3278	2	10.74	1456	1	87	101	
A.IIDQDNSGFIEEEE.L	N	16.99	1636.7103	0.3	819.3627	2	12.36	1738	1	50	63	

total 7 peptides

tr|A0A1A8J4D2|A0A1A8J4D2_NOTKU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDNSGFIEEEELK.L	N	67.46	1877.8894	-1.0	939.9510	2	12.28	1724	1	50	65	
A.GDSDGDGKIGVDEF.A	N	35.47	1409.5946	-1.1	705.8038	2	11.99	1675	1	90	103	
S.GFIEEEELK.L	N	31.42	1092.5338	-0.1	547.2741	2	11.80	1641	1	57	65	
A.IIDQDNSGFIEEEELKLF.L	N	30.80	2138.0417	0.6	1070.0288	2	14.58	2119	1	50	67	
F.AIIDQDNSGFIE.E	N	26.76	1320.6198	-0.6	661.3168	2	12.86	1825	1	49	60	
F.LAAGDSDGDGKIGVD.E	N	25.04	1388.6418	-0.5	695.3278	2	10.74	1456	1	87	101	
A.IIDQDNSGFIEEEE.L	N	16.99	1636.7103	0.3	819.3627	2	12.36	1738	1	50	63	

total 7 peptides

tr|A0A672Y4P6|A0A672Y4P6_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.LGETNPADSKPGSIR.G	Y	61.86	1540.7844	4.9	771.4033	2	10.00	1349	1	88	102	
H.YLDLKDMPFYA.G	Y	42.76	1374.6530	-0.5	688.3334	2	14.24	2059	1	49	59	
H.YLDLKDMPFYAGL.C	Y	24.94	1544.7584	-0.8	773.3859	2	14.97	2184	1	49	61	
E.VDLWFK.A	Y	19.10	806.4326	-0.8	404.2233	2	13.17	1879	1	127	132	
Y.LDLKDMPFY.A	Y	18.92	1140.5525	0.0	571.2835	2	14.02	2023	1	50	58	
E.VDLWFKA.E	Y	17.14	877.4697	-1.0	439.7417	2	13.37	1915	1	127	133	

total 6 peptides

tr|A0A2I4CF45|A0A2I4CF45_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.LGETNPADSKPGSIR.G	Y	61.86	1540.7844	4.9	771.4033	2	10.00	1349	1	88	102	
H.YLDLKDMPFYA.G	Y	42.76	1374.6530	-0.5	688.3334	2	14.24	2059	1	49	59	
H.YLDLKDMPFYAGL.C	Y	24.94	1544.7584	-0.8	773.3859	2	14.97	2184	1	49	61	
E.VDLWFK.A	Y	19.10	806.4326	-0.8	404.2233	2	13.17	1879	1	127	132	
Y.LDLKDMPFY.A	Y	18.92	1140.5525	0.0	571.2835	2	14.02	2023	1	50	58	
E.VDLWFKA.E	Y	17.14	877.4697	-1.0	439.7417	2	13.37	1915	1	127	133	

total 6 peptides

tr|A0A6P7ISB4|A0A6P7ISB4_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.LGETNPADSKPGSIR.G	Y	61.86	1540.7844	4.9	771.4033	2	10.00	1349	1	88	102	
H.YLDLKDMPFYA.G	Y	42.76	1374.6530	-0.5	688.3334	2	14.24	2059	1	49	59	
H.YLDLKDMPFYAGL.C	Y	24.94	1544.7584	-0.8	773.3859	2	14.97	2184	1	49	61	
E.VDLWFK.A	Y	19.10	806.4326	-0.8	404.2233	2	13.17	1879	1	127	132	
Y.LDLKDMPFY.A	Y	18.92	1140.5525	0.0	571.2835	2	14.02	2023	1	50	58	
E.VDLWFKA.E	Y	17.14	877.4697	-1.0	439.7417	2	13.37	1915	1	127	133	

total 6 peptides

tr|A0A3Q4I698|A0A3Q4I698_NEOBR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.LGETNPADSKPGSIR.G	Y	61.86	1540.7844	4.9	771.4033	2	10.00	1349	1	88	102	
H.YLDLKDMPFYA.G	Y	42.76	1374.6530	-0.5	688.3334	2	14.24	2059	1	49	59	
H.YLDLKDMPFYAGL.C	Y	24.94	1544.7584	-0.8	773.3859	2	14.97	2184	1	49	61	
E.VDLWFK.A	Y	19.10	806.4326	-0.8	404.2233	2	13.17	1879	1	127	132	
Y.LDLKDMPFY.A	Y	18.92	1140.5525	0.0	571.2835	2	14.02	2023	1	50	58	
E.VDLWFKA.E	Y	17.14	877.4697	-1.0	439.7417	2	13.37	1915	1	127	133	

total 6 peptides

tr|A0A3B3Z6H5|A0A3B3Z6H5_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.LGETNPADSKPGSIR.G	Y	61.86	1540.7844	4.9	771.4033	2	10.00	1349	1	88	102	
H.YLDLKDMPFYA.G	Y	42.76	1374.6530	-0.5	688.3334	2	14.24	2059	1	49	59	
H.YLDLKDMPFYAGL.C	Y	24.94	1544.7584	-0.8	773.3859	2	14.97	2184	1	49	61	
E.VDLWFK.A	Y	19.10	806.4326	-0.8	404.2233	2	13.17	1879	1	127	132	
Y.LDLKDMPFY.A	Y	18.92	1140.5525	0.0	571.2835	2	14.02	2023	1	50	58	
E.VDLWFKA.E	Y	17.14	877.4697	-1.0	439.7417	2	13.37	1915	1	127	133	

total 6 peptides

tr|A0A3Q3A341|A0A3Q3A341_KRYMA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.LGETNPADSKPGSIR.G	Y	61.86	1540.7844	4.9	771.4033	2	10.00	1349	1	88	102	
H.YLDLKDMPFYA.G	Y	42.76	1374.6530	-0.5	688.3334	2	14.24	2059	1	49	59	
H.YLDLKDMPFYAGL.C	Y	24.94	1544.7584	-0.8	773.3859	2	14.97	2184	1	49	61	
E.VDLWFK.A	Y	19.10	806.4326	-0.8	404.2233	2	13.17	1879	1	127	132	
Y.LDLKDMPFY.A	Y	18.92	1140.5525	0.0	571.2835	2	14.02	2023	1	50	58	
E.VDLWFKA.E	Y	17.14	877.4697	-1.0	439.7417	2	13.37	1915	1	127	133	

total 6 peptides

tr|A0A3P8Q104|A0A3P8Q104_ASTCA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.LGETNPADSKPGSIR.G	Y	61.86	1540.7844	4.9	771.4033	2	10.00	1349	1	90	104	
H.YLDLKDMPFYA.G	Y	42.76	1374.6530	-0.5	688.3334	2	14.24	2059	1	51	61	
H.YLDLKDMPFYAGL.C	Y	24.94	1544.7584	-0.8	773.3859	2	14.97	2184	1	51	63	
E.VDLWFK.A	Y	19.10	806.4326	-0.8	404.2233	2	13.17	1879	1	129	134	
Y.LDLKDMPFY.A	Y	18.92	1140.5525	0.0	571.2835	2	14.02	2023	1	52	60	
E.VDLWFKA.E	Y	17.14	877.4697	-1.0	439.7417	2	13.37	1915	1	129	135	

total 6 peptides

tr|A0A3Q3CUD8|A0A3Q3CUD8_HAPBU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.LGETNPADSKPGSIR.G	Y	61.86	1540.7844	4.9	771.4033	2	10.00	1349	1	90	104	
H.YLDLKDMPFYA.G	Y	42.76	1374.6530	-0.5	688.3334	2	14.24	2059	1	51	61	
H.YLDLKDMPFYAGL.C	Y	24.94	1544.7584	-0.8	773.3859	2	14.97	2184	1	51	63	
E.VDLWFK.A	Y	19.10	806.4326	-0.8	404.2233	2	13.17	1879	1	129	134	
Y.LDLKDMPFY.A	Y	18.92	1140.5525	0.0	571.2835	2	14.02	2023	1	52	60	
E.VDLWFKA.E	Y	17.14	877.4697	-1.0	439.7417	2	13.37	1915	1	129	135	

total 6 peptides

tr|A0A3Q4I6B8|A0A3Q4I6B8_NEOBR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.LGETNPADSKPGSIR.G	Y	61.86	1540.7844	4.9	771.4033	2	10.00	1349	1	90	104	
H.YLDLKDMPFYA.G	Y	42.76	1374.6530	-0.5	688.3334	2	14.24	2059	1	51	61	
H.YLDLKDMPFYAGL.C	Y	24.94	1544.7584	-0.8	773.3859	2	14.97	2184	1	51	63	
E.VDLWFK.A	Y	19.10	806.4326	-0.8	404.2233	2	13.17	1879	1	129	134	
Y.LDLKDMPFY.A	Y	18.92	1140.5525	0.0	571.2835	2	14.02	2023	1	52	60	
E.VDLWFKA.E	Y	17.14	877.4697	-1.0	439.7417	2	13.37	1915	1	129	135	

total 6 peptides

tr|M4ADR4|M4ADR4_XIPMA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.LGETNPADSKPGSIR.G	Y	61.86	1540.7844	4.9	771.4033	2	10.00	1349	1	101	115	
H.YLDLKDMPFYA.G	Y	42.76	1374.6530	-0.5	688.3334	2	14.24	2059	1	62	72	
H.YLDLKDMPFYAGL.C	Y	24.94	1544.7584	-0.8	773.3859	2	14.97	2184	1	62	74	
E.VDLWFK.A	Y	19.10	806.4326	-0.8	404.2233	2	13.17	1879	1	140	145	
Y.LDLKDMPFY.A	Y	18.92	1140.5525	0.0	571.2835	2	14.02	2023	1	63	71	
E.VDLWFKA.E	Y	17.14	877.4697	-1.0	439.7417	2	13.37	1915	1	140	146	

total 6 peptides

tr|A0A3B3Z5H2|A0A3B3Z5H2_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.LGETNPADSKPGSIR.G	Y	61.86	1540.7844	4.9	771.4033	2	10.00	1349	1	102	116	
H.YLDLKDMPFYA.G	Y	42.76	1374.6530	-0.5	688.3334	2	14.24	2059	1	63	73	
H.YLDLKDMPFYAGL.C	Y	24.94	1544.7584	-0.8	773.3859	2	14.97	2184	1	63	75	
E.VDLWFK.A	Y	19.10	806.4326	-0.8	404.2233	2	13.17	1879	1	141	146	
Y.LDLKDMPFY.A	Y	18.92	1140.5525	0.0	571.2835	2	14.02	2023	1	64	72	
E.VDLWFKA.E	Y	17.14	877.4697	-1.0	439.7417	2	13.37	1915	1	141	147	

total 6 peptides

tr|A0A087YID2|A0A087YID2_POEFO
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.LGETNPADSKPGSIR.G	Y	61.86	1540.7844	4.9	771.4033	2	10.00	1349	1	102	116	
H.YLDLKDMPFYA.G	Y	42.76	1374.6530	-0.5	688.3334	2	14.24	2059	1	63	73	
H.YLDLKDMPFYAGL.C	Y	24.94	1544.7584	-0.8	773.3859	2	14.97	2184	1	63	75	
E.VDLWFK.A	Y	19.10	806.4326	-0.8	404.2233	2	13.17	1879	1	141	146	
Y.LDLKDMPFY.A	Y	18.92	1140.5525	0.0	571.2835	2	14.02	2023	1	64	72	
E.VDLWFKA.E	Y	17.14	877.4697	-1.0	439.7417	2	13.37	1915	1	141	147	

total 6 peptides

tr|A0A3Q2PNK7|A0A3Q2PNK7_FUNHE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.LGETNPADSKPGSIR.G	Y	61.86	1540.7844	4.9	771.4033	2	10.00	1349	1	181	195	
H.YLDLKDMPFYA.G	Y	42.76	1374.6530	-0.5	688.3334	2	14.24	2059	1	142	152	
H.YLDLKDMPFYAGL.C	Y	24.94	1544.7584	-0.8	773.3859	2	14.97	2184	1	142	154	
E.VDLWFK.A	Y	19.10	806.4326	-0.8	404.2233	2	13.17	1879	1	220	225	
Y.LDLKDMPFY.A	Y	18.92	1140.5525	0.0	571.2835	2	14.02	2023	1	143	151	
E.VDLWFKA.E	Y	17.14	877.4697	-1.0	439.7417	2	13.37	1915	1	220	226	

total 6 peptides

tr|A0A4W4EA72|A0A4W4EA72_ELEEL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.VLDRDKSGFIEEEELK.L	Y	60.50	1905.9683	-23.1	953.9694	2	11.67	1618	2	50	65	
F.TVLDRDKSGFIEEEE.L	Y	32.23	1765.8369	-27.6	883.9014	2	12.46	1756	1	49	63	
S.GFIEEEELK.L	N	31.42	1092.5338	-0.1	547.2741	2	11.80	1641	1	57	65	
R.DKSGFIEEEELK.L	N	25.85	1422.6877	-0.4	712.3508	2	11.40	1570	1	54	65	
F.TVLDRDKSGFIE.E	Y	20.41	1378.7092	-34.7	690.3380	2	15.47	2282	4	49	60	
T.VLDRDKSGFIEEEE.L	Y	17.77	1664.7893	-22.2	833.3835	2	11.56	1599	1	50	63	
T.VLDRDKSGFIEEEEL.K	Y	15.17	1777.8733	-21.4	889.9249	2	12.64	1787	1	50	64	

total 7 peptides

tr|A0A3B4TLJ3|A0A3B4TLJ3_SERDU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDKSGFIEEEELK.L	N	49.57	1891.9414	-0.6	946.9774	2	11.72	1627	1	46	61	
A.IIDQDKSGFIE.E	N	44.01	1263.6346	-0.5	632.8243	2	11.60	1605	1	46	56	
A.GDSDGDGKIGVDEF.A	N	35.47	1409.5946	-1.1	705.8038	2	11.99	1675	1	86	99	
S.GFIEEEELK.L	N	31.42	1092.5338	-0.1	547.2741	2	11.80	1641	1	53	61	
Q.DKSGFIEEEELK.L	N	25.85	1422.6877	-0.4	712.3508	2	11.40	1570	1	50	61	

total 5 peptides

tr|A9ZTF1|A9ZTF1_KATPE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDKSGFIEEEELK.L	N	49.57	1891.9414	-0.6	946.9774	2	11.72	1627	1	49	64	
A.IIDQDKSGFIE.E	N	44.01	1263.6346	-0.5	632.8243	2	11.60	1605	1	49	59	
A.GDSDGDGKIGVDEF.A	N	35.47	1409.5946	-1.1	705.8038	2	11.99	1675	1	89	102	
S.GFIEEEELK.L	N	31.42	1092.5338	-0.1	547.2741	2	11.80	1641	1	56	64	
Q.DKSGFIEEEELK.L	N	25.85	1422.6877	-0.4	712.3508	2	11.40	1570	1	53	64	

total 5 peptides

tr|G8GWA1|G8GWA1_CARAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDKSGFIEEEELK.L	N	49.57	1891.9414	-0.6	946.9774	2	11.72	1627	1	50	65	
A.IIDQDKSGFIE.E	N	44.01	1263.6346	-0.5	632.8243	2	11.60	1605	1	50	60	
A.GDSDGDGKIGVDEF.T	N	35.47	1409.5946	-1.1	705.8038	2	11.99	1675	1	90	103	
S.GFIEEEELK.L	N	31.42	1092.5338	-0.1	547.2741	2	11.80	1641	1	57	65	
Q.DKSGFIEEEELK.L	N	25.85	1422.6877	-0.4	712.3508	2	11.40	1570	1	54	65	

total 5 peptides

tr|A0A3B4TM81|A0A3B4TM81_SERDU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDKSGFIEEEELK.L	N	49.57	1891.9414	-0.6	946.9774	2	11.72	1627	1	50	65	
A.IIDQDKSGFIE.E	N	44.01	1263.6346	-0.5	632.8243	2	11.60	1605	1	50	60	
A.GDSDGDGKIGVDEF.A	N	35.47	1409.5946	-1.1	705.8038	2	11.99	1675	1	90	103	
S.GFIEEEELK.L	N	31.42	1092.5338	-0.1	547.2741	2	11.80	1641	1	57	65	
Q.DKSGFIEEEELK.L	N	25.85	1422.6877	-0.4	712.3508	2	11.40	1570	1	54	65	

total 5 peptides

tr|A0A6P6KMF1|A0A6P6KMF1_CARAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.IIDQDKSGFIEEEELK.L	N	49.57	1891.9414	-0.6	946.9774	2	11.72	1627	1	50	65	
A.IIDQDKSGFIE.E	N	44.01	1263.6346	-0.5	632.8243	2	11.60	1605	1	50	60	
A.GDSDGDGKIGVDEF.T	N	35.47	1409.5946	-1.1	705.8038	2	11.99	1675	1	90	103	
S.GFIEEEELK.L	N	31.42	1092.5338	-0.1	547.2741	2	11.80	1641	1	57	65	
Q.DKSGFIEEEELK.L	N	25.85	1422.6877	-0.4	712.3508	2	11.40	1570	1	54	65	

total 5 peptides

tr|A0A6G0IXD3|A0A6G0IXD3_LARCR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SKIEDEQSLGAQ.L	N	35.68	1303.6255	4.7	652.8231	2	10.20	1374	1	1059	1070	
K.LEQQVDDLEGSLE.Q	N	32.76	1473.6835	-0.5	737.8486	2	12.65	1789	1	994	1006	
K.NDENVRQ.M	N	29.03	873.3940	-0.4	437.7041	2	8.49	1190	1	1230	1236	
A.EWKQKYEEGQAELE.G	N	26.99	1765.8158	-0.6	883.9147	2	11.00	1500	1	1422	1435	
Q.GEVDDTVQEAR.N	N	25.82	1217.5524	4.7	609.7863	2	10.04	1355	1	1706	1716	
K.KMEGDLNEM.E	N	25.67	1065.4470	-0.7	533.7304	2	11.02	1504	1	1584	1592	
K.FDKIEDM.A	N	23.34	896.3950	-0.6	449.2045	2	11.46	1581	2	86	92	
Q.GEVDDTVQEA.R	N	20.03	1061.4513	-0.3	531.7328	2	10.64	1439	1	1706	1715	
K.GFPSRIPY.A	Y	19.70	935.4865	6.1	468.7534	2	12.11	1693	1	683	690	
Q.TALEEAEGTL.E	N	19.11	1032.4974	-0.7	517.2556	2	12.43	1750	1	1509	1518	
M.AEELKKE.Q	N	18.25	845.4494	-0.4	423.7318	2	8.54	1200	1	1733	1739	
M.NPPKFDKIEDM.A	N	17.32	1332.6383	-0.5	667.3261	2	11.50	1587	1	82	92	

total 12 peptides

tr|A0A6G0IXM2|A0A6G0IXM2_LARCR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SKIEDEQSLGAQ.L	N	35.68	1303.6255	4.7	652.8231	2	10.20	1374	1	1069	1080	
K.LEQQVDDLEGSLE.Q	N	32.76	1473.6835	-0.5	737.8486	2	12.65	1789	1	1004	1016	
K.NDENVRQ.I	N	29.03	873.3940	-0.4	437.7041	2	8.49	1190	1	1240	1246	
A.EWKQKYEEGQAELE.G	N	26.99	1765.8158	-0.6	883.9147	2	11.00	1500	1	1432	1445	
Q.GEVDDTVQEAR.N	N	25.82	1217.5524	4.7	609.7863	2	10.04	1355	1	1716	1726	
K.KMEGDLNEM.E	N	25.67	1065.4470	-0.7	533.7304	2	11.02	1504	1	1594	1602	
K.FDKIEDM.A	N	23.34	896.3950	-0.6	449.2045	2	11.46	1581	2	86	92	
Q.GEVDDTVQEA.R	N	20.03	1061.4513	-0.3	531.7328	2	10.64	1439	1	1716	1725	

total 12 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.GFPSRIPY.A	Y	19.70	935.4865	6.1	468.7534	2	12.11	1693	1	685	692	
Q.TALEEAEGTL.E	N	19.11	1032.4974	-0.7	517.2556	2	12.43	1750	1	1519	1528	
M.AEELKKE.Q	N	18.25	845.4494	-0.4	423.7318	2	8.54	1200	1	1743	1749	
M.NPPKFDKIEDM.A	N	17.32	1332.6383	-0.5	667.3261	2	11.50	1587	1	82	92	

total 12 peptides

tr|A0A6G0IXG4|A0A6G0IXG4_LARCR
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SKIEDEQSLGAQ.L	N	35.68	1303.6255	4.7	652.8231	2	10.20	1374	1	1079	1090	
K.LEQQVDDLEGSLE.Q	N	32.76	1473.6835	-0.5	737.8486	2	12.65	1789	1	1014	1026	
K.NDENVRQ.M	N	29.03	873.3940	-0.4	437.7041	2	8.49	1190	1	1250	1256	
A.EWKQKYEEGQAELE.G	N	26.99	1765.8158	-0.6	883.9147	2	11.00	1500	1	1442	1455	
Q.GEVDDTVQEAR.N	N	25.82	1217.5524	4.7	609.7863	2	10.04	1355	1	1726	1736	
K.KMEGDLNEM.E	N	25.67	1065.4470	-0.7	533.7304	2	11.02	1504	1	1604	1612	
K.FDKIEDM.A	N	23.34	896.3950	-0.6	449.2045	2	11.46	1581	2	86	92	
Q.GEVDDTVQEA.R	N	20.03	1061.4513	-0.3	531.7328	2	10.64	1439	1	1726	1735	
K.GFPSRIPY.A	Y	19.70	935.4865	6.1	468.7534	2	12.11	1693	1	703	710	
Q.TALEEAEGTL.E	N	19.11	1032.4974	-0.7	517.2556	2	12.43	1750	1	1529	1538	
M.AEELKKE.Q	N	18.25	845.4494	-0.4	423.7318	2	8.54	1200	1	1753	1759	
M.NPPKFDKIEDM.A	N	17.32	1332.6383	-0.5	667.3261	2	11.50	1587	1	82	92	

total 12 peptides

tr|G3NEV3|G3NEV3_GASAC
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SKIEDEQSLGAQ.L	N	35.68	1303.6255	4.7	652.8231	2	10.20	1374	1	1082	1093	
K.LEQQVDDLEGSLE.Q	N	32.76	1473.6835	-0.5	737.8486	2	12.65	1789	1	1017	1029	
K.NDENVRQ.I	N	29.03	873.3940	-0.4	437.7041	2	8.49	1190	1	1253	1259	
A.EWKQKYEEGQAELE.G	N	26.99	1765.8158	-0.6	883.9147	2	11.00	1500	1	1447	1460	
Q.GEVDDTVQEAR.N	N	25.82	1217.5524	4.7	609.7863	2	10.04	1355	1	1731	1741	
K.KMEGDLNEM.E	N	25.67	1065.4470	-0.7	533.7304	2	11.02	1504	1	1609	1617	
E.LKKEQDTSAH.L	N	22.49	1155.5884	-0.2	578.8013	2	7.77	1050	1	1761	1770	
Q.GEVDDTVQEA.R	N	20.03	1061.4513	-0.3	531.7328	2	10.64	1439	1	1731	1740	
Q.TALEEAEGTL.E	N	19.11	1032.4974	-0.7	517.2556	2	12.43	1750	1	1534	1543	
M.AEELKKE.Q	N	18.25	845.4494	-0.4	423.7318	2	8.54	1200	1	1758	1764	

total 10 peptides

tr|A0A6P8W5C3|A0A6P8W5C3_GYMAC
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SKIEDEQSLGAQ.L	N	35.68	1303.6255	4.7	652.8231	2	10.20	1374	1	1086	1097	
K.LEQQVDDLEGSLE.Q	N	32.76	1473.6835	-0.5	737.8486	2	12.65	1789	1	1021	1033	
K.NDENVRQ.I	N	29.03	873.3940	-0.4	437.7041	2	8.49	1190	1	1257	1263	
A.EWKQKYEEGQAELE.G	N	26.99	1765.8158	-0.6	883.9147	2	11.00	1500	1	1449	1462	
Q.GEVDDTVQEAR.N	N	25.82	1217.5524	4.7	609.7863	2	10.04	1355	1	1733	1743	
K.KMEGDLNEM.E	N	25.67	1065.4470	-0.7	533.7304	2	11.02	1504	1	1611	1619	
E.LKKEQDTSAH.L	N	22.49	1155.5884	-0.2	578.8013	2	7.77	1050	1	1763	1772	
Q.GEVDDTVQEA.R	N	20.03	1061.4513	-0.3	531.7328	2	10.64	1439	1	1733	1742	
Q.TALEEAEGTL.E	N	19.11	1032.4974	-0.7	517.2556	2	12.43	1750	1	1536	1545	
M.AEELKKE.Q	N	18.25	845.4494	-0.4	423.7318	2	8.54	1200	1	1760	1766	

total 10 peptides

tr|A0A6P8VS48|A0A6P8VS48_GYMAC
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SKIEDEQSLGAQ.L	N	35.68	1303.6255	4.7	652.8231	2	10.20	1374	1	1086	1097	
K.LEQQVDDLEGSLE.Q	N	32.76	1473.6835	-0.5	737.8486	2	12.65	1789	1	1021	1033	
K.NDENVRQ.I	N	29.03	873.3940	-0.4	437.7041	2	8.49	1190	1	1257	1263	
A.EWKQKYEEGQAELE.G	N	26.99	1765.8158	-0.6	883.9147	2	11.00	1500	1	1449	1462	
Q.GEVDDTVQEAR.N	N	25.82	1217.5524	4.7	609.7863	2	10.04	1355	1	1733	1743	
K.KMEGDLNEM.E	N	25.67	1065.4470	-0.7	533.7304	2	11.02	1504	1	1611	1619	
E.LKKEQDTSAH.L	N	22.49	1155.5884	-0.2	578.8013	2	7.77	1050	1	1763	1772	
Q.GEVDDTVQEA.R	N	20.03	1061.4513	-0.3	531.7328	2	10.64	1439	1	1733	1742	
Q.TALEEAEGTL.E	N	19.11	1032.4974	-0.7	517.2556	2	12.43	1750	1	1536	1545	
M.AEELKKE.Q	N	18.25	845.4494	-0.4	423.7318	2	8.54	1200	1	1760	1766	

total 10 peptides

tr|A0A3Q3W464|A0A3Q3W464_MOLML
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.FDIIDQDKSGFIE.K	N	51.87	1525.7300	-1.4	763.8712	2	13.28	1898	1	48	60	
D.IIDQDKSGFIE.K	N	44.01	1263.6346	-0.5	632.8243	2	11.60	1605	1	50	60	
S.DELKKAFDIIDQDKSGFIE.K	Y	33.36	2210.1106	-17.3	1106.0435	2	13.70	1970	1	42	60	

total 3 peptides

tr|A0A3Q3WAG3|A0A3Q3WAG3_MOLML
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.FDIIDQDKSGFIE.K	N	51.87	1525.7300	-1.4	763.8712	2	13.28	1898	1	48	60	
D.IIDQDKSGFIE.K	N	44.01	1263.6346	-0.5	632.8243	2	11.60	1605	1	50	60	
S.DELKKAFDIIDQDKSGFIE.K	Y	33.36	2210.1106	-17.3	1106.0435	2	13.70	1970	1	42	60	

total 3 peptides

tr|A0A3Q4AW30|A0A3Q4AW30_MOLML
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.FDIIDQDKSGFIE.K	N	51.87	1525.7300	-1.4	763.8712	2	13.28	1898	1	48	60	
D.IIDQDKSGFIE.K	N	44.01	1263.6346	-0.5	632.8243	2	11.60	1605	1	50	60	
S.DELKKAFDIIDQDKSGFIE.K	Y	33.36	2210.1106	-17.3	1106.0435	2	13.70	1970	1	42	60	

total 3 peptides

tr|A0A3Q3W3Y6|A0A3Q3W3Y6_MOLML
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.FDIIDQDKSGFIE.K	N	51.87	1525.7300	-1.4	763.8712	2	13.28	1898	1	48	60	
D.IIDQDKSGFIE.K	N	44.01	1263.6346	-0.5	632.8243	2	11.60	1605	1	50	60	
S.DELKKAFDIIDQDKSGFIE.K	Y	33.36	2210.1106	-17.3	1106.0435	2	13.70	1970	1	42	60	

total 3 peptides

tr|A0A6P8GNA2|A0A6P8GNA2_CLUHA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SKIEDEQSLGAQ.L	N	35.68	1303.6255	4.7	652.8231	2	10.20	1374	1	1092	1103	
K.LEQQVDDLEGSLE.Q	N	32.76	1473.6835	-0.5	737.8486	2	12.65	1789	1	1027	1039	
A.EWKQKYEEGQAELE.G	N	26.99	1765.8158	-0.6	883.9147	2	11.00	1500	1	1455	1468	
K.KMEGDLNEM.E	N	25.67	1065.4470	-0.7	533.7304	2	11.02	1504	1	1617	1625	
P.VLYPPVVEE.T	Y	25.37	1043.5538	-0.5	522.7839	2	12.77	1809	1	621	629	

total 9 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.FDKIEDM.A	N	23.34	896.3950	-0.6	449.2045	2	11.46	1581	2	85	91	
Q.TALEEAEGTL.E	N	19.11	1032.4974	-0.7	517.2556	2	12.43	1750	1	1542	1551	
M.AEELKKE.Q	N	18.25	845.4494	-0.4	423.7318	2	8.54	1200	1	1766	1772	
M.NPPKFDKIEDM.A	N	17.32	1332.6383	-0.5	667.3261	2	11.50	1587	1	81	91	

total 9 peptides

tr|A0A3Q1HW42|A0A3Q1HW42_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VDSELPVDDVFGQ.V	Y	49.54	1418.6565	-1.0	710.3348	2	13.82	1991	1	173	185	
P.LDTVLDMIKDA.M	N	20.90	1232.6322	-0.8	617.3229	2	14.44	2094	1	69	79	
L.DTVLDMIK.D	N	17.70	933.4841	-1.1	467.7488	2	13.23	1891	1	70	77	
D.TVLDMIKDA.M	N	16.00	1004.5212	-1.1	503.2673	2	13.42	1923	1	71	79	
K.VDSELPVDDVF.G	N	15.68	1233.5764	-0.5	617.7952	2	14.17	2049	1	173	183	

total 5 peptides

tr|A0A3B5BIY5|A0A3B5BIY5_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VDSELPVDDVFGQ.V	Y	49.54	1418.6565	-1.0	710.3348	2	13.82	1991	1	173	185	
P.LDTVLDMIKDA.M	N	20.90	1232.6322	-0.8	617.3229	2	14.44	2094	1	69	79	
L.DTVLDMIK.D	N	17.70	933.4841	-1.1	467.7488	2	13.23	1891	1	70	77	
D.TVLDMIKDA.M	N	16.00	1004.5212	-1.1	503.2673	2	13.42	1923	1	71	79	
K.VDSELPVDDVF.G	N	15.68	1233.5764	-0.5	617.7952	2	14.17	2049	1	173	183	

total 5 peptides

tr|A0A4U5UZN8|A0A4U5UZN8_COLLU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.S	Y	42.46	1329.6638	-0.6	665.8388	2	12.27	1723	1	225	236	
D.VIEDPVEIIDN.S	Y	35.61	1254.6343	-0.3	628.3242	2	13.52	1941	1	145	155	
D.VIEDPVEIIDNSRE.L	Y	22.59	1626.8101	-0.5	814.4119	2	13.15	1877	1	145	158	

total 3 peptides

tr|A0A7N8YD85|A0A7N8YD85_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	Y	42.46	1329.6638	-0.6	665.8388	2	12.27	1723	1	219	230	
D.VLEDPVEILDN.S	Y	35.61	1254.6343	-0.3	628.3242	2	13.52	1941	1	145	155	
D.VLEDPVEILDNSRE.L	Y	22.59	1626.8101	-0.5	814.4119	2	13.15	1877	1	145	158	

total 3 peptides

tr|A0A7N8Y4P6|A0A7N8Y4P6_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	Y	42.46	1329.6638	-0.6	665.8388	2	12.27	1723	1	222	233	
D.VLEDPVEILDN.S	Y	35.61	1254.6343	-0.3	628.3242	2	13.52	1941	1	142	152	
D.VLEDPVEILDNSRE.L	Y	22.59	1626.8101	-0.5	814.4119	2	13.15	1877	1	142	155	

total 3 peptides

tr|A0A7N8XJX7|A0A7N8XJX7_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	Y	42.46	1329.6638	-0.6	665.8388	2	12.27	1723	1	225	236	
D.VLEDPVEILDN.S	Y	35.61	1254.6343	-0.3	628.3242	2	13.52	1941	1	145	155	
D.VLEDPVEILDNSRE.L	Y	22.59	1626.8101	-0.5	814.4119	2	13.15	1877	1	145	158	

total 3 peptides

tr|A0A3Q3SHA7|A0A3Q3SHA7_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	Y	42.46	1329.6638	-0.6	665.8388	2	12.27	1723	1	237	248	
D.VLEDPVEILDN.S	Y	35.61	1254.6343	-0.3	628.3242	2	13.52	1941	1	157	167	
D.VLEDPVEILDNSRE.L	Y	22.59	1626.8101	-0.5	814.4119	2	13.15	1877	1	157	170	

total 3 peptides

tr|A0A7N8XSZ9|A0A7N8XSZ9_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	Y	42.46	1329.6638	-0.6	665.8388	2	12.27	1723	1	237	248	
D.VLEDPVEILDN.S	Y	35.61	1254.6343	-0.3	628.3242	2	13.52	1941	1	157	167	
D.VLEDPVEILDNSRE.L	Y	22.59	1626.8101	-0.5	814.4119	2	13.15	1877	1	157	170	

total 3 peptides

tr|A0A7N8XRW1|A0A7N8XRW1_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	Y	42.46	1329.6638	-0.6	665.8388	2	12.27	1723	1	238	249	
D.VLEDPVEILDN.S	Y	35.61	1254.6343	-0.3	628.3242	2	13.52	1941	1	158	168	
D.VLEDPVEILDNSRE.L	Y	22.59	1626.8101	-0.5	814.4119	2	13.15	1877	1	158	171	

total 3 peptides

tr|A0A7N8Y2R6|A0A7N8Y2R6_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	Y	42.46	1329.6638	-0.6	665.8388	2	12.27	1723	1	238	249	
D.VLEDPVEILDN.S	Y	35.61	1254.6343	-0.3	628.3242	2	13.52	1941	1	158	168	
D.VLEDPVEILDNSRE.L	Y	22.59	1626.8101	-0.5	814.4119	2	13.15	1877	1	158	171	

total 3 peptides

tr|A0A7N8Y336|A0A7N8Y336_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	Y	42.46	1329.6638	-0.6	665.8388	2	12.27	1723	1	241	252	
D.VLEDPVEILDN.S	Y	35.61	1254.6343	-0.3	628.3242	2	13.52	1941	1	161	171	
D.VLEDPVEILDNSRE.L	Y	22.59	1626.8101	-0.5	814.4119	2	13.15	1877	1	161	174	

total 3 peptides

tr|A0A1A8GBU0|A0A1A8GBU0_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.GDSDGDGKIGVDEF.A	N	35.47	1409.5946	-1.1	705.8038	2	11.99	1675	1	90	103	

total 4 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.GFIEEEELK.L	N	31.42	1092.5338	-0.1	547.2741	2	11.80	1641	1	57	65	
F.AVIDQDKSGFIEEEELK.L	Y	29.62	1948.9629	-18.8	975.4704	2	12.63	1786	1	49	65	
Q.DKSGFIEEEELK.L	N	25.85	1422.6877	-0.4	712.3508	2	11.40	1570	1	54	65	

total 4 peptides

tr|A0A3B3ZS88|A0A3B3ZS88_9GOBI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	56.63	1457.7725	5.3	729.8974	2	10.03	1354	2	157	168	
R.AERAEQQR.V	Y	20.06	986.4893	-0.1	494.2519	2	7.59	1018	1	66	73	

total 2 peptides

tr|A0A3Q1CJW7|A0A3Q1CJW7_AMPOC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	56.63	1457.7725	5.3	729.8974	2	10.03	1354	2	157	168	
R.AERAEQQR.V	Y	20.06	986.4893	-0.1	494.2519	2	7.59	1018	1	66	73	

total 2 peptides

tr|A0A3Q3EFK1|A0A3Q3EFK1_9LABR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	56.63	1457.7725	5.3	729.8974	2	10.03	1354	2	162	173	
R.AERAEQQR.I	Y	20.06	986.4893	-0.1	494.2519	2	7.59	1018	1	71	78	

total 2 peptides

tr|A0A3Q3AF19|A0A3Q3AF19_KRYMA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	56.63	1457.7725	5.3	729.8974	2	10.03	1354	2	162	173	
R.AERAEQQR.V	Y	20.06	986.4893	-0.1	494.2519	2	7.59	1018	1	71	78	

total 2 peptides

tr|A0A3Q3AF32|A0A3Q3AF32_KRYMA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	56.63	1457.7725	5.3	729.8974	2	10.03	1354	2	171	182	
R.AERAEQQR.V	Y	20.06	986.4893	-0.1	494.2519	2	7.59	1018	1	80	87	

total 2 peptides

tr|A0A3P8UNE3|A0A3P8UNE3_CYNSE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	56.63	1457.7725	5.3	729.8974	2	10.03	1354	2	168	179	
R.AERAEQQR.V	Y	20.06	986.4893	-0.1	494.2519	2	7.59	1018	1	77	84	

total 2 peptides

tr|A0A672Y3T4|A0A672Y3T4_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	56.63	1457.7725	5.3	729.8974	2	10.03	1354	2	168	179	
R.AERAEQQR.V	Y	20.06	986.4893	-0.1	494.2519	2	7.59	1018	1	77	84	

total 2 peptides

tr|A0A3P8UNF6|A0A3P8UNF6_CYNSE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	56.63	1457.7725	5.3	729.8974	2	10.03	1354	2	190	201	
R.AERAEQQR.V	Y	20.06	986.4893	-0.1	494.2519	2	7.59	1018	1	99	106	

total 2 peptides

tr|A0A3B4UYC0|A0A3B4UYC0_SERDU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	56.63	1457.7725	5.3	729.8974	2	10.03	1354	2	159	170	
R.AERAEQQR.V	Y	20.06	986.4893	-0.1	494.2519	2	7.59	1018	1	68	75	

total 2 peptides

tr|A0A3P8URR7|A0A3P8URR7_CYNSE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	56.63	1457.7725	5.3	729.8974	2	10.03	1354	2	169	180	
R.AERAEQQR.V	Y	20.06	986.4893	-0.1	494.2519	2	7.59	1018	1	78	85	

total 2 peptides

tr|A0A3P8URM3|A0A3P8URM3_CYNSE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	56.63	1457.7725	5.3	729.8974	2	10.03	1354	2	193	204	
R.AERAEQQR.V	Y	20.06	986.4893	-0.1	494.2519	2	7.59	1018	1	102	109	

total 2 peptides

tr|A0A3Q3XL97|A0A3Q3XL97_MOLML
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	56.63	1457.7725	5.3	729.8974	2	10.03	1354	2	204	215	
R.AERAEQQR.V	Y	20.06	986.4893	-0.1	494.2519	2	7.59	1018	1	113	120	

total 2 peptides

tr|A0A3P8ULW6|A0A3P8ULW6_CYNSE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	56.63	1457.7725	5.3	729.8974	2	10.03	1354	2	206	217	
R.AERAEQQR.V	Y	20.06	986.4893	-0.1	494.2519	2	7.59	1018	1	115	122	

total 2 peptides

tr|A0A5C6P7G2|A0A5C6P7G2_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	56.63	1457.7725	5.3	729.8974	2	10.03	1354	2	211	222	
R.AERAEQQR.I	Y	20.06	986.4893	-0.1	494.2519	2	7.59	1018	1	120	127	

total 2 peptides

tr|A0A3Q1CRB3|A0A3Q1CRB3_AMPOC
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	56.63	1457.7725	5.3	729.8974	2	10.03	1354	2	214	225	
R.AERAEQQR.V	Y	20.06	986.4893	-0.1	494.2519	2	7.59	1018	1	123	130	

total 2 peptides

tr|A0A665T7Y2|A0A665T7Y2_ECHNA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	56.63	1457.7725	5.3	729.8974	2	10.03	1354	2	220	231	
R.AERAEQQR.I	Y	20.06	986.4893	-0.1	494.2519	2	7.59	1018	1	129	136	

total 2 peptides

tr|A0A3Q1BEW8|A0A3Q1BEW8_AMPOC
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	56.63	1457.7725	5.3	729.8974	2	10.03	1354	2	220	231	
R.AERAEQQR.V	Y	20.06	986.4893	-0.1	494.2519	2	7.59	1018	1	129	136	

total 2 peptides

tr|A0A3P8THB6|A0A3P8THB6_AMPPE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	56.63	1457.7725	5.3	729.8974	2	10.03	1354	2	229	240	
R.AERAEQQR.V	Y	20.06	986.4893	-0.1	494.2519	2	7.59	1018	1	138	145	

total 2 peptides

tr|A0A672YCL7|A0A672YCL7_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	56.63	1457.7725	5.3	729.8974	2	10.03	1354	2	223	234	
R.AERAEQQR.V	Y	20.06	986.4893	-0.1	494.2519	2	7.59	1018	1	132	139	

total 2 peptides

tr|A0A672YCL2|A0A672YCL2_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	56.63	1457.7725	5.3	729.8974	2	10.03	1354	2	229	240	
R.AERAEQQR.V	Y	20.06	986.4893	-0.1	494.2519	2	7.59	1018	1	138	145	

total 2 peptides

tr|A0A6P7KCL6|A0A6P7KCL6_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	56.63	1457.7725	5.3	729.8974	2	10.03	1354	2	233	244	
R.AERAEQQR.V	Y	20.06	986.4893	-0.1	494.2519	2	7.59	1018	1	142	149	

total 2 peptides

tr|A0A6P7KCQ1|A0A6P7KCQ1_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	56.63	1457.7725	5.3	729.8974	2	10.03	1354	2	236	247	
R.AERAEQQR.V	Y	20.06	986.4893	-0.1	494.2519	2	7.59	1018	1	145	152	

total 2 peptides

tr|A0A6P7KDL5|A0A6P7KDL5_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEKTIDDLEDELY.A	Y	35.82	1594.7614	-1.1	798.3871	2	13.31	1904	1	249	261	
K.AAEDRSKQLEDDLVAL.Q	Y	28.57	1771.8951	-1.0	886.9540	2	12.87	1828	1	31	46	
K.LEKTIDDLEDE.L	Y	23.72	1318.6140	-0.4	660.3140	2	11.50	1588	1	249	259	
K.LKGTEDELDKY.S	Y	18.29	1309.6401	-0.1	437.5539	3	10.75	1459	1	50	60	
K.LEKTIDDLEDELYAQ.K	Y	15.24	1793.8571	-1.4	897.9346	2	13.29	1900	1	249	263	

total 5 peptides

tr|A0A6P7MR93|A0A6P7MR93_BETSP
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEKTIDDLEDELY.A	Y	35.82	1594.7614	-1.1	798.3871	2	13.31	1904	1	249	261	
K.AAEDRSKQLEDDLVAL.Q	Y	28.57	1771.8951	-1.0	886.9540	2	12.87	1828	1	31	46	
K.LEKTIDDLEDE.L	Y	23.72	1318.6140	-0.4	660.3140	2	11.50	1588	1	249	259	
K.LKGTEDELDKY.S	Y	18.29	1309.6401	-0.1	437.5539	3	10.75	1459	1	50	60	
K.LEKTIDDLEDELYAQ.K	Y	15.24	1793.8571	-1.4	897.9346	2	13.29	1900	1	249	263	

total 5 peptides

tr|X2J4M2|X2J4M2_PAROL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEKTIDDLEDELY.A	Y	35.82	1594.7614	-1.1	798.3871	2	13.31	1904	1	249	261	
K.AAEDRSKQLEDDLVAL.Q	Y	28.57	1771.8951	-1.0	886.9540	2	12.87	1828	1	31	46	
K.LEKTIDDLEDE.L	Y	23.72	1318.6140	-0.4	660.3140	2	11.50	1588	1	249	259	
K.LKGTEDELDKY.S	Y	18.29	1309.6401	-0.1	437.5539	3	10.75	1459	1	50	60	
K.LEKTIDDLEDELYAQ.K	Y	15.24	1793.8571	-1.4	897.9346	2	13.29	1900	1	249	263	

total 5 peptides

tr|A0A3P9D7I0|A0A3P9D7I0_9CICH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEKTIDDLEDELY.A	Y	35.82	1594.7614	-1.1	798.3871	2	13.31	1904	1	249	261	
K.AAEDRSKQLEDDLVAL.Q	Y	28.57	1771.8951	-1.0	886.9540	2	12.87	1828	1	31	46	
K.LEKTIDDLEDE.L	Y	23.72	1318.6140	-0.4	660.3140	2	11.50	1588	1	249	259	
K.LKGTEDELDKY.S	Y	18.29	1309.6401	-0.1	437.5539	3	10.75	1459	1	50	60	
K.LEKTIDDLEDELYAQ.K	Y	15.24	1793.8571	-1.4	897.9346	2	13.29	1900	1	249	263	

total 5 peptides

tr|A0A665VR95|A0A665VR95_ECHNA
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEKTIDDLEDELY.A	Y	35.82	1594.7614	-1.1	798.3871	2	13.31	1904	1	249	261	
K.AAEDRSKQLEDDLVAL.Q	Y	28.57	1771.8951	-1.0	886.9540	2	12.87	1828	1	31	46	
K.LEKTIDDLEDE.L	Y	23.72	1318.6140	-0.4	660.3140	2	11.50	1588	1	249	259	
K.LKGTEDELDKY.S	Y	18.29	1309.6401	-0.1	437.5539	3	10.75	1459	1	50	60	
K.LEKTIDDLEDELYAQ.K	Y	15.24	1793.8571	-1.4	897.9346	2	13.29	1900	1	249	263	

total 5 peptides

tr|A0A3P9LRU7|A0A3P9LRU7_ORYLA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.GIDNPGHPFIM.T	Y	41.01	1196.5648	-0.7	599.2892	2	12.79	1813	1	60	70	
N.LKGGDDLDPNY.V	N	26.11	1205.5564	-0.8	603.7850	2	11.03	1505	1	115	125	
T.GIDNPGHPF.I	Y	19.24	952.4402	-0.2	477.2273	2	11.27	1547	2	60	68	
Q.LVVDGVKL.M	N	18.62	841.5273	-1.0	421.7705	2	12.90	1832	1	352	359	

total 4 peptides

tr|A0A2I4BW49|A0A2I4BW49_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.GIDNPGHPFIM.T	Y	41.01	1196.5648	-0.7	599.2892	2	12.79	1813	1	60	70	
N.LKGGDDLDPNY.V	N	26.11	1205.5564	-0.8	603.7850	2	11.03	1505	1	115	125	
T.GIDNPGHPF.I	Y	19.24	952.4402	-0.2	477.2273	2	11.27	1547	2	60	68	
Q.LVVDGVKL.M	N	18.62	841.5273	-1.0	421.7705	2	12.90	1832	1	352	359	

total 4 peptides

tr|A0A3B3I369|A0A3B3I369_ORYLA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.GIDNPGHPFIM.T	Y	41.01	1196.5648	-0.7	599.2892	2	12.79	1813	1	60	70	
N.LKGGDDLDPNY.V	N	26.11	1205.5564	-0.8	603.7850	2	11.03	1505	1	115	125	
T.GIDNPGHPF.I	Y	19.24	952.4402	-0.2	477.2273	2	11.27	1547	2	60	68	
Q.LVVDGVKL.M	N	18.62	841.5273	-1.0	421.7705	2	12.90	1832	1	352	359	

total 4 peptides

tr|A0A3P9HLZ1|A0A3P9HLZ1_ORYLA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.GIDNPGHPFIM.T	Y	41.01	1196.5648	-0.7	599.2892	2	12.79	1813	1	60	70	
N.LKGGDDLDPNY.V	N	26.11	1205.5564	-0.8	603.7850	2	11.03	1505	1	115	125	
T.GIDNPGHPF.I	Y	19.24	952.4402	-0.2	477.2273	2	11.27	1547	2	60	68	
Q.LVVDGVKL.M	N	18.62	841.5273	-1.0	421.7705	2	12.90	1832	1	352	359	

total 4 peptides

tr|A0A3P8WTN2|A0A3P8WTN2_CYNSE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.GIDNPGHPFIM.T	Y	41.01	1196.5648	-0.7	599.2892	2	12.79	1813	1	60	70	
N.LKGGDDLDPNY.V	N	26.11	1205.5564	-0.8	603.7850	2	11.03	1505	1	115	125	
T.GIDNPGHPF.I	Y	19.24	952.4402	-0.2	477.2273	2	11.27	1547	2	60	68	
Q.LVVDGVKL.M	N	18.62	841.5273	-1.0	421.7705	2	12.90	1832	1	352	359	

total 4 peptides

tr|A0A3P8Q9R4|A0A3P8Q9R4_ASTCA

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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.GVDNPGHPF.I	Y	34.94	938.4246	-0.6	470.2193	2	10.88	1479	2	59	67	
T.GVDNPGHPFIM.T	Y	27.25	1182.5492	-0.4	592.2816	2	12.47	1757	1	59	69	
N.LKGGDDLDPNY.V	N	26.11	1205.5564	-0.8	603.7850	2	11.03	1505	1	114	124	
Q.LVVDGVKL.M	N	18.62	841.5273	-1.0	421.7705	2	12.90	1832	1	351	358	

total 4 peptides

tr|A0A6P7JDS0|A0A6P7JDS0_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.GVDNPGHPF.I	Y	34.94	938.4246	-0.6	470.2193	2	10.88	1479	2	141	149	
T.GVDNPGHPFIM.T	Y	27.25	1182.5492	-0.4	592.2816	2	12.47	1757	1	141	151	
N.LKGGDDLDPNY.V	N	26.11	1205.5564	-0.8	603.7850	2	11.03	1505	1	196	206	
Q.LVVDGVKL.M	N	18.62	841.5273	-1.0	421.7705	2	12.90	1832	1	433	440	

total 4 peptides

tr|A0A3Q2Q7Q3|A0A3Q2Q7Q3_FUNHE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.GVDNPGHPF.I	Y	34.94	938.4246	-0.6	470.2193	2	10.88	1479	2	61	69	
T.GVDNPGHPFIM.T	Y	27.25	1182.5492	-0.4	592.2816	2	12.47	1757	1	61	71	
N.LKGGDDLDPNY.V	N	26.11	1205.5564	-0.8	603.7850	2	11.03	1505	1	116	126	
Q.LVVDGVKL.M	N	18.62	841.5273	-1.0	421.7705	2	12.90	1832	1	315	322	

total 4 peptides

tr|A0A3B4BZV1|A0A3B4BZV1_PYGNA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.GVDNPGHPF.I	Y	34.94	938.4246	-0.6	470.2193	2	10.88	1479	2	59	67	
T.GVDNPGHPFIM.T	Y	27.25	1182.5492	-0.4	592.2816	2	12.47	1757	1	59	69	
N.LKGGDDLDPNY.V	N	26.11	1205.5564	-0.8	603.7850	2	11.03	1505	1	114	124	
Q.LVVDGVKL.M	N	18.62	841.5273	-1.0	421.7705	2	12.90	1832	1	351	358	

total 4 peptides

tr|A0A6P7PB38|A0A6P7PB38_BETSP
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.GVDNPGHPF.I	Y	34.94	938.4246	-0.6	470.2193	2	10.88	1479	2	59	67	
T.GVDNPGHPFIM.T	Y	27.25	1182.5492	-0.4	592.2816	2	12.47	1757	1	59	69	
N.LKGGDDLDPNY.V	N	26.11	1205.5564	-0.8	603.7850	2	11.03	1505	1	114	124	
Q.LVVDGVKL.M	N	18.62	841.5273	-1.0	421.7705	2	12.90	1832	1	351	358	

total 4 peptides

tr|A0A3P8NKE2|A0A3P8NKE2_ASTCA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.GVDNPGHPF.I	Y	34.94	938.4246	-0.6	470.2193	2	10.88	1479	2	60	68	
T.GVDNPGHPFIM.T	Y	27.25	1182.5492	-0.4	592.2816	2	12.47	1757	1	60	70	
N.LKGGDDLDPNY.V	N	26.11	1205.5564	-0.8	603.7850	2	11.03	1505	1	115	125	

total 4 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.LVVDGVKL.M	N	18.62	841.5273	-1.0	421.7705	2	12.90	1832	1	352	359	

total 4 peptides

tr|A0A6P7JIX2|A0A6P7JIX2_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.GVDNPGHPF.I	Y	34.94	938.4246	-0.6	470.2193	2	10.88	1479	2	60	68	
T.GVDNPGHPFIM.T	Y	27.25	1182.5492	-0.4	592.2816	2	12.47	1757	1	60	70	
N.LKGGDDLDPNY.V	N	26.11	1205.5564	-0.8	603.7850	2	11.03	1505	1	115	125	
Q.LVVDGVKL.M	N	18.62	841.5273	-1.0	421.7705	2	12.90	1832	1	352	359	

total 4 peptides

tr|A0A6P7PLI8|A0A6P7PLI8_BETSP
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.GVDNPGHPF.I	Y	34.94	938.4246	-0.6	470.2193	2	10.88	1479	2	60	68	
T.GVDNPGHPFIM.T	Y	27.25	1182.5492	-0.4	592.2816	2	12.47	1757	1	60	70	
N.LKGGDDLDPNY.V	N	26.11	1205.5564	-0.8	603.7850	2	11.03	1505	1	115	125	
Q.LVVDGVKL.M	N	18.62	841.5273	-1.0	421.7705	2	12.90	1832	1	352	359	

total 4 peptides

tr|A0A674PS54|A0A674PS54_TAKRU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.GVDNPGHPF.I	Y	34.94	938.4246	-0.6	470.2193	2	10.88	1479	2	54	62	
T.GVDNPGHPFIM.T	Y	27.25	1182.5492	-0.4	592.2816	2	12.47	1757	1	54	64	
N.LKGGDDLDPNY.V	N	26.11	1205.5564	-0.8	603.7850	2	11.03	1505	1	109	119	
Q.LVVDGVKL.M	N	18.62	841.5273	-1.0	421.7705	2	12.90	1832	1	334	341	

total 4 peptides

tr|A0A437CN94|A0A437CN94_ORYJA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.GVDNPGHPF.I	Y	34.94	938.4246	-0.6	470.2193	2	10.88	1479	2	60	68	
T.GVDNPGHPFIM.T	Y	27.25	1182.5492	-0.4	592.2816	2	12.47	1757	1	60	70	
N.LKGGDDLDPNY.V	N	26.11	1205.5564	-0.8	603.7850	2	11.03	1505	1	115	125	
Q.LVVDGVKL.M	N	18.62	841.5273	-1.0	421.7705	2	12.90	1832	1	352	359	

total 4 peptides

tr|A0A6J2R235|A0A6J2R235_COTGO
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.GVDNPGHPF.I	Y	34.94	938.4246	-0.6	470.2193	2	10.88	1479	2	60	68	
T.GVDNPGHPFIM.T	Y	27.25	1182.5492	-0.4	592.2816	2	12.47	1757	1	60	70	
N.LKGGDDLDPNY.V	N	26.11	1205.5564	-0.8	603.7850	2	11.03	1505	1	115	125	
Q.LVVDGVKL.M	N	18.62	841.5273	-1.0	421.7705	2	12.90	1832	1	352	359	

total 4 peptides

tr|A0A4U5VU95|A0A4U5VU95_COLLU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.AFPPDVAGN.V	Y	29.50	886.4185	-0.5	444.2163	2	11.38	1567	3	122	130	
T.IIDQNRDGIISKD.D	Y	24.69	1485.7787	0.3	743.8969	2	10.47	1413	1	16	28	
S.KDDLRDVLAS.M	Y	24.23	1130.5931	-0.5	566.3036	2	11.55	1597	1	27	36	
K.LKGADPEDVILS.A	Y	19.92	1255.6659	-0.1	628.8401	2	12.66	1790	2	71	82	
K.GADPEDVILS.A	Y	15.25	1014.4869	-0.1	508.2507	2	12.72	1801	1	73	82	
F.GEKLKGADPEDVILS.A	Y	15.24	1569.8250	-0.6	785.9193	2	11.75	1631	1	68	82	

total 6 peptides

tr|A0A6P7II88|A0A6P7II88_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.AFPPDVAGN.V	Y	29.50	886.4185	-0.5	444.2163	2	11.38	1567	3	144	152	
T.IIDQNRDGIISKD.D	Y	24.69	1485.7787	0.3	743.8969	2	10.47	1413	1	38	50	
S.KDDLRDVLAS.M	Y	24.23	1130.5931	-0.5	566.3036	2	11.55	1597	1	49	58	
K.LKGADPEDVILS.A	Y	19.92	1255.6659	-0.1	628.8401	2	12.66	1790	2	93	104	
K.GADPEDVILS.A	Y	15.25	1014.4869	-0.1	508.2507	2	12.72	1801	1	95	104	
F.GEKLKGADPEDVILS.A	Y	15.24	1569.8250	-0.6	785.9193	2	11.75	1631	1	90	104	

total 6 peptides

tr|A0A672MA11|A0A672MA11_SINGR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.AFPPDVAGN.V	Y	29.50	886.4185	-0.5	444.2163	2	11.38	1567	3	116	124	
T.IIDQNRDGIISKD.D	Y	24.69	1485.7787	0.3	743.8969	2	10.47	1413	1	10	22	
S.KDDLRDVLAS.M	Y	24.23	1130.5931	-0.5	566.3036	2	11.55	1597	1	21	30	
K.LKGADPEDVILS.A	Y	19.92	1255.6659	-0.1	628.8401	2	12.66	1790	2	65	76	
K.GADPEDVILS.A	Y	15.25	1014.4869	-0.1	508.2507	2	12.72	1801	1	67	76	
F.GEKLKGADPEDVILS.A	Y	15.24	1569.8250	-0.6	785.9193	2	11.75	1631	1	62	76	

total 6 peptides

tr|A0A669DZW9|A0A669DZW9_ORENI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.AFPPDVAGN.V	Y	29.50	886.4185	-0.5	444.2163	2	11.38	1567	3	135	143	
T.IIDQNRDGIISKD.D	Y	24.69	1485.7787	0.3	743.8969	2	10.47	1413	1	29	41	
S.KDDLRDVLAS.M	Y	24.23	1130.5931	-0.5	566.3036	2	11.55	1597	1	40	49	
K.LKGADPEDVILS.A	Y	19.92	1255.6659	-0.1	628.8401	2	12.66	1790	2	84	95	
K.GADPEDVILS.A	Y	15.25	1014.4869	-0.1	508.2507	2	12.72	1801	1	86	95	
F.GEKLKGADPEDVILS.A	Y	15.24	1569.8250	-0.6	785.9193	2	11.75	1631	1	81	95	

total 6 peptides

tr|A0A3B4BW75|A0A3B4BW75_PYGNA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.AFPPDVAGN.V	Y	29.50	886.4185	-0.5	444.2163	2	11.38	1567	3	136	144	
T.IIDQNRDGIISKD.D	Y	24.69	1485.7787	0.3	743.8969	2	10.47	1413	1	30	42	
S.KDDLRDVLAS.M	Y	24.23	1130.5931	-0.5	566.3036	2	11.55	1597	1	41	50	
K.LKGADPEDVILS.G	Y	19.92	1255.6659	-0.1	628.8401	2	12.66	1790	2	85	96	
K.GADPEDVILS.G	Y	15.25	1014.4869	-0.1	508.2507	2	12.72	1801	1	87	96	
F.GEKLKGADPEDVILS.G	Y	15.24	1569.8250	-0.6	785.9193	2	11.75	1631	1	82	96	

total 6 peptides

tr|I3JU24|I3JU24_ORENI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.AFPPDVAGN.V	Y	29.50	886.4185	-0.5	444.2163	2	11.38	1567	3	137	145	
T.IIDQNRDGIISKD.D	Y	24.69	1485.7787	0.3	743.8969	2	10.47	1413	1	31	43	
S.KDDLRDVLAS.M	Y	24.23	1130.5931	-0.5	566.3036	2	11.55	1597	1	42	51	
K.LKGADPEDVILS.A	Y	19.92	1255.6659	-0.1	628.8401	2	12.66	1790	2	86	97	
K.GADPEDVILS.A	Y	15.25	1014.4869	-0.1	508.2507	2	12.72	1801	1	88	97	
F.GEKLKGADPEDVILS.A	Y	15.24	1569.8250	-0.6	785.9193	2	11.75	1631	1	83	97	

total 6 peptides

tr|A0A7J6CHK6|A0A7J6CHK6_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.AFPPDVAGN.V	Y	29.50	886.4185	-0.5	444.2163	2	11.38	1567	3	143	151	
T.IIDQNRDGIISKD.D	Y	24.69	1485.7787	0.3	743.8969	2	10.47	1413	1	37	49	
S.KDDLRDVLAS.M	Y	24.23	1130.5931	-0.5	566.3036	2	11.55	1597	1	48	57	
K.LKGADPEDVILS.A	Y	19.92	1255.6659	-0.1	628.8401	2	12.66	1790	2	92	103	
K.GADPEDVILS.A	Y	15.25	1014.4869	-0.1	508.2507	2	12.72	1801	1	94	103	
F.GEKLKGADPEDVILS.A	Y	15.24	1569.8250	-0.6	785.9193	2	11.75	1631	1	89	103	

total 6 peptides

tr|A0A0F8CBC9|A0A0F8CBC9_LARCR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.AFPPDVAGN.V	Y	29.50	886.4185	-0.5	444.2163	2	11.38	1567	3	144	152	
T.IIDQNRDGIISKD.D	Y	24.69	1485.7787	0.3	743.8969	2	10.47	1413	1	38	50	
S.KDDLRDVLAS.M	Y	24.23	1130.5931	-0.5	566.3036	2	11.55	1597	1	49	58	
K.LKGADPEDVILS.A	Y	19.92	1255.6659	-0.1	628.8401	2	12.66	1790	2	93	104	
K.GADPEDVILS.A	Y	15.25	1014.4869	-0.1	508.2507	2	12.72	1801	1	95	104	
F.GEKLKGADPEDVILS.A	Y	15.24	1569.8250	-0.6	785.9193	2	11.75	1631	1	90	104	

total 6 peptides

tr|A0A7N8XBQ9|A0A7N8XBQ9_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.AFPPDVAGN.V	Y	29.50	886.4185	-0.5	444.2163	2	11.38	1567	3	166	174	
T.IIDQNRDGIISKD.D	Y	24.69	1485.7787	0.3	743.8969	2	10.47	1413	1	60	72	
S.KDDLRDVLAS.M	Y	24.23	1130.5931	-0.5	566.3036	2	11.55	1597	1	71	80	
K.LKGADPEDVILS.A	Y	19.92	1255.6659	-0.1	628.8401	2	12.66	1790	2	115	126	
K.GADPEDVILS.A	Y	15.25	1014.4869	-0.1	508.2507	2	12.72	1801	1	117	126	
F.GEKLKGADPEDVILS.A	Y	15.24	1569.8250	-0.6	785.9193	2	11.75	1631	1	112	126	

total 6 peptides

tr|F8U029|F8U029_EPIBR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.AFPPDVAGN.V	Y	29.50	886.4185	-0.5	444.2163	2	11.38	1567	3	144	152	
T.IIDQNRDGIISKD.D	Y	24.69	1485.7787	0.3	743.8969	2	10.47	1413	1	38	50	
S.KDDLRDVLAS.L	Y	24.23	1130.5931	-0.5	566.3036	2	11.55	1597	1	49	58	
K.LKGADPEDVILS.S	Y	19.92	1255.6659	-0.1	628.8401	2	12.66	1790	2	93	104	
K.GADPEDVILS.S	Y	15.25	1014.4869	-0.1	508.2507	2	12.72	1801	1	95	104	
F.GEKLKGADPEDVILS.S	Y	15.24	1569.8250	-0.6	785.9193	2	11.75	1631	1	90	104	

total 6 peptides

tr|A0A3B5RBY4|A0A3B5RBY4_XIPMA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.AFPPDVAGN.V	Y	29.50	886.4185	-0.5	444.2163	2	11.38	1567	3	223	231	
T.IIDQNRDGIISKD.D	Y	24.69	1485.7787	0.3	743.8969	2	10.47	1413	1	117	129	
S.KDDLRDVLAS.M	Y	24.23	1130.5931	-0.5	566.3036	2	11.55	1597	1	128	137	
K.LKGADPEDVILS.A	Y	19.92	1255.6659	-0.1	628.8401	2	12.66	1790	2	172	183	
K.GADPEDVILS.A	Y	15.25	1014.4869	-0.1	508.2507	2	12.72	1801	1	174	183	
F.GEKLKGADPEDVILS.A	Y	15.24	1569.8250	-0.6	785.9193	2	11.75	1631	1	169	183	

total 6 peptides

tr|G3N515|G3N515_GASAC
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.ILPPGPPTPW.I	N	38.27	1073.5909	0.1	537.8028	2	13.74	1976	1	3917	3926	
L.IVEELPVKW.L	N	27.75	1111.6277	-1.0	556.8206	2	13.27	1897	1	130	138	
N.LDVIDVPAPVKN.L	Y	17.46	1278.7183	-0.5	640.3661	2	12.62	1784	1	1994	2005	

total 3 peptides

tr|Q4T444|Q4T444_TETNG
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.ILPPGPPTPW.I	N	38.27	1073.5909	0.1	537.8028	2	13.74	1976	1	4399	4408	
L.IVEELPVKW.V	N	27.75	1111.6277	-1.0	556.8206	2	13.27	1897	1	625	633	
F.LLWEPPK.Y	Y	16.69	881.5010	-0.4	441.7576	2	11.92	1663	1	3071	3077	

total 3 peptides

tr|D2KQG3|D2KQG3_SINCH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.EVIDQDKSGFIE.E	Y	45.95	1378.6616	-0.9	690.3375	2	12.49	1760	7	49	60	
A.FEVIDQDKSGFIE.E	Y	21.69	1525.7300	-1.1	763.8714	2	12.69	1796	1	48	60	

total 2 peptides

tr|B9VJM3|B9VJM3_SINCH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.EVIDQDKSGFIE.E	Y	45.95	1378.6616	-0.9	690.3375	2	12.49	1760	7	49	60	
A.FEVIDQDKSGFIE.E	Y	21.69	1525.7300	-1.1	763.8714	2	12.69	1796	1	48	60	

total 2 peptides

tr|A0A3P8TDG8|A0A3P8TDG8_AMPPE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VDSELPVDDVFAQV.S	Y	30.65	1531.7406	0.1	766.8776	2	14.97	2185	1	173	186	
P.LDTVLDMIKDA.M	N	20.90	1232.6322	-0.8	617.3229	2	14.44	2094	1	69	79	
L.DTVLDMIK.D	N	17.70	933.4841	-1.1	467.7488	2	13.23	1891	1	70	77	
D.TVLDMIKDA.M	N	16.00	1004.5212	-1.1	503.2673	2	13.42	1923	1	71	79	
K.VDSELPVDDVF.A	N	15.68	1233.5764	-0.5	617.7952	2	14.17	2049	1	173	183	

total 5 peptides

tr|A0A556TIT9|A0A556TIT9_BAGYA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.GFIEEEELK.L	N	31.42	1092.5338	-0.1	547.2741	2	11.80	1641	1	57	65	
Q.DKSGFIEEEELK.L	N	25.85	1422.6877	-0.4	712.3508	2	11.40	1570	1	54	65	
F.LAAGDSDGDGKIGVD.A	N	25.04	1388.6418	-0.5	695.3278	2	10.74	1456	1	87	101	

total 3 peptides

tr|A0A484CUS5|A0A484CUS5_PERFV
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.ILPPGPPTPW.I	N	38.27	1073.5909	0.1	537.8028	2	13.74	1976	1	1746	1755	
T.VVDRPTPPVGPVVF.E	Y	27.22	1477.8292	-1.8	739.9206	2	13.07	1861	1	3654	3667	

total 2 peptides

tr|A0A2I4CWS8|A0A2I4CWS8_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.TGREFDDLPLHEQ.S	Y	28.57	1555.7267	-0.4	778.8703	2	11.70	1623	1	651	663	
E.IVPGDIVEV.S	Y	24.00	939.5276	-0.7	470.7708	2	13.35	1910	1	145	153	
E.FDDLPLHEQ.S	Y	19.12	1112.5138	-0.1	557.2641	2	11.86	1652	1	655	663	

total 3 peptides

tr|A0A3P9C9M1|A0A3P9C9M1_9CICH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.TGREFDDLPLHEQ.S	Y	28.57	1555.7267	-0.4	778.8703	2	11.70	1623	1	651	663	
E.IVPGDIVEV.S	Y	24.00	939.5276	-0.7	470.7708	2	13.35	1910	1	145	153	
E.FDDLPLHEQ.S	Y	19.12	1112.5138	-0.1	557.2641	2	11.86	1652	1	655	663	

total 3 peptides

tr|A0A7J6CZM2|A0A7J6CZM2_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.TVEDPFDQDDWE.A	Y	43.01	1494.5786	-0.2	748.2964	2	14.25	2062	1	344	355	

total 1 peptides

tr|A0A0F8AZU0|A0A0F8AZU0_LARCR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.GFIEEEELK.L	N	31.42	1092.5338	-0.1	547.2741	2	11.80	1641	1	57	65	
R.EGEEEK.K	N	16.22	719.2973	0.9	360.6562	2	7.44	989	1	269	274	

total 2 peptides

tr|A0A4W4GVK8|A0A4W4GVK8_ELEEL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	92	102	

total 1 peptides

tr|A0A4W4GPW6|A0A4W4GPW6_ELEEL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	94	104	

total 1 peptides

tr|A0A4W4GW96|A0A4W4GW96_ELEEL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	95	105	

total 1 peptides

tr|A0A665WHZ7|A0A665WHZ7_ECHNA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	89	99	

total 1 peptides

tr|A0A3B4FQL1|A0A3B4FQL1_9CICH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	94	104	

total 1 peptides

tr|A0A3P8PB88|A0A3P8PB88_ASTCA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	94	104	

total 1 peptides

tr|A0A665WHJ1|A0A665WHJ1_ECHNA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	94	104	

total 1 peptides

tr|F2WR27|F2WR27_EPICO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	94	104	

total 1 peptides

tr|A0A4W6FFD1|A0A4W6FFD1_LATCA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	94	104	

total 1 peptides

tr|A0A3B3C1H6|A0A3B3C1H6_ORYME
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	94	104	

total 1 peptides

tr|A0A3Q1B309|A0A3Q1B309_AMPOC
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	94	104	

total 1 peptides

tr|A0A3B4VIP0|A0A3B4VIP0_SERDU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	103	113	

total 1 peptides

tr|A0A3B5RBB9|A0A3B5RBB9_XIPMA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	104	114	

total 1 peptides

tr|A0A3B5R1L0|A0A3B5R1L0_XIPMA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	105	115	

total 1 peptides

tr|A0A3P9CCX0|A0A3P9CCX0_9CICH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	94	104	

total 1 peptides

tr|A0A665WHZ4|A0A665WHZ4_ECHNA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	108	118	

total 1 peptides

tr|A0A4W6FCG2|A0A4W6FCG2_LATCA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	89	99	

total 1 peptides

tr|A0A4W6FFD6|A0A4W6FFD6_LATCA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	91	101	

total 1 peptides

tr|A0A665WI19|A0A665WI19_ECHNA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	115	125	

total 1 peptides

tr|B9V2Y1|B9V2Y1_EPICO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	115	125	

total 1 peptides

tr|A0A4W6FDH6|A0A4W6FDH6_LATCA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	101	111	

total 1 peptides

tr|A0A669EYH8|A0A669EYH8_ORENI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	94	104	

total 1 peptides

tr|A0A3B4VK07|A0A3B4VK07_SERDU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	163	173	

total 1 peptides

tr|A0A3B4VK38|A0A3B4VK38_SERDU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	163	173	

total 1 peptides

tr|A0A834C4M6|A0A834C4M6_ORYME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	106	116	

total 1 peptides

tr|A0A315W7Q8|A0A315W7Q8_GAMAF

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	128	138	

total 1 peptides

tr|A0A672K127|A0A672K127_SINGR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	95	105	

total 1 peptides

tr|A0A7J6DIX6|A0A7J6DIX6_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	95	105	

total 1 peptides

tr|A0A4W5MNE5|A0A4W5MNE5_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	87	97	

total 1 peptides

tr|A0A4W5MRK6|A0A4W5MRK6_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	96	106	

total 1 peptides

tr|A0A4W5MMD2|A0A4W5MMD2_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	122	132	

total 1 peptides

tr|A0A3Q3JIG8|A0A3Q3JIG8_MONAL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	137	147	

total 1 peptides

tr|Q90332|Q90332_CYPCA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	137	147	

total 1 peptides

tr|Q90WC7|Q90WC7_ONCMY
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	137	147	

total 1 peptides

tr|A0A7J6CQG1|A0A7J6CQG1_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	137	147	

total 1 peptides

tr|Q90W52|Q90W52_PSEDN

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	138	148	

total 1 peptides

tr|Q90W46|Q90W46_DECMR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	141	151	

total 1 peptides

tr|A0A4W5MQC0|A0A4W5MQC0_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	131	141	

total 1 peptides

tr|A0A0P7TY12|A0A0P7TY12_SCLFO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	93	103	

total 1 peptides

tr|A0A672GTD6|A0A672GTD6_SALFA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	93	103	

total 1 peptides

tr|A0A3P8V7S6|A0A3P8V7S6_CYNSE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	94	104	

total 1 peptides

tr|A0A671WWZ3|A0A671WWZ3_SPAAU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	97	107	

total 1 peptides

tr|A0A672GWW2|A0A672GWW2_SALFA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	99	109	

total 1 peptides

tr|A0A671X3G3|A0A671X3G3_SPAAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	102	112	

total 1 peptides

tr|A0A672H327|A0A672H327_SALFA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	102	112	

total 1 peptides

tr|A0A7N8Y8C7|A0A7N8Y8C7_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	95	105	

total 1 peptides

tr|A0A672GRY1|A0A672GRY1_SALFA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	109	119	

total 1 peptides

tr|A0A3Q2XPR8|A0A3Q2XPR8_HIPCM
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	126	136	

total 1 peptides

tr|A0A6J2QQE0|A0A6J2QQE0_COTGO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	126	136	

total 1 peptides

tr|A0A3Q3D9S9|A0A3Q3D9S9_HIPCM
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFDKEGNGTVM.G	Y	37.84	1195.5543	-0.9	598.7839	2	11.12	1522	1	139	149	

total 1 peptides

tr|A0A4Z2CI05|A0A4Z2CI05_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.IVEELPVKW.I	N	27.75	1111.6277	-1.0	556.8206	2	13.27	1897	1	770	778	
K.EGEEEK.K	N	16.22	719.2973	0.9	360.6562	2	7.44	989	1	4321	4326	

total 2 peptides

tr|Q4RE90|Q4RE90_TETNG
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.VVDRPQPPEGPVVF.N	Y	27.46	1534.8143	-1.0	768.4137	2	12.56	1774	1	4491	4504	
K.EGEEEK.K	N	16.22	719.2973	0.9	360.6562	2	7.44	989	1	2532	2537	

total 2 peptides

tr|A0A6F9CEX9|A0A6F9CEX9_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.IVEELPVKW.V	N	27.75	1111.6277	-1.0	556.8206	2	13.27	1897	1	577	585	
D.VFEPPGSDIVFE.V	Y	15.16	1334.6394	-0.2	668.3268	2	13.99	2019	1	2259	2270	

total 2 peptides

tr|A0A060W3X5|A0A060W3X5_ONCMY
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.IVEELPVKW.V	N	27.75	1111.6277	-1.0	556.8206	2	13.27	1897	1	1746	1754	
D.VFEPPGSDIVFE.V	Y	15.16	1334.6394	-0.2	668.3268	2	13.99	2019	1	3457	3468	

total 2 peptides

tr|A0A6P3W3B1|A0A6P3W3B1_CLUHA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.GYPDKIIIGM.D	Y	23.66	1105.5841	-1.5	553.7985	2	12.99	1847	1	235	244	
A.GYPDKIIIGMD.V	Y	15.88	1220.6111	-0.6	611.3124	2	12.77	1810	1	235	245	

total 2 peptides

tr|F5BZS7|F5BZS7_EPIBR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.GYPDKIIIGM.D	Y	23.66	1105.5841	-1.5	553.7985	2	12.99	1847	1	235	244	
A.GYPDKIIIGMD.V	Y	15.88	1220.6111	-0.6	611.3124	2	12.77	1810	1	235	245	

total 2 peptides

tr|A0A668V8T6|A0A668V8T6_OREAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.GYPDKIIIGM.D	Y	23.66	1105.5841	-1.5	553.7985	2	12.99	1847	1	235	244	
A.GYPDKIIIGMD.V	Y	15.88	1220.6111	-0.6	611.3124	2	12.77	1810	1	235	245	

total 2 peptides

tr|A0A4W4FGS3|A0A4W4FGS3_ELEEL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.GYPDKIIIGM.D	Y	23.66	1105.5841	-1.5	553.7985	2	12.99	1847	1	233	242	
A.GYPDKIIIGMD.V	Y	15.88	1220.6111	-0.6	611.3124	2	12.77	1810	1	233	243	

total 2 peptides

tr|A0A3B4CPC9|A0A3B4CPC9_PYGNA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.GYPDKIIIGM.D	Y	23.66	1105.5841	-1.5	553.7985	2	12.99	1847	1	235	244	
A.GYPDKIIIGMD.V	Y	15.88	1220.6111	-0.6	611.3124	2	12.77	1810	1	235	245	

total 2 peptides

tr|A0A3P8TVY9|A0A3P8TVY9_AMPPE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.GYPDKIIIGM.D	Y	23.66	1105.5841	-1.5	553.7985	2	12.99	1847	1	235	244	
A.GYPDKIIIGMD.V	Y	15.88	1220.6111	-0.6	611.3124	2	12.77	1810	1	235	245	

total 2 peptides

tr|A0A3P8NTT0|A0A3P8NTT0_ASTCA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.GYPDKIIIGM.D	Y	23.66	1105.5841	-1.5	553.7985	2	12.99	1847	1	246	255	
A.GYPDKIIIGMD.V	Y	15.88	1220.6111	-0.6	611.3124	2	12.77	1810	1	246	256	

total 2 peptides

tr|A0A7J6BP23|A0A7J6BP23_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	20	33	

total 1 peptides

tr|A0A4Z2FMJ8|A0A4Z2FMJ8_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	63	76	

total 1 peptides

tr|A0A1A8D9W7|A0A1A8D9W7_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	38	51	

total 1 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM

total 1 peptides

tr|A0A6P3VH61|A0A6P3VH61_CLUHA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	48	61	

total 1 peptides

tr|A0A3B4CI86|A0A3B4CI86_PYGNA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	48	61	

total 1 peptides

tr|A0A3B4E1V9|A0A3B4E1V9_PYGNA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	59	72	

total 1 peptides

tr|A0A6J2Q142|A0A6J2Q142_COTGO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	63	76	

total 1 peptides

tr|A0A3B4E4D7|A0A3B4E4D7_PYGNA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	63	76	

total 1 peptides

tr|H2SBN2|H2SBN2_TAKRU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	63	76	

total 1 peptides

tr|A0A2R8QMW7|A0A2R8QMW7_DANRE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	63	76	

total 1 peptides

tr|A0A4W4EUJ0|A0A4W4EUJ0_ELEEL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	63	76	

total 1 peptides

tr|A0A3Q3G540|A0A3Q3G540_9LABR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	63	76	

total 1 peptides

tr|G3NJM6|G3NJM6_GASAC
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	63	76	

total 1 peptides

tr|W5UMX1|W5UMX1_ICTPU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	63	76	

total 1 peptides

tr|A0A3P8P1R5|A0A3P8P1R5_ASTCA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	64	77	

total 1 peptides

tr|A0A4W4EW29|A0A4W4EW29_ELEEL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	64	77	

total 1 peptides

tr|A0A6P7IM54|A0A6P7IM54_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	64	77	

total 1 peptides

tr|A0A4W4EVB1|A0A4W4EVB1_ELEEL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	64	77	

total 1 peptides

tr|I3IZI3|I3IZI3_ORENI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	64	77	

total 1 peptides

tr|A0A3Q1CAA4|A0A3Q1CAA4_AMPOC
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	64	77	

total 1 peptides

tr|A0A3Q3G8Q9|A0A3Q3G8Q9_9LABR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	64	77	

total 1 peptides

tr|A0A4W5NYP8|A0A4W5NYP8_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	64	77	

total 1 peptides

tr|A0A672J300|A0A672J300_SALFA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	64	77	

total 1 peptides

tr|A0A3Q2W3W0|A0A3Q2W3W0_HAPBU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	64	77	

total 1 peptides

tr|A0A3Q2WC94|A0A3Q2WC94_HAPBU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	63	76	

total 1 peptides

tr|A0A669E7L6|A0A669E7L6_ORENI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	64	77	

total 1 peptides

tr|A0A3B3TEJ6|A0A3B3TEJ6_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	64	77	

total 1 peptides

tr|A0A3P8P1N2|A0A3P8P1N2_ASTCA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	87	100	

total 1 peptides

tr|A0A3P9N7Z1|A0A3P9N7Z1_POERE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	64	77	

total 1 peptides

tr|A0A6F9C7M8|A0A6F9C7M8_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDEDGSGTIDFEEF.L	Y	29.88	1558.6311	0.0	780.3228	2	13.98	2017	1	274	287	

total 1 peptides

tr|A0A315VUM5|A0A315VUM5_GAMAF

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.LGNPIPHIVW.R	Y	24.10	1144.6393	-43.6	573.3019	2	15.20	2226	1	919	928	

total 1 peptides

tr|A0A3Q0S4A7|A0A3Q0S4A7_AMPCI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	738	749	

total 1 peptides

tr|A0A3B4V2S1|A0A3B4V2S1_SERDU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	741	752	

total 1 peptides

tr|A0A4W4FZE0|A0A4W4FZE0_ELEEL

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	830	841	

total 1 peptides

tr|A0A1A8RP46|A0A1A8RP46_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	947	958	

total 1 peptides

tr|A0A6Q2ZPR8|A0A6Q2ZPR8_ESOLU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	897	908	

total 1 peptides

tr|A0A674AQG9|A0A674AQG9_SALTR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	894	905	

total 1 peptides

tr|A0A3P8T5S7|A0A3P8T5S7_AMPPE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	925	936	

total 1 peptides

tr|A0A4W4FZ81|A0A4W4FZ81_ELEEL

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	929	940	

total 1 peptides

tr|A0A4W5QGX5|A0A4W5QGX5_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	931	942	

total 1 peptides

tr|A0A3B3DDJ3|A0A3B3DDJ3_ORYME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	937	948	

total 1 peptides

tr|A0A4W4FW94|A0A4W4FW94_ELEEL

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	935	946	

total 1 peptides

tr|A0A674AP52|A0A674AP52_SALTR

back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	935	946	

total 1 peptides

tr|A0A834KWF7|A0A834KWF7_ORYME
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	925	936	

total 1 peptides

tr|A0A667ZHJ6|A0A667ZHJ6_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	944	955	

total 1 peptides

tr|A0A3B4DWJ2|A0A3B4DWJ2_PYGNA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	947	958	

total 1 peptides

tr|A0A3Q2XWS4|A0A3Q2XWS4_HIPCM
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	947	958	

total 1 peptides

tr|A0A667ZHH4|A0A667ZHH4_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	947	958	

total 1 peptides

tr|A0A3Q3G3V8|A0A3Q3G3V8_KRYMA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	947	958	

total 1 peptides

tr|A0A3P8R774|A0A3P8R774_ASTCA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	947	958	

total 1 peptides

tr|A0A484CLN2|A0A484CLN2_PERFV
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	947	958	

total 1 peptides

tr|A0A4W4FZM1|A0A4W4FZM1_ELEEL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	950	961	

total 1 peptides

tr|A0A4W5M1U7|A0A4W5M1U7_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	952	963	

total 1 peptides

tr|A0A674ARJ6|A0A674ARJ6_SALTR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	952	963	

total 1 peptides

tr|A0A4W4FZR2|A0A4W4FZR2_ELEEL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	952	963	

total 1 peptides

tr|A0A4W5M1X7|A0A4W5M1X7_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	953	964	

total 1 peptides

tr|A0A3Q3Q182|A0A3Q3Q182_MONAL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	957	968	

total 1 peptides

tr|A0A4W5QMX9|A0A4W5QMX9_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	954	965	

total 1 peptides

tr|A0A673Z592|A0A673Z592_SALTR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	964	975	

total 1 peptides

tr|A0A5N5JWC6|A0A5N5JWC6_PANHP

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	984	995	

total 1 peptides

tr|A0A4W4FWH2|A0A4W4FWH2_ELEEL

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.DLATICSVLLEN.G	Y	23.39	1289.6537	-2.6	645.8325	2	15.41	2264	1	988	999	

total 1 peptides

tr|A0A2D0QGH0|A0A2D0QGH0_ICTPU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.LTGFANILGQ.S	Y	22.34	1032.5604	-11.7	517.2814	2	14.98	2187	1	1362	1371	

total 1 peptides

tr|A0A2D0QIP4|A0A2D0QIP4_ICTPU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.LTGFANILGQ.S	Y	22.34	1032.5604	-11.7	517.2814	2	14.98	2187	1	1362	1371	

total 1 peptides

tr|A0A2D0QFG9|A0A2D0QFG9_ICTPU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.LTGFANILGQ.S	Y	22.34	1032.5604	-11.7	517.2814	2	14.98	2187	1	1362	1371	

total 1 peptides

tr|A0EXC6|A0EXC6_DANRE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.NKFLSGEI.V	Y	21.77	906.4811	-13.0	454.2419	2	14.84	2162	1	152	159	

total 1 peptides

tr|A4FUP0|A4FUP0_DANRE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM

total 1 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.NKFLSGEI.V	Y	21.77	906.4811	-13.0	454.2419	2	14.84	2162	1	152	159	

total 1 peptides

tr|A0A4V6ASI9|A0A4V6ASI9_COLLU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.AGPGGPAGPVGAA.G	Y	20.00	977.4930	0.2	489.7538	2	10.68	1446	1	974	986	

total 1 peptides

tr|A0A5J6XX13|A0A5J6XX13_NIBCO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.AGPGGPAGPVGAA.G	Y	20.00	977.4930	0.2	489.7538	2	10.68	1446	1	971	983	

total 1 peptides

Protein List

1. Notes

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)

Table 1. Statistics of data.

# of MS Scans	1037
# of MS/MS Scans	2802

Table 2. Result filtration parameters.

Peptide -10lgP	≥15
Protein -10lgP	≥20
Proteins unique peptides	≥0
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	92
Peptide Sequences	88
Protein Groups	34
Proteins	221
Proteins (#Unique Peptides)	31 (>2); 57 (=2); 130 (=1);
FDR (Peptide-Spectrum Matches)	12.0%
FDR (Peptide Sequences)	12.5%
FDR (Protein)	0.5%
De Novo Only Spectra	1033

Table 4. PTM profile.

Name	**ΔMass**	**#PSM**	**Position**

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)

Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Orbi2222	0	0	0	0	88

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS 7.0
Parent Mass Error Tolerance: 0.03 Da
Fragment Mass Error Tolerance: 0.1 Da
Precursor Mass Search Type: monoisotopic
Enzyme: None
Max Missed Cleavages: 100
Non-specific Cleavage: both
Max variable PTM per peptide: 3
Database: Teleosteo
Taxon: All
Searched Entry: 4529691
FDR Estimation: Enabled
Merge Options: 0.1 min. 0.03 Da
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB_PIMENTA_MA_20220211_02.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID/ECD
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
1	66811	tr|A0A3P9CRE7|A0A3P9CRE7_9CICH	97.15	4	11	1	N	219343	Myosin heavy chain, fast skeletal muscle OS=Maylandia zebra OX=106582 PE=3 SV=1
1	69465	tr|A0A669BHT6|A0A669BHT6_ORENI	97.15	4	11	1	N	221312	Uncharacterized protein OS=Oreochromis niloticus OX=8128 GN=LOC100712344 PE=3 SV=1
1	66813	tr|A0A3P8Q1P8|A0A3P8Q1P8_ASTCA	97.15	4	11	1	N	221800	Myosin heavy chain, fast skeletal muscle-like OS=Astatotilapia calliptera OX=8154 PE=3 SV=1
1	66814	tr|A0A3P8QMC2|A0A3P8QMC2_ASTCA	97.15	4	11	1	N	222125	Myosin heavy chain, fast skeletal muscle-like OS=Astatotilapia calliptera OX=8154 PE=3 SV=1
1	66815	tr|A0A3P8Q1G5|A0A3P8Q1G5_ASTCA	97.15	4	11	1	N	222421	Myosin heavy chain, fast skeletal muscle-like OS=Astatotilapia calliptera OX=8154 PE=3 SV=1
3	69467	tr|I3IZY8|I3IZY8_ORENI	93.85	4	10	0	N	218461	Uncharacterized protein OS=Oreochromis niloticus OX=8128 GN=LOC100707599 PE=3 SV=2
3	69468	tr|I3IZU1|I3IZU1_ORENI	93.85	4	10	0	N	218648	Uncharacterized protein OS=Oreochromis niloticus OX=8128 GN=LOC100707599 PE=3 SV=2
2	12040	tr|A0A3S2MUF9|A0A3S2MUF9_ORYJA	87.01	15	10	10	N	41945	Uncharacterized protein OS=Oryzias javanicus OX=123683 GN=OJAV_G00024300 PE=3 SV=1
2	66846	tr|A0A7J6C441|A0A7J6C441_9TELE	87.01	15	10	10	N	41959	Uncharacterized protein OS=Onychostoma macrolepis OX=369639 GN=G5714_016621 PE=3 SV=1
4	69474	tr|A0A3B4YLK9|A0A3B4YLK9_SERLL	77.19	3	9	0	N	222756	Myosin heavy chain, fast skeletal muscle-like OS=Seriola lalandi dorsalis OX=1841481 PE=3 SV=1
11	67380	tr|A0A671XZM8|A0A671XZM8_SPAAU	64.75	9	3	3	N	45256	Calsequestrin OS=Sparus aurata OX=8175 GN=LOC115572796 PE=3 SV=1
11	67381	tr|A0A671Y6A5|A0A671Y6A5_SPAAU	64.75	8	3	3	N	50365	Calsequestrin OS=Sparus aurata OX=8175 GN=LOC115572796 PE=3 SV=1
11	67384	tr|A0A671XZM4|A0A671XZM4_SPAAU	64.75	8	3	3	N	51763	Calsequestrin OS=Sparus aurata OX=8175 GN=LOC115572796 PE=3 SV=1
11	67389	tr|A0A671XZK3|A0A671XZK3_SPAAU	64.75	8	3	3	N	52734	Calsequestrin OS=Sparus aurata OX=8175 GN=LOC115572796 PE=3 SV=1
11	67395	tr|A0A671XZP8|A0A671XZP8_SPAAU	64.75	7	3	3	N	55189	Calsequestrin OS=Sparus aurata OX=8175 GN=LOC115572796 PE=3 SV=1
8	69471	tr|A0A834CTG4|A0A834CTG4_ORYME	63.38	1	3	3	N	850198	Titin OS=Oryzias melastigma OX=30732 GN=FQA47_016182 PE=4 SV=1
6	69487	tr|A0A315VR11|A0A315VR11_GAMAF	58.47	4	5	5	N	93743	Creatine kinase (Fragment) OS=Gambusia affinis OX=33528 GN=CCH79_00019883 PE=3 SV=1

total 221 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
9	66962	tr|A0A6G0IP12|A0A6G0IP12_LARCR	57.75	12	3	3	N	18230	Troponin C, skeletal muscle OS=Larimichthys crocea OX=215358 GN=D5F01_LYC08192 PE=4 SV=1
9	67020	tr|A0A1A8D9W7|A0A1A8D9W7_9TELE	57.75	15	3	3	N	15353	Troponin C type 2 (Fast) OS=Nothobranchius kadleci OX=1051664 GN=TNNC2 PE=4 SV=1
9	67021	tr|A0A1A8CTF6|A0A1A8CTF6_9TELE	57.75	12	3	3	N	18199	Troponin C type 2 (Fast) OS=Nothobranchius kadleci OX=1051664 GN=TNNC2 PE=4 SV=1
9	67022	tr|A0A1A8QW41|A0A1A8QW41_9TELE	57.75	12	3	3	N	18199	Troponin C type 2 (Fast) OS=Nothobranchius rachovii OX=451742 GN=TNNC2 PE=4 SV=1
9	67023	tr|A0A1A8B5H7|A0A1A8B5H7_NOTFU	57.75	12	3	3	N	18199	Troponin C type 2 (Fast) OS=Nothobranchius furzeri OX=105023 GN=TNNC2 PE=4 SV=1
9	67397	tr|A0A1A8IG78|A0A1A8IG78_NOTKU	57.75	22	3	3	N	10482	Troponin C type 2 (Fast) (Fragment) OS=Nothobranchius kuhntae OX=321403 GN=TNNC2 PE=4 SV=1
9	67398	tr|A0A1A8ML32|A0A1A8ML32_9TELE	57.75	22	3	3	N	10482	Troponin C type 2 (Fast) (Fragment) OS=Nothobranchius pienaari OX=704102 GN=TNNC2 PE=4 SV=1
9	67210	tr|A0A1A8SNN3|A0A1A8SNN3_9TELE	57.75	21	3	3	N	11028	Troponin C type 2 (Fast) (Fragment) OS=Nothobranchius rachovii OX=451742 GN=TNNC2 PE=4 SV=1
9	66963	tr|A0A1A8Q0J1|A0A1A8Q0J1_9TELE	57.75	12	3	3	N	18215	Troponin C type 2 (Fast) OS=Nothobranchius pienaari OX=704102 GN=TNNC2 PE=4 SV=1
5	66958	tr|A0A6J2PW36|A0A6J2PW36_COTGO	56.57	3	7	1	N	221235	myosin heavy chain, fast skeletal muscle-like OS=Cottoperca gobio OX=56716 GN=LOC115009632 PE=3 SV=1
21	68363	tr|A0A6A5EZU1|A0A6A5EZU1_PERFL	50.73	1	1	1	N	136636	Uncharacterized protein OS=Perca fluviatilis OX=8168 GN=PFLUV_G00182780 PE=4 SV=1
21	69488	tr|A0A4Z2EZH8|A0A4Z2EZH8_9TELE	50.73	2	1	1	N	72089	Collagen alpha-2(I) chain OS=Liparis tanakae OX=230148 GN=Col1a2_1 PE=4 SV=1
21	69489	tr|A0A6A4S346|A0A6A4S346_SCOMX	50.73	1	1	1	N	152271	Uncharacterized protein OS=Scophthalmus maximus OX=52904 GN=F2P81_022633 PE=4 SV=1
15	69486	tr|C6GKU3|C6GKU3_THUAL	48.28	21	2	2	N	11548	Parvalbumin OS=Thunnus albacares OX=8236 GN=pvalb1 PE=2 SV=1
15	67518	tr|D2KQG3|D2KQG3_SINCH	48.28	21	2	2	N	11617	Parvalbumin OS=Siniperca chuatsi OX=119488 PE=2 SV=1
15	67527	tr|A0A7J6CHT3|A0A7J6CHT3_9TELE	48.28	21	2	2	N	11577	Parvalbumin OS=Onychostoma macrolepis OX=369639 GN=G5714_012686 PE=3 SV=1
15	21897	P05941|PRVB_OPSTA	48.28	21	2	2	N	11757	Parvalbumin beta OS=Opsanus tau OX=8068 PE=1 SV=2
15	67519	tr|B9VJM3|B9VJM3_SINCH	48.28	21	2	2	N	11589	Parvalbumin OS=Siniperca chuatsi OX=119488 PE=2 SV=1
12	69544	tr|A0A668SJD1|A0A668SJD1_OREAU	46.28	2	3	1	N	123810	Myosin binding protein C, fast type b OS=Oreochromis aureus OX=47969 PE=4 SV=1
12	69545	tr|A0A6P7L5W1|A0A6P7L5W1_BETSP	46.28	2	3	1	N	124685	myosin-binding protein C, fast-type-like isoform X8 OS=Betta splendens OX=158456 GN=LOC114845484 PE=4 SV=1
12	69546	tr|A0A3P9C2F1|A0A3P9C2F1_9CICH	46.28	2	3	1	N	124875	Myosin-binding protein C, fast-type OS=Maylandia zebra OX=106582 PE=4 SV=1
12	69547	tr|A0A6P7L5V6|A0A6P7L5V6_BETSP	46.28	2	3	1	N	125396	myosin-binding protein C, fast-type-like isoform X6 OS=Betta splendens OX=158456 GN=LOC114845484 PE=4 SV=1
12	69548	tr|A0A668SIT2|A0A668SIT2_OREAU	46.28	2	3	1	N	126234	Myosin binding protein C, fast type b OS=Oreochromis aureus OX=47969 PE=4 SV=1

total 221 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
12	69549	tr|A0A6P7L5V2|A0A6P7L5V2_BETSP	46.28	2	3	1	N	126921	myosin-binding protein C, fast-type-like isoform X2 OS=Betta splendens OX=158456 GN=LOC114845484 PE=4 SV=1
20	67265	tr|A0A6P7INY3|A0A6P7INY3_9TELE	46.23	1	1	1	N	123690	collagen alpha-1(I) chain-like isoform X2 OS=Parambassis ranga OX=210632 GN=LOC114439468 PE=4 SV=1
20	67266	tr|A0A6P7IU28|A0A6P7IU28_9TELE	46.23	1	1	1	N	136458	collagen alpha-1(I) chain-like isoform X1 OS=Parambassis ranga OX=210632 GN=LOC114439468 PE=4 SV=1
20	67009	tr|A0A2I4D9D9|A0A2I4D9D9_9TELE	46.23	1	1	1	N	133831	collagen alpha-1(I) chain-like isoform X2 OS=Austrofundulus limnaeus OX=52670 GN=LOC106536191 PE=4 SV=1
20	67267	tr|A0A7J6DBF9|A0A7J6DBF9_9TELE	46.23	1	1	1	N	136989	Uncharacterized protein OS=Onychostoma macrolepis OX=369639 GN=G5714_003834 PE=4 SV=1
20	67010	tr|A0A2I4D9D6|A0A2I4D9D6_9TELE	46.23	1	1	1	N	136808	collagen alpha-1(I) chain-like isoform X1 OS=Austrofundulus limnaeus OX=52670 GN=LOC106536191 PE=4 SV=1
20	67268	tr|A0A6P6JU61|A0A6P6JU61_CARAU	46.23	1	1	1	N	137216	collagen alpha-1(I) chain-like OS=Carassius auratus OX=7957 GN=LOC113046705 PE=4 SV=1
20	67012	tr|A0A3B4UIY5|A0A3B4UIY5_SERDU	46.23	1	1	1	N	132549	Collagen alpha-1(I) chain-like OS=Seriola dumerili OX=41447 PE=4 SV=1
20	67281	tr|A0A2I4D9D4|A0A2I4D9D4_9TELE	46.23	1	1	1	N	114299	collagen alpha-1(I) chain-like isoform X3 OS=Austrofundulus limnaeus OX=52670 GN=LOC106536191 PE=4 SV=1
20	67571	tr|A0A060WU51|A0A060WU51_ONCMY	46.23	7	1	1	N	22546	VWFC domain-containing protein OS=Oncorhynchus mykiss OX=8022 GN=GSONMT00040585001 PE=4 SV=1
20	67572	tr|A0A6F9C010|A0A6F9C010_9TELE	46.23	5	1	1	N	27312	VWFC domain-containing protein OS=Coregonus sp. 'balchen' OX=861768 GN=CSTEINMANNI_LOCUS3426487 PE=4 SV=1
20	67573	tr|A0A060X5H1|A0A060X5H1_ONCMY	46.23	4	1	1	N	41631	VWFC domain-containing protein OS=Oncorhynchus mykiss OX=8022 GN=GSONMT00019804001 PE=4 SV=1
20	67574	tr|A0A4W5KL14|A0A4W5KL14_9TELE	46.23	3	1	1	N	59489	Collagen, type I, alpha 1a OS=Hucho hucho OX=62062 PE=4 SV=1
20	67284	tr|A0A673A8U8|A0A673A8U8_9TELE	46.23	1	1	1	N	111385	Collagen, type I, alpha 1b OS=Sphaeramia orbicularis OX=375764 PE=4 SV=1
20	67018	tr|I3JGN1|I3JGN1_ORENI	46.23	1	1	1	N	121918	Uncharacterized protein OS=Oreochromis niloticus OX=8128 GN=col1a1 PE=4 SV=2
20	67417	tr|A0A671YED8|A0A671YED8_SPAAU	46.23	1	1	1	N	131412	Collagen, type I, alpha 1b OS=Sparus aurata OX=8175 PE=4 SV=1
20	67418	tr|A0A671YFV1|A0A671YFV1_SPAAU	46.23	1	1	1	N	132045	Collagen, type I, alpha 1b OS=Sparus aurata OX=8175 PE=4 SV=1
20	67275	tr|A0A3Q2W9Y5|A0A3Q2W9Y5_HAPBU	46.23	1	1	1	N	135591	Collagen type I alpha 1 chain OS=Haplochromis burtoni OX=8153 PE=4 SV=1
20	67575	tr|A0A674DLV9|A0A674DLV9_SALTR	46.23	1	1	1	N	135355	Collagen alpha-1(I) chain-like OS=Salmo trutta OX=8032 GN=LOC115170991 PE=4 SV=1
20	67276	tr|A0A3Q3CY74|A0A3Q3CY74_HAPBU	46.23	1	1	1	N	137155	Collagen type I alpha 1 chain OS=Haplochromis burtoni OX=8153 PE=4 SV=1
20	67019	tr|G9M6I5|G9M6I5_ORENI	46.23	1	1	1	N	137283	Collagen type I alpha 1 OS=Oreochromis niloticus OX=8128 GN=COL1A1 PE=2 SV=1

total 221 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
20	67576	tr|A0A674DL09|A0A674DL09_SALTR	46.23	1	1	1	N	136924	Collagen alpha-1(I) chain-like OS=Salmo trutta OX=8032 GN=LOC115170991 PE=4 SV=1
20	67577	tr|Q910C0|Q910C0_ONCMY	46.23	1	1	1	N	137117	Collagen a1(I) OS=Oncorhynchus mykiss OX=8022 GN=COL1A1 PE=2 SV=1
20	67578	tr|A0A1S3S6G4|A0A1S3S6G4_SALSA	46.23	1	1	1	N	136936	collagen alpha-1(I) chain OS=Salmo salar OX=8030 GN=LOC100286406 PE=4 SV=1
20	67579	tr|A0A6J2RRG5|A0A6J2RRG5_COTGO	46.23	1	1	1	N	136726	collagen alpha-1(I) chain-like OS=Cottoperca gobio OX=56716 GN=LOC115024512 PE=4 SV=1
20	67580	tr|A0A1S3R8F9|A0A1S3R8F9_SALSA	46.23	1	1	1	N	136917	collagen alpha-1(I) chain-like OS=Salmo salar OX=8030 GN=LOC106600852 PE=4 SV=1
10	69550	tr|A0A1S3NGD5|A0A1S3NGD5_SALSA	45.17	2	3	1	N	127246	myosin-binding protein C, fast-type-like OS=Salmo salar OX=8030 GN=LOC106579178 PE=4 SV=1
10	69563	tr|A0A1A7W9Y4|A0A1A7W9Y4_9TELE	45.17	2	3	1	N	124706	Myosin binding protein C, fast type b OS=Iconisemion striatum OX=60296 GN=MYBPC2B PE=4 SV=1
7	69552	tr|A0A0F8B178|A0A0F8B178_LARCR	44.42	4	4	4	N	108080	Calcium-transporting ATPase OS=Larimichthys crocea OX=215358 GN=EH28_02549 PE=3 SV=1
7	69553	tr|A0A3P8PD71|A0A3P8PD71_ASTCA	44.42	4	4	4	N	108538	Calcium-transporting ATPase OS=Astatotilapia calliptera OX=8154 PE=3 SV=1
7	67215	tr|A0A3Q2WQG2|A0A3Q2WQG2_HAPBU	44.42	4	4	4	N	108554	Calcium-transporting ATPase OS=Haplochromis burtoni OX=8153 PE=3 SV=1
7	69554	tr|A0A6G0HZ09|A0A6G0HZ09_LARCR	44.42	4	4	4	N	108647	Calcium-transporting ATPase OS=Larimichthys crocea OX=215358 GN=D5F01_LYC17582 PE=3 SV=1
7	69555	tr|A0A3B4GKY8|A0A3B4GKY8_9CICH	44.42	4	4	4	N	108592	Calcium-transporting ATPase OS=Pundamilia nyererei OX=303518 PE=3 SV=1
7	69556	tr|A0A3P9C8S8|A0A3P9C8S8_9CICH	44.42	4	4	4	N	108556	Calcium-transporting ATPase OS=Maylandia zebra OX=106582 PE=3 SV=1
7	69557	tr|A0A3P8PD17|A0A3P8PD17_ASTCA	44.42	4	4	4	N	109053	Calcium-transporting ATPase OS=Astatotilapia calliptera OX=8154 PE=3 SV=1
7	69558	tr|A0A3B4GL15|A0A3B4GL15_9CICH	44.42	4	4	4	N	109107	Calcium-transporting ATPase OS=Pundamilia nyererei OX=303518 PE=3 SV=1
7	67219	tr|A0A3P9C9M1|A0A3P9C9M1_9CICH	44.42	4	4	4	N	109087	Calcium-transporting ATPase OS=Maylandia zebra OX=106582 PE=3 SV=1
7	69559	tr|A0A3Q2WG66|A0A3Q2WG66_HAPBU	44.42	4	4	4	N	109069	Calcium-transporting ATPase OS=Haplochromis burtoni OX=8153 PE=3 SV=1
7	69560	tr|A0A3P8PDJ9|A0A3P8PDJ9_ASTCA	44.42	4	4	4	N	110865	Calcium-transporting ATPase OS=Astatotilapia calliptera OX=8154 PE=3 SV=1
7	69561	tr|A0A3P8PDC7|A0A3P8PDC7_ASTCA	44.42	4	4	4	N	111173	Calcium-transporting ATPase OS=Astatotilapia calliptera OX=8154 PE=3 SV=1
7	69562	tr|A0A3Q2WG59|A0A3Q2WG59_HAPBU	44.42	4	4	4	N	111189	Calcium-transporting ATPase OS=Haplochromis burtoni OX=8153 PE=3 SV=1
27	69493	tr|A0A3P8P4C2|A0A3P8P4C2_ASTCA	35.05	1	1	1	N	157122	Myomesin-2-like OS=Astatotilapia calliptera OX=8154 GN=MYOM2 PE=4 SV=1
27	69494	tr|A0A3Q1D109|A0A3Q1D109_AMPOC	35.05	1	1	1	N	156426	Myomesin-2-like OS=Amphiprion ocellaris OX=80972 GN=MYOM2 PE=4 SV=1
27	69495	tr|A0A3Q2WWP1|A0A3Q2WWP1_HAPBU	35.05	1	1	1	N	156996	Myomesin-2-like OS=Haplochromis burtoni OX=8153 PE=4 SV=1
27	69519	tr|A0A3Q4GHK3|A0A3Q4GHK3_NEOBR	35.05	2	1	1	N	99617	Myomesin-2-like OS=Neolamprologus brichardi OX=32507 GN=MYOM2 PE=4 SV=1

total 221 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
27	69520	tr|A0A672ZI78|A0A672ZI78_9TELE	35.05	1	1	1	N	126360	Uncharacterized protein OS=Sphaeramia orbicularis OX=375764 GN=LOC115437523 PE=4 SV=1
27	69521	tr|A0A669ELF6|A0A669ELF6_ORENI	35.05	1	1	1	N	132152	Uncharacterized protein OS=Oreochromis niloticus OX=8128 GN=LOC100698303 PE=4 SV=1
27	69522	tr|A0A4U5U6X9|A0A4U5U6X9_COLLU	35.05	1	1	1	N	136304	Myomesin-2 165 kDa connectin-associated protein 165 kDa titin-associated protein M-protein OS=Collichthys lucidus OX=240159 GN=D9C73_004091 PE=4 SV=1
27	69523	tr|A0A3Q4GXU7|A0A3Q4GXU7_NEOBR	35.05	1	1	1	N	139979	Myomesin-2-like OS=Neolamprologus brichardi OX=32507 GN=MYOM2 PE=4 SV=1
27	69524	tr|A0A669CKL2|A0A669CKL2_ORENI	35.05	1	1	1	N	141158	Uncharacterized protein OS=Oreochromis niloticus OX=8128 GN=LOC100698303 PE=4 SV=1
27	69525	tr|A0A671Y401|A0A671Y401_SPAAU	35.05	1	1	1	N	145648	Myomesin-2-like OS=Sparus aurata OX=8175 GN=MYOM2 PE=4 SV=1
27	69526	tr|A0A672FNF5|A0A672FNF5_SALFA	35.05	1	1	1	N	148203	Uncharacterized protein OS=Salarias fasciatus OX=181472 GN=LOC115388674 PE=4 SV=1
27	69527	tr|A0A6G0J0W8|A0A6G0J0W8_LARCR	35.05	1	1	1	N	152797	Myomesin-2 165 kDa connectin-associated protein OS=Larimichthys crocea OX=215358 GN=D5F01_LYC03862 PE=4 SV=1
27	69528	tr|A0A671Y575|A0A671Y575_SPAAU	35.05	1	1	1	N	154320	Myomesin-2-like OS=Sparus aurata OX=8175 GN=MYOM2 PE=4 SV=1
27	69529	tr|A0A3B3IJA0|A0A3B3IJA0_ORYLA	35.05	1	1	1	N	155226	Uncharacterized protein OS=Oryzias latipes OX=8090 GN=LOC101163890 PE=4 SV=1
27	69530	tr|A0A6G1P7U8|A0A6G1P7U8_9TELE	35.05	1	1	1	N	156806	Myomesin-2 165 kDa connectin-associated protein OS=Channa argus OX=215402 GN=EXN66_Car002007 PE=4 SV=1
27	69531	tr|A0A087YFH0|A0A087YFH0_POEFO	35.05	1	1	1	N	156966	Myomesin-2-like OS=Poecilia formosa OX=48698 GN=MYOM2 PE=4 SV=2
27	69532	tr|A0A3P9PGW1|A0A3P9PGW1_POERE	35.05	1	1	1	N	156917	Myomesin-2-like OS=Poecilia reticulata OX=8081 PE=4 SV=1
27	69533	tr|A0A672ZHV0|A0A672ZHV0_9TELE	35.05	1	1	1	N	156079	Uncharacterized protein OS=Sphaeramia orbicularis OX=375764 GN=LOC115437523 PE=4 SV=1
27	69534	tr|I3JDJ1|I3JDJ1_ORENI	35.05	1	1	1	N	157148	Uncharacterized protein OS=Oreochromis niloticus OX=8128 GN=LOC100698303 PE=4 SV=2
27	69535	tr|A0A2I4AP94|A0A2I4AP94_9TELE	35.05	1	1	1	N	156788	M-protein, striated muscle-like OS=Austrofundulus limnaeus OX=52670 GN=LOC106513170 PE=4 SV=1
27	69536	tr|A0A834CMG6|A0A834CMG6_ORYME	35.05	1	1	1	N	157078	Myomesin-2 OS=Oryzias melastigma OX=30732 GN=FQA47_006815 PE=4 SV=1
27	69537	tr|A0A3B3BCL7|A0A3B3BCL7_ORYME	35.05	1	1	1	N	157034	Myomesin-2-like OS=Oryzias melastigma OX=30732 PE=4 SV=1
27	69538	tr|A0A3P9IT90|A0A3P9IT90_ORYLA	35.05	1	1	1	N	156872	Uncharacterized protein OS=Oryzias latipes OX=8090 PE=4 SV=1
27	69539	tr|H2M2B3|H2M2B3_ORYLA	35.05	1	1	1	N	156953	Uncharacterized protein OS=Oryzias latipes OX=8090 GN=LOC101163890 PE=4 SV=2
27	69540	tr|A0A3P9LTE0|A0A3P9LTE0_ORYLA	35.05	1	1	1	N	157011	Uncharacterized protein OS=Oryzias latipes OX=8090 PE=4 SV=1
27	69541	tr|A0A3B3D3C5|A0A3B3D3C5_ORYME	35.05	1	1	1	N	157566	Myomesin-2-like OS=Oryzias melastigma OX=30732 PE=4 SV=1
27	69542	tr|A0A6P7LYN0|A0A6P7LYN0_BETSP	35.05	1	1	1	N	158082	myomesin-2-like isoform X1 OS=Betta splendens OX=158456 GN=LOC114852036 PE=4 SV=1
27	69543	tr|A0A3B3HWS2|A0A3B3HWS2_ORYLA	35.05	1	1	1	N	158285	Uncharacterized protein OS=Oryzias latipes OX=8090 GN=LOC101163890 PE=4 SV=1

total 221 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
16	69651	tr|A0A665WT54|A0A665WT54_ECHNA	34.94	7	2	2	N	12976	LIM domain-binding protein 3-like OS=Echeneis naucrates OX=173247 GN=LOC115060026 PE=4 SV=1
16	69652	tr|A0A671N228|A0A671N228_9TELE	34.94	3	2	2	N	28684	LIM domain-binding protein 3-like OS=Sinocyclocheilus anshuiensis OX=1608454 GN=LOC107698793 PE=4 SV=1
16	69653	tr|A0A3Q3Q7K2|A0A3Q3Q7K2_MONAL	34.94	3	2	2	N	29692	Synuclein-like OS=Monopterus albus OX=43700 PE=4 SV=1
16	69654	tr|A0A671MU99|A0A671MU99_9TELE	34.94	3	2	2	N	29538	LIM domain-binding protein 3-like OS=Sinocyclocheilus anshuiensis OX=1608454 GN=LOC107698793 PE=4 SV=1
16	69655	tr|A0A672KK19|A0A672KK19_SINGR	34.94	3	2	2	N	30329	LIM domain-binding protein 3-like OS=Sinocyclocheilus grahami OX=75366 GN=LOC107552745 PE=4 SV=1
16	69656	tr|A0A673LYE6|A0A673LYE6_9TELE	34.94	3	2	2	N	30316	LIM domain-binding protein 3-like OS=Sinocyclocheilus rhinocerous OX=307959 GN=LOC107749342 PE=4 SV=1
16	69657	tr|A0A3P8VEA1|A0A3P8VEA1_CYNSE	34.94	3	2	2	N	30334	LIM domain-binding protein 3-like OS=Cynoglossus semilaevis OX=244447 PE=4 SV=1
16	69658	tr|A0A3Q1II99|A0A3Q1II99_ANATE	34.94	3	2	2	N	30310	LIM domain binding 3b OS=Anabas testudineus OX=64144 PE=4 SV=1
16	69659	tr|A0A6P7L9I7|A0A6P7L9I7_BETSP	34.94	3	2	2	N	30536	LIM domain-binding protein 3-like isoform X2 OS=Betta splendens OX=158456 GN=LOC114846412 PE=4 SV=1
16	69660	tr|A0A3P8X8T4|A0A3P8X8T4_ESOLU	34.94	3	2	2	N	30572	LIM domain-binding protein 3 OS=Esox lucius OX=8010 PE=4 SV=1
16	69661	tr|A0A3Q0R4X6|A0A3Q0R4X6_AMPCI	34.94	3	2	2	N	30403	LIM domain binding 3b OS=Amphilophus citrinellus OX=61819 PE=4 SV=1
16	69662	tr|A0A3P8VK01|A0A3P8VK01_CYNSE	34.94	3	2	2	N	30591	LIM domain-binding protein 3-like OS=Cynoglossus semilaevis OX=244447 PE=4 SV=1
16	69663	tr|A0A3P8XBI5|A0A3P8XBI5_ESOLU	34.94	3	2	2	N	30957	LIM domain-binding protein 3 OS=Esox lucius OX=8010 PE=4 SV=2
16	69664	tr|A0A3Q1H919|A0A3Q1H919_ANATE	34.94	3	2	2	N	31065	LIM domain binding 3b OS=Anabas testudineus OX=64144 PE=4 SV=1
16	69665	tr|A0A3Q3KN21|A0A3Q3KN21_9TELE	34.94	3	2	2	N	31352	LIM domain binding 3b OS=Mastacembelus armatus OX=205130 PE=4 SV=2
16	69666	tr|A0A6P7L9I9|A0A6P7L9I9_BETSP	34.94	3	2	2	N	31290	LIM domain-binding protein 3-like isoform X1 OS=Betta splendens OX=158456 GN=LOC114846412 PE=4 SV=1
16	69667	tr|A0A3P8VE68|A0A3P8VE68_CYNSE	34.94	3	2	2	N	31336	LIM domain-binding protein 3-like OS=Cynoglossus semilaevis OX=244447 PE=4 SV=1
16	69668	tr|A0A6G0HYN5|A0A6G0HYN5_LARCR	34.94	3	2	2	N	31123	LIM domain-binding protein 3 Protein cypher Z-band alternatively spliced PDZ-motif protein OS=Larimichthys crocea OX=215358 GN=D5F01_LYC17526 PE=4 SV=1
16	69669	tr|A0A3P8ZCR8|A0A3P8ZCR8_ESOLU	34.94	3	2	2	N	31398	LIM domain-binding protein 3 OS=Esox lucius OX=8010 PE=4 SV=1
16	69670	tr|A0A3Q3IQV7|A0A3Q3IQV7_MONAL	34.94	3	2	2	N	31456	Synuclein-like OS=Monopterus albus OX=43700 PE=4 SV=1
16	69671	tr|A0A665WTS5|A0A665WTS5_ECHNA	34.94	3	2	2	N	31290	LIM domain-binding protein 3-like OS=Echeneis naucrates OX=173247 GN=LOC115060026 PE=4 SV=1
16	69672	tr|A0A7N8Y585|A0A7N8Y585_9TELE	34.94	3	2	2	N	31804	LIM domain binding 3b OS=Mastacembelus armatus OX=205130 PE=4 SV=1

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Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
16	69673	tr|A0A6P6QFT2|A0A6P6QFT2_CARAU	34.94	3	2	2	N	31663	LIM domain-binding protein 3-like isoform X2 OS=Carassius auratus OX=7957 GN=LOC113111546 PE=4 SV=1
16	69674	tr|A0A672KNU9|A0A672KNU9_SINGR	34.94	3	2	2	N	31638	LIM domain-binding protein 3-like OS=Sinocyclocheilus grahami OX=75366 GN=LOC107552745 PE=4 SV=1
16	69675	tr|A0A673M1Q3|A0A673M1Q3_9TELE	34.94	3	2	2	N	31625	LIM domain-binding protein 3-like OS=Sinocyclocheilus rhinocerous OX=307959 GN=LOC107749342 PE=4 SV=1
16	69676	tr|A0A7J6CGV6|A0A7J6CGV6_9TELE	34.94	3	2	2	N	31765	PDZ domain-containing protein OS=Onychostoma macrolepis OX=369639 GN=G5714_012537 PE=4 SV=1
16	69677	tr|A0A6P6QIW1|A0A6P6QIW1_CARAU	34.94	3	2	2	N	34204	LIM domain-binding protein 3-like isoform X1 OS=Carassius auratus OX=7957 GN=LOC113111546 PE=4 SV=1
16	69678	tr|A0A6Q2XWF7|A0A6Q2XWF7_ESOLU	34.94	3	2	2	N	35095	LIM domain-binding protein 3 OS=Esox lucius OX=8010 PE=4 SV=1
16	69679	tr|A0A0F8AMH6|A0A0F8AMH6_LARCR	34.94	2	2	2	N	43721	LIM domain-binding protein 3 OS=Larimichthys crocea OX=215358 GN=EH28_03737 PE=4 SV=1
16	69680	tr|A0A6G0HYU6|A0A6G0HYU6_LARCR	34.94	1	2	2	N	80212	Melanopsin-A Mammalian-like melanopsin Melanopsin-M Opsin-4-A Opsin-4M OS=Larimichthys crocea OX=215358 GN=D5F01_LYC17520 PE=4 SV=1
23	69577	tr|A0A0P7UGN8|A0A0P7UGN8_SCLFO	30.17	2	1	1	N	52152	Arrestin domain-containing protein 1-like OS=Scleropages formosus OX=113540 GN=Z043_114076 PE=3 SV=1
23	69587	tr|A0A3P8UKD4|A0A3P8UKD4_CYNSE	30.17	6	1	1	N	15153	Ig-like domain-containing protein OS=Cynoglossus semilaevis OX=244447 PE=4 SV=1
23	69588	tr|A0A668SIM0|A0A668SIM0_OREAU	30.17	2	1	1	N	39658	Ig-like domain-containing protein OS=Oreochromis aureus OX=47969 PE=4 SV=1
23	69589	tr|A0A6P7NE86|A0A6P7NE86_BETSP	30.17	2	1	1	N	40039	arrestin domain-containing protein 1 isoform X2 OS=Betta splendens OX=158456 GN=arrdc1 PE=3 SV=1
23	69590	tr|A0A5J5CFY0|A0A5J5CFY0_9PERO	30.17	2	1	1	N	43851	Uncharacterized protein (Fragment) OS=Etheostoma spectabile OX=54343 GN=FQN60_006042 PE=4 SV=1
23	69591	tr|A0A315V5I0|A0A315V5I0_GAMAF	30.17	2	1	1	N	48027	Arrestin_C domain-containing protein (Fragment) OS=Gambusia affinis OX=33528 GN=CCH79_00009980 PE=3 SV=1
23	69592	tr|A0A6P7NIN0|A0A6P7NIN0_BETSP	30.17	2	1	1	N	48523	arrestin domain-containing protein 1 isoform X1 OS=Betta splendens OX=158456 GN=arrdc1 PE=3 SV=1
23	69593	tr|A0A6J2QDT9|A0A6J2QDT9_COTGO	30.17	2	1	1	N	48759	arrestin domain-containing protein 1-like OS=Cottoperca gobio OX=56716 GN=LOC115013564 PE=3 SV=1
23	69594	tr|M3ZP84|M3ZP84_XIPMA	30.17	2	1	1	N	49386	Arrestin_C domain-containing protein OS=Xiphophorus maculatus OX=8083 PE=3 SV=2
23	69595	tr|A0A3P9PCX4|A0A3P9PCX4_POERE	30.17	2	1	1	N	49543	Arrestin domain-containing protein 1-like OS=Poecilia reticulata OX=8081 PE=3 SV=1
23	69596	tr|A0A3B3WUC6|A0A3B3WUC6_9TELE	30.17	2	1	1	N	49610	Arrestin domain-containing protein 1-like OS=Poecilia mexicana OX=48701 PE=3 SV=1
23	69612	tr|A0A6G0J5Q9|A0A6G0J5Q9_LARCR	30.17	0	1	1	N	928406	Titin OS=Larimichthys crocea OX=215358 GN=D5F01_LYC01467 PE=4 SV=1
13	69619	tr|A0A6J2RVQ6|A0A6J2RVQ6_COTGO	28.13	0	2	2	N	676713	nebulin isoform X14 OS=Cottoperca gobio OX=56716 GN=neb PE=4 SV=1

total 221 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
13	69620	tr|A0A6J2RYJ1|A0A6J2RYJ1_COTGO	28.13	0	2	2	N	678455	nebulin isoform X13 OS=Cottoperca gobio OX=56716 GN=neb PE=4 SV=1
13	69621	tr|A0A6J2RTY3|A0A6J2RTY3_COTGO	28.13	0	2	2	N	691692	nebulin isoform X12 OS=Cottoperca gobio OX=56716 GN=neb PE=4 SV=1
13	69622	tr|A0A6J2RY66|A0A6J2RY66_COTGO	28.13	0	2	2	N	698051	nebulin isoform X11 OS=Cottoperca gobio OX=56716 GN=neb PE=4 SV=1
13	69623	tr|A0A6J2RVQ1|A0A6J2RVQ1_COTGO	28.13	0	2	2	N	701558	nebulin isoform X10 OS=Cottoperca gobio OX=56716 GN=neb PE=4 SV=1
13	69624	tr|A0A3Q1HC41|A0A3Q1HC41_ANATE	28.13	0	2	2	N	704841	Nebulin OS=Anabas testudineus OX=64144 GN=NEB PE=4 SV=2
13	69625	tr|A0A6J2RYI7|A0A6J2RYI7_COTGO	28.13	0	2	2	N	705639	nebulin isoform X9 OS=Cottoperca gobio OX=56716 GN=neb PE=4 SV=1
13	69626	tr|A0A6J2RWT1|A0A6J2RWT1_COTGO	28.13	0	2	2	N	712677	nebulin isoform X8 OS=Cottoperca gobio OX=56716 GN=neb PE=4 SV=1
13	69627	tr|A0A6J2RY61|A0A6J2RY61_COTGO	28.13	0	2	2	N	715609	nebulin isoform X6 OS=Cottoperca gobio OX=56716 GN=neb PE=4 SV=1
13	69628	tr|A0A6J2RYI1|A0A6J2RYI1_COTGO	28.13	0	2	2	N	716207	nebulin isoform X4 OS=Cottoperca gobio OX=56716 GN=neb PE=4 SV=1
13	69629	tr|A0A6J2RVP6|A0A6J2RVP6_COTGO	28.13	0	2	2	N	716181	nebulin isoform X5 OS=Cottoperca gobio OX=56716 GN=neb PE=4 SV=1
13	69630	tr|A0A6J2RY55|A0A6J2RY55_COTGO	28.13	0	2	2	N	716421	nebulin isoform X3 OS=Cottoperca gobio OX=56716 GN=neb PE=4 SV=1
13	69631	tr|A0A6J2RVP0|A0A6J2RVP0_COTGO	28.13	0	2	2	N	717944	nebulin isoform X2 OS=Cottoperca gobio OX=56716 GN=neb PE=4 SV=1
13	69632	tr|A0A6J2RWS0|A0A6J2RWS0_COTGO	28.13	0	2	2	N	719690	nebulin isoform X1 OS=Cottoperca gobio OX=56716 GN=neb PE=4 SV=1
13	69633	tr|A0A6G0J8D3|A0A6G0J8D3_LARCR	28.13	0	2	2	N	592244	Nebulin OS=Larimichthys crocea OX=215358 GN=D5F01_LYC02135 PE=4 SV=1
13	69634	tr|A0A5C6PNB9|A0A5C6PNB9_9TELE	28.13	0	2	2	N	690778	Nebulin OS=Takifugu flavidus OX=433684 GN=D4764_01G0002010 PE=4 SV=1
13	69635	tr|A0A669CKX5|A0A669CKX5_ORENI	28.13	0	2	2	N	700756	Nebulin OS=Oreochromis niloticus OX=8128 PE=4 SV=1
13	69636	tr|I3KK23|I3KK23_ORENI	28.13	0	2	2	N	705912	Nebulin OS=Oreochromis niloticus OX=8128 PE=4 SV=2
13	18868	tr|A0A3P8QJ88|A0A3P8QJ88_ASTCA	28.13	0	2	2	N	709333	Nebulin OS=Astatotilapia calliptera OX=8154 PE=4 SV=1
13	69637	tr|A0A3P9CU79|A0A3P9CU79_9CICH	28.13	0	2	2	N	709930	Nebulin OS=Maylandia zebra OX=106582 PE=4 SV=1
13	69638	tr|A0A6J2RTX8|A0A6J2RTX8_COTGO	28.13	0	2	2	N	715423	nebulin isoform X7 OS=Cottoperca gobio OX=56716 GN=neb PE=4 SV=1
13	69639	tr|A0A4U5U1Y5|A0A4U5U1Y5_COLLU	28.13	0	2	2	N	731042	Nebulin OS=Collichthys lucidus OX=240159 GN=D9C73_000886 PE=4 SV=1
24	69583	tr|A0A4W4F305|A0A4W4F305_ELEEL	28.12	0	1	1	N	373023	Uncharacterized protein OS=Electrophorus electricus OX=8005 GN=LOC113571677 PE=4 SV=1
24	69611	tr|W5KZP4|W5KZP4_ASTMX	28.12	1	1	1	N	116741	Collagen, type XXVIII, alpha 2b OS=Astyanax mexicanus OX=7994 PE=4 SV=2
22	67639	tr|A0A6P3VUU5|A0A6P3VUU5_CLUHA	26.91	1	1	1	N	141605	collagen alpha-1(II) chain-like isoform X1 OS=Clupea harengus OX=7950 GN=LOC105899289 PE=4 SV=1

total 221 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
28	68490	tr|A0A6J2PWT2|A0A6J2PWT2_COTGO	26.90	4	1	1	N	27686	troponin T, fast skeletal muscle isoforms-like isoform X4 OS=Cottoperca gobio OX=56716 GN=LOC115009585 PE=3 SV=1
28	68487	tr|A0A6J2PTP5|A0A6J2PTP5_COTGO	26.90	4	1	1	N	27279	troponin T, fast skeletal muscle isoforms-like isoform X5 OS=Cottoperca gobio OX=56716 GN=LOC115009585 PE=3 SV=1
28	68543	tr|A0A6J2PW38|A0A6J2PW38_COTGO	26.90	4	1	1	N	33340	troponin T, fast skeletal muscle isoforms-like isoform X3 OS=Cottoperca gobio OX=56716 GN=LOC115009585 PE=3 SV=1
28	68546	tr|A0A6J2PTY9|A0A6J2PTY9_COTGO	26.90	3	1	1	N	33991	LOW QUALITY PROTEIN: troponin T, fast skeletal muscle isoforms-like OS=Cottoperca gobio OX=56716 GN=LOC115009631 PE=3 SV=1
28	68547	tr|A0A6J2PVR7|A0A6J2PVR7_COTGO	26.90	3	1	1	N	33971	troponin T, fast skeletal muscle isoforms-like isoform X2 OS=Cottoperca gobio OX=56716 GN=LOC115009585 PE=3 SV=1
28	68549	tr|A0A6J2PTN9|A0A6J2PTN9_COTGO	26.90	3	1	1	N	34378	troponin T, fast skeletal muscle isoforms-like isoform X1 OS=Cottoperca gobio OX=56716 GN=LOC115009585 PE=3 SV=1
28	69618	tr|A0A5A9PG84|A0A5A9PG84_9TELE	26.90	3	1	1	N	39345	Troponin T, cardiac muscle OS=Triplophysa tibetana OX=1572043 GN=E1301_Tti002088 PE=3 SV=1
29	67404	tr|A0A6F9CEX9|A0A6F9CEX9_9TELE	26.71	0	1	1	N	1022296	Uncharacterized protein OS=Coregonus sp. 'balchen' OX=861768 GN=CSTEINMANNI_LOCUS3957823 PE=4 SV=1
19	69734	tr|A0A3B3ICW0|A0A3B3ICW0_ORYLA	24.32	4	2	1	N	47229	2-phospho-D-glycerate hydro-lyase OS=Oryzias latipes OX=8090 GN=eno1 PE=3 SV=1
30	67800	tr|A0A3Q4GK85|A0A3Q4GK85_NEOBR	24.20	6	1	1	N	21230	Adenylate kinase isoenzyme 1 OS=Neolamprologus brichardi OX=32507 GN=AK1 PE=3 SV=1
30	67801	tr|A0A3Q4GS43|A0A3Q4GS43_NEOBR	24.20	6	1	1	N	21240	Adenylate kinase isoenzyme 1 OS=Neolamprologus brichardi OX=32507 GN=AK1 PE=3 SV=1
30	67802	tr|A0A3P8P8S3|A0A3P8P8S3_ASTCA	24.20	6	1	1	N	21228	Adenylate kinase isoenzyme 1 OS=Astatotilapia calliptera OX=8154 GN=AK1 PE=3 SV=1
30	67795	tr|A0A3Q1HW42|A0A3Q1HW42_9TELE	24.20	6	1	1	N	21205	Adenylate kinase isoenzyme 1 OS=Acanthochromis polyacanthus OX=80966 GN=AK1 PE=3 SV=1
30	67803	tr|A0A3P9CWL7|A0A3P9CWL7_9CICH	24.20	6	1	1	N	21258	Adenylate kinase isoenzyme 1 OS=Maylandia zebra OX=106582 GN=AK1 PE=3 SV=1
30	67796	tr|A0A3B5BIY5|A0A3B5BIY5_9TELE	24.20	6	1	1	N	21206	Adenylate kinase isoenzyme 1 OS=Stegastes partitus OX=144197 GN=AK1 PE=3 SV=1
30	67804	tr|A0A3Q2VY92|A0A3Q2VY92_HAPBU	24.20	6	1	1	N	21228	Adenylate kinase isoenzyme 1 OS=Haplochromis burtoni OX=8153 GN=AK1 PE=3 SV=1
30	67805	tr|A0A3B4FMK3|A0A3B4FMK3_9CICH	24.20	6	1	1	N	21228	Adenylate kinase isoenzyme 1 OS=Pundamilia nyererei OX=303518 GN=AK1 PE=3 SV=1
30	67806	tr|A0A3Q3CWR9|A0A3Q3CWR9_HAPBU	24.20	5	1	1	N	23163	Adenylate kinase isoenzyme 1 OS=Haplochromis burtoni OX=8153 GN=AK1 PE=3 SV=1
30	67807	tr|A0A3P8P8V3|A0A3P8P8V3_ASTCA	24.20	5	1	1	N	23216	Adenylate kinase isoenzyme 1 OS=Astatotilapia calliptera OX=8154 GN=AK1 PE=3 SV=1
14	69881	tr|A0A3Q1FHQ1|A0A3Q1FHQ1_9TELE	23.71	0	2	1	N	545809	Ryanodine receptor 3-like OS=Acanthochromis polyacanthus OX=80966 GN=RYR3 PE=4 SV=1
14	69882	tr|G3NYZ7|G3NYZ7_GASAC	23.71	0	2	1	N	545639	Ryanodine receptor 3 OS=Gasterosteus aculeatus OX=69293 PE=4 SV=1

total 221 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
14	69883	tr|A0A674BRX0|A0A674BRX0_SALTR	23.71	0	2	1	N	549015	Ryanodine receptor 3-like OS=Salmo trutta OX=8032 GN=RYR3 PE=4 SV=1
31	69681	tr|A0A0F8B8T7|A0A0F8B8T7_LARCR	23.41	1	1	1	N	158653	Collagen alpha-1(IV) chain OS=Larimichthys crocea OX=215358 GN=EH28_07982 PE=4 SV=1
39	69682	tr|A0A665TL93|A0A665TL93_ECHNA	22.82	2	1	1	N	107933	Uncharacterized protein OS=Echeneis naucrates OX=173247 PE=4 SV=1
39	69683	tr|A0A7J5Y3X5|A0A7J5Y3X5_DISMA	22.82	1	1	1	N	148241	Uncharacterized protein OS=Dissostichus mawsoni OX=36200 GN=F7725_002632 PE=4 SV=1
40	69686	tr|A0A3Q1G4M0|A0A3Q1G4M0_9TELE	22.56	2	1	1	N	62757	Collagen alpha chain-like OS=Acanthochromis polyacanthus OX=80966 PE=4 SV=1
41	69687	tr|A0A834FMH6|A0A834FMH6_ORYME	21.61	3	1	1	N	29285	DNA polymerase eta OS=Oryzias melastigma OX=30732 GN=FQA47_004450 PE=4 SV=1
42	69694	tr|A0A673HU84|A0A673HU84_9TELE	21.18	5	1	1	N	26537	Uncharacterized protein OS=Sinocyclocheilus rhinocerous OX=307959 PE=3 SV=1
42	69696	tr|A0A2Z4XFW9|A0A2Z4XFW9_CTEID	21.18	4	1	1	N	33893	G-protein coupled estrogen receptor 1b (Fragment) OS=Ctenopharyngodon idella OX=7959 PE=2 SV=1
42	69697	tr|A0A4W4E5X7|A0A4W4E5X7_ELEEL	21.18	3	1	1	N	37717	G_PROTEIN_RECEP_F1_2 domain-containing protein OS=Electrophorus electricus OX=8005 PE=3 SV=1
42	69698	tr|A0A672KLI0|A0A672KLI0_SINGR	21.18	3	1	1	N	38253	G_PROTEIN_RECEP_F1_2 domain-containing protein OS=Sinocyclocheilus grahami OX=75366 PE=3 SV=1
42	69699	tr|A0A671RDB8|A0A671RDB8_9TELE	21.18	3	1	1	N	39470	G_PROTEIN_RECEP_F1_2 domain-containing protein OS=Sinocyclocheilus anshuiensis OX=1608454 PE=3 SV=1
42	69700	tr|W5LSJ6|W5LSJ6_ASTMX	21.18	3	1	1	N	40447	G_PROTEIN_RECEP_F1_2 domain-containing protein OS=Astyanax mexicanus OX=7994 PE=3 SV=2
42	69701	tr|A0A3B4C497|A0A3B4C497_PYGNA	21.18	3	1	1	N	41083	G-protein coupled estrogen receptor 1-like OS=Pygocentrus nattereri OX=42514 PE=3 SV=1
42	69702	tr|A0A6P3WBU3|A0A6P3WBU3_CLUHA	21.18	3	1	1	N	41861	G-protein coupled estrogen receptor 1-like OS=Clupea harengus OX=7950 GN=LOC105910498 PE=3 SV=1
42	69703	tr|A0A6P6J7W1|A0A6P6J7W1_CARAU	21.18	3	1	1	N	43164	G-protein coupled estrogen receptor 1-like isoform X2 OS=Carassius auratus OX=7957 GN=LOC113042077 PE=3 SV=1
42	69704	tr|A0A5A9N4U0|A0A5A9N4U0_9TELE	21.18	3	1	1	N	43365	G-protein coupled estrogen receptor 1 G protein-coupled estrogen receptor 1 OS=Triplophysa tibetana OX=1572043 GN=E1301_Tti017821 PE=3 SV=1
42	69705	tr|A0A3N0XI69|A0A3N0XI69_ANAGA	21.18	3	1	1	N	43107	G-protein coupled estrogen receptor 1 OS=Anabarilius grahami OX=495550 GN=DPX16_4475 PE=3 SV=1
42	69706	tr|A0A6J2UVU6|A0A6J2UVU6_CHACN	21.18	3	1	1	N	44149	G-protein coupled estrogen receptor 1-like OS=Chanos chanos OX=29144 GN=LOC115807694 PE=3 SV=1
42	69707	tr|A0A6P6JAH3|A0A6P6JAH3_CARAU	21.18	3	1	1	N	47039	G-protein coupled estrogen receptor 1-like isoform X1 OS=Carassius auratus OX=7957 GN=LOC113042077 PE=3 SV=1
42	69708	tr|A0A6P6JAN8|A0A6P6JAN8_CARAU	21.18	3	1	1	N	47299	G-protein coupled estrogen receptor 1-like OS=Carassius auratus OX=7957 GN=LOC113042127 PE=3 SV=1
42	69709	tr|A0A498LK34|A0A498LK34_LABRO	21.18	2	1	1	N	54338	G-coupled estrogen receptor 1-like protein OS=Labeo rohita OX=84645 GN=ROHU_006898 PE=3 SV=1

total 221 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
43	69695	tr|A0A4W6ESI4|A0A4W6ESI4_LATCA	20.60	1	1	1	N	116901	Collagen, type I, alpha 2 OS=Lates calcarifer OX=8187 PE=4 SV=1
44	69710	tr|A0A7J6A7M3|A0A7J6A7M3_AMEME	20.39	0	1	1	N	242148	Separase OS=Ameiurus melas OX=219545 GN=AMELA_G00185210 PE=4 SV=1
17	69711	tr|A0A6G1P920|A0A6G1P920_9TELE	20.06	1	1	1	N	161430	WD repeat and HMG-box DNA-binding protein 1 Acidic nucleoplasmic DNA-binding protein 1 OS=Channa argus OX=215402 GN=EXN66_Car002427 PE=4 SV=1

total 221 proteins

tr|A0A3P9CRE7|A0A3P9CRE7_9CICH
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TKTPGLME.N	N	44.96	875.4423	-1.2	438.7279	2	10.50	1395	1	650	657	
W.LDKNKDPLNDSVVQ.L	N	37.14	1583.8154	-1.9	792.9135	2	10.88	1463	1	571	584	
E.VADKIAY.L	N	25.34	778.4225	-1.1	390.2181	2	10.49	1394	1	357	363	
L.SKIEDEQSL.G	N	24.72	1047.5084	-0.8	524.7610	2	10.24	1352	1	1064	1072	
E.APPHIF.S	N	22.93	680.3646	-1.5	341.1891	2	11.68	1610	1	144	149	
Q.TEEDKKNLVRL.Q	N	22.80	1343.7408	-0.9	448.9205	3	10.25	1353	1	1826	1836	
K.RIEAPPHIF.S	Y	22.23	1078.5923	-1.5	540.3026	2	11.79	1629	3	141	149	
K.QRNFDKVL.A	N	20.14	1018.5560	-1.1	340.5255	3	10.65	1421	1	1418	1425	
L.KKDIDDLE.L	N	16.50	974.4920	-0.8	488.2529	2	9.80	1275	1	923	930	
T.LEHEE.A	N	16.09	655.2813	3.2	328.6490	2	8.51	1054	1	1523	1527	
T.GWLDKNKDPLNDS.V	N	15.99	1500.7208	4.7	751.3712	2	11.80	1632	1	569	581	

total 11 peptides

tr|A0A669BHT6|A0A669BHT6_ORENI
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TKTPGLME.N	N	44.96	875.4423	-1.2	438.7279	2	10.50	1395	1	671	678	
W.LDKNKDPLNDSVVQ.L	N	37.14	1583.8154	-1.9	792.9135	2	10.88	1463	1	589	602	
E.VADKIAY.L	N	25.34	778.4225	-1.1	390.2181	2	10.49	1394	1	375	381	
L.SKIEDEQSL.G	N	24.72	1047.5084	-0.8	524.7610	2	10.24	1352	1	1085	1093	
E.APPHIF.S	N	22.93	680.3646	-1.5	341.1891	2	11.68	1610	1	144	149	
Q.TEEDKKNLVRL.Q	N	22.80	1343.7408	-0.9	448.9205	3	10.25	1353	1	1847	1857	
K.RIEAPPHIF.S	Y	22.23	1078.5923	-1.5	540.3026	2	11.79	1629	3	141	149	
K.QRNFDKVL.A	N	20.14	1018.5560	-1.1	340.5255	3	10.65	1421	1	1439	1446	
L.KKDIDDLE.L	N	16.50	974.4920	-0.8	488.2529	2	9.80	1275	1	944	951	
T.LEHEE.A	N	16.09	655.2813	3.2	328.6490	2	8.51	1054	1	1544	1548	
S.GWLDKNKDPLNDS.V	N	15.99	1500.7208	4.7	751.3712	2	11.80	1632	1	587	599	

total 11 peptides

tr|A0A3P8Q1P8|A0A3P8Q1P8_ASTCA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TKTPGLME.N	N	44.96	875.4423	-1.2	438.7279	2	10.50	1395	1	679	686	
W.LDKNKDPLNDSVVQ.L	N	37.14	1583.8154	-1.9	792.9135	2	10.88	1463	1	596	609	
E.VADKIAY.L	N	25.34	778.4225	-1.1	390.2181	2	10.49	1394	1	382	388	
L.SKIEDEQSL.G	N	24.72	1047.5084	-0.8	524.7610	2	10.24	1352	1	1093	1101	
E.APPHIF.S	N	22.93	680.3646	-1.5	341.1891	2	11.68	1610	1	151	156	
Q.TEEDKKNLVRL.Q	N	22.80	1343.7408	-0.9	448.9205	3	10.25	1353	1	1855	1865	
K.RIEAPPHIF.S	Y	22.23	1078.5923	-1.5	540.3026	2	11.79	1629	3	148	156	
K.QRNFDKVL.A	N	20.14	1018.5560	-1.1	340.5255	3	10.65	1421	1	1447	1454	
L.KKDIDDLE.L	N	16.50	974.4920	-0.8	488.2529	2	9.80	1275	1	952	959	
T.LEHEE.A	N	16.09	655.2813	3.2	328.6490	2	8.51	1054	1	1552	1556	

total 11 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.GWLDKNKDPLNDS.V	N	15.99	1500.7208	4.7	751.3712	2	11.80	1632	1	594	606	

total 11 peptides

tr|A0A3P8QMC2|A0A3P8QMC2_ASTCA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TKTPGLME.N	N	44.96	875.4423	-1.2	438.7279	2	10.50	1395	1	676	683	
W.LDKNKDPLNDSVVQ.L	N	37.14	1583.8154	-1.9	792.9135	2	10.88	1463	1	596	609	
E.VADKIAY.L	N	25.34	778.4225	-1.1	390.2181	2	10.49	1394	1	382	388	
L.SKIEDEQSL.G	N	24.72	1047.5084	-0.8	524.7610	2	10.24	1352	1	1090	1098	
E.APPHIF.S	N	22.93	680.3646	-1.5	341.1891	2	11.68	1610	1	151	156	
Q.TEEDKKNLVRL.Q	N	22.80	1343.7408	-0.9	448.9205	3	10.25	1353	1	1852	1862	
K.RIEAPPHIF.S	Y	22.23	1078.5923	-1.5	540.3026	2	11.79	1629	3	148	156	
K.QRNFDKVL.A	N	20.14	1018.5560	-1.1	340.5255	3	10.65	1421	1	1444	1451	
L.KKDIDDLE.L	N	16.50	974.4920	-0.8	488.2529	2	9.80	1275	1	949	956	
T.LEHEE.A	N	16.09	655.2813	3.2	328.6490	2	8.51	1054	1	1549	1553	
T.GWLDKNKDPLNDS.V	N	15.99	1500.7208	4.7	751.3712	2	11.80	1632	1	594	606	

total 11 peptides

tr|A0A3P8Q1G5|A0A3P8Q1G5_ASTCA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TKTPGLME.N	N	44.96	875.4423	-1.2	438.7279	2	10.50	1395	1	677	684	
W.LDKNKDPLNDSVVQ.L	N	37.14	1583.8154	-1.9	792.9135	2	10.88	1463	1	596	609	
E.VADKIAY.L	N	25.34	778.4225	-1.1	390.2181	2	10.49	1394	1	382	388	
L.SKIEDEQSL.G	N	24.72	1047.5084	-0.8	524.7610	2	10.24	1352	1	1091	1099	
E.APPHIF.S	N	22.93	680.3646	-1.5	341.1891	2	11.68	1610	1	151	156	
Q.TEEDKKNLVRL.Q	N	22.80	1343.7408	-0.9	448.9205	3	10.25	1353	1	1853	1863	
K.RIEAPPHIF.S	Y	22.23	1078.5923	-1.5	540.3026	2	11.79	1629	3	148	156	
K.QRNFDKVL.A	N	20.14	1018.5560	-1.1	340.5255	3	10.65	1421	1	1445	1452	
L.KKDIDDLE.L	N	16.50	974.4920	-0.8	488.2529	2	9.80	1275	1	950	957	
T.LEHEE.A	N	16.09	655.2813	3.2	328.6490	2	8.51	1054	1	1550	1554	
T.GWLDKNKDPLNDS.V	N	15.99	1500.7208	4.7	751.3712	2	11.80	1632	1	594	606	

total 11 peptides

tr|I3IZY8|I3IZY8_ORENI
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TKTPGLME.N	N	44.96	875.4423	-1.2	438.7279	2	10.50	1395	1	680	687	
W.LDKNKDPLNDSVVQ.L	N	37.14	1583.8154	-1.9	792.9135	2	10.88	1463	1	596	609	
E.VADKIAY.L	N	25.34	778.4225	-1.1	390.2181	2	10.49	1394	1	382	388	
E.APPHIF.S	N	22.93	680.3646	-1.5	341.1891	2	11.68	1610	1	151	156	
Q.TEEDKKNLVRL.Q	N	22.80	1343.7408	-0.9	448.9205	3	10.25	1353	1	1831	1841	
K.QRNFDKVL.A	N	20.14	1018.5560	-1.1	340.5255	3	10.65	1421	1	1423	1430	
K.RVEAPPHIF.S	N	19.35	1064.5767	-1.6	533.2947	2	11.56	1588	1	148	156	
L.KKDIDDLE.L	N	16.50	974.4920	-0.8	488.2529	2	9.80	1275	1	953	960	
T.LEHEE.A	N	16.09	655.2813	3.2	328.6490	2	8.51	1054	1	1528	1532	
T.GWLDKNKDPLNDS.V	N	15.99	1500.7208	4.7	751.3712	2	11.80	1632	1	594	606	

total 10 peptides

tr|I3IZU1|I3IZU1_ORENI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TKTPGLME.N	N	44.96	875.4423	-1.2	438.7279	2	10.50	1395	1	678	685	

total 10 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.LDKNKDPLNDSVVQ.L	N	37.14	1583.8154	-1.9	792.9135	2	10.88	1463	1	596	609	
E.VADKIAY.L	N	25.34	778.4225	-1.1	390.2181	2	10.49	1394	1	382	388	
E.APPHIF.S	N	22.93	680.3646	-1.5	341.1891	2	11.68	1610	1	151	156	
Q.TEEDKKNLVRL.Q	N	22.80	1343.7408	-0.9	448.9205	3	10.25	1353	1	1829	1839	
K.QRNFDKVL.A	N	20.14	1018.5560	-1.1	340.5255	3	10.65	1421	1	1421	1428	
K.RVEAPPHIF.S	N	19.35	1064.5767	-1.6	533.2947	2	11.56	1588	1	148	156	
L.KKDIDDLE.L	N	16.50	974.4920	-0.8	488.2529	2	9.80	1275	1	951	958	
T.LEHEE.A	N	16.09	655.2813	3.2	328.6490	2	8.51	1054	1	1526	1530	
T.GWLDKNKDPLNDS.V	N	15.99	1500.7208	4.7	751.3712	2	11.80	1632	1	594	606	

total 10 peptides

tr|A0A3S2MUF9|A0A3S2MUF9_ORYJA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.GFAGDDAPRA.V	Y	37.63	975.4410	-1.4	488.7271	2	10.18	1340	1	22	31	
T.MYPGIADRM.Q	Y	36.60	1052.4783	-1.8	527.2455	2	11.84	1640	1	307	315	
G.FAGDDAPRA.V	Y	28.57	918.4195	-1.0	460.2166	2	9.82	1278	1	23	31	
L.DAGDGVTH.N	Y	22.86	770.3195	0.3	386.1671	2	8.70	1091	2	156	163	
K.IIAPPERKY.S	Y	22.73	1085.6233	-2.0	543.8178	2	10.01	1311	2	331	339	
K.IIAPPERK.Y	Y	18.76	922.5599	-1.4	308.5268	3	9.49	1222	1	331	338	
Y.ELPDGQVI.T	Y	18.22	869.4494	-1.6	435.7313	2	12.46	1756	1	243	250	
M.KIKIIAPPERKY.S	Y	18.16	1454.8972	-1.2	485.9724	3	9.98	1305	1	328	339	
E.KSYELPDGQVITI.G	Y	15.76	1461.7715	-0.4	731.8927	2	13.67	1973	1	240	252	
E.EHPTLL.T	Y	15.28	708.3806	-1.3	355.1971	2	11.27	1532	1	102	107	

total 10 peptides

tr|A0A7J6C441|A0A7J6C441_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.GFAGDDAPRA.V	Y	37.63	975.4410	-1.4	488.7271	2	10.18	1340	1	22	31	
T.MYPGIADRM.Q	Y	36.60	1052.4783	-1.8	527.2455	2	11.84	1640	1	307	315	
G.FAGDDAPRA.V	Y	28.57	918.4195	-1.0	460.2166	2	9.82	1278	1	23	31	
L.DAGDGVTH.N	Y	22.86	770.3195	0.3	386.1671	2	8.70	1091	2	156	163	
K.IIAPPERKY.S	Y	22.73	1085.6233	-2.0	543.8178	2	10.01	1311	2	331	339	
K.IIAPPERK.Y	Y	18.76	922.5599	-1.4	308.5268	3	9.49	1222	1	331	338	
Y.ELPDGQVI.T	Y	18.22	869.4494	-1.6	435.7313	2	12.46	1756	1	243	250	
M.KIKIIAPPERKY.S	Y	18.16	1454.8972	-1.2	485.9724	3	9.98	1305	1	328	339	
E.KSYELPDGQVITI.G	Y	15.76	1461.7715	-0.4	731.8927	2	13.67	1973	1	240	252	
E.EHPTLL.T	Y	15.28	708.3806	-1.3	355.1971	2	11.27	1532	1	102	107	

total 10 peptides

tr|A0A3B4YLK9|A0A3B4YLK9_SERLL
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.LDKNKDPLNDSVVQ.L	N	37.14	1583.8154	-1.9	792.9135	2	10.88	1463	1	595	608	
E.VADKIAY.L	N	25.34	778.4225	-1.1	390.2181	2	10.49	1394	1	381	387	
L.SKIEDEQSL.S	N	24.72	1047.5084	-0.8	524.7610	2	10.24	1352	1	1093	1101	
E.APPHIF.S	N	22.93	680.3646	-1.5	341.1891	2	11.68	1610	1	150	155	
K.QRNFDKVL.A	N	20.14	1018.5560	-1.1	340.5255	3	10.65	1421	1	1447	1454	
K.RVEAPPHIF.S	N	19.35	1064.5767	-1.6	533.2947	2	11.56	1588	1	147	155	
L.KKDIDDLE.L	N	16.50	974.4920	-0.8	488.2529	2	9.80	1275	1	952	959	
T.LEHEE.S	N	16.09	655.2813	3.2	328.6490	2	8.51	1054	1	1552	1556	
L.GWLDKNKDPLNDS.V	N	15.99	1500.7208	4.7	751.3712	2	11.80	1632	1	593	605	

total 9 peptides

tr|A0A671XZM8|A0A671XZM8_SPAAU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.WIDPDDFPLLLPH.W	Y	40.97	1576.7925	-1.3	789.4025	2	15.34	2265	1	309	321	
F.MDDPVVIPGKPY.T	Y	30.08	1329.6638	-1.8	665.8380	2	12.26	1718	1	225	236	
E.LEDWIEDVLS.V	Y	26.20	1217.5815	-0.3	609.7979	2	15.35	2267	1	362	371	

total 3 peptides

tr|A0A671Y6A5|A0A671Y6A5_SPAAU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.WIDPDDFPLLLPH.W	Y	40.97	1576.7925	-1.3	789.4025	2	15.34	2265	1	286	298	
F.MDDPVVIPGKPY.T	Y	30.08	1329.6638	-1.8	665.8380	2	12.26	1718	1	211	222	
E.LEDWIEDVLS.G	Y	26.20	1217.5815	-0.3	609.7979	2	15.35	2267	1	339	348	

total 3 peptides

tr|A0A671XZM4|A0A671XZM4_SPAAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.WIDPDDFPLLLPH.W	Y	40.97	1576.7925	-1.3	789.4025	2	15.34	2265	1	299	311	
F.MDDPVVIPGKPY.T	Y	30.08	1329.6638	-1.8	665.8380	2	12.26	1718	1	224	235	
E.LEDWIEDVLS.G	Y	26.20	1217.5815	-0.3	609.7979	2	15.35	2267	1	352	361	

total 3 peptides

tr|A0A671XZK3|A0A671XZK3_SPAAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.WIDPDDFPLLLPH.W	Y	40.97	1576.7925	-1.3	789.4025	2	15.34	2265	1	309	321	
F.MDDPVVIPGKPY.T	Y	30.08	1329.6638	-1.8	665.8380	2	12.26	1718	1	225	236	
E.LEDWIEDVLS.G	Y	26.20	1217.5815	-0.3	609.7979	2	15.35	2267	1	362	371	

total 3 peptides

tr|A0A671XZP8|A0A671XZP8_SPAAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.WIDPDDFPLLLPH.W	Y	40.97	1576.7925	-1.3	789.4025	2	15.34	2265	1	328	340	
F.MDDPVVIPGKPY.T	Y	30.08	1329.6638	-1.8	665.8380	2	12.26	1718	1	253	264	
E.LEDWIEDVLS.G	Y	26.20	1217.5815	-0.3	609.7979	2	15.35	2267	1	381	390	

total 3 peptides

tr|A0A834CTG4|A0A834CTG4_ORYME
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.MNPLFPPGPPKDL.H	Y	36.23	1421.7377	-3.1	711.8739	2	13.54	1950	2	1811	1823	
E.VGAGDPSPPSKPVFA.K	Y	35.36	1424.7299	-2.2	713.3707	2	11.38	1554	1	1499	1513	
L.GPPGPPVGPIKF.T	Y	28.36	1161.6545	-1.2	581.8339	2	12.78	1814	1	595	606	

total 3 peptides

tr|A0A315VR11|A0A315VR11_GAMAF
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.FDKPVSPL.L	Y	29.51	901.4908	-1.7	451.7520	2	11.53	1581	2	628	635	

total 5 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.HGGYKPT.D	Y	24.75	758.3711	-0.1	380.1928	2	8.43	1038	1	531	537	
L.VVDGVKLM.V	Y	21.72	859.4837	-1.9	430.7483	2	11.82	1636	1	787	794	
L.VVDGVKL.M	Y	21.20	728.4432	-1.5	365.2283	2	11.24	1526	1	787	793	
T.GVDNPGHPF.I	Y	20.20	938.4246	-0.2	470.2195	2	16.17	2408	3	494	502	

total 5 peptides

tr|A0A6G0IP12|A0A6G0IP12_LARCR
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.SDGMLDFDEFLKM.M	Y	35.71	1546.6683	-0.5	774.3411	2	15.25	2249	1	143	155	
N.SDGMLDFDEFLK.M	Y	33.64	1415.6278	-0.2	708.8210	2	14.54	2125	1	143	154	
L.MKDGDKNSDGMLDFDEFLK.M	Y	15.63	2203.9766	-2.0	735.6647	3	13.43	1932	1	136	154	

total 3 peptides

tr|A0A1A8D9W7|A0A1A8D9W7_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.SDGMLDFDEFLKM.M	Y	35.71	1546.6683	-0.5	774.3411	2	15.25	2249	1	118	130	
N.SDGMLDFDEFLK.M	Y	33.64	1415.6278	-0.2	708.8210	2	14.54	2125	1	118	129	
L.MKDGDKNSDGMLDFDEFLK.M	Y	15.63	2203.9766	-2.0	735.6647	3	13.43	1932	1	111	129	

total 3 peptides

tr|A0A1A8CTF6|A0A1A8CTF6_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.SDGMLDFDEFLKM.M	Y	35.71	1546.6683	-0.5	774.3411	2	15.25	2249	1	143	155	
N.SDGMLDFDEFLK.M	Y	33.64	1415.6278	-0.2	708.8210	2	14.54	2125	1	143	154	
L.MKDGDKNSDGMLDFDEFLK.M	Y	15.63	2203.9766	-2.0	735.6647	3	13.43	1932	1	136	154	

total 3 peptides

tr|A0A1A8QW41|A0A1A8QW41_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.SDGMLDFDEFLKM.M	Y	35.71	1546.6683	-0.5	774.3411	2	15.25	2249	1	143	155	
N.SDGMLDFDEFLK.M	Y	33.64	1415.6278	-0.2	708.8210	2	14.54	2125	1	143	154	
L.MKDGDKNSDGMLDFDEFLK.M	Y	15.63	2203.9766	-2.0	735.6647	3	13.43	1932	1	136	154	

total 3 peptides

tr|A0A1A8B5H7|A0A1A8B5H7_NOTFU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.SDGMLDFDEFLKM.M	Y	35.71	1546.6683	-0.5	774.3411	2	15.25	2249	1	143	155	
N.SDGMLDFDEFLK.M	Y	33.64	1415.6278	-0.2	708.8210	2	14.54	2125	1	143	154	
L.MKDGDKNSDGMLDFDEFLK.M	Y	15.63	2203.9766	-2.0	735.6647	3	13.43	1932	1	136	154	

total 3 peptides

tr|A0A1A8IG78|A0A1A8IG78_NOTKU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.SDGMLDFDEFLKM.M	Y	35.71	1546.6683	-0.5	774.3411	2	15.25	2249	1	73	85	

total 3 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.SDGMLDFDEFLK.M	Y	33.64	1415.6278	-0.2	708.8210	2	14.54	2125	1	73	84	
L.MKDGDKNSDGMLDFDEFLK.M	Y	15.63	2203.9766	-2.0	735.6647	3	13.43	1932	1	66	84	

total 3 peptides

tr|A0A1A8ML32|A0A1A8ML32_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.SDGMLDFDEFLKM.M	Y	35.71	1546.6683	-0.5	774.3411	2	15.25	2249	1	73	85	
N.SDGMLDFDEFLK.M	Y	33.64	1415.6278	-0.2	708.8210	2	14.54	2125	1	73	84	
L.MKDGDKNSDGMLDFDEFLK.M	Y	15.63	2203.9766	-2.0	735.6647	3	13.43	1932	1	66	84	

total 3 peptides

tr|A0A1A8SNN3|A0A1A8SNN3_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.SDGMLDFDEFLKM.M	Y	35.71	1546.6683	-0.5	774.3411	2	15.25	2249	1	79	91	
N.SDGMLDFDEFLK.M	Y	33.64	1415.6278	-0.2	708.8210	2	14.54	2125	1	79	90	
L.MKDGDKNSDGMLDFDEFLK.M	Y	15.63	2203.9766	-2.0	735.6647	3	13.43	1932	1	72	90	

total 3 peptides

tr|A0A1A8Q0J1|A0A1A8Q0J1_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.SDGMLDFDEFLKM.M	Y	35.71	1546.6683	-0.5	774.3411	2	15.25	2249	1	144	156	
N.SDGMLDFDEFLK.M	Y	33.64	1415.6278	-0.2	708.8210	2	14.54	2125	1	144	155	
L.MKDGDKNSDGMLDFDEFLK.M	Y	15.63	2203.9766	-2.0	735.6647	3	13.43	1932	1	137	155	

total 3 peptides

tr|A0A6J2PW36|A0A6J2PW36_COTGO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SKIEDEQSL.G	N	24.72	1047.5084	-0.8	524.7610	2	10.24	1352	1	1088	1096	
E.APPHIF.S	N	22.93	680.3646	-1.5	341.1891	2	11.68	1610	1	152	157	
N.MENVAK.A	Y	21.24	690.3370	-0.7	346.1756	2	9.03	1148	1	1231	1236	
K.QRNFDKVL.A	N	20.14	1018.5560	-1.1	340.5255	3	10.65	1421	1	1442	1449	
L.KKDIDDLE.L	N	16.50	974.4920	-0.8	488.2529	2	9.80	1275	1	947	954	
T.LEHEE.S	N	16.09	655.2813	3.2	328.6490	2	8.51	1054	1	1547	1551	
N.GWLDKNKDPLNDS.V	N	15.99	1500.7208	4.7	751.3712	2	11.80	1632	1	590	602	

total 7 peptides

tr|A0A6A5EZU1|A0A6A5EZU1_PERFL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGSPGSSGPQ.G	Y	50.73	1333.6375	-1.1	667.8253	2	9.41	1210	1	169	183	

total 1 peptides

tr|A0A4Z2EZH8|A0A4Z2EZH8_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGSPGSSGPQ.G	Y	50.73	1333.6375	-1.1	667.8253	2	9.41	1210	1	71	85	

total 1 peptides

tr|A0A6A4S346|A0A6A4S346_SCOMX

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGSPGSSGPQ.G	Y	50.73	1333.6375	-1.1	667.8253	2	9.41	1210	1	200	214	

total 1 peptides

tr|C6GKU3|C6GKU3_THUAL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.GDSDGDGKIGID.E	Y	36.13	1147.4993	-1.2	574.7562	2	10.59	1412	1	90	101	
A.VIDQDKSGFIE.E	Y	24.31	1249.6190	-2.1	625.8155	2	11.36	1550	1	50	60	

total 2 peptides

tr|D2KQG3|D2KQG3_SINCH

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.GDSDGDGKIGID.E	Y	36.13	1147.4993	-1.2	574.7562	2	10.59	1412	1	90	101	
E.VIDQDKSGFIE.E	Y	24.31	1249.6190	-2.1	625.8155	2	11.36	1550	1	50	60	

total 2 peptides

tr|A0A7J6CHT3|A0A7J6CHT3_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.GDSDGDGKIGID.E	Y	36.13	1147.4993	-1.2	574.7562	2	10.59	1412	1	90	101	
A.VIDQDKSGFIE.E	Y	24.31	1249.6190	-2.1	625.8155	2	11.36	1550	1	50	60	

total 2 peptides

P05941|PRVB_OPSTA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.GDSDGDGKIGID.E	Y	36.13	1147.4993	-1.2	574.7562	2	10.59	1412	1	89	100	
Y.VIDQDKSGFIE.E	Y	24.31	1249.6190	-2.1	625.8155	2	11.36	1550	1	49	59	

total 2 peptides

tr|B9VJM3|B9VJM3_SINCH

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.GDSDGDGKIGID.E	Y	36.13	1147.4993	-1.2	574.7562	2	10.59	1412	1	90	101	
E.VIDQDKSGFIE.E	Y	24.31	1249.6190	-2.1	625.8155	2	11.36	1550	1	50	60	

total 2 peptides

tr|A0A668SJD1|A0A668SJD1_OREAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IDYVPR.Q	N	27.60	761.4072	-1.1	381.7104	2	10.67	1426	1	472	477	
K.MIIGEDPKYL.M	Y	23.06	1177.6052	-1.8	589.8088	2	12.67	1793	1	1025	1034	
F.VKEPPVTIT.K	N	21.46	982.5699	-1.7	492.2914	2	10.81	1449	1	285	293	

total 3 peptides

tr|A0A6P7L5W1|A0A6P7L5W1_BETSP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IDYVPR.Q	N	27.60	761.4072	-1.1	381.7104	2	10.67	1426	1	490	495	
K.MIIGEDPKYL.M	Y	23.06	1177.6052	-1.8	589.8088	2	12.67	1793	1	1047	1056	
F.VKEPPVTIT.K	N	21.46	982.5699	-1.7	492.2914	2	10.81	1449	1	303	311	

total 3 peptides

tr|A0A3P9C2F1|A0A3P9C2F1_9CICH

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IDYVPR.Q	N	27.60	761.4072	-1.1	381.7104	2	10.67	1426	1	495	500	
K.MIIGEDPKYL.M	Y	23.06	1177.6052	-1.8	589.8088	2	12.67	1793	1	1052	1061	
F.VKEPPVTIT.K	N	21.46	982.5699	-1.7	492.2914	2	10.81	1449	1	308	316	

total 3 peptides

tr|A0A6P7L5V6|A0A6P7L5V6_BETSP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IDYVPR.Q	N	27.60	761.4072	-1.1	381.7104	2	10.67	1426	1	497	502	
K.MIIGEDPKYL.M	Y	23.06	1177.6052	-1.8	589.8088	2	12.67	1793	1	1054	1063	
F.VKEPPVTIT.K	N	21.46	982.5699	-1.7	492.2914	2	10.81	1449	1	310	318	

total 3 peptides

tr|A0A668SIT2|A0A668SIT2_OREAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IDYVPR.Q	N	27.60	761.4072	-1.1	381.7104	2	10.67	1426	1	482	487	
K.MIIGEDPKYL.M	Y	23.06	1177.6052	-1.8	589.8088	2	12.67	1793	1	1052	1061	
F.VKEPPVTIT.K	N	21.46	982.5699	-1.7	492.2914	2	10.81	1449	1	295	303	

total 3 peptides

tr|A0A6P7L5V2|A0A6P7L5V2_BETSP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IDYVPR.Q	N	27.60	761.4072	-1.1	381.7104	2	10.67	1426	1	510	515	
K.MIIGEDPKYL.M	Y	23.06	1177.6052	-1.8	589.8088	2	12.67	1793	1	1067	1076	
F.VKEPPVTIT.K	N	21.46	982.5699	-1.7	492.2914	2	10.81	1449	1	323	331	

total 3 peptides

tr|A0A6P7INY3|A0A6P7INY3_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	169	183	

total 1 peptides

tr|A0A6P7IU28|A0A6P7IU28_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	169	183	

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM

total 1 peptides

tr|A0A2I4D9D9|A0A2I4D9D9_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	169	183	

total 1 peptides

tr|A0A7J6DBF9|A0A7J6DBF9_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	169	183	

total 1 peptides

tr|A0A2I4D9D6|A0A2I4D9D6_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	169	183	

total 1 peptides

tr|A0A6P6JU61|A0A6P6JU61_CARAU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	170	184	

total 1 peptides

tr|A0A3B4UIY5|A0A3B4UIY5_SERDU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	149	163	

total 1 peptides

tr|A0A2I4D9D4|A0A2I4D9D4_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	169	183	

total 1 peptides

tr|A0A060WU51|A0A060WU51_ONCMY
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	170	184	

total 1 peptides

tr|A0A6F9C010|A0A6F9C010_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	170	184	

total 1 peptides

tr|A0A060X5H1|A0A060X5H1_ONCMY
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	170	184	

total 1 peptides

tr|A0A4W5KL14|A0A4W5KL14_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	170	184	

total 1 peptides

tr|A0A673A8U8|A0A673A8U8_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	78	92	

total 1 peptides

tr|I3JGN1|I3JGN1_ORENI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	163	177	

total 1 peptides

tr|A0A671YED8|A0A671YED8_SPAAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	108	122	

total 1 peptides

tr|A0A671YFV1|A0A671YFV1_SPAAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	169	183	

total 1 peptides

tr|A0A3Q2W9Y5|A0A3Q2W9Y5_HAPBU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	169	183	

total 1 peptides

tr|A0A674DLV9|A0A674DLV9_SALTR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	170	184	

total 1 peptides

tr|A0A3Q3CY74|A0A3Q3CY74_HAPBU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	169	183	

total 1 peptides

tr|G9M6I5|G9M6I5_ORENI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	169	183	

total 1 peptides

tr|A0A674DL09|A0A674DL09_SALTR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	170	184	

total 1 peptides

tr|Q910C0|Q910C0_ONCMY
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	170	184	

total 1 peptides

tr|A0A1S3S6G4|A0A1S3S6G4_SALSA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	170	184	

total 1 peptides

tr|A0A6J2RRG5|A0A6J2RRG5_COTGO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	170	184	

total 1 peptides

tr|A0A1S3R8F9|A0A1S3R8F9_SALSA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQ.G	Y	46.23	1343.6582	-1.5	672.8354	2	9.65	1250	1	170	184	

total 1 peptides

tr|A0A1S3NGD5|A0A1S3NGD5_SALSA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IDYVPR.Q	N	27.60	761.4072	-1.1	381.7104	2	10.67	1426	1	513	518	
F.VKEPPVTIT.K	N	21.46	982.5699	-1.7	492.2914	2	10.81	1449	1	327	335	
R.VGDKINL.T	Y	20.52	757.4333	-1.1	379.7235	2	11.14	1509	1	838	844	

total 3 peptides

tr|A0A1A7W9Y4|A0A1A7W9Y4_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IDYVPR.Q	N	27.60	761.4072	-1.1	381.7104	2	10.67	1426	1	497	502	
Y.VKEPPVTIT.K	N	21.46	982.5699	-1.7	492.2914	2	10.81	1449	1	309	317	
K.VGDKINL.T	Y	20.52	757.4333	-1.1	379.7235	2	11.14	1509	1	822	828	

total 3 peptides

tr|A0A0F8B178|A0A0F8B178_LARCR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TVDGDHVDLD.A	Y	22.82	1084.4673	-1.3	543.2402	2	10.79	1446	1	365	374	
Q.SLVRMPPWSNF.W	Y	21.63	1332.6648	-1.9	667.3384	2	14.19	2063	1	912	922	
L.IDEVLKFF.A	Y	20.20	1009.5484	-0.4	505.7813	2	14.37	2094	1	971	978	
E.VSVGDKVPADIR.I	Y	16.19	1254.6931	-1.0	419.2379	3	10.68	1427	2	147	158	

total 4 peptides

tr|A0A3P8PD71|A0A3P8PD71_ASTCA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TVDGDHVDLD.A	Y	22.82	1084.4673	-1.3	543.2402	2	10.79	1446	1	371	380	
Q.SLVRMPPWSNF.W	Y	21.63	1332.6648	-1.9	667.3384	2	14.19	2063	1	918	928	
A.IDEVLKFF.A	Y	20.20	1009.5484	-0.4	505.7813	2	14.37	2094	1	977	984	
E.VSVGDKVPADIR.I	Y	16.19	1254.6931	-1.0	419.2379	3	10.68	1427	2	153	164	

total 4 peptides

tr|A0A3Q2WQG2|A0A3Q2WQG2_HAPBU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TVDGDHVDLD.A	Y	22.82	1084.4673	-1.3	543.2402	2	10.79	1446	1	371	380	
Q.SLVRMPPWSNF.W	Y	21.63	1332.6648	-1.9	667.3384	2	14.19	2063	1	918	928	
A.IDEVLKFF.A	Y	20.20	1009.5484	-0.4	505.7813	2	14.37	2094	1	977	984	
E.VSVGDKVPADIR.I	Y	16.19	1254.6931	-1.0	419.2379	3	10.68	1427	2	153	164	

total 4 peptides

tr|A0A6G0HZ09|A0A6G0HZ09_LARCR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TVDGDHVDLD.A	Y	22.82	1084.4673	-1.3	543.2402	2	10.79	1446	1	371	380	
Q.SLVRMPPWSNF.W	Y	21.63	1332.6648	-1.9	667.3384	2	14.19	2063	1	918	928	
L.IDEVLKFF.A	Y	20.20	1009.5484	-0.4	505.7813	2	14.37	2094	1	977	984	
E.VSVGDKVPADIR.I	Y	16.19	1254.6931	-1.0	419.2379	3	10.68	1427	2	153	164	

total 4 peptides

tr|A0A3B4GKY8|A0A3B4GKY8_9CICH

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TVDGDHVDLD.A	Y	22.82	1084.4673	-1.3	543.2402	2	10.79	1446	1	371	380	
Q.SLVRMPPWSNF.W	Y	21.63	1332.6648	-1.9	667.3384	2	14.19	2063	1	918	928	
A.IDEVLKFF.A	Y	20.20	1009.5484	-0.4	505.7813	2	14.37	2094	1	977	984	
E.VSVGDKVPADIR.I	Y	16.19	1254.6931	-1.0	419.2379	3	10.68	1427	2	153	164	

total 4 peptides

tr|A0A3P9C8S8|A0A3P9C8S8_9CICH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TVDGDHVDLD.A	Y	22.82	1084.4673	-1.3	543.2402	2	10.79	1446	1	371	380	
Q.SLVRMPPWSNF.W	Y	21.63	1332.6648	-1.9	667.3384	2	14.19	2063	1	918	928	
A.IDEVLKFF.A	Y	20.20	1009.5484	-0.4	505.7813	2	14.37	2094	1	977	984	
E.VSVGDKVPADIR.I	Y	16.19	1254.6931	-1.0	419.2379	3	10.68	1427	2	153	164	

total 4 peptides

tr|A0A3P8PD17|A0A3P8PD17_ASTCA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TVDGDHVDLD.A	Y	22.82	1084.4673	-1.3	543.2402	2	10.79	1446	1	371	380	
Q.SLVRMPPWSNF.W	Y	21.63	1332.6648	-1.9	667.3384	2	14.19	2063	1	918	928	
A.IDEVLKFF.A	Y	20.20	1009.5484	-0.4	505.7813	2	14.37	2094	1	977	984	
E.VSVGDKVPADIR.I	Y	16.19	1254.6931	-1.0	419.2379	3	10.68	1427	2	153	164	

total 4 peptides

tr|A0A3B4GL15|A0A3B4GL15_9CICH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TVDGDHVDLD.A	Y	22.82	1084.4673	-1.3	543.2402	2	10.79	1446	1	371	380	
Q.SLVRMPPWSNF.W	Y	21.63	1332.6648	-1.9	667.3384	2	14.19	2063	1	918	928	
A.IDEVLKFF.A	Y	20.20	1009.5484	-0.4	505.7813	2	14.37	2094	1	977	984	
E.VSVGDKVPADIR.I	Y	16.19	1254.6931	-1.0	419.2379	3	10.68	1427	2	153	164	

total 4 peptides

tr|A0A3P9C9M1|A0A3P9C9M1_9CICH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TVDGDHVDLD.A	Y	22.82	1084.4673	-1.3	543.2402	2	10.79	1446	1	371	380	
Q.SLVRMPPWSNF.W	Y	21.63	1332.6648	-1.9	667.3384	2	14.19	2063	1	918	928	
A.IDEVLKFF.A	Y	20.20	1009.5484	-0.4	505.7813	2	14.37	2094	1	977	984	
E.VSVGDKVPADIR.I	Y	16.19	1254.6931	-1.0	419.2379	3	10.68	1427	2	153	164	

total 4 peptides

tr|A0A3Q2WG66|A0A3Q2WG66_HAPBU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TVDGDHVDLD.A	Y	22.82	1084.4673	-1.3	543.2402	2	10.79	1446	1	371	380	
Q.SLVRMPPWSNF.W	Y	21.63	1332.6648	-1.9	667.3384	2	14.19	2063	1	918	928	
A.IDEVLKFF.A	Y	20.20	1009.5484	-0.4	505.7813	2	14.37	2094	1	977	984	
E.VSVGDKVPADIR.I	Y	16.19	1254.6931	-1.0	419.2379	3	10.68	1427	2	153	164	

total 4 peptides

tr|A0A3P8PDJ9|A0A3P8PDJ9_ASTCA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TVDGDHVDLD.A	Y	22.82	1084.4673	-1.3	543.2402	2	10.79	1446	1	369	378	
Q.SLVRMPPWSNF.W	Y	21.63	1332.6648	-1.9	667.3384	2	14.19	2063	1	916	926	
A.IDEVLKFF.A	Y	20.20	1009.5484	-0.4	505.7813	2	14.37	2094	1	975	982	
E.VSVGDKVPADIR.I	Y	16.19	1254.6931	-1.0	419.2379	3	10.68	1427	2	151	162	

total 4 peptides

tr|A0A3P8PDC7|A0A3P8PDC7_ASTCA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TVDGDHVDLD.A	Y	22.82	1084.4673	-1.3	543.2402	2	10.79	1446	1	371	380	
Q.SLVRMPPWSNF.W	Y	21.63	1332.6648	-1.9	667.3384	2	14.19	2063	1	918	928	
A.IDEVLKFF.A	Y	20.20	1009.5484	-0.4	505.7813	2	14.37	2094	1	977	984	
E.VSVGDKVPADIR.I	Y	16.19	1254.6931	-1.0	419.2379	3	10.68	1427	2	153	164	

total 4 peptides

tr|A0A3Q2WG59|A0A3Q2WG59_HAPBU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TVDGDHVDLD.A	Y	22.82	1084.4673	-1.3	543.2402	2	10.79	1446	1	371	380	
Q.SLVRMPPWSNF.W	Y	21.63	1332.6648	-1.9	667.3384	2	14.19	2063	1	918	928	
A.IDEVLKFF.A	Y	20.20	1009.5484	-0.4	505.7813	2	14.37	2094	1	977	984	
E.VSVGDKVPADIR.I	Y	16.19	1254.6931	-1.0	419.2379	3	10.68	1427	2	153	164	

total 4 peptides

tr|A0A3P8P4C2|A0A3P8P4C2_ASTCA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1366	1380	

total 1 peptides

tr|A0A3Q1D109|A0A3Q1D109_AMPOC
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1366	1380	

total 1 peptides

tr|A0A3Q2WWP1|A0A3Q2WWP1_HAPBU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1366	1380	

total 1 peptides

tr|A0A3Q4GHK3|A0A3Q4GHK3_NEOBR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.P	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	858	872	

total 1 peptides

tr|A0A672ZI78|A0A672ZI78_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1101	1115	

total 1 peptides

tr|A0A669ELF6|A0A669ELF6_ORENI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1146	1160	

total 1 peptides

tr|A0A4U5U6X9|A0A4U5U6X9_COLLU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1190	1204	

total 1 peptides

tr|A0A3Q4GXU7|A0A3Q4GXU7_NEOBR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.P	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1184	1198	

total 1 peptides

tr|A0A669CKL2|A0A669CKL2_ORENI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1224	1238	

total 1 peptides

tr|A0A671Y401|A0A671Y401_SPAAU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1268	1282	

total 1 peptides

tr|A0A672FNF5|A0A672FNF5_SALFA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1294	1308	

total 1 peptides

tr|A0A6G0J0W8|A0A6G0J0W8_LARCR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1335	1349	

total 1 peptides

tr|A0A671Y575|A0A671Y575_SPAAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1349	1363	

total 1 peptides

tr|A0A3B3IJA0|A0A3B3IJA0_ORYLA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1351	1365	

total 1 peptides

tr|A0A6G1P7U8|A0A6G1P7U8_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1366	1380	

total 1 peptides

tr|A0A087YFH0|A0A087YFH0_POEFO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1365	1379	

total 1 peptides

tr|A0A3P9PGW1|A0A3P9PGW1_POERE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1365	1379	

total 1 peptides

tr|A0A672ZHV0|A0A672ZHV0_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1366	1380	

total 1 peptides

tr|I3JDJ1|I3JDJ1_ORENI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1366	1380	

total 1 peptides

tr|A0A2I4AP94|A0A2I4AP94_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM

total 1 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1366	1380	

total 1 peptides

tr|A0A834CMG6|A0A834CMG6_ORYME
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1366	1380	

total 1 peptides

tr|A0A3B3BCL7|A0A3B3BCL7_ORYME
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1366	1380	

total 1 peptides

tr|A0A3P9IT90|A0A3P9IT90_ORYLA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1366	1380	

total 1 peptides

tr|H2M2B3|H2M2B3_ORYLA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1366	1380	

total 1 peptides

tr|A0A3P9LTE0|A0A3P9LTE0_ORYLA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1366	1380	

total 1 peptides

tr|A0A3B3D3C5|A0A3B3D3C5_ORYME
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1371	1385	

total 1 peptides

tr|A0A6P7LYN0|A0A6P7LYN0_BETSP
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIELPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1382	1396	

total 1 peptides

tr|A0A3B3HWS2|A0A3B3HWS2_ORYLA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TIIPPKLPIEIPQPK.T	Y	35.05	1683.0334	0.1	842.5240	2	13.77	1991	1	1378	1392	

total 1 peptides

tr|A0A665WT54|A0A665WT54_ECHNA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A671N228|A0A671N228_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A3Q3Q7K2|A0A3Q3Q7K2_MONAL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A671MU99|A0A671MU99_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A672KK19|A0A672KK19_SINGR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A673LYE6|A0A673LYE6_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A3P8VEA1|A0A3P8VEA1_CYNSE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A3Q1II99|A0A3Q1II99_ANATE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A6P7L9I7|A0A6P7L9I7_BETSP
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A3P8X8T4|A0A3P8X8T4_ESOLU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	97	105	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	98	105	

total 2 peptides

tr|A0A3Q0R4X6|A0A3Q0R4X6_AMPCI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A3P8VK01|A0A3P8VK01_CYNSE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A3P8XBI5|A0A3P8XBI5_ESOLU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	97	105	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	98	105	

total 2 peptides

tr|A0A3Q1H919|A0A3Q1H919_ANATE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A3Q3KN21|A0A3Q3KN21_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A6P7L9I9|A0A6P7L9I9_BETSP
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A3P8VE68|A0A3P8VE68_CYNSE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A6G0HYN5|A0A6G0HYN5_LARCR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A3P8ZCR8|A0A3P8ZCR8_ESOLU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	97	105	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	98	105	

total 2 peptides

tr|A0A3Q3IQV7|A0A3Q3IQV7_MONAL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A665WTS5|A0A665WTS5_ECHNA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A7N8Y585|A0A7N8Y585_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	101	109	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	102	109	

total 2 peptides

tr|A0A6P6QFT2|A0A6P6QFT2_CARAU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A672KNU9|A0A672KNU9_SINGR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A673M1Q3|A0A673M1Q3_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A7J6CGV6|A0A7J6CGV6_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A6P6QIW1|A0A6P6QIW1_CARAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A6Q2XWF7|A0A6Q2XWF7_ESOLU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	97	105	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	98	105	

total 2 peptides

tr|A0A0F8AMH6|A0A0F8AMH6_LARCR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	98	106	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	99	106	

total 2 peptides

tr|A0A6G0HYU6|A0A6G0HYU6_LARCR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.DSPMPIIPH.Q	Y	23.87	1005.4954	-1.3	503.7543	2	12.27	1720	1	545	553	
D.SPMPIIPH.Q	Y	22.14	890.4684	-2.1	446.2405	2	11.82	1635	1	546	553	

total 2 peptides

tr|A0A0P7UGN8|A0A0P7UGN8_SCLFO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.IIVPALPQ.S	Y	30.17	849.5323	-1.3	425.7729	2	13.25	1898	1	263	270	

total 1 peptides

tr|A0A3P8UKD4|A0A3P8UKD4_CYNSE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.IIVPALPQ.D	Y	30.17	849.5323	-1.3	425.7729	2	13.25	1898	1	102	109	

total 1 peptides

tr|A0A668SIM0|A0A668SIM0_OREAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.IIVPALPQ.D	Y	30.17	849.5323	-1.3	425.7729	2	13.25	1898	1	262	269	

total 1 peptides

tr|A0A6P7NE86|A0A6P7NE86_BETSP
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.IIVPALPQ.S	Y	30.17	849.5323	-1.3	425.7729	2	13.25	1898	1	164	171	

total 1 peptides

tr|A0A5J5CFY0|A0A5J5CFY0_9PERO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.IIVPALPQ.D	Y	30.17	849.5323	-1.3	425.7729	2	13.25	1898	1	164	171	

total 1 peptides

tr|A0A315V5I0|A0A315V5I0_GAMAF
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.IIVPALPQ.S	Y	30.17	849.5323	-1.3	425.7729	2	13.25	1898	1	242	249	

total 1 peptides

tr|A0A6P7NIN0|A0A6P7NIN0_BETSP

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.IIVPALPQ.S	Y	30.17	849.5323	-1.3	425.7729	2	13.25	1898	1	242	249	

total 1 peptides

tr|A0A6J2QDT9|A0A6J2QDT9_COTGO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.IIVPALPQ.S	Y	30.17	849.5323	-1.3	425.7729	2	13.25	1898	1	242	249	

total 1 peptides

tr|M3ZP84|M3ZP84_XIPMA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.IIVPALPQ.S	Y	30.17	849.5323	-1.3	425.7729	2	13.25	1898	1	242	249	

total 1 peptides

tr|A0A3P9PCX4|A0A3P9PCX4_POERE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.IIVPALPQ.S	Y	30.17	849.5323	-1.3	425.7729	2	13.25	1898	1	242	249	

total 1 peptides

tr|A0A3B3WUC6|A0A3B3WUC6_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.IIVPALPQ.S	Y	30.17	849.5323	-1.3	425.7729	2	13.25	1898	1	242	249	

total 1 peptides

tr|A0A6G0J5Q9|A0A6G0J5Q9_LARCR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.IIVPALPQ.D	Y	30.17	849.5323	-1.3	425.7729	2	13.25	1898	1	1289	1296	

total 1 peptides

tr|A0A6J2RVQ6|A0A6J2RVQ6_COTGO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SIQDDPLLVH.Y	Y	20.27	1135.5873	-1.5	568.8000	2	12.24	1715	1	835	844	
C.VIPVVDDKLTL.L	Y	15.71	1210.7173	-1.2	606.3652	2	13.28	1904	1	5321	5331	

total 2 peptides

tr|A0A6J2RYJ1|A0A6J2RYJ1_COTGO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SIQDDPLLVH.Y	Y	20.27	1135.5873	-1.5	568.8000	2	12.24	1715	1	835	844	
C.VIPVVDDKLTL.L	Y	15.71	1210.7173	-1.2	606.3652	2	13.28	1904	1	5321	5331	

total 2 peptides

tr|A0A6J2RTY3|A0A6J2RTY3_COTGO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SIQDDPLLVH.Y	Y	20.27	1135.5873	-1.5	568.8000	2	12.24	1715	1	835	844	
C.VIPVVDDKLTL.L	Y	15.71	1210.7173	-1.2	606.3652	2	13.28	1904	1	5077	5087	

total 2 peptides

tr|A0A6J2RY66|A0A6J2RY66_COTGO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SIQDDPLLVH.Y	Y	20.27	1135.5873	-1.5	568.8000	2	12.24	1715	1	835	844	
C.VIPVVDDKLTL.L	Y	15.71	1210.7173	-1.2	606.3652	2	13.28	1904	1	5321	5331	

total 2 peptides

tr|A0A6J2RVQ1|A0A6J2RVQ1_COTGO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SIQDDPLLVH.Y	Y	20.27	1135.5873	-1.5	568.8000	2	12.24	1715	1	835	844	
C.VIPVVDDKLTL.L	Y	15.71	1210.7173	-1.2	606.3652	2	13.28	1904	1	5321	5331	

total 2 peptides

tr|A0A3Q1HC41|A0A3Q1HC41_ANATE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SLQDDPLLVH.Y	Y	20.27	1135.5873	-1.5	568.8000	2	12.24	1715	1	777	786	
C.VIPVVDDKLTL.L	Y	15.71	1210.7173	-1.2	606.3652	2	13.28	1904	1	5240	5250	

total 2 peptides

tr|A0A6J2RYI7|A0A6J2RYI7_COTGO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SIQDDPLLVH.Y	Y	20.27	1135.5873	-1.5	568.8000	2	12.24	1715	1	835	844	
C.VIPVVDDKLTL.L	Y	15.71	1210.7173	-1.2	606.3652	2	13.28	1904	1	5321	5331	

total 2 peptides

tr|A0A6J2RWT1|A0A6J2RWT1_COTGO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SIQDDPLLVH.Y	Y	20.27	1135.5873	-1.5	568.8000	2	12.24	1715	1	835	844	
C.VIPVVDDKLTL.L	Y	15.71	1210.7173	-1.2	606.3652	2	13.28	1904	1	5321	5331	

total 2 peptides

tr|A0A6J2RY61|A0A6J2RY61_COTGO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SIQDDPLLVH.Y	Y	20.27	1135.5873	-1.5	568.8000	2	12.24	1715	1	835	844	
C.VIPVVDDKLTL.L	Y	15.71	1210.7173	-1.2	606.3652	2	13.28	1904	1	5321	5331	

total 2 peptides

tr|A0A6J2RYI1|A0A6J2RYI1_COTGO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SIQDDPLLVH.Y	Y	20.27	1135.5873	-1.5	568.8000	2	12.24	1715	1	835	844	
C.VIPVVDDKLTL.L	Y	15.71	1210.7173	-1.2	606.3652	2	13.28	1904	1	5321	5331	

total 2 peptides

tr|A0A6J2RVP6|A0A6J2RVP6_COTGO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SIQDDPLLVH.Y	Y	20.27	1135.5873	-1.5	568.8000	2	12.24	1715	1	835	844	
C.VIPVVDDKLTL.L	Y	15.71	1210.7173	-1.2	606.3652	2	13.28	1904	1	5321	5331	

total 2 peptides

tr|A0A6J2RY55|A0A6J2RY55_COTGO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SIQDDPLLVH.Y	Y	20.27	1135.5873	-1.5	568.8000	2	12.24	1715	1	835	844	
C.VIPVVDDKLTL.L	Y	15.71	1210.7173	-1.2	606.3652	2	13.28	1904	1	5321	5331	

total 2 peptides

tr|A0A6J2RVP0|A0A6J2RVP0_COTGO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SIQDDPLLVH.Y	Y	20.27	1135.5873	-1.5	568.8000	2	12.24	1715	1	819	828	
C.VIPVVDDKLTL.L	Y	15.71	1210.7173	-1.2	606.3652	2	13.28	1904	1	5305	5315	

total 2 peptides

tr|A0A6J2RWS0|A0A6J2RWS0_COTGO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SIQDDPLLVH.Y	Y	20.27	1135.5873	-1.5	568.8000	2	12.24	1715	1	835	844	
C.VIPVVDDKLTL.L	Y	15.71	1210.7173	-1.2	606.3652	2	13.28	1904	1	5321	5331	

total 2 peptides

tr|A0A6G0J8D3|A0A6G0J8D3_LARCR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SLQDDPLLVH.Y	Y	20.27	1135.5873	-1.5	568.8000	2	12.24	1715	1	830	839	
C.VIPVVDDKLTL.L	Y	15.71	1210.7173	-1.2	606.3652	2	13.28	1904	1	4101	4111	

total 2 peptides

tr|A0A5C6PNB9|A0A5C6PNB9_9TELE

back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SLQDDPLLVH.Y	Y	20.27	1135.5873	-1.5	568.8000	2	12.24	1715	1	788	797	
C.VIPVVDDKLTL.L	Y	15.71	1210.7173	-1.2	606.3652	2	13.28	1904	1	4995	5005	

total 2 peptides

tr|A0A669CKX5|A0A669CKX5_ORENI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SLQDDPLLVH.Y	Y	20.27	1135.5873	-1.5	568.8000	2	12.24	1715	1	733	742	
C.VIPVVDDKLTL.L	Y	15.71	1210.7173	-1.2	606.3652	2	13.28	1904	1	5207	5217	

total 2 peptides

tr|I3KK23|I3KK23_ORENI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SLQDDPLLVH.Y	Y	20.27	1135.5873	-1.5	568.8000	2	12.24	1715	1	777	786	
C.VIPVVDDKLTL.L	Y	15.71	1210.7173	-1.2	606.3652	2	13.28	1904	1	5251	5261	

total 2 peptides

tr|A0A3P8QJ88|A0A3P8QJ88_ASTCA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SLQDDPLLVH.Y	Y	20.27	1135.5873	-1.5	568.8000	2	12.24	1715	1	799	808	
C.VIPVVDDKLTL.L	Y	15.71	1210.7173	-1.2	606.3652	2	13.28	1904	1	5273	5283	

total 2 peptides

tr|A0A3P9CU79|A0A3P9CU79_9CICH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SLQDDPLLVH.Y	Y	20.27	1135.5873	-1.5	568.8000	2	12.24	1715	1	818	827	
C.VIPVVDDKLTL.L	Y	15.71	1210.7173	-1.2	606.3652	2	13.28	1904	1	5292	5302	

total 2 peptides

tr|A0A6J2RTX8|A0A6J2RTX8_COTGO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SIQDDPLLVH.Y	Y	20.27	1135.5873	-1.5	568.8000	2	12.24	1715	1	835	844	
C.VIPVVDDKLTL.L	Y	15.71	1210.7173	-1.2	606.3652	2	13.28	1904	1	5321	5331	

total 2 peptides

tr|A0A4U5U1Y5|A0A4U5U1Y5_COLLU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SLQDDPLLVH.Y	Y	20.27	1135.5873	-1.5	568.8000	2	12.24	1715	1	912	921	
C.VIPVVDDKLTL.L	Y	15.71	1210.7173	-1.2	606.3652	2	13.28	1904	1	5403	5413	

total 2 peptides

tr|A0A4W4F305|A0A4W4F305_ELEEL
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.RGLPGPAGPPGE.S	Y	28.12	1103.5723	-1.5	552.7926	2	10.58	1409	1	3336	3347	

total 1 peptides

tr|W5KZP4|W5KZP4_ASTMX

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.RGLPGPAGPPGE.G	Y	28.12	1103.5723	-1.5	552.7926	2	10.58	1409	1	590	601	

total 1 peptides

tr|A0A6P3VUU5|A0A6P3VUU5_CLUHA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.AGPPGSDGQPGAK.G	Y	26.91	1137.5414	-1.0	569.7774	2	9.07	1156	1	837	849	

total 1 peptides

tr|A0A6J2PWT2|A0A6J2PWT2_COTGO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.APKLPDGEKV.D	Y	26.90	1052.5865	-1.2	527.2999	2	10.12	1331	1	24	33	

total 1 peptides

tr|A0A6J2PTP5|A0A6J2PTP5_COTGO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.APKLPDGEKV.D	Y	26.90	1052.5865	-1.2	527.2999	2	10.12	1331	1	21	30	

total 1 peptides

tr|A0A6J2PW38|A0A6J2PW38_COTGO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.APKLPDGEKV.D	Y	26.90	1052.5865	-1.2	527.2999	2	10.12	1331	1	78	87	

total 1 peptides

tr|A0A6J2PTY9|A0A6J2PTY9_COTGO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.APKLPDGEKV.D	Y	26.90	1052.5865	-1.2	527.2999	2	10.12	1331	1	84	93	

total 1 peptides

tr|A0A6J2PVR7|A0A6J2PVR7_COTGO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.APKLPDGEKV.D	Y	26.90	1052.5865	-1.2	527.2999	2	10.12	1331	1	84	93	

total 1 peptides

tr|A0A6J2PTN9|A0A6J2PTN9_COTGO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.APKLPDGEKV.D	Y	26.90	1052.5865	-1.2	527.2999	2	10.12	1331	1	87	96	

total 1 peptides

tr|A0A5A9PG84|A0A5A9PG84_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.APKLPDGEKV.D	Y	26.90	1052.5865	-1.2	527.2999	2	10.12	1331	1	127	136	

total 1 peptides

tr|A0A6F9CEX9|A0A6F9CEX9_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.LDPIDAPGKPDVISIT.R	Y	26.71	1649.8876	-1.8	825.9496	2	12.83	1822	1	8748	8763	

total 1 peptides

tr|A0A3B3ICW0|A0A3B3ICW0_ORYLA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VILPVPAF.N	Y	16.42	854.5266	-0.2	428.2704	2	14.94	2196	1	143	150	
V.GDDLTVTNPK.R	N	15.81	1058.5244	-0.4	530.2693	2	10.15	1336	1	317	326	

total 2 peptides

tr|A0A3Q4GK85|A0A3Q4GK85_NEOBR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.SELPVDDVFGQ.V	Y	24.20	1204.5612	0.4	603.2881	2	13.63	1966	1	174	184	

total 1 peptides

tr|A0A3Q4GS43|A0A3Q4GS43_NEOBR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.SELPVDDVFGQ.V	Y	24.20	1204.5612	0.4	603.2881	2	13.63	1966	1	175	185	

total 1 peptides

tr|A0A3P8P8S3|A0A3P8P8S3_ASTCA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.SELPVDDVFGQ.V	Y	24.20	1204.5612	0.4	603.2881	2	13.63	1966	1	175	185	

total 1 peptides

tr|A0A3Q1HW42|A0A3Q1HW42_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.SELPVDDVFGQ.V	Y	24.20	1204.5612	0.4	603.2881	2	13.63	1966	1	175	185	

total 1 peptides

tr|A0A3P9CWL7|A0A3P9CWL7_9CICH

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.SELPVDDVFGQ.V	Y	24.20	1204.5612	0.4	603.2881	2	13.63	1966	1	175	185	

total 1 peptides

tr|A0A3B5BIY5|A0A3B5BIY5_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.SELPVDDVFGQ.V	Y	24.20	1204.5612	0.4	603.2881	2	13.63	1966	1	175	185	

total 1 peptides

tr|A0A3Q2VY92|A0A3Q2VY92_HAPBU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.SELPVDDVFGQ.V	Y	24.20	1204.5612	0.4	603.2881	2	13.63	1966	1	175	185	

total 1 peptides

tr|A0A3B4FMK3|A0A3B4FMK3_9CICH

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.SELPVDDVFGQ.V	Y	24.20	1204.5612	0.4	603.2881	2	13.63	1966	1	175	185	

total 1 peptides

tr|A0A3Q3CWR9|A0A3Q3CWR9_HAPBU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.SELPVDDVFGQ.V	Y	24.20	1204.5612	0.4	603.2881	2	13.63	1966	1	193	203	

total 1 peptides

tr|A0A3P8P8V3|A0A3P8P8V3_ASTCA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.SELPVDDVFGQ.V	Y	24.20	1204.5612	0.4	603.2881	2	13.63	1966	1	193	203	

total 1 peptides

tr|A0A3Q1FHQ1|A0A3Q1FHQ1_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.LEHEE.R	N	16.09	655.2813	3.2	328.6490	2	8.51	1054	1	446	450	
L.MIDGLGDI.M	Y	15.23	832.4000	-3.9	417.2057	2	14.21	2067	1	2023	2030	

total 2 peptides

tr|G3NYZ7|G3NYZ7_GASAC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM

total 2 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.LEHEE.K	N	16.09	655.2813	3.2	328.6490	2	8.51	1054	1	440	444	
L.MIDGLGDI.M	Y	15.23	832.4000	-3.9	417.2057	2	14.21	2067	1	1963	1970	

total 2 peptides

tr|A0A674BRX0|A0A674BRX0_SALTR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.LEHEE.K	N	16.09	655.2813	3.2	328.6490	2	8.51	1054	1	446	450	
L.MIDGLGDI.M	Y	15.23	832.4000	-3.9	417.2057	2	14.21	2067	1	2017	2024	

total 2 peptides

tr|A0A0F8B8T7|A0A0F8B8T7_LARCR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.KGESGLPGPPG.R	Y	23.41	994.5083	-2.0	498.2604	2	11.00	1484	1	338	348	

total 1 peptides

tr|A0A665TL93|A0A665TL93_ECHNA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.EDTIFQPGPPGNPRVL.D	Y	22.82	1735.8893	-2.1	868.9501	2	12.93	1840	1	272	287	

total 1 peptides

tr|A0A7J5Y3X5|A0A7J5Y3X5_DISMA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.EDTIFQPGPPGNPRVL.D	Y	22.82	1735.8893	-2.1	868.9501	2	12.93	1840	1	543	558	

total 1 peptides

tr|A0A3Q1G4M0|A0A3Q1G4M0_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.AGDPGKGLPGLDGPQ.G	Y	22.56	1377.6887	6.6	689.8562	2	10.47	1391	1	551	565	

total 1 peptides

tr|A0A834FMH6|A0A834FMH6_ORYME
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.FGPAAKRQ.R	Y	21.61	873.4821	-4.9	437.7462	2	12.19	1706	1	250	257	

total 1 peptides

tr|A0A673HU84|A0A673HU84_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.ALADLVLVLDS.L	Y	21.18	1127.6438	22.2	564.8417	2	17.39	2610	1	90	100	

total 1 peptides

tr|A0A2Z4XFW9|A0A2Z4XFW9_CTEID
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.ALADLVLVLDS.L	Y	21.18	1127.6438	22.2	564.8417	2	17.39	2610	1	5	15	

total 1 peptides

tr|A0A4W4E5X7|A0A4W4E5X7_ELEEL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.ALADLVLVLDS.L	Y	21.18	1127.6438	22.2	564.8417	2	17.39	2610	1	81	91	

total 1 peptides

tr|A0A672KLI0|A0A672KLI0_SINGR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.ALADLVLVLDS.L	Y	21.18	1127.6438	22.2	564.8417	2	17.39	2610	1	79	89	

total 1 peptides

tr|A0A671RDB8|A0A671RDB8_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.ALADLVLVLDS.L	Y	21.18	1127.6438	22.2	564.8417	2	17.39	2610	1	84	94	

total 1 peptides

tr|W5LSJ6|W5LSJ6_ASTMX
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.ALADLVLVLDS.L	Y	21.18	1127.6438	22.2	564.8417	2	17.39	2610	1	76	86	

total 1 peptides

tr|A0A3B4C497|A0A3B4C497_PYGNA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.ALADLVLVLDS.L	Y	21.18	1127.6438	22.2	564.8417	2	17.39	2610	1	78	88	

total 1 peptides

tr|A0A6P3WBU3|A0A6P3WBU3_CLUHA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.ALADLVLVLDS.L	Y	21.18	1127.6438	22.2	564.8417	2	17.39	2610	1	80	90	

total 1 peptides

tr|A0A6P6J7W1|A0A6P6J7W1_CARAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.ALADLVLVLDS.L	Y	21.18	1127.6438	22.2	564.8417	2	17.39	2610	1	87	97	

total 1 peptides

tr|A0A5A9N4U0|A0A5A9N4U0_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.ALADLVLVLDS.L	Y	21.18	1127.6438	22.2	564.8417	2	17.39	2610	1	85	95	

total 1 peptides

tr|A0A3N0XI69|A0A3N0XI69_ANAGA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.ALADLVLVLDS.L	Y	21.18	1127.6438	22.2	564.8417	2	17.39	2610	1	87	97	

total 1 peptides

tr|A0A6J2UVU6|A0A6J2UVU6_CHACN
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.ALADLVLVLDS.L	Y	21.18	1127.6438	22.2	564.8417	2	17.39	2610	1	80	90	

total 1 peptides

tr|A0A6P6JAH3|A0A6P6JAH3_CARAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.ALADLVLVLDS.L	Y	21.18	1127.6438	22.2	564.8417	2	17.39	2610	1	122	132	

total 1 peptides

tr|A0A6P6JAN8|A0A6P6JAN8_CARAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.ALADLVLVLDS.L	Y	21.18	1127.6438	22.2	564.8417	2	17.39	2610	1	125	135	

total 1 peptides

tr|A0A498LK34|A0A498LK34_LABRO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.ALADLVLVLDS.L	Y	21.18	1127.6438	22.2	564.8417	2	17.39	2610	1	80	90	

total 1 peptides

tr|A0A4W6ESI4|A0A4W6ESI4_LATCA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.SGPGGPAGPVGA.A	Y	20.60	922.4508	-1.2	462.2321	2	10.46	1389	1	840	851	

total 1 peptides

tr|A0A7J6A7M3|A0A7J6A7M3_AMEME
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.DEEVCLRLL.E	Y	20.39	1088.5536	29.5	545.3001	2	12.18	1703	1	590	598	

total 1 peptides

tr|A0A6G1P920|A0A6G1P920_9TELE
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.TEAPLKPN.V	Y	20.06	868.4654	-0.2	435.2399	2	22.56	3493	2	186	193	

total 1 peptides

1. Notes

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)

Table 1. Statistics of data.

# of MS Scans	1013
# of MS/MS Scans	2952

Table 4. PTM profile.

Name	ΔMass	#PSM	Position

Table 2. Result filtration parameters.

Peptide -10lgP	≥15
Protein -10lgP	≥20
Proteins unique peptides	≥0
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	159
Peptide Sequences	144
Protein Groups	64
Proteins	327
Proteins (#Unique Peptides)	141 (>2); 46 (=2); 42 (=1);
FDR (Peptide-Spectrum Matches)	10.1%
FDR (Peptide Sequences)	11.1%
FDR (Protein)	0.0%
De Novo Only Spectra	1323

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)

Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Orbi2222	0	0	0	0	144

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS 7.0
Parent Mass Error Tolerance: 0.03 Da
Fragment Mass Error Tolerance: 0.1 Da
Precursor Mass Search Type: monoisotopic
Enzyme: None
Max Missed Cleavages: 100
Non-specific Cleavage: both
Max variable PTM per peptide: 3
Database: Teleosteo
Taxon: All
Searched Entry: 4529691
FDR Estimation: Enabled
Merge Options: 0.1 min. 0.03 Da
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB_PIMENTA_MP_20220211_05.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID/ECD
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
1	66837	tr|A0A3B4T4B1|A0A3B4T4B1_SERDU	158.76	24	23	20	N	41596	Actin, alpha skeletal muscle A OS=Seriola dumerili OX=41447 PE=3 SV=1
1	66838	tr|A0A3Q3BBJ2|A0A3Q3BBJ2_KRYMA	158.76	23	23	20	N	41945	Actin, alpha skeletal muscle A OS=Kryptolebias marmoratus OX=37003 GN=ACTA1 PE=3 SV=1
1	66839	tr|Q76MZ4|Q76MZ4_9TELE	158.76	23	23	20	N	41959	Skeletal alpha-actin type-1 OS=Coryphaenoides cinereus OX=83391 PE=2 SV=1
1	12040	tr|A0A3S2MUF9|A0A3S2MUF9_ORYJA	158.76	23	23	20	N	41945	Uncharacterized protein OS=Oryzias javanicus OX=123683 GN=OJAV_G00024300 PE=3 SV=1
1	66840	tr|A0A3Q0RI14|A0A3Q0RI14_AMPCI	158.76	23	23	20	N	41945	Actin alpha 1, skeletal muscle OS=Amphilophus citrinellus OX=61819 GN=ACTA1 PE=3 SV=1
1	66841	tr|M4AKR3|M4AKR3_XIPMA	158.76	23	23	20	N	41945	Uncharacterized protein OS=Xiphophorus maculatus OX=8083 GN=ACTA1 PE=3 SV=2
1	66842	tr|C0LLE8|C0LLE8_DICLA	158.76	23	23	20	N	41929	Alpha actin OS=Dicentrarchus labrax OX=13489 PE=2 SV=1
1	66843	tr|A0A3Q3N432|A0A3Q3N432_9TELE	158.76	23	23	20	N	41945	Actin alpha 1, skeletal muscle b OS=Mastacembelus armatus OX=205130 GN=ACTA1 PE=3 SV=1
1	12049	tr|Q76LU1|Q76LU1_GADCH	158.76	23	23	20	N	41959	Alpha skeletal actin-1 OS=Gadus chalcogrammus OX=1042646 PE=2 SV=1
1	12038	tr|F5BZL8|F5BZL8_EPIBR	158.76	23	23	20	N	41945	Alpha actin (Fragment) OS=Epinephelus bruneus OX=323802 PE=2 SV=1
1	66844	tr|A0A3Q4BGG8|A0A3Q4BGG8_MOLML	158.76	23	23	20	N	41945	Actin alpha 1, skeletal muscle OS=Mola mola OX=94237 PE=3 SV=1
1	66845	tr|A0A3Q1DE47|A0A3Q1DE47_AMPOC	158.76	23	23	20	N	41945	Actin, alpha skeletal muscle A OS=Amphiprion ocellaris OX=80972 GN=ACTA1 PE=3 SV=1
1	66846	tr|A0A7J6C441|A0A7J6C441_9TELE	158.76	23	23	20	N	41959	Uncharacterized protein OS=Onychostoma macrolepis OX=369639 GN=G5714_016621 PE=3 SV=1
1	66847	tr|A0A6P7M219|A0A6P7M219_BETSP	158.76	23	23	20	N	41959	actin, alpha skeletal muscle OS=Betta splendens OX=158456 GN=acta1 PE=3 SV=1
1	66848	tr|A0A3Q2P9J5|A0A3Q2P9J5_FUNHE	158.76	23	23	20	N	41945	Actin, alpha skeletal muscle A OS=Fundulus heteroclitus OX=8078 GN=ACTA1 PE=3 SV=1
1	66849	tr|D4P4P1|D4P4P1_COBCH	158.76	23	23	20	N	41920	Skeletal alpha-actin 1.2 OS=Cobitis choii OX=457511 GN=acta1.2 PE=2 SV=1
1	66850	tr|A3F5V3|A3F5V3_ORENI	158.76	25	23	20	N	39189	Alpha actin (Fragment) OS=Oreochromis niloticus OX=8128 PE=2 SV=1

total 327 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
3	66792	tr|A0A3P8QM38|A0A3P8QM38_ASTCA	116.80	8	16	0	N	221264	Uncharacterized protein OS=Astatotilapia calliptera OX=8154 PE=3 SV=1
2	66795	tr|A0A6G0HED4|A0A6G0HED4_LARCR	115.75	9	17	0	N	221587	Myosin heavy chain, fast skeletal muscle OS=Larimichthys crocea OX=215358 GN=D5F01_LYC24499 PE=3 SV=1
2	66797	tr|A0A665X5K8|A0A665X5K8_ECHNA	115.75	9	17	0	N	223744	Myosin heavy chain, fast skeletal muscle-like OS=Echeneis naucrates OX=173247 GN=LOC115047598 PE=3 SV=1
10	66791	tr|A0A6J2PN08|A0A6J2PN08_COTGO	115.41	7	12	0	N	223516	myosin heavy chain, fast skeletal muscle-like isoform X1 OS=Cottoperca gobio OX=56716 GN=LOC115007825 PE=3 SV=1
8	66793	tr|A0A6P7NC66|A0A6P7NC66_BETSP	114.09	8	15	0	N	221411	myosin heavy chain, fast skeletal muscle-like OS=Betta splendens OX=158456 GN=LOC114860972 PE=3 SV=1
5	66801	tr|Q90YF6|Q90YF6_PARFO	113.36	8	16	0	N	221374	Myosin heavy chain OS=Paracirrhites forsteri OX=100206 GN=MyoHC-T54 PE=2 SV=1
6	66798	tr|A0A665WXF0|A0A665WXF0_ECHNA	113.26	7	15	0	N	221777	Myosin heavy chain, fast skeletal muscle-like OS=Echeneis naucrates OX=173247 GN=LOC115047599 PE=3 SV=1
4	66903	tr|A0A7N8X0U0|A0A7N8X0U0_9TELE	112.54	9	17	0	N	220309	Myosin heavy chain, fast skeletal muscle-like OS=Mastacembelus armatus OX=205130 PE=3 SV=1
4	66904	tr|A0A7N8WLS2|A0A7N8WLS2_9TELE	112.54	8	17	0	N	221458	Myosin heavy chain, fast skeletal muscle-like OS=Mastacembelus armatus OX=205130 PE=3 SV=1
27	66962	tr|A0A6G0IP12|A0A6G0IP12_LARCR	110.62	31	6	6	N	18230	Troponin C, skeletal muscle OS=Larimichthys crocea OX=215358 GN=D5F01_LYC08192 PE=4 SV=1
27	66963	tr|A0A1A8Q0J1|A0A1A8Q0J1_9TELE	110.62	31	6	6	N	18215	Troponin C type 2 (Fast) OS=Nothobranchius pienaari OX=704102 GN=TNNC2 PE=4 SV=1
7	66912	tr|A0A3P8SK70|A0A3P8SK70_AMPPE	110.05	8	16	0	N	221849	Uncharacterized protein OS=Amphiprion percula OX=161767 PE=3 SV=1
7	66913	tr|A0A3P8SLP0|A0A3P8SLP0_AMPPE	110.05	8	16	0	N	221886	Uncharacterized protein OS=Amphiprion percula OX=161767 PE=3 SV=1
9	66910	tr|A0A3Q3WZY2|A0A3Q3WZY2_MOLML	108.37	8	15	0	N	205901	Uncharacterized protein OS=Mola mola OX=94237 PE=3 SV=1
12	66820	tr|A0A6P6KAZ0|A0A6P6KAZ0_CARAU	106.22	6	11	0	N	222556	myosin heavy chain, fast skeletal muscle-like OS=Carassius auratus OX=7957 GN=LOC113050383 PE=3 SV=1
15	66863	tr|A0A3Q3EJE1|A0A3Q3EJE1_9LABR	104.70	5	11	0	N	220889	Myosin heavy chain, fast skeletal muscle-like OS=Labrus bergylta OX=56723 PE=3 SV=1
15	66864	tr|A0A6P8GH29|A0A6P8GH29_CLUHA	104.70	5	11	0	N	220733	myosin heavy chain, fast skeletal muscle-like OS=Clupea harengus OX=7950 GN=LOC105894483 PE=3 SV=1
11	66961	tr|A0A7N8XS20|A0A7N8XS20_9TELE	103.67	8	16	0	N	222388	Myosin heavy chain, fast skeletal muscle OS=Mastacembelus armatus OX=205130 PE=3 SV=1
13	66862	tr|A0A6P8FM41|A0A6P8FM41_CLUHA	102.05	4	9	0	N	222593	myosin heavy chain, fast skeletal muscle OS=Clupea harengus OX=7950 GN=LOC105889197 PE=3 SV=1
14	66867	tr|A0A6P8G2F8|A0A6P8G2F8_CLUHA	101.68	4	9	0	N	212617	myosin heavy chain, fast skeletal muscle-like OS=Clupea harengus OX=7950 GN=LOC105902796 PE=3 SV=1
14	66868	tr|A0A6P8G1S8|A0A6P8G1S8_CLUHA	101.68	4	9	0	N	212837	myosin heavy chain, fast skeletal muscle-like OS=Clupea harengus OX=7950 GN=LOC105902797 PE=3 SV=1

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Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
20	67069	tr|A0A2U9CMP6|A0A2U9CMP6_SCOMX	98.55	17	5	3	N	11876	Parvalbumin OS=Scophthalmus maximus OX=52904 GN=SMAX5B_020129 PE=3 SV=1
20	67070	tr|A0A6A4RT91|A0A6A4RT91_SCOMX	98.55	1	5	3	N	177174	Parvalbumin OS=Scophthalmus maximus OX=52904 GN=F2P81_022114 PE=3 SV=1
20	67087	tr|A0A3B3XMC4|A0A3B3XMC4_9TELE	98.55	17	5	3	N	11357	Parvalbumin OS=Poecilia mexicana OX=48701 PE=3 SV=1
20	67088	tr|A0A3B5LQ20|A0A3B5LQ20_9TELE	98.55	17	5	3	N	11419	Parvalbumin OS=Xiphophorus couchianus OX=32473 PE=3 SV=1
20	67089	tr|A0A3B3Z292|A0A3B3Z292_9TELE	98.55	17	5	3	N	11593	Parvalbumin OS=Poecilia mexicana OX=48701 PE=3 SV=1
20	67090	tr|A0A671XKN2|A0A671XKN2_SPAAU	98.55	17	5	3	N	11732	Parvalbumin OS=Sparus aurata OX=8175 GN=LOC115574776 PE=3 SV=1
20	67091	tr|A0A672Z6Y0|A0A672Z6Y0_9TELE	98.55	17	5	3	N	11480	Parvalbumin OS=Sphaeramia orbicularis OX=375764 GN=LOC115424708 PE=3 SV=1
20	67092	tr|D0VB96|D0VB96_SPAAU	98.55	17	5	3	N	11500	Parvalbumin OS=Sparus aurata OX=8175 GN=LOC115574776 PE=2 SV=1
20	67093	tr|A0A087Y091|A0A087Y091_POEFO	98.55	17	5	3	N	11775	Parvalbumin OS=Poecilia formosa OX=48698 PE=3 SV=1
20	67094	tr|A0A5N5MFD7|A0A5N5MFD7_PANHP	98.55	17	5	3	N	11727	Parvalbumin OS=Pangasianodon hypophthalmus OX=310915 GN=PHYPO_G00043940 PE=3 SV=1
20	67095	tr|A0A087Y0W0|A0A087Y0W0_POEFO	98.55	17	5	3	N	11793	Parvalbumin OS=Poecilia formosa OX=48698 PE=3 SV=1
20	67096	tr|A0A668AEA1|A0A668AEA1_9TELE	98.55	17	5	3	N	11577	Parvalbumin OS=Myripristis murdjan OX=586833 GN=LOC115377764 PE=3 SV=1
20	67097	tr|C6GKU4|C6GKU4_9TELE	98.55	17	5	3	N	11446	Parvalbumin OS=Sebastes marinus OX=34821 GN=pvalb1 PE=2 SV=1
20	67098	tr|A0A087Y5E9|A0A087Y5E9_POEFO	98.55	17	5	3	N	11413	Parvalbumin OS=Poecilia formosa OX=48698 PE=3 SV=2
20	67099	tr|A0A1A8GBU0|A0A1A8GBU0_9TELE	98.55	17	5	3	N	11460	Parvalbumin OS=Nothobranchius korthausae OX=1143690 GN=PVALB4 PE=3 SV=1
20	67100	tr|E0WD96|E0WD96_9TELE	98.55	17	5	3	N	11402	Parvalbumin OS=Sebastes marinus OX=34821 GN=pvalb1 PE=3 SV=1
20	67101	tr|A0A1A7WES6|A0A1A7WES6_9TELE	98.55	17	5	3	N	11426	Parvalbumin OS=Iconisemion striatum OX=60296 GN=PVALB4 PE=3 SV=1
20	67102	tr|A0A1A8EAV3|A0A1A8EAV3_9TELE	98.55	17	5	3	N	11414	Parvalbumin OS=Nothobranchius kadleci OX=1051664 GN=PVALB4 PE=3 SV=1
20	67103	tr|A0A1A8PM62|A0A1A8PM62_9TELE	98.55	17	5	3	N	11414	Parvalbumin OS=Nothobranchius rachovii OX=451742 GN=PVALB4 PE=3 SV=1
20	67104	tr|A0A3B3TQ55|A0A3B3TQ55_9TELE	98.55	17	5	3	N	11413	Parvalbumin OS=Poecilia latipinna OX=48699 PE=3 SV=1
20	67105	tr|A0A1A8JGR3|A0A1A8JGR3_NOTKU	98.55	17	5	3	N	11414	Parvalbumin OS=Nothobranchius kuhntae OX=321403 GN=PVALB4 PE=3 SV=1
20	67106	tr|A0A3B3XME4|A0A3B3XME4_9TELE	98.55	16	5	3	N	11973	Parvalbumin OS=Poecilia mexicana OX=48701 PE=3 SV=1
20	67107	tr|A0A668AEA6|A0A668AEA6_9TELE	98.55	15	5	3	N	12474	Parvalbumin OS=Myripristis murdjan OX=586833 GN=LOC115377764 PE=3 SV=1
20	67108	tr|A0A5N5MKE2|A0A5N5MKE2_PANHP	98.55	15	5	3	N	12804	Parvalbumin OS=Pangasianodon hypophthalmus OX=310915 GN=PHYPO_G00034490 PE=3 SV=1
20	67109	tr|A0A668ANA4|A0A668ANA4_9TELE	98.55	14	5	3	N	13836	Parvalbumin OS=Myripristis murdjan OX=586833 GN=LOC115377764 PE=3 SV=1
20	67110	tr|A0A3B3UHS0|A0A3B3UHS0_9TELE	98.55	13	5	3	N	14779	Parvalbumin OS=Poecilia latipinna OX=48699 PE=3 SV=1
20	67111	tr|A0A556TIT9|A0A556TIT9_BAGYA	98.55	9	5	3	N	21698	Parvalbumin OS=Bagarius yarrelli OX=175774 GN=Baya_0626 PE=3 SV=1

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Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
20	67112	tr|A0A7J6BCR9|A0A7J6BCR9_AMEME	98.55	7	5	3	N	26250	Parvalbumin OS=Ameiurus melas OX=219545 GN=AMELA_G00025130 PE=3 SV=1
20	67113	tr|A0A315V786|A0A315V786_GAMAF	98.55	6	5	3	N	35443	Parvalbumin OS=Gambusia affinis OX=33528 GN=CCH79_00014604 PE=3 SV=1
16	66956	tr|A0A1S3QJI3|A0A1S3QJI3_SALSA	96.89	5	10	0	N	222009	myosin heavy chain, fast skeletal muscle-like OS=Salmo salar OX=8030 GN=LOC106593382 PE=3 SV=1
17	66957	tr|A0A6J2PWE3|A0A6J2PWE3_COTGO	95.55	3	9	0	N	221042	myosin heavy chain, fast skeletal muscle-like OS=Cottoperca gobio OX=56716 GN=LOC115009637 PE=3 SV=1
21	67118	tr|A0A3Q3WCX3|A0A3Q3WCX3_MOLML	95.06	16	8	2	N	42571	Creatine kinase OS=Mola mola OX=94237 PE=3 SV=1
21	67119	tr|A0A0S7H3J1|A0A0S7H3J1_9TELE	95.06	15	8	2	N	42849	Creatine kinase OS=Poeciliopsis prolifica OX=188132 GN=KCRM PE=3 SV=1
21	67120	tr|A0A3B3XY74|A0A3B3XY74_9TELE	95.06	15	8	2	N	42904	Creatine kinase OS=Poecilia mexicana OX=48701 PE=3 SV=1
21	67121	tr|A0A3B3W291|A0A3B3W291_9TELE	95.06	15	8	2	N	42860	Creatine kinase OS=Poecilia latipinna OX=48699 PE=3 SV=1
21	67122	tr|A0A087YG46|A0A087YG46_POEFO	95.06	15	8	2	N	43062	Creatine kinase OS=Poecilia formosa OX=48698 GN=CKM PE=3 SV=2
24	67007	tr|A0A3Q2D194|A0A3Q2D194_CYPVA	91.50	16	7	1	N	42846	Creatine kinase OS=Cyprinodon variegatus OX=28743 GN=CKM PE=3 SV=1
24	67008	tr|A0A3Q2D1K7|A0A3Q2D1K7_CYPVA	91.50	17	7	1	N	39261	Creatine kinase OS=Cyprinodon variegatus OX=28743 GN=CKM PE=3 SV=1
19	67115	tr|C7ASM1|C7ASM1_SINCH	91.47	18	8	1	N	42922	Creatine kinase OS=Siniperca chuatsi OX=119488 PE=2 SV=1
19	67116	tr|M4AU26|M4AU26_XIPMA	91.47	18	8	1	N	42994	Creatine kinase OS=Xiphophorus maculatus OX=8083 PE=3 SV=1
19	67117	tr|A0A3B5M9I5|A0A3B5M9I5_9TELE	91.47	18	8	1	N	42994	Creatine kinase OS=Xiphophorus couchianus OX=32473 PE=3 SV=1
18	66970	tr|A0A6J2Q2L7|A0A6J2Q2L7_COTGO	90.05	4	9	0	N	224430	myosin heavy chain, fast skeletal muscle-like OS=Cottoperca gobio OX=56716 GN=LOC115011664 PE=3 SV=1
22	66980	tr|A0A6P3WCZ7|A0A6P3WCZ7_CLUHA	86.02	4	7	0	N	224559	myosin heavy chain, fast skeletal muscle-like OS=Clupea harengus OX=7950 GN=LOC105910910 PE=3 SV=1
23	66971	tr|A0A4W4E3Q5|A0A4W4E3Q5_ELEEL	85.58	7	6	0	N	116476	Myosin_tail_1 domain-containing protein OS=Electrophorus electricus OX=8005 PE=4 SV=1
25	66978	tr|A0A3B4FY50|A0A3B4FY50_9CICH	83.82	3	6	0	N	222437	Myosin heavy chain, fast skeletal muscle-like OS=Pundamilia nyererei OX=303518 PE=3 SV=1
25	66979	tr|A0A3P9ART7|A0A3P9ART7_9CICH	83.82	3	6	0	N	222529	Myosin heavy chain, fast skeletal muscle-like OS=Maylandia zebra OX=106582 PE=3 SV=1
32	67518	tr|D2KQG3|D2KQG3_SINCH	75.08	12	2	1	N	11617	Parvalbumin OS=Siniperca chuatsi OX=119488 PE=2 SV=1
32	67519	tr|B9VJM3|B9VJM3_SINCH	75.08	12	2	1	N	11589	Parvalbumin OS=Siniperca chuatsi OX=119488 PE=2 SV=1
34	67240	tr|A0A3Q0QYR9|A0A3Q0QYR9_AMPCI	73.47	11	4	4	N	13728	Nucleoside diphosphate kinase B OS=Amphilophus citrinellus OX=61819 PE=3 SV=1
34	30118	P85280|NDKB_MERME	73.47	10	4	4	N	14207	Nucleoside diphosphate kinase B (Fragments) OS=Merluccius merluccius OX=8063 GN=nme2 PE=1 SV=1
34	30119	P85284|NDKB_MERPA	73.47	10	4	4	N	14207	Nucleoside diphosphate kinase B (Fragments) OS=Merluccius paradoxus OX=89950 GN=nme2 PE=1 SV=1

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Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
34	30114	P85292|NDKB_MACMG	73.47	10	4	4	N	14118	Nucleoside diphosphate kinase B (Fragments) OS=Macruronus magellanicus OX=92050 GN=nme2 PE=1 SV=1
34	30115	P85282|NDKB_MERSE	73.47	10	4	4	N	14207	Nucleoside diphosphate kinase B (Fragments) OS=Merluccius senegalensis OX=89953 GN=nme2 PE=1 SV=1
34	30116	P85283|NDKB_MERPO	73.47	10	4	4	N	14207	Nucleoside diphosphate kinase B (Fragments) OS=Merluccius polli OX=89951 GN=nme2 PE=1 SV=1
34	30123	P85287|NDKB_MERAP	73.47	10	4	4	N	14393	Nucleoside diphosphate kinase B (Fragments) OS=Merluccius australis polylepis OX=307685 GN=nme2 PE=1 SV=1
34	30124	P85289|NDKB_MERPR	73.47	10	4	4	N	14393	Nucleoside diphosphate kinase B (Fragments) OS=Merluccius productus OX=89952 GN=nme2 PE=1 SV=1
34	30121	P85290|NDKB_MERBI	73.47	10	4	4	N	14407	Nucleoside diphosphate kinase B (Fragments) OS=Merluccius bilinearis OX=79698 GN=nme2 PE=1 SV=1
34	67241	tr|A0A672Y4P6|A0A672Y4P6_9TELE	73.47	9	4	4	N	17050	Nucleoside diphosphate kinase B OS=Sphaeramia orbicularis OX=375764 GN=LOC115423821 PE=3 SV=1
34	67242	tr|A0A2I4CF45|A0A2I4CF45_9TELE	73.47	9	4	4	N	16890	Nucleoside diphosphate kinase B OS=Austrofundulus limnaeus OX=52670 GN=LOC106528082 PE=3 SV=1
34	67243	tr|A0A3Q1K2U7|A0A3Q1K2U7_ANATE	73.47	9	4	4	N	17020	Nucleoside diphosphate kinase B OS=Anabas testudineus OX=64144 PE=3 SV=1
34	67244	tr|A0A1A8C566|A0A1A8C566_9TELE	73.47	9	4	4	N	16875	Nucleoside diphosphate kinase B OS=Nothobranchius kadleci OX=1051664 GN=NME2B.2 PE=3 SV=1
34	67245	tr|A0A6P7ISB4|A0A6P7ISB4_9TELE	73.47	9	4	4	N	16935	Nucleoside diphosphate kinase B OS=Parambassis ranga OX=210632 GN=LOC114440125 PE=3 SV=1
34	67246	tr|A0A3Q4I698|A0A3Q4I698_NEOBR	73.47	9	4	4	N	16950	Nucleoside diphosphate kinase B OS=Neolamprologus brichardi OX=32507 PE=3 SV=1
34	67247	tr|A0A3Q3L2T8|A0A3Q3L2T8_9TELE	73.47	9	4	4	N	17100	Nucleoside diphosphate kinase B OS=Mastacembelus armatus OX=205130 PE=3 SV=2
34	67248	tr|A0A6P7NDJ7|A0A6P7NDJ7_BETSP	73.47	9	4	4	N	17113	Nucleoside diphosphate kinase B OS=Betta splendens OX=158456 GN=LOC114861025 PE=3 SV=1
34	67249	tr|A0A3Q3A341|A0A3Q3A341_KRYMA	73.47	9	4	4	N	16887	Nucleoside diphosphate kinase B OS=Kryptolebias marmoratus OX=37003 PE=3 SV=1
34	67250	tr|A0A3Q4HQ85|A0A3Q4HQ85_NEOBR	73.47	9	4	4	N	16851	Nucleoside diphosphate kinase B OS=Neolamprologus brichardi OX=32507 PE=3 SV=1
34	67251	tr|A0A3P8Q104|A0A3P8Q104_ASTCA	73.47	9	4	4	N	17195	Nucleoside diphosphate kinase B OS=Astatotilapia calliptera OX=8154 PE=3 SV=1
34	67252	tr|A0A3Q3CUD8|A0A3Q3CUD8_HAPBU	73.47	9	4	4	N	17195	Nucleoside diphosphate kinase B OS=Haplochromis burtoni OX=8153 PE=3 SV=1
34	67253	tr|A0A3Q4I6B8|A0A3Q4I6B8_NEOBR	73.47	9	4	4	N	17195	Nucleoside diphosphate kinase B OS=Neolamprologus brichardi OX=32507 PE=3 SV=1
34	67254	tr|A0A3Q0QSW6|A0A3Q0QSW6_AMPCI	73.47	9	4	4	N	17238	Nucleoside diphosphate kinase B OS=Amphilophus citrinellus OX=61819 PE=3 SV=1
34	67255	tr|A0A3Q0QYR1|A0A3Q0QYR1_AMPCI	73.47	9	4	4	N	17278	Nucleoside diphosphate kinase B OS=Amphilophus citrinellus OX=61819 PE=3 SV=1

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Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
34	67256	tr|A0A3Q3R7S1|A0A3Q3R7S1_MONAL	73.47	9	4	4	N	17252	Nucleoside diphosphate kinase B OS=Monopterus albus OX=43700 PE=3 SV=1
34	67257	tr|A0A3Q0QXA4|A0A3Q0QXA4_AMPCI	73.47	8	4	4	N	17296	Nucleoside diphosphate kinase B OS=Amphilophus citrinellus OX=61819 PE=3 SV=1
34	67258	tr|M4ADR4|M4ADR4_XIPMA	73.47	8	4	4	N	18277	Nucleoside diphosphate kinase B OS=Xiphophorus maculatus OX=8083 PE=3 SV=2
34	67259	tr|A0A1A8J8K8|A0A1A8J8K8_NOTKU	73.47	8	4	4	N	18247	Nucleoside diphosphate kinase B (Fragment) OS=Nothobranchius kuhntae OX=321403 GN=NME2B.2 PE=3 SV=1
34	67260	tr|A0A1A7XFD3|A0A1A7XFD3_9TELE	73.47	7	4	4	N	20309	Nucleoside diphosphate kinase B (Fragment) OS=Iconisemion striatum OX=60296 GN=NME2B.2 PE=3 SV=1
34	67261	tr|A0A0S7LYJ8|A0A0S7LYJ8_9TELE	73.47	7	4	4	N	20062	Nucleoside diphosphate kinase B (Fragment) OS=Poeciliopsis prolifica OX=188132 GN=NDKB PE=3 SV=1
28	67031	tr|H3CAK5|H3CAK5_TETNG	71.68	14	4	4	N	37106	2-phospho-D-glycerate hydro-lyase OS=Tetraodon nigroviridis OX=99883 PE=3 SV=1
28	67032	tr|A0A3B3D6F1|A0A3B3D6F1_ORYME	71.68	12	4	4	N	42602	2-phospho-D-glycerate hydro-lyase OS=Oryzias melastigma OX=30732 PE=3 SV=1
28	67033	tr|A0A3B3BLA1|A0A3B3BLA1_ORYME	71.68	11	4	4	N	47528	2-phospho-D-glycerate hydro-lyase OS=Oryzias melastigma OX=30732 GN=FQA47_002919 PE=3 SV=1
28	67034	tr|A0A3B4CPC9|A0A3B4CPC9_PYGNA	71.68	11	4	4	N	47482	2-phospho-D-glycerate hydro-lyase OS=Pygocentrus nattereri OX=42514 PE=3 SV=1
28	67035	tr|A0A6M4C6H3|A0A6M4C6H3_DIOHY	71.68	11	4	4	N	47513	2-phospho-D-glycerate hydro-lyase OS=Diodon hystrix OX=223145 GN=ENO3 PE=2 SV=1
28	67036	tr|A0A0F8AN77|A0A0F8AN77_LARCR	71.68	11	4	4	N	47431	2-phospho-D-glycerate hydro-lyase OS=Larimichthys crocea OX=215358 GN=EH28_01590 PE=3 SV=1
28	67037	tr|A0A437CFA6|A0A437CFA6_ORYJA	71.68	9	4	4	N	58417	2-phospho-D-glycerate hydro-lyase OS=Oryzias javanicus OX=123683 GN=OJAV_G00185520 PE=3 SV=1
28	67040	tr|A0A671TWQ7|A0A671TWQ7_SPAAU	71.68	13	4	4	N	38363	2-phospho-D-glycerate hydro-lyase OS=Sparus aurata OX=8175 PE=3 SV=1
28	67041	tr|A0A671TWN1|A0A671TWN1_SPAAU	71.68	13	4	4	N	39726	2-phospho-D-glycerate hydro-lyase OS=Sparus aurata OX=8175 PE=3 SV=1
28	67042	tr|A0A671TZ14|A0A671TZ14_SPAAU	71.68	12	4	4	N	41134	2-phospho-D-glycerate hydro-lyase OS=Sparus aurata OX=8175 PE=3 SV=1
28	67043	tr|F5BZS7|F5BZS7_EPIBR	71.68	12	4	4	N	43226	2-phospho-D-glycerate hydro-lyase (Fragment) OS=Epinephelus bruneus OX=323802 PE=2 SV=1
28	67044	tr|Q4TBD1|Q4TBD1_TETNG	71.68	11	4	4	N	47111	2-phospho-D-glycerate hydro-lyase (Fragment) OS=Tetraodon nigroviridis OX=99883 GN=GSTENG00003809001 PE=3 SV=1
28	67045	tr|A0A2U9B0J8|A0A2U9B0J8_SCOMX	71.68	11	4	4	N	47494	2-phospho-D-glycerate hydro-lyase OS=Scophthalmus maximus OX=52904 GN=SMAX5B_008009 PE=3 SV=1
28	67046	tr|A0A6J2P9G6|A0A6J2P9G6_COTGO	71.68	11	4	4	N	47397	2-phospho-D-glycerate hydro-lyase OS=Cottoperca gobio OX=56716 GN=LOC115004495 PE=3 SV=1
28	67047	tr|D6PVP1|D6PVP1_EPICO	71.68	11	4	4	N	47516	2-phospho-D-glycerate hydro-lyase OS=Epinephelus coioides OX=94232 PE=2 SV=1
28	67048	tr|A0A6A4S9A7|A0A6A4S9A7_SCOMX	71.68	7	4	4	N	70779	2-phospho-D-glycerate hydro-lyase OS=Scophthalmus maximus OX=52904 GN=F2P81_017933 PE=3 SV=1

total 327 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
31	67269	tr|A0A6P7KDL5|A0A6P7KDL5_9TELE	71.63	8	4	4	N	32714	tropomyosin alpha-1 chain isoform X1 OS=Parambassis ranga OX=210632 GN=LOC114452528 PE=3 SV=1
31	67270	tr|A0A6P7MR93|A0A6P7MR93_BETSP	71.63	8	4	4	N	32714	tropomyosin alpha-1 chain isoform X1 OS=Betta splendens OX=158456 GN=tpm1 PE=3 SV=1
31	67271	tr|A0A3P9D7I0|A0A3P9D7I0_9CICH	71.63	8	4	4	N	32822	Tropomyosin 1 OS=Maylandia zebra OX=106582 GN=TPM1 PE=3 SV=1
31	67272	tr|A0A665VR95|A0A665VR95_ECHNA	71.63	8	4	4	N	32714	Tropomyosin 1 OS=Echeneis naucrates OX=173247 GN=tpm1 PE=3 SV=1
31	67273	tr|A0A3P8SLC6|A0A3P8SLC6_AMPPE	71.63	8	4	4	N	32754	Uncharacterized protein OS=Amphiprion percula OX=161767 PE=3 SV=1
31	67274	tr|A0A668UDB6|A0A668UDB6_OREAU	71.63	7	4	4	N	38586	Tropomyosin 1 OS=Oreochromis aureus OX=47969 PE=3 SV=1
31	67282	tr|X2J4M2|X2J4M2_PAROL	71.63	8	4	4	N	32670	Tropomyosin alpha-1 OS=Paralichthys olivaceus OX=8255 PE=2 SV=1
31	67283	tr|H2SQV9|H2SQV9_TAKRU	71.63	8	4	4	N	31672	Uncharacterized protein OS=Takifugu rubripes OX=31033 PE=3 SV=3
31	67311	tr|A0A4U5UG20|A0A4U5UG20_COLLU	71.63	6	4	4	N	39015	Tropomyosin alpha-1 chain OS=Collichthys lucidus OX=240159 GN=D9C73_007538 PE=3 SV=1
31	67337	tr|A0A6P3VQ87|A0A6P3VQ87_CLUHA	71.63	8	4	4	N	32706	tropomyosin alpha-3 chain isoform X5 OS=Clupea harengus OX=7950 GN=LOC105896158 PE=3 SV=1
31	67340	tr|A0A4W4GLX2|A0A4W4GLX2_ELEEL	71.63	8	4	4	N	32017	Uncharacterized protein OS=Electrophorus electricus OX=8005 GN=LOC113589122 PE=3 SV=1
33	67009	tr|A0A2I4D9D9|A0A2I4D9D9_9TELE	63.49	4	4	1	N	133831	collagen alpha-1(I) chain-like isoform X2 OS=Austrofundulus limnaeus OX=52670 GN=LOC106536191 PE=4 SV=1
33	67010	tr|A0A2I4D9D6|A0A2I4D9D6_9TELE	63.49	4	4	1	N	136808	collagen alpha-1(I) chain-like isoform X1 OS=Austrofundulus limnaeus OX=52670 GN=LOC106536191 PE=4 SV=1
26	67071	tr|A0A3P8WWA2|A0A3P8WWA2_CYNSE	63.15	7	4	1	N	28542	Actin-85C-like OS=Cynoglossus semilaevis OX=244447 PE=3 SV=1
26	67072	tr|A0A3P8X278|A0A3P8X278_CYNSE	63.15	5	4	1	N	41692	Actin-85C-like OS=Cynoglossus semilaevis OX=244447 PE=3 SV=1
26	67073	tr|A0A3P8X031|A0A3P8X031_CYNSE	63.15	5	4	1	N	42049	Actin-85C-like OS=Cynoglossus semilaevis OX=244447 PE=3 SV=1
26	67074	tr|A0A3P8WTX4|A0A3P8WTX4_CYNSE	63.15	17	4	1	N	12782	Actin-85C-like OS=Cynoglossus semilaevis OX=244447 PE=4 SV=1
26	67075	tr|A0A3P8WU36|A0A3P8WU36_CYNSE	63.15	14	4	1	N	15094	Actin-85C-like OS=Cynoglossus semilaevis OX=244447 PE=4 SV=1
26	67076	tr|A0A3P8WUR0|A0A3P8WUR0_CYNSE	63.15	13	4	1	N	16136	Actin-85C-like OS=Cynoglossus semilaevis OX=244447 PE=4 SV=1
29	67212	tr|A0A7N8WP58|A0A7N8WP58_9TELE	63.04	4	5	5	N	104947	Calcium-transporting ATPase OS=Mastacembelus armatus OX=205130 PE=3 SV=1
29	67213	tr|A0A668SKK1|A0A668SKK1_OREAU	63.04	4	5	5	N	108090	Calcium-transporting ATPase OS=Oreochromis aureus OX=47969 PE=3 SV=1
29	67214	tr|A0A3Q3BHF7|A0A3Q3BHF7_KRYMA	63.04	4	5	5	N	108762	Calcium-transporting ATPase OS=Kryptolebias marmoratus OX=37003 PE=3 SV=1
29	67215	tr|A0A3Q2WQG2|A0A3Q2WQG2_HAPBU	63.04	4	5	5	N	108554	Calcium-transporting ATPase OS=Haplochromis burtoni OX=8153 PE=3 SV=1
29	67216	tr|A0A3B3DXK1|A0A3B3DXK1_ORYME	63.04	4	5	5	N	108606	Calcium-transporting ATPase OS=Oryzias melastigma OX=30732 PE=3 SV=1
29	67217	tr|A0A3Q3BR63|A0A3Q3BR63_HAPBU	63.04	4	5	5	N	108978	Calcium-transporting ATPase OS=Haplochromis burtoni OX=8153 PE=3 SV=1

total 327 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
29	67218	tr|A0A3Q3H0F6|A0A3Q3H0F6_KRYMA	63.04	4	5	5	N	109277	Calcium-transporting ATPase OS=Kryptolebias marmoratus OX=37003 PE=3 SV=1
29	67219	tr|A0A3P9C9M1|A0A3P9C9M1_9CICH	63.04	4	5	5	N	109087	Calcium-transporting ATPase OS=Maylandia zebra OX=106582 PE=3 SV=1
29	67220	tr|A0A668SKH5|A0A668SKH5_OREAU	63.04	4	5	5	N	109261	Calcium-transporting ATPase OS=Oreochromis aureus OX=47969 PE=3 SV=1
29	67221	tr|A0A669D951|A0A669D951_ORENI	63.04	4	5	5	N	109951	Calcium-transporting ATPase OS=Oreochromis niloticus OX=8128 GN=LOC100706607 PE=3 SV=1
29	67222	tr|A0A674PDV8|A0A674PDV8_TAKRU	63.04	4	5	5	N	109836	Calcium-transporting ATPase OS=Takifugu rubripes OX=31033 GN=LOC101069346 PE=3 SV=1
29	67223	tr|A0A674P4B1|A0A674P4B1_TAKRU	63.04	4	5	5	N	111179	Calcium-transporting ATPase OS=Takifugu rubripes OX=31033 GN=LOC101069346 PE=3 SV=1
30	67156	tr|A0A3Q1CVI2|A0A3Q1CVI2_AMPOC	62.38	23	4	4	N	16402	Myosin light chain, phosphorylatable, fast skeletal muscle OS=Amphiprion ocellaris OX=80972 PE=4 SV=1
30	67157	tr|A0A4U5VU95|A0A4U5VU95_COLLU	62.38	23	4	4	N	16791	Myosin regulatory light chain 2, skeletal muscle isoform DTNB OS=Collichthys lucidus OX=240159 GN=D9C73_025504 PE=4 SV=1
30	67158	tr|A0A6P7II88|A0A6P7II88_9TELE	62.38	20	4	4	N	18948	myosin regulatory light chain 2, skeletal muscle isoform OS=Parambassis ranga OX=210632 GN=mylpf PE=4 SV=1
30	67159	tr|A0A3Q4GCJ7|A0A3Q4GCJ7_NEOBR	62.38	20	4	4	N	19081	Myosin regulatory light chain 2, skeletal muscle isoform-like OS=Neolamprologus brichardi OX=32507 PE=4 SV=1
30	67160	tr|A0A3P9IWY3|A0A3P9IWY3_ORYLA	62.38	20	4	4	N	18979	Uncharacterized protein OS=Oryzias latipes OX=8090 PE=4 SV=1
30	67161	tr|H3C4G7|H3C4G7_TETNG	62.38	20	4	4	N	19008	Myosin light chain, phosphorylatable, fast skeletal muscle a OS=Tetraodon nigroviridis OX=99883 PE=4 SV=1
30	67162	tr|A0A3B4VIC8|A0A3B4VIC8_SERDU	62.38	20	4	4	N	19032	Myosin light chain, phosphorylatable, fast skeletal muscle OS=Seriola dumerili OX=41447 PE=4 SV=1
30	67163	tr|I6U9W3|I6U9W3_ORYJA	62.38	20	4	4	N	19039	Myosin light chain 2 polypeptide OS=Oryzias javanicus OX=123683 GN=OJAV_G00082200 PE=2 SV=1
30	67164	tr|A0A3P9KRI4|A0A3P9KRI4_ORYLA	62.38	18	4	4	N	21414	Myosin light chain, phosphorylatable, fast skeletal muscle a OS=Oryzias latipes OX=8090 PE=4 SV=1
30	67165	tr|A0A3B3HA26|A0A3B3HA26_ORYLA	62.38	13	4	4	N	28219	Uncharacterized protein OS=Oryzias latipes OX=8090 GN=mylpf PE=4 SV=1
54	67200	tr|A0A7N8YD85|A0A7N8YD85_9TELE	62.16	7	2	0	N	50163	Calsequestrin OS=Mastacembelus armatus OX=205130 PE=3 SV=1
54	67201	tr|A0A7N8XIB6|A0A7N8XIB6_9TELE	62.16	7	2	0	N	50507	Calsequestrin OS=Mastacembelus armatus OX=205130 PE=3 SV=1
54	67202	tr|A0A7N8Y4P6|A0A7N8Y4P6_9TELE	62.16	7	2	0	N	50544	Calsequestrin OS=Mastacembelus armatus OX=205130 PE=3 SV=1
54	67203	tr|A0A7N8WMA4|A0A7N8WMA4_9TELE	62.16	7	2	0	N	50567	Calsequestrin OS=Mastacembelus armatus OX=205130 PE=3 SV=1
54	67204	tr|A0A7N8XJX7|A0A7N8XJX7_9TELE	62.16	6	2	0	N	52431	Calsequestrin OS=Mastacembelus armatus OX=205130 PE=3 SV=1
54	67205	tr|A0A3Q3SHA7|A0A3Q3SHA7_9TELE	62.16	6	2	0	N	52425	Calsequestrin OS=Mastacembelus armatus OX=205130 PE=3 SV=2
54	67206	tr|A0A7N8XSZ9|A0A7N8XSZ9_9TELE	62.16	6	2	0	N	52256	Calsequestrin OS=Mastacembelus armatus OX=205130 PE=3 SV=1
54	67207	tr|A0A7N8XRW1|A0A7N8XRW1_9TELE	62.16	6	2	0	N	52191	Calsequestrin OS=Mastacembelus armatus OX=205130 PE=3 SV=1
54	67208	tr|A0A7N8Y2R6|A0A7N8Y2R6_9TELE	62.16	6	2	0	N	52373	Calsequestrin OS=Mastacembelus armatus OX=205130 PE=3 SV=1
54	67209	tr|A0A7N8Y336|A0A7N8Y336_9TELE	62.16	6	2	0	N	52793	Calsequestrin OS=Mastacembelus armatus OX=205130 PE=3 SV=1

total 327 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
41	67018	tr|I3JGN1|I3JGN1_ORENI	56.43	4	3	0	N	121918	Uncharacterized protein OS=Oreochromis niloticus OX=8128 GN=col1a1 PE=4 SV=2
41	67019	tr|G9M6I5|G9M6I5_ORENI	56.43	3	3	0	N	137283	Collagen type I alpha 1 OS=Oreochromis niloticus OX=8128 GN=COL1A1 PE=2 SV=1
37	67005	tr|Q4RE90|Q4RE90_TETNG	55.57	1	3	3	N	863297	Chromosome undetermined SCAF15134, whole genome shotgun sequence (Fragment) OS=Tetraodon nigroviridis OX=99883 GN=GSTENG00035871001 PE=4 SV=1
48	67341	tr|A0A484CUS5|A0A484CUS5_PERFV	55.47	0	2	1	N	867139	Uncharacterized protein OS=Perca flavescens OX=8167 GN=EPR50_G00113850 PE=4 SV=1
38	67211	tr|A0A6G0I8D2|A0A6G0I8D2_LARCR	53.80	2	3	3	N	97204	Alpha-1,4 glucan phosphorylase OS=Larimichthys crocea OX=215358 GN=D5F01_LYC13586 PE=3 SV=1
38	67322	tr|A0A669CG83|A0A669CG83_ORENI	53.80	2	3	3	N	91665	Alpha-1,4 glucan phosphorylase OS=Oreochromis niloticus OX=8128 PE=3 SV=1
38	67323	tr|A0A3P8QJ74|A0A3P8QJ74_ASTCA	53.80	2	3	3	N	91586	Alpha-1,4 glucan phosphorylase OS=Astatotilapia calliptera OX=8154 PE=3 SV=1
38	67324	tr|A0A669E543|A0A669E543_ORENI	53.80	2	3	3	N	93767	Alpha-1,4 glucan phosphorylase OS=Oreochromis niloticus OX=8128 PE=3 SV=1
38	67325	tr|A0A3B4C8L5|A0A3B4C8L5_PYGNA	53.80	2	3	3	N	93768	Alpha-1,4 glucan phosphorylase OS=Pygocentrus nattereri OX=42514 PE=3 SV=1
38	67326	tr|A0A669F5E7|A0A669F5E7_ORENI	53.80	2	3	3	N	94615	Alpha-1,4 glucan phosphorylase OS=Oreochromis niloticus OX=8128 PE=3 SV=1
38	67327	tr|A0A672GIA2|A0A672GIA2_SALFA	53.80	2	3	3	N	96233	Alpha-1,4 glucan phosphorylase OS=Salarias fasciatus OX=181472 GN=LOC115395314 PE=3 SV=1
38	67328	tr|A0A3B4B6P0|A0A3B4B6P0_9GOBI	53.80	2	3	3	N	97017	Alpha-1,4 glucan phosphorylase OS=Periophthalmus magnuspinnatus OX=409849 PE=3 SV=1
38	67329	tr|A0A6P7PB25|A0A6P7PB25_BETSP	53.80	2	3	3	N	97104	Alpha-1,4 glucan phosphorylase OS=Betta splendens OX=158456 GN=LOC114869705 PE=3 SV=1
38	67330	tr|M4A9F5|M4A9F5_XIPMA	53.80	2	3	3	N	97256	Alpha-1,4 glucan phosphorylase OS=Xiphophorus maculatus OX=8083 PE=3 SV=1
38	67331	tr|A0A498LG69|A0A498LG69_LABRO	53.80	2	3	3	N	97018	Alpha-1,4 glucan phosphorylase OS=Labeo rohita OX=84645 GN=ROHU_012033 PE=3 SV=1
38	67332	tr|A0A0S7H0F8|A0A0S7H0F8_9TELE	53.80	2	3	3	N	97085	Alpha-1,4 glucan phosphorylase OS=Poeciliopsis prolifica OX=188132 GN=PYGM PE=3 SV=1
38	67335	tr|A0A5J5D262|A0A5J5D262_9PERO	53.80	2	3	3	N	98712	Alpha-1,4 glucan phosphorylase (Fragment) OS=Etheostoma spectabile OX=54343 GN=FQN60_000806 PE=3 SV=1
49	67343	tr|A0A6I9P2J6|A0A6I9P2J6_9TELE	52.39	6	2	0	N	51099	Calsequestrin OS=Notothenia coriiceps OX=8208 GN=LOC104956576 PE=3 SV=1
49	67344	tr|A0A2U9BKK8|A0A2U9BKK8_SCOMX	52.39	6	2	0	N	52892	Calsequestrin OS=Scophthalmus maximus OX=52904 GN=SMAX5B_006105 PE=3 SV=1
49	67345	tr|A0A6J2RKV3|A0A6J2RKV3_COTGO	52.39	6	2	0	N	53535	Calsequestrin OS=Cottoperca gobio OX=56716 GN=LOC115023113 PE=3 SV=1
49	67346	tr|A0A6P8WKA1|A0A6P8WKA1_GYMAC	52.39	6	2	0	N	55298	Calsequestrin OS=Gymnodraco acuticeps OX=8218 GN=casq1a PE=3 SV=1
49	67347	tr|A0A6A4TIJ9|A0A6A4TIJ9_SCOMX	52.39	4	2	0	N	89028	Calsequestrin OS=Scophthalmus maximus OX=52904 GN=F2P81_000969 PE=3 SV=1
49	67436	tr|A0A3P8VNQ7|A0A3P8VNQ7_CYNSE	52.39	6	2	0	N	49877	Calsequestrin OS=Cynoglossus semilaevis OX=244447 PE=3 SV=1

total 327 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
49	67437	tr|A0A3P8VQY9|A0A3P8VQY9_CYNSE	52.39	6	2	0	N	52455	Calsequestrin OS=Cynoglossus semilaevis OX=244447 PE=3 SV=1
49	67438	tr|A0A2I4B9K0|A0A2I4B9K0_9TELE	52.39	5	2	0	N	59100	Calsequestrin OS=Austrofundulus limnaeus OX=52670 GN=LOC106517901 PE=3 SV=1
55	67284	tr|A0A673A8U8|A0A673A8U8_9TELE	51.18	3	2	1	N	111385	Collagen, type I, alpha 1b OS=Sphaeramia orbicularis OX=375764 PE=4 SV=1
51	67439	tr|A0A671U7M6|A0A671U7M6_SPAAU	49.51	4	2	2	N	39670	Troponin T, fast skeletal muscle isoforms-like OS=Sparus aurata OX=8175 GN=LOC115587311 PE=4 SV=1
51	67449	tr|A0A3B3ZS88|A0A3B3ZS88_9GOBI	49.51	7	2	2	N	25528	Uncharacterized protein OS=Periophthalmus magnuspinnatus OX=409849 PE=3 SV=1
51	67450	tr|A0A3Q1CJW7|A0A3Q1CJW7_AMPOC	49.51	7	2	2	N	26282	Troponin T, fast skeletal muscle isoforms-like OS=Amphiprion ocellaris OX=80972 PE=3 SV=1
51	67451	tr|A0A3Q3EFK1|A0A3Q3EFK1_9LABR	49.51	7	2	2	N	26666	Troponin T, fast skeletal muscle isoforms-like OS=Labrus bergylta OX=56723 PE=3 SV=1
51	67452	tr|A0A3Q3AF19|A0A3Q3AF19_KRYMA	49.51	7	2	2	N	26771	Troponin T, fast skeletal muscle isoforms-like OS=Kryptolebias marmoratus OX=37003 PE=3 SV=1
51	67453	tr|A0A3Q3AF32|A0A3Q3AF32_KRYMA	49.51	7	2	2	N	26884	Troponin T, fast skeletal muscle isoforms-like OS=Kryptolebias marmoratus OX=37003 PE=3 SV=1
51	67454	tr|A0A3P8UNE3|A0A3P8UNE3_CYNSE	49.51	7	2	2	N	27351	Troponin T, fast skeletal muscle isoforms-like OS=Cynoglossus semilaevis OX=244447 PE=3 SV=1
51	67455	tr|A0SJB3|A0SJB3_SPAAU	49.51	7	2	2	N	27348	Fast/white muscle troponin T larval isoform OS=Sparus aurata OX=8175 PE=2 SV=1
51	67456	tr|A0A672Y3T4|A0A672Y3T4_9TELE	49.51	7	2	2	N	27423	Uncharacterized protein OS=Sphaeramia orbicularis OX=375764 GN=LOC115421585 PE=3 SV=1
51	67457	tr|A0SJB2|A0SJB2_SPAAU	49.51	6	2	2	N	27755	Fast/white muscle troponin T adult isoform OS=Sparus aurata OX=8175 PE=2 SV=1
51	67458	tr|A0A3P8UNF6|A0A3P8UNF6_CYNSE	49.51	6	2	2	N	28353	Troponin T, fast skeletal muscle isoforms-like OS=Cynoglossus semilaevis OX=244447 PE=3 SV=1
51	67459	tr|A0A3B4UYC0|A0A3B4UYC0_SERDU	49.51	6	2	2	N	29388	Troponin T type 3a (skeletal, fast) OS=Seriola dumerili OX=41447 PE=3 SV=1
51	67460	tr|A0A3P8URR7|A0A3P8URR7_CYNSE	49.51	6	2	2	N	29425	Troponin T, fast skeletal muscle isoforms-like OS=Cynoglossus semilaevis OX=244447 PE=3 SV=1
51	67461	tr|A0A3P8URM3|A0A3P8URM3_CYNSE	49.51	6	2	2	N	30206	Troponin T, fast skeletal muscle isoforms-like OS=Cynoglossus semilaevis OX=244447 PE=3 SV=1
51	67462	tr|A0A3Q3XL97|A0A3Q3XL97_MOLML	49.51	6	2	2	N	30493	Troponin T type 3a (skeletal, fast) OS=Mola mola OX=94237 PE=3 SV=1
51	67463	tr|A0A3P8ULW6|A0A3P8ULW6_CYNSE	49.51	6	2	2	N	31797	Troponin T, fast skeletal muscle isoforms-like OS=Cynoglossus semilaevis OX=244447 PE=3 SV=1
51	67464	tr|A0A5C6P7G2|A0A5C6P7G2_9TELE	49.51	6	2	2	N	32128	Troponin T, fast skeletal muscle isoforms OS=Takifugu flavidus OX=433684 GN=D4764_13G0000270 PE=3 SV=1
51	67465	tr|A0A3Q1CRB3|A0A3Q1CRB3_AMPOC	49.51	5	2	2	N	32379	Troponin T, fast skeletal muscle isoforms-like OS=Amphiprion ocellaris OX=80972 PE=3 SV=1
51	67466	tr|A0A665T7Y2|A0A665T7Y2_ECHNA	49.51	5	2	2	N	33067	Troponin T type 3a (skeletal, fast) OS=Echeneis naucrates OX=173247 PE=3 SV=1
51	67467	tr|A0A3Q1BEW8|A0A3Q1BEW8_AMPOC	49.51	5	2	2	N	33080	Troponin T, fast skeletal muscle isoforms-like OS=Amphiprion ocellaris OX=80972 PE=3 SV=1

total 327 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
51	67468	tr|A0A3P8THB6|A0A3P8THB6_AMPPE	49.51	5	2	2	N	33365	Troponin T type 3a (skeletal, fast) OS=Amphiprion percula OX=161767 PE=3 SV=1
51	67469	tr|A0A671U7Q2|A0A671U7Q2_SPAAU	49.51	5	2	2	N	33456	Troponin T, fast skeletal muscle isoforms-like OS=Sparus aurata OX=8175 GN=LOC115587311 PE=3 SV=1
51	67470	tr|A0A672YCL7|A0A672YCL7_9TELE	49.51	5	2	2	N	33478	Uncharacterized protein OS=Sphaeramia orbicularis OX=375764 GN=LOC115421585 PE=3 SV=1
51	67471	tr|A0A672YCL2|A0A672YCL2_9TELE	49.51	5	2	2	N	34165	Uncharacterized protein OS=Sphaeramia orbicularis OX=375764 GN=LOC115421585 PE=3 SV=1
51	67472	tr|A0A6P7KCL6|A0A6P7KCL6_9TELE	49.51	5	2	2	N	34619	troponin T, fast skeletal muscle isoforms-like isoform X3 OS=Parambassis ranga OX=210632 GN=LOC114452235 PE=3 SV=1
51	67473	tr|A0A6P7KCQ1|A0A6P7KCQ1_9TELE	49.51	5	2	2	N	35105	troponin T, fast skeletal muscle isoforms-like isoform X2 OS=Parambassis ranga OX=210632 GN=LOC114452235 PE=3 SV=1
51	67474	tr|A0A671UB90|A0A671UB90_SPAAU	49.51	4	2	2	N	38604	Troponin T, fast skeletal muscle isoforms-like OS=Sparus aurata OX=8175 GN=LOC115587311 PE=3 SV=1
51	67475	tr|A0A671U8G8|A0A671U8G8_SPAAU	49.51	4	2	2	N	39011	Troponin T, fast skeletal muscle isoforms-like OS=Sparus aurata OX=8175 GN=LOC115587311 PE=3 SV=1
51	67545	tr|A0A671U7M0|A0A671U7M0_SPAAU	49.51	5	2	2	N	36576	Troponin T, fast skeletal muscle isoforms-like OS=Sparus aurata OX=8175 GN=LOC115587311 PE=4 SV=1
51	67546	tr|A0A671UB76|A0A671UB76_SPAAU	49.51	4	2	2	N	38011	Troponin T, fast skeletal muscle isoforms-like OS=Sparus aurata OX=8175 GN=LOC115587311 PE=4 SV=1
36	67357	tr|A0A6A5F2V4|A0A6A5F2V4_PERFL	48.73	0	3	1	N	1083091	Uncharacterized protein OS=Perca fluviatilis OX=8168 GN=PFLUV_G00150840 PE=4 SV=1
45	67277	tr|A0A0S7EPU5|A0A0S7EPU5_9TELE	48.44	0	2	0	N	534030	TITIN OS=Poeciliopsis prolifica OX=188132 GN=TITIN PE=4 SV=1
45	67278	tr|A0A0S7ETZ8|A0A0S7ETZ8_9TELE	48.44	0	2	0	N	536335	TITIN (Fragment) OS=Poeciliopsis prolifica OX=188132 GN=TITIN PE=4 SV=1
45	67279	tr|A0A0S7EQ56|A0A0S7EQ56_9TELE	48.44	0	2	0	N	555084	TITIN OS=Poeciliopsis prolifica OX=188132 GN=TITIN PE=4 SV=1
45	67280	tr|A0A0S7F0D9|A0A0S7F0D9_9TELE	48.44	0	2	0	N	557390	TITIN (Fragment) OS=Poeciliopsis prolifica OX=188132 GN=TITIN PE=4 SV=1
57	67596	tr|A0A146UF80|A0A146UF80_FUNHE	47.30	5	2	2	N	29240	Phosphoglycerate mutase (Fragment) OS=Fundulus heteroclitus OX=8078 PE=3 SV=1
39	67077	tr|A0A671YMU3|A0A671YMU3_SPAAU	47.29	3	3	0	N	118161	Collagen alpha-1(I) chain-like OS=Sparus aurata OX=8175 GN=LOC115575148 PE=4 SV=1
39	67078	tr|A0A671YMZ1|A0A671YMZ1_SPAAU	47.29	3	3	0	N	120762	Collagen alpha-1(I) chain-like OS=Sparus aurata OX=8175 GN=LOC115575148 PE=4 SV=1
39	67079	tr|A0A671YQ85|A0A671YQ85_SPAAU	47.29	3	3	0	N	120531	Collagen alpha-1(I) chain-like OS=Sparus aurata OX=8175 GN=LOC115575148 PE=4 SV=1
39	67080	tr|A0A671YMZ6|A0A671YMZ6_SPAAU	47.29	3	3	0	N	122692	Collagen alpha-1(I) chain-like OS=Sparus aurata OX=8175 GN=LOC115575148 PE=4 SV=1
39	67081	tr|A0A671YNQ4|A0A671YNQ4_SPAAU	47.29	3	3	0	N	122121	Collagen alpha-1(I) chain-like OS=Sparus aurata OX=8175 GN=LOC115575148 PE=4 SV=1

total 327 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
39	67082	tr|A0A671YN33|A0A671YN33_SPAAU	47.29	3	3	0	N	129109	Collagen alpha-1(I) chain-like OS=Sparus aurata OX=8175 GN=LOC115575148 PE=4 SV=1
39	67083	tr|A0A671YQA1|A0A671YQA1_SPAAU	47.29	3	3	0	N	128328	Collagen alpha-1(I) chain-like OS=Sparus aurata OX=8175 GN=LOC115575148 PE=4 SV=1
39	67084	tr|A0A671YNR4|A0A671YNR4_SPAAU	47.29	3	3	0	N	130557	Collagen alpha-1(I) chain-like OS=Sparus aurata OX=8175 GN=LOC115575148 PE=4 SV=1
39	67085	tr|A0A671YPG6|A0A671YPG6_SPAAU	47.29	3	3	0	N	134738	Collagen alpha-1(I) chain-like OS=Sparus aurata OX=8175 GN=LOC115575148 PE=4 SV=1
39	67086	tr|A0A671YMN4|A0A671YMN4_SPAAU	47.29	3	3	0	N	136688	Collagen alpha-1(I) chain-like OS=Sparus aurata OX=8175 GN=LOC115575148 PE=4 SV=1
39	67114	tr|A0A3Q3RR05|A0A3Q3RR05_9TELE	47.29	3	3	0	N	117109	Collagen, type I, alpha 1a OS=Mastacembelus armatus OX=205130 PE=4 SV=2
39	67147	tr|A0A0F8B7E5|A0A0F8B7E5_LARCR	47.29	3	3	0	N	133708	Collagen alpha-1(I) chain OS=Larimichthys crocea OX=215358 GN=EH28_11446 PE=4 SV=1
39	67148	tr|A0A6G0HX74|A0A6G0HX74_LARCR	47.29	3	3	0	N	136864	Collagen alpha-1(I) chain Alpha-1 type I collagen OS=Larimichthys crocea OX=215358 GN=D5F01_LYC19014 PE=4 SV=1
39	67149	tr|A0A5J6XWD3|A0A5J6XWD3_NIBCO	47.29	3	3	0	N	136596	Collagen type I alpha 1 chain OS=Nibea coibor OX=396775 GN=COL1A1 PE=2 SV=1
39	67150	tr|A0A7N8XDE6|A0A7N8XDE6_9TELE	47.29	3	3	0	N	116695	Collagen, type I, alpha 1a OS=Mastacembelus armatus OX=205130 PE=4 SV=1
39	67151	tr|A0A7N8WW01|A0A7N8WW01_9TELE	47.29	3	3	0	N	123048	Collagen, type I, alpha 1a OS=Mastacembelus armatus OX=205130 PE=4 SV=1
39	67152	tr|A0A7N8XAN7|A0A7N8XAN7_9TELE	47.29	3	3	0	N	126162	Collagen, type I, alpha 1a OS=Mastacembelus armatus OX=205130 PE=4 SV=1
35	67400	tr|A0A4W4EA72|A0A4W4EA72_ELEEL	44.91	17	2	1	N	11756	Parvalbumin OS=Electrophorus electricus OX=8005 GN=LOC113569881 PE=3 SV=1
47	67404	tr|A0A6F9CEX9|A0A6F9CEX9_9TELE	44.31	0	2	1	N	1022296	Uncharacterized protein OS=Coregonus sp. 'balchen' OX=861768 GN=CSTEINMANNI_LOCUS3957823 PE=4 SV=1
42	67348	tr|A0A668V0Q0|A0A668V0Q0_OREAU	44.26	6	2	1	N	37062	Glyceraldehyde-3-phosphate dehydrogenase OS=Oreochromis aureus OX=47969 PE=3 SV=1
42	67355	tr|Q8AWX8|Q8AWX8_GADMO	44.26	6	2	1	N	36092	Glyceraldehyde-3-phosphate dehydrogenase OS=Gadus morhua OX=8049 PE=2 SV=1
42	67356	tr|A0A6P7KWB3|A0A6P7KWB3_BETSP	44.26	6	2	1	N	35917	Glyceraldehyde-3-phosphate dehydrogenase OS=Betta splendens OX=158456 GN=gapdh PE=3 SV=1
42	67507	tr|Q4VKA7|Q4VKA7_PARLE	44.26	18	2	1	N	12254	Glyceraldehyde-3-phosphate dehydrogenase (Fragment) OS=Paralichthys lethostigma OX=141886 GN=GAPDH PE=2 SV=1
50	67379	tr|A0A4W6CL45|A0A4W6CL45_LATCA	43.11	6	2	0	N	43959	Calsequestrin OS=Lates calcarifer OX=8187 GN=LOC108883924 PE=3 SV=1
50	67380	tr|A0A671XZM8|A0A671XZM8_SPAAU	43.11	6	2	0	N	45256	Calsequestrin OS=Sparus aurata OX=8175 GN=LOC115572796 PE=3 SV=1
50	67381	tr|A0A671Y6A5|A0A671Y6A5_SPAAU	43.11	5	2	0	N	50365	Calsequestrin OS=Sparus aurata OX=8175 GN=LOC115572796 PE=3 SV=1
50	67382	tr|A0A672HWD2|A0A672HWD2_SALFA	43.11	5	2	0	N	50618	Calsequestrin OS=Salarias fasciatus OX=181472 PE=3 SV=1
50	67383	tr|A0A672HWL2|A0A672HWL2_SALFA	43.11	5	2	0	N	51610	Calsequestrin OS=Salarias fasciatus OX=181472 PE=3 SV=1

total 327 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
50	67384	tr|A0A671XZM4|A0A671XZM4_SPAAU	43.11	5	2	0	N	51763	Calsequestrin OS=Sparus aurata OX=8175 GN=LOC115572796 PE=3 SV=1
50	67385	tr|A0A672HWC2|A0A672HWC2_SALFA	43.11	5	2	0	N	52548	Calsequestrin OS=Salarias fasciatus OX=181472 PE=3 SV=1
50	67386	tr|A0A672HXH8|A0A672HXH8_SALFA	43.11	5	2	0	N	52344	Calsequestrin OS=Salarias fasciatus OX=181472 PE=3 SV=1
50	67387	tr|A0A672HWL0|A0A672HWL0_SALFA	43.11	5	2	0	N	52538	Calsequestrin OS=Salarias fasciatus OX=181472 PE=3 SV=1
50	67388	tr|A0A672HXF4|A0A672HXF4_SALFA	43.11	5	2	0	N	52636	Calsequestrin OS=Salarias fasciatus OX=181472 PE=3 SV=1
50	67389	tr|A0A671XZK3|A0A671XZK3_SPAAU	43.11	5	2	0	N	52734	Calsequestrin OS=Sparus aurata OX=8175 GN=LOC115572796 PE=3 SV=1
50	67390	tr|A0A672HWP0|A0A672HWP0_SALFA	43.11	5	2	0	N	52933	Calsequestrin OS=Salarias fasciatus OX=181472 PE=3 SV=1
50	67391	tr|A0A4W6CL16|A0A4W6CL16_LATCA	43.11	5	2	0	N	52990	Calsequestrin OS=Lates calcarifer OX=8187 GN=LOC108883924 PE=3 SV=1
50	67392	tr|A0A4W6CL41|A0A4W6CL41_LATCA	43.11	5	2	0	N	53391	Calsequestrin OS=Lates calcarifer OX=8187 GN=LOC108883924 PE=3 SV=1
50	67393	tr|A0A672HXA9|A0A672HXA9_SALFA	43.11	5	2	0	N	53688	Calsequestrin OS=Salarias fasciatus OX=181472 PE=3 SV=1
50	67394	tr|A0A672HW84|A0A672HW84_SALFA	43.11	5	2	0	N	53918	Calsequestrin OS=Salarias fasciatus OX=181472 PE=3 SV=1
50	67395	tr|A0A671XZP8|A0A671XZP8_SPAAU	43.11	5	2	0	N	55189	Calsequestrin OS=Sparus aurata OX=8175 GN=LOC115572796 PE=3 SV=1
50	67396	tr|A0A4U5UZN8|A0A4U5UZN8_COLLU	43.11	3	2	0	N	98899	Calsequestrin OS=Collichthys lucidus OX=240159 GN=D9C73_013496 PE=3 SV=1
50	67508	tr|A0A3Q3JCJ6|A0A3Q3JCJ6_MONAL	43.11	5	2	0	N	49224	Calsequestrin OS=Monopterus albus OX=43700 PE=3 SV=1
50	67509	tr|A0A3B4WCW4|A0A3B4WCW4_SERLL	43.11	5	2	0	N	50048	Calsequestrin OS=Seriola lalandi dorsalis OX=1841481 PE=3 SV=1
50	67510	tr|A0A3B4UFZ1|A0A3B4UFZ1_SERDU	43.11	5	2	0	N	50935	Calsequestrin OS=Seriola dumerili OX=41447 PE=3 SV=1
50	67511	tr|A0A3B4WCV3|A0A3B4WCV3_SERLL	43.11	5	2	0	N	51404	Calsequestrin OS=Seriola lalandi dorsalis OX=1841481 PE=3 SV=1
40	67440	tr|A0A484CIB2|A0A484CIB2_PERFV	41.48	3	3	0	N	136760	Uncharacterized protein OS=Perca flavescens OX=8167 GN=EPR50_G00163440 PE=4 SV=1
52	67489	tr|A0A6A4SNF9|A0A6A4SNF9_SCOMX	41.47	3	2	1	N	77468	Parvalbumin OS=Scophthalmus maximus OX=52904 GN=F2P81_014924 PE=3 SV=1
56	67550	tr|A0A3B3CIU5|A0A3B3CIU5_ORYME	39.53	2	2	0	N	111992	Collagen type II alpha 1 chain OS=Oryzias melastigma OX=30732 GN=COL2A1 PE=4 SV=1
56	67551	tr|A0A834FQR3|A0A834FQR3_ORYME	39.53	2	2	0	N	140416	Collagen alpha-1(II) chain OS=Oryzias melastigma OX=30732 GN=FQA47_017639 PE=4 SV=1
56	67552	tr|A0A437DEJ9|A0A437DEJ9_ORYJA	39.53	2	2	0	N	142714	Uncharacterized protein OS=Oryzias javanicus OX=123683 GN=OJAV_G00046120 PE=4 SV=1
46	67490	tr|G3N515|G3N515_GASAC	38.85	0	2	0	N	451257	Uncharacterized protein OS=Gasterosteus aculeatus OX=69293 PE=4 SV=1
46	67497	tr|Q4T444|Q4T444_TETNG	38.85	0	2	0	N	1041680	Chromosome undetermined SCAF9829, whole genome shotgun sequence (Fragment) OS=Tetraodon nigroviridis OX=99883 GN=GSTENG00007498001 PE=4 SV=1
75	67581	tr|A0A6P7IXE2|A0A6P7IXE2_9TELE	37.39	4	1	1	N	48050	keratin, type I cytoskeletal 13-like OS=Parambassis ranga OX=210632 GN=LOC114440068 PE=4 SV=1
53	67795	tr|A0A3Q1HW42|A0A3Q1HW42_9TELE	36.31	7	2	2	N	21205	Adenylate kinase isoenzyme 1 OS=Acanthochromis polyacanthus OX=80966 GN=AK1 PE=3 SV=1

total 327 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
53	67796	tr|A0A3B5BIY5|A0A3B5BIY5_9TELE	36.31	7	2	2	N	21206	Adenylate kinase isoenzyme 1 OS=Stegastes partitus OX=144197 GN=AK1 PE=3 SV=1
53	67800	tr|A0A3Q4GK85|A0A3Q4GK85_NEOBR	36.31	7	2	2	N	21230	Adenylate kinase isoenzyme 1 OS=Neolamprologus brichardi OX=32507 GN=AK1 PE=3 SV=1
53	67801	tr|A0A3Q4GS43|A0A3Q4GS43_NEOBR	36.31	7	2	2	N	21240	Adenylate kinase isoenzyme 1 OS=Neolamprologus brichardi OX=32507 GN=AK1 PE=3 SV=1
53	67802	tr|A0A3P8P8S3|A0A3P8P8S3_ASTCA	36.31	7	2	2	N	21228	Adenylate kinase isoenzyme 1 OS=Astatotilapia calliptera OX=8154 GN=AK1 PE=3 SV=1
53	67803	tr|A0A3P9CWL7|A0A3P9CWL7_9CICH	36.31	7	2	2	N	21258	Adenylate kinase isoenzyme 1 OS=Maylandia zebra OX=106582 GN=AK1 PE=3 SV=1
53	67804	tr|A0A3Q2VY92|A0A3Q2VY92_HAPBU	36.31	7	2	2	N	21228	Adenylate kinase isoenzyme 1 OS=Haplochromis burtoni OX=8153 GN=AK1 PE=3 SV=1
53	67805	tr|A0A3B4FMK3|A0A3B4FMK3_9CICH	36.31	7	2	2	N	21228	Adenylate kinase isoenzyme 1 OS=Pundamilia nyererei OX=303518 GN=AK1 PE=3 SV=1
53	67806	tr|A0A3Q3CWR9|A0A3Q3CWR9_HAPBU	36.31	6	2	2	N	23163	Adenylate kinase isoenzyme 1 OS=Haplochromis burtoni OX=8153 GN=AK1 PE=3 SV=1
53	67807	tr|A0A3P8P8V3|A0A3P8P8V3_ASTCA	36.31	6	2	2	N	23216	Adenylate kinase isoenzyme 1 OS=Astatotilapia calliptera OX=8154 GN=AK1 PE=3 SV=1
44	67549	tr|A0A3Q3WSG6|A0A3Q3WSG6_MOLML	33.08	7	2	1	N	35991	Glyceraldehyde-3-phosphate dehydrogenase OS=Mola mola OX=94237 PE=3 SV=1
43	67850	tr|A0A6P7K206|A0A6P7K206_9TELE	23.54	6	2	0	N	35440	Glyceraldehyde-3-phosphate dehydrogenase OS=Parambassis ranga OX=210632 GN=LOC114449667 PE=3 SV=1
43	67852	tr|F5BZT7|F5BZT7_EPIBR	23.54	10	2	0	N	21481	Glyceraldehyde 3-phosphate dehydrogenase (Fragment) OS=Epinephelus bruneus OX=323802 PE=2 SV=1
43	67876	tr|A0A076U5J2|A0A076U5J2_SALFO	23.54	12	2	0	N	17964	Glyceraldehyde 3-phosphate dehydrogenase (Fragment) OS=Salvelinus fontinalis OX=8038 GN=GAPDH PE=2 SV=1
76	67808	tr|A0A1A8SH28|A0A1A8SH28_9TELE	23.48	1	1	1	N	120560	Collagen, type XI, alpha 1a (Fragment) OS=Nothobranchius rachovii OX=451742 GN=COL11A1A PE=4 SV=1
76	67809	tr|A0A1A8AFF3|A0A1A8AFF3_NOTFU	23.48	1	1	1	N	141734	Collagen, type XI, alpha 1a (Fragment) OS=Nothobranchius furzeri OX=105023 GN=COL11A1A PE=4 SV=1
76	67810	tr|A0A6P6JF49|A0A6P6JF49_CARAU	23.48	1	1	1	N	166733	collagen alpha-1(XI) chain-like isoform X5 OS=Carassius auratus OX=7957 GN=LOC113042513 PE=4 SV=1
76	67811	tr|A0A1A7ZX47|A0A1A7ZX47_NOTFU	23.48	1	1	1	N	169593	Collagen, type XI, alpha 1a OS=Nothobranchius furzeri OX=105023 GN=COL11A1A PE=4 SV=1
76	67812	tr|A0A6P6JAI8|A0A6P6JAI8_CARAU	23.48	1	1	1	N	169942	collagen alpha-1(XI) chain-like isoform X4 OS=Carassius auratus OX=7957 GN=LOC113042513 PE=4 SV=1
76	67813	tr|A0A1A8VA48|A0A1A8VA48_NOTFU	23.48	1	1	1	N	167925	Collagen, type XI, alpha 1a OS=Nothobranchius furzeri OX=105023 GN=COL11A1A PE=4 SV=1
76	67814	tr|A0A6P6JA06|A0A6P6JA06_CARAU	23.48	1	1	1	N	172657	collagen alpha-1(XI) chain-like isoform X3 OS=Carassius auratus OX=7957 GN=LOC113042513 PE=4 SV=1

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Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
76	67815	tr|A0A6P6J9V5|A0A6P6J9V5_CARAU	23.48	1	1	1	N	177532	collagen alpha-1(XI) chain-like isoform X2 OS=Carassius auratus OX=7957 GN=LOC113042513 PE=4 SV=1
76	67816	tr|A0A1A8S1T5|A0A1A8S1T5_9TELE	23.48	1	1	1	N	179570	Collagen, type XI, alpha 1a OS=Nothobranchius rachovii OX=451742 GN=COL11A1A PE=4 SV=1
76	67817	tr|A0A6P6JCL5|A0A6P6JCL5_CARAU	23.48	1	1	1	N	180741	collagen alpha-1(XI) chain-like isoform X1 OS=Carassius auratus OX=7957 GN=LOC113042513 PE=4 SV=1
77	67825	tr|A0A3P8TNL0|A0A3P8TNL0_AMPPE	22.74	1	1	1	N	151454	ATP-binding cassette, sub-family C (CFTR/MRP), member 5 OS=Amphiprion percula OX=161767 PE=4 SV=1
59	67827	tr|A0A6P6M1S2|A0A6P6M1S2_CARAU	22.02	1	1	1	N	109031	ankycorbin-like isoform X2 OS=Carassius auratus OX=7957 GN=LOC113064207 PE=4 SV=1
58	67890	tr|A0A315V5V2|A0A315V5V2_GAMAF	21.66	1	1	1	N	130242	Uncharacterized protein OS=Gambusia affinis OX=33528 GN=CCH79_00005593 PE=4 SV=1
78	67958	tr|A0A3P8PXL3|A0A3P8PXL3_ASTCA	21.04	1	1	1	N	126408	SEC24 homolog A, COPII coat complex component OS=Astatotilapia calliptera OX=8154 PE=3 SV=1
61	67894	tr|A0A674A9W5|A0A674A9W5_SALTR	20.23	3	1	1	N	39767	Fructose-bisphosphate aldolase OS=Salmo trutta OX=8032 GN=ALDOA PE=3 SV=1

total 327 proteins

tr|A0A3B4T4B1|A0A3B4T4B1_SERDU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.LEKSYELPDGQVITIGNE.R	Y	62.40	2004.0051	-0.7	1003.0091	2	13.51	2043	1	235	252	
S.LEKSYELPDGQVITIG.N	Y	47.00	1760.9196	-0.2	881.4669	2	13.63	2063	2	235	250	
E.KSYELPDGQVITIGNE.R	Y	42.86	1761.8784	-1.3	881.9453	2	13.39	2022	2	237	252	
L.EKSYELPDGQVITIG.N	Y	40.62	1647.8356	-0.1	824.9250	2	13.49	2040	1	236	250	
G.IVLDAGDGVTH.N	Y	40.00	1095.5560	0.0	548.7853	2	11.28	1650	1	150	160	
A.GFAGDDAPRA.V	N	39.52	975.4410	-0.2	488.7277	2	10.22	1469	4	19	28	
D.LAGRDLTDYLMK.I	Y	35.48	1394.7228	-0.4	698.3684	2	12.53	1874	1	179	190	
L.EKSYELPDGQVIT.I	Y	34.60	1477.7300	-1.0	739.8715	2	12.16	1807	1	236	248	
E.KSYELPDGQ.V	Y	29.74	1035.4873	4.6	518.7533	2	10.72	1551	1	237	245	
L.DAGDGVTH.N	Y	29.15	770.3195	0.0	386.1670	2	8.66	1223	3	153	160	
E.KSYELPDGQVITIG.N	Y	29.00	1518.7930	-0.3	760.4036	2	13.49	2039	2	237	250	
E.KSYELPDGQVIT.I	Y	28.67	1348.6874	-0.9	675.3503	2	11.98	1776	1	237	248	
S.LEKSYELPDGQVI.T	Y	28.05	1489.7664	-1.6	745.8893	2	12.81	1923	1	235	247	
Y.VGDEAQSK.R	N	26.03	832.3926	0.0	417.2036	2	8.09	1115	1	53	60	
S.LEKSYELPDGQVITI.G	Y	22.10	1703.8981	1.1	852.9572	2	13.95	2115	1	235	249	
L.DLAGRDLTDYLM.K	Y	21.76	1381.6548	0.3	691.8349	2	14.01	2125	1	178	189	
T.MYPGIADRM.Q	Y	19.69	1052.4783	-1.2	527.2458	2	11.85	1751	1	304	312	
R.VAPEEHPTL.L	Y	19.35	991.4974	0.6	496.7563	2	10.69	1547	1	95	103	
G.IITNWDDMEK.I	Y	19.16	1263.5806	-1.2	632.7968	2	12.15	1805	1	74	83	
G.FAGDDAPRA.V	N	18.34	918.4195	0.1	460.2171	2	17.21	2654	7	20	28	
S.LEKSYELPDGQ.V	Y	16.48	1277.6139	-0.9	639.8137	2	11.17	1631	1	235	245	
L.DLAGRDLTDYLMK.I	Y	15.77	1509.7498	-1.3	755.8812	2	13.04	1962	1	178	190	
L.EKSYELPDGQVITI.G	Y	15.45	1590.8141	-0.6	796.4139	2	13.72	2078	1	236	249	

total 23 peptides

tr|A0A3Q3BBJ2|A0A3Q3BBJ2_KRYMA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM

total 23 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.LEKSYELPDGQVITIGNE.R	Y	62.40	2004.0051	-0.7	1003.0091	2	13.51	2043	1	238	255	
S.LEKSYELPDGQVITIG.N	Y	47.00	1760.9196	-0.2	881.4669	2	13.63	2063	2	238	253	
E.KSYELPDGQVITIGNE.R	Y	42.86	1761.8784	-1.3	881.9453	2	13.39	2022	2	240	255	
L.EKSYELPDGQVITIG.N	Y	40.62	1647.8356	-0.1	824.9250	2	13.49	2040	1	239	253	
G.IVLDAGDGVTH.N	Y	40.00	1095.5560	0.0	548.7853	2	11.28	1650	1	153	163	
A.GFAGDDAPRA.V	N	39.52	975.4410	-0.2	488.7277	2	10.22	1469	4	22	31	
D.LAGRDLTDYLMK.I	Y	35.48	1394.7228	-0.4	698.3684	2	12.53	1874	1	182	193	
L.EKSYELPDGQVIT.I	Y	34.60	1477.7300	-1.0	739.8715	2	12.16	1807	1	239	251	
E.KSYELPDGQ.V	Y	29.74	1035.4873	4.6	518.7533	2	10.72	1551	1	240	248	
L.DAGDGVTH.N	Y	29.15	770.3195	0.0	386.1670	2	8.66	1223	3	156	163	
E.KSYELPDGQVITIG.N	Y	29.00	1518.7930	-0.3	760.4036	2	13.49	2039	2	240	253	
E.KSYELPDGQVIT.I	Y	28.67	1348.6874	-0.9	675.3503	2	11.98	1776	1	240	251	
S.LEKSYELPDGQVI.T	Y	28.05	1489.7664	-1.6	745.8893	2	12.81	1923	1	238	250	
Y.VGDEAQSK.R	N	26.03	832.3926	0.0	417.2036	2	8.09	1115	1	56	63	
S.LEKSYELPDGQVITI.G	Y	22.10	1703.8981	1.1	852.9572	2	13.95	2115	1	238	252	
L.DLAGRDLTDYLM.K	Y	21.76	1381.6548	0.3	691.8349	2	14.01	2125	1	181	192	
T.MYPGIADRM.Q	Y	19.69	1052.4783	-1.2	527.2458	2	11.85	1751	1	307	315	
R.VAPEEHPTL.L	Y	19.35	991.4974	0.6	496.7563	2	10.69	1547	1	98	106	
G.IITNWDDMEK.I	Y	19.16	1263.5806	-1.2	632.7968	2	12.15	1805	1	77	86	
G.FAGDDAPRA.V	N	18.34	918.4195	0.1	460.2171	2	17.21	2654	7	23	31	
S.LEKSYELPDGQ.V	Y	16.48	1277.6139	-0.9	639.8137	2	11.17	1631	1	238	248	
L.DLAGRDLTDYLMK.I	Y	15.77	1509.7498	-1.3	755.8812	2	13.04	1962	1	181	193	
L.EKSYELPDGQVITI.G	Y	15.45	1590.8141	-0.6	796.4139	2	13.72	2078	1	239	252	

total 23 peptides

tr|Q76MZ4|Q76MZ4_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.LEKSYELPDGQVITIGNE.R	Y	62.40	2004.0051	-0.7	1003.0091	2	13.51	2043	1	238	255	
S.LEKSYELPDGQVITIG.N	Y	47.00	1760.9196	-0.2	881.4669	2	13.63	2063	2	238	253	
E.KSYELPDGQVITIGNE.R	Y	42.86	1761.8784	-1.3	881.9453	2	13.39	2022	2	240	255	
L.EKSYELPDGQVITIG.N	Y	40.62	1647.8356	-0.1	824.9250	2	13.49	2040	1	239	253	
G.IVLDAGDGVTH.N	Y	40.00	1095.5560	0.0	548.7853	2	11.28	1650	1	153	163	
A.GFAGDDAPRA.V	N	39.52	975.4410	-0.2	488.7277	2	10.22	1469	4	22	31	
D.LAGRDLTDYLMK.I	Y	35.48	1394.7228	-0.4	698.3684	2	12.53	1874	1	182	193	
L.EKSYELPDGQVIT.I	Y	34.60	1477.7300	-1.0	739.8715	2	12.16	1807	1	239	251	
E.KSYELPDGQ.V	Y	29.74	1035.4873	4.6	518.7533	2	10.72	1551	1	240	248	
L.DAGDGVTH.N	Y	29.15	770.3195	0.0	386.1670	2	8.66	1223	3	156	163	
E.KSYELPDGQVITIG.N	Y	29.00	1518.7930	-0.3	760.4036	2	13.49	2039	2	240	253	
E.KSYELPDGQVIT.I	Y	28.67	1348.6874	-0.9	675.3503	2	11.98	1776	1	240	251	
S.LEKSYELPDGQVI.T	Y	28.05	1489.7664	-1.6	745.8893	2	12.81	1923	1	238	250	
Y.VGDEAQSK.R	N	26.03	832.3926	0.0	417.2036	2	8.09	1115	1	56	63	
S.LEKSYELPDGQVITI.G	Y	22.10	1703.8981	1.1	852.9572	2	13.95	2115	1	238	252	
L.DLAGRDLTDYLM.K	Y	21.76	1381.6548	0.3	691.8349	2	14.01	2125	1	181	192	
T.MYPGIADRM.Q	Y	19.69	1052.4783	-1.2	527.2458	2	11.85	1751	1	307	315	
R.VAPEEHPTL.L	Y	19.35	991.4974	0.6	496.7563	2	10.69	1547	1	98	106	
G.IITNWDDMEK.I	Y	19.16	1263.5806	-1.2	632.7968	2	12.15	1805	1	77	86	
G.FAGDDAPRA.V	N	18.34	918.4195	0.1	460.2171	2	17.21	2654	7	23	31	
S.LEKSYELPDGQ.V	Y	16.48	1277.6139	-0.9	639.8137	2	11.17	1631	1	238	248	
L.DLAGRDLTDYLMK.I	Y	15.77	1509.7498	-1.3	755.8812	2	13.04	1962	1	181	193	
L.EKSYELPDGQVITI.G	Y	15.45	1590.8141	-0.6	796.4139	2	13.72	2078	1	239	252	

total 23 peptides

tr|A0A3S2MUF9|A0A3S2MUF9_ORYJA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.LEKSYELPDGQVITIGNE.R	Y	62.40	2004.0051	-0.7	1003.0091	2	13.51	2043	1	238	255	
S.LEKSYELPDGQVITIG.N	Y	47.00	1760.9196	-0.2	881.4669	2	13.63	2063	2	238	253	
E.KSYELPDGQVITIGNE.R	Y	42.86	1761.8784	-1.3	881.9453	2	13.39	2022	2	240	255	
L.EKSYELPDGQVITIG.N	Y	40.62	1647.8356	-0.1	824.9250	2	13.49	2040	1	239	253	

total 23 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.IVLDAGDGVTH.N	Y	40.00	1095.5560	0.0	548.7853	2	11.28	1650	1	153	163	
A.GFAGDDAPRA.V	N	39.52	975.4410	-0.2	488.7277	2	10.22	1469	4	22	31	
D.LAGRDLTDYLMK.I	Y	35.48	1394.7228	-0.4	698.3684	2	12.53	1874	1	182	193	
L.EKSYELPDGQVIT.I	Y	34.60	1477.7300	-1.0	739.8715	2	12.16	1807	1	239	251	
E.KSYELPDGQ.V	Y	29.74	1035.4873	4.6	518.7533	2	10.72	1551	1	240	248	
L.DAGDGVTH.N	Y	29.15	770.3195	0.0	386.1670	2	8.66	1223	3	156	163	
E.KSYELPDGQVITIG.N	Y	29.00	1518.7930	-0.3	760.4036	2	13.49	2039	2	240	253	
E.KSYELPDGQVIT.I	Y	28.67	1348.6874	-0.9	675.3503	2	11.98	1776	1	240	251	
S.LEKSYELPDGQVI.T	Y	28.05	1489.7664	-1.6	745.8893	2	12.81	1923	1	238	250	
Y.VGDEAQSK.R	N	26.03	832.3926	0.0	417.2036	2	8.09	1115	1	56	63	
S.LEKSYELPDGQVITI.G	Y	22.10	1703.8981	1.1	852.9572	2	13.95	2115	1	238	252	
L.DLAGRDLTDYLM.K	Y	21.76	1381.6548	0.3	691.8349	2	14.01	2125	1	181	192	
T.MYPGIADRM.Q	Y	19.69	1052.4783	-1.2	527.2458	2	11.85	1751	1	307	315	
R.VAPEEHPTL.L	Y	19.35	991.4974	0.6	496.7563	2	10.69	1547	1	98	106	
G.IITNWDDMEK.I	Y	19.16	1263.5806	-1.2	632.7968	2	12.15	1805	1	77	86	
G.FAGDDAPRA.V	N	18.34	918.4195	0.1	460.2171	2	17.21	2654	7	23	31	
S.LEKSYELPDGQ.V	Y	16.48	1277.6139	-0.9	639.8137	2	11.17	1631	1	238	248	
L.DLAGRDLTDYLMK.I	Y	15.77	1509.7498	-1.3	755.8812	2	13.04	1962	1	181	193	
L.EKSYELPDGQVITI.G	Y	15.45	1590.8141	-0.6	796.4139	2	13.72	2078	1	239	252	

total 23 peptides

tr|A0A3Q0RI14|A0A3Q0RI14_AMPCI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.LEKSYELPDGQVITIGNE.R	Y	62.40	2004.0051	-0.7	1003.0091	2	13.51	2043	1	238	255	
S.LEKSYELPDGQVITIG.N	Y	47.00	1760.9196	-0.2	881.4669	2	13.63	2063	2	238	253	
E.KSYELPDGQVITIGNE.R	Y	42.86	1761.8784	-1.3	881.9453	2	13.39	2022	2	240	255	
L.EKSYELPDGQVITIG.N	Y	40.62	1647.8356	-0.1	824.9250	2	13.49	2040	1	239	253	
G.IVLDAGDGVTH.N	Y	40.00	1095.5560	0.0	548.7853	2	11.28	1650	1	153	163	
A.GFAGDDAPRA.V	N	39.52	975.4410	-0.2	488.7277	2	10.22	1469	4	22	31	
D.LAGRDLTDYLMK.I	Y	35.48	1394.7228	-0.4	698.3684	2	12.53	1874	1	182	193	
L.EKSYELPDGQVIT.I	Y	34.60	1477.7300	-1.0	739.8715	2	12.16	1807	1	239	251	
E.KSYELPDGQ.V	Y	29.74	1035.4873	4.6	518.7533	2	10.72	1551	1	240	248	
L.DAGDGVTH.N	Y	29.15	770.3195	0.0	386.1670	2	8.66	1223	3	156	163	
E.KSYELPDGQVITIG.N	Y	29.00	1518.7930	-0.3	760.4036	2	13.49	2039	2	240	253	
E.KSYELPDGQVIT.I	Y	28.67	1348.6874	-0.9	675.3503	2	11.98	1776	1	240	251	
S.LEKSYELPDGQVI.T	Y	28.05	1489.7664	-1.6	745.8893	2	12.81	1923	1	238	250	
Y.VGDEAQSK.R	N	26.03	832.3926	0.0	417.2036	2	8.09	1115	1	56	63	
S.LEKSYELPDGQVITI.G	Y	22.10	1703.8981	1.1	852.9572	2	13.95	2115	1	238	252	
L.DLAGRDLTDYLM.K	Y	21.76	1381.6548	0.3	691.8349	2	14.01	2125	1	181	192	
T.MYPGIADRM.Q	Y	19.69	1052.4783	-1.2	527.2458	2	11.85	1751	1	307	315	
R.VAPEEHPTL.L	Y	19.35	991.4974	0.6	496.7563	2	10.69	1547	1	98	106	
G.IITNWDDMEK.I	Y	19.16	1263.5806	-1.2	632.7968	2	12.15	1805	1	77	86	
G.FAGDDAPRA.V	N	18.34	918.4195	0.1	460.2171	2	17.21	2654	7	23	31	
S.LEKSYELPDGQ.V	Y	16.48	1277.6139	-0.9	639.8137	2	11.17	1631	1	238	248	
L.DLAGRDLTDYLMK.I	Y	15.77	1509.7498	-1.3	755.8812	2	13.04	1962	1	181	193	
L.EKSYELPDGQVITI.G	Y	15.45	1590.8141	-0.6	796.4139	2	13.72	2078	1	239	252	

total 23 peptides

tr|M4AKR3|M4AKR3_XIPMA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.LEKSYELPDGQVITIGNE.R	Y	62.40	2004.0051	-0.7	1003.0091	2	13.51	2043	1	238	255	
S.LEKSYELPDGQVITIG.N	Y	47.00	1760.9196	-0.2	881.4669	2	13.63	2063	2	238	253	
E.KSYELPDGQVITIGNE.R	Y	42.86	1761.8784	-1.3	881.9453	2	13.39	2022	2	240	255	
L.EKSYELPDGQVITIG.N	Y	40.62	1647.8356	-0.1	824.9250	2	13.49	2040	1	239	253	
G.IVLDAGDGVTH.N	Y	40.00	1095.5560	0.0	548.7853	2	11.28	1650	1	153	163	
A.GFAGDDAPRA.V	N	39.52	975.4410	-0.2	488.7277	2	10.22	1469	4	22	31	
D.LAGRDLTDYLMK.I	Y	35.48	1394.7228	-0.4	698.3684	2	12.53	1874	1	182	193	
L.EKSYELPDGQVIT.I	Y	34.60	1477.7300	-1.0	739.8715	2	12.16	1807	1	239	251	

total 23 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.KSYELPDGQ.V	Y	29.74	1035.4873	4.6	518.7533	2	10.72	1551	1	240	248	
L.DAGDGVTH.N	Y	29.15	770.3195	0.0	386.1670	2	8.66	1223	3	156	163	
E.KSYELPDGQVITIG.N	Y	29.00	1518.7930	-0.3	760.4036	2	13.49	2039	2	240	253	
E.KSYELPDGQVIT.I	Y	28.67	1348.6874	-0.9	675.3503	2	11.98	1776	1	240	251	
S.LEKSYELPDGQVI.T	Y	28.05	1489.7664	-1.6	745.8893	2	12.81	1923	1	238	250	
Y.VGDEAQSK.R	N	26.03	832.3926	0.0	417.2036	2	8.09	1115	1	56	63	
S.LEKSYELPDGQVITI.G	Y	22.10	1703.8981	1.1	852.9572	2	13.95	2115	1	238	252	
L.DLAGRDLTDYLM.K	Y	21.76	1381.6548	0.3	691.8349	2	14.01	2125	1	181	192	
T.MYPGIADRM.Q	Y	19.69	1052.4783	-1.2	527.2458	2	11.85	1751	1	307	315	
R.VAPEEHPTL.L	Y	19.35	991.4974	0.6	496.7563	2	10.69	1547	1	98	106	
G.IITNWDDMEK.I	Y	19.16	1263.5806	-1.2	632.7968	2	12.15	1805	1	77	86	
G.FAGDDAPRA.V	N	18.34	918.4195	0.1	460.2171	2	17.21	2654	7	23	31	
S.LEKSYELPDGQ.V	Y	16.48	1277.6139	-0.9	639.8137	2	11.17	1631	1	238	248	
L.DLAGRDLTDYLMK.I	Y	15.77	1509.7498	-1.3	755.8812	2	13.04	1962	1	181	193	
L.EKSYELPDGQVITI.G	Y	15.45	1590.8141	-0.6	796.4139	2	13.72	2078	1	239	252	

total 23 peptides

tr|C0LLE8|C0LLE8_DICLA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.LEKSYELPDGQVITIGNE.R	Y	62.40	2004.0051	-0.7	1003.0091	2	13.51	2043	1	238	255	
S.LEKSYELPDGQVITIG.N	Y	47.00	1760.9196	-0.2	881.4669	2	13.63	2063	2	238	253	
E.KSYELPDGQVITIGNE.R	Y	42.86	1761.8784	-1.3	881.9453	2	13.39	2022	2	240	255	
L.EKSYELPDGQVITIG.N	Y	40.62	1647.8356	-0.1	824.9250	2	13.49	2040	1	239	253	
G.IVLDAGDGVTH.N	Y	40.00	1095.5560	0.0	548.7853	2	11.28	1650	1	153	163	
A.GFAGDDAPRA.V	N	39.52	975.4410	-0.2	488.7277	2	10.22	1469	4	22	31	
D.LAGRDLTDYLMK.I	Y	35.48	1394.7228	-0.4	698.3684	2	12.53	1874	1	182	193	
L.EKSYELPDGQVIT.I	Y	34.60	1477.7300	-1.0	739.8715	2	12.16	1807	1	239	251	
E.KSYELPDGQ.V	Y	29.74	1035.4873	4.6	518.7533	2	10.72	1551	1	240	248	
L.DAGDGVTH.N	Y	29.15	770.3195	0.0	386.1670	2	8.66	1223	3	156	163	
E.KSYELPDGQVITIG.N	Y	29.00	1518.7930	-0.3	760.4036	2	13.49	2039	2	240	253	
E.KSYELPDGQVIT.I	Y	28.67	1348.6874	-0.9	675.3503	2	11.98	1776	1	240	251	
S.LEKSYELPDGQVI.T	Y	28.05	1489.7664	-1.6	745.8893	2	12.81	1923	1	238	250	
Y.VGDEAQSK.R	N	26.03	832.3926	0.0	417.2036	2	8.09	1115	1	56	63	
S.LEKSYELPDGQVITI.G	Y	22.10	1703.8981	1.1	852.9572	2	13.95	2115	1	238	252	
L.DLAGRDLTDYLM.K	Y	21.76	1381.6548	0.3	691.8349	2	14.01	2125	1	181	192	
T.MYPGIADRM.Q	Y	19.69	1052.4783	-1.2	527.2458	2	11.85	1751	1	307	315	
R.VAPEEHPTL.L	Y	19.35	991.4974	0.6	496.7563	2	10.69	1547	1	98	106	
G.IITNWDDMEK.I	Y	19.16	1263.5806	-1.2	632.7968	2	12.15	1805	1	77	86	
G.FAGDDAPRA.V	N	18.34	918.4195	0.1	460.2171	2	17.21	2654	7	23	31	
S.LEKSYELPDGQ.V	Y	16.48	1277.6139	-0.9	639.8137	2	11.17	1631	1	238	248	
L.DLAGRDLTDYLMK.I	Y	15.77	1509.7498	-1.3	755.8812	2	13.04	1962	1	181	193	
L.EKSYELPDGQVITI.G	Y	15.45	1590.8141	-0.6	796.4139	2	13.72	2078	1	239	252	

total 23 peptides

tr|A0A3Q3N432|A0A3Q3N432_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.LEKSYELPDGQVITIGNE.R	Y	62.40	2004.0051	-0.7	1003.0091	2	13.51	2043	1	238	255	
S.LEKSYELPDGQVITIG.N	Y	47.00	1760.9196	-0.2	881.4669	2	13.63	2063	2	238	253	
E.KSYELPDGQVITIGNE.R	Y	42.86	1761.8784	-1.3	881.9453	2	13.39	2022	2	240	255	
L.EKSYELPDGQVITIG.N	Y	40.62	1647.8356	-0.1	824.9250	2	13.49	2040	1	239	253	
G.IVLDAGDGVTH.N	Y	40.00	1095.5560	0.0	548.7853	2	11.28	1650	1	153	163	
A.GFAGDDAPRA.V	N	39.52	975.4410	-0.2	488.7277	2	10.22	1469	4	22	31	
D.LAGRDLTDYLMK.I	Y	35.48	1394.7228	-0.4	698.3684	2	12.53	1874	1	182	193	
L.EKSYELPDGQVIT.I	Y	34.60	1477.7300	-1.0	739.8715	2	12.16	1807	1	239	251	
E.KSYELPDGQ.V	Y	29.74	1035.4873	4.6	518.7533	2	10.72	1551	1	240	248	
L.DAGDGVTH.N	Y	29.15	770.3195	0.0	386.1670	2	8.66	1223	3	156	163	
E.KSYELPDGQVITIG.N	Y	29.00	1518.7930	-0.3	760.4036	2	13.49	2039	2	240	253	
E.KSYELPDGQVIT.I	Y	28.67	1348.6874	-0.9	675.3503	2	11.98	1776	1	240	251	

total 23 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.LEKSYELPDGQVI.T	Y	28.05	1489.7664	-1.6	745.8893	2	12.81	1923	1	238	250	
Y.VGDEAQSK.R	N	26.03	832.3926	0.0	417.2036	2	8.09	1115	1	56	63	
S.LEKSYELPDGQVITI.G	Y	22.10	1703.8981	1.1	852.9572	2	13.95	2115	1	238	252	
L.DLAGRDLTDYLM.K	Y	21.76	1381.6548	0.3	691.8349	2	14.01	2125	1	181	192	
T.MYPGIADRM.Q	Y	19.69	1052.4783	-1.2	527.2458	2	11.85	1751	1	307	315	
R.VAPEEHPTL.L	Y	19.35	991.4974	0.6	496.7563	2	10.69	1547	1	98	106	
G.IITNWDDMEK.I	Y	19.16	1263.5806	-1.2	632.7968	2	12.15	1805	1	77	86	
G.FAGDDAPRA.V	N	18.34	918.4195	0.1	460.2171	2	17.21	2654	7	23	31	
S.LEKSYELPDGQ.V	Y	16.48	1277.6139	-0.9	639.8137	2	11.17	1631	1	238	248	
L.DLAGRDLTDYLMK.I	Y	15.77	1509.7498	-1.3	755.8812	2	13.04	1962	1	181	193	
L.EKSYELPDGQVITI.G	Y	15.45	1590.8141	-0.6	796.4139	2	13.72	2078	1	239	252	

total 23 peptides

tr|Q76LU1|Q76LU1_GADCH

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.LEKSYELPDGQVITIGNE.R	Y	62.40	2004.0051	-0.7	1003.0091	2	13.51	2043	1	238	255	
S.LEKSYELPDGQVITIG.N	Y	47.00	1760.9196	-0.2	881.4669	2	13.63	2063	2	238	253	
E.KSYELPDGQVITIGNE.R	Y	42.86	1761.8784	-1.3	881.9453	2	13.39	2022	2	240	255	
L.EKSYELPDGQVITIG.N	Y	40.62	1647.8356	-0.1	824.9250	2	13.49	2040	1	239	253	
G.IVLDAGDGVTH.N	Y	40.00	1095.5560	0.0	548.7853	2	11.28	1650	1	153	163	
A.GFAGDDAPRA.V	N	39.52	975.4410	-0.2	488.7277	2	10.22	1469	4	22	31	
D.LAGRDLTDYLMK.I	Y	35.48	1394.7228	-0.4	698.3684	2	12.53	1874	1	182	193	
L.EKSYELPDGQVIT.I	Y	34.60	1477.7300	-1.0	739.8715	2	12.16	1807	1	239	251	
E.KSYELPDGQ.V	Y	29.74	1035.4873	4.6	518.7533	2	10.72	1551	1	240	248	
L.DAGDGVTH.N	Y	29.15	770.3195	0.0	386.1670	2	8.66	1223	3	156	163	
E.KSYELPDGQVITIG.N	Y	29.00	1518.7930	-0.3	760.4036	2	13.49	2039	2	240	253	
E.KSYELPDGQVIT.I	Y	28.67	1348.6874	-0.9	675.3503	2	11.98	1776	1	240	251	
S.LEKSYELPDGQVI.T	Y	28.05	1489.7664	-1.6	745.8893	2	12.81	1923	1	238	250	
Y.VGDEAQSK.R	N	26.03	832.3926	0.0	417.2036	2	8.09	1115	1	56	63	
S.LEKSYELPDGQVITI.G	Y	22.10	1703.8981	1.1	852.9572	2	13.95	2115	1	238	252	
L.DLAGRDLTDYLM.K	Y	21.76	1381.6548	0.3	691.8349	2	14.01	2125	1	181	192	
T.MYPGIADRM.Q	Y	19.69	1052.4783	-1.2	527.2458	2	11.85	1751	1	307	315	
R.VAPEEHPTL.L	Y	19.35	991.4974	0.6	496.7563	2	10.69	1547	1	98	106	
G.IITNWDDMEK.I	Y	19.16	1263.5806	-1.2	632.7968	2	12.15	1805	1	77	86	
G.FAGDDAPRA.V	N	18.34	918.4195	0.1	460.2171	2	17.21	2654	7	23	31	
S.LEKSYELPDGQ.V	Y	16.48	1277.6139	-0.9	639.8137	2	11.17	1631	1	238	248	
L.DLAGRDLTDYLMK.I	Y	15.77	1509.7498	-1.3	755.8812	2	13.04	1962	1	181	193	
L.EKSYELPDGQVITI.G	Y	15.45	1590.8141	-0.6	796.4139	2	13.72	2078	1	239	252	

total 23 peptides

tr|F5BZL8|F5BZL8_EPIBR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.LEKSYELPDGQVITIGNE.R	Y	62.40	2004.0051	-0.7	1003.0091	2	13.51	2043	1	238	255	
S.LEKSYELPDGQVITIG.N	Y	47.00	1760.9196	-0.2	881.4669	2	13.63	2063	2	238	253	
E.KSYELPDGQVITIGNE.R	Y	42.86	1761.8784	-1.3	881.9453	2	13.39	2022	2	240	255	
L.EKSYELPDGQVITIG.N	Y	40.62	1647.8356	-0.1	824.9250	2	13.49	2040	1	239	253	
G.IVLDAGDGVTH.N	Y	40.00	1095.5560	0.0	548.7853	2	11.28	1650	1	153	163	
A.GFAGDDAPRA.V	N	39.52	975.4410	-0.2	488.7277	2	10.22	1469	4	22	31	
D.LAGRDLTDYLMK.I	Y	35.48	1394.7228	-0.4	698.3684	2	12.53	1874	1	182	193	
L.EKSYELPDGQVIT.I	Y	34.60	1477.7300	-1.0	739.8715	2	12.16	1807	1	239	251	
E.KSYELPDGQ.V	Y	29.74	1035.4873	4.6	518.7533	2	10.72	1551	1	240	248	
L.DAGDGVTH.N	Y	29.15	770.3195	0.0	386.1670	2	8.66	1223	3	156	163	
E.KSYELPDGQVITIG.N	Y	29.00	1518.7930	-0.3	760.4036	2	13.49	2039	2	240	253	
E.KSYELPDGQVIT.I	Y	28.67	1348.6874	-0.9	675.3503	2	11.98	1776	1	240	251	
S.LEKSYELPDGQVI.T	Y	28.05	1489.7664	-1.6	745.8893	2	12.81	1923	1	238	250	
Y.VGDEAQSK.R	N	26.03	832.3926	0.0	417.2036	2	8.09	1115	1	56	63	
S.LEKSYELPDGQVITI.G	Y	22.10	1703.8981	1.1	852.9572	2	13.95	2115	1	238	252	
L.DLAGRDLTDYLM.K	Y	21.76	1381.6548	0.3	691.8349	2	14.01	2125	1	181	192	

total 23 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.MYPGIADRM.Q	Y	19.69	1052.4783	-1.2	527.2458	2	11.85	1751	1	307	315	
R.VAPEEHPTL.L	Y	19.35	991.4974	0.6	496.7563	2	10.69	1547	1	98	106	
G.IITNWDDMEK.I	Y	19.16	1263.5806	-1.2	632.7968	2	12.15	1805	1	77	86	
G.FAGDDAPRA.V	N	18.34	918.4195	0.1	460.2171	2	17.21	2654	7	23	31	
S.LEKSYELPDGQ.V	Y	16.48	1277.6139	-0.9	639.8137	2	11.17	1631	1	238	248	
L.DLAGRDLTDYLMK.I	Y	15.77	1509.7498	-1.3	755.8812	2	13.04	1962	1	181	193	
L.EKSYELPDGQVITI.G	Y	15.45	1590.8141	-0.6	796.4139	2	13.72	2078	1	239	252	

total 23 peptides

tr|A0A3Q4BGG8|A0A3Q4BGG8_MOLML
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.LEKSYELPDGQVITIGNE.R	Y	62.40	2004.0051	-0.7	1003.0091	2	13.51	2043	1	238	255	
S.LEKSYELPDGQVITIG.N	Y	47.00	1760.9196	-0.2	881.4669	2	13.63	2063	2	238	253	
E.KSYELPDGQVITIGNE.R	Y	42.86	1761.8784	-1.3	881.9453	2	13.39	2022	2	240	255	
L.EKSYELPDGQVITIG.N	Y	40.62	1647.8356	-0.1	824.9250	2	13.49	2040	1	239	253	
G.IVLDAGDGVTH.N	Y	40.00	1095.5560	0.0	548.7853	2	11.28	1650	1	153	163	
A.GFAGDDAPRA.V	N	39.52	975.4410	-0.2	488.7277	2	10.22	1469	4	22	31	
D.LAGRDLTDYLMK.I	Y	35.48	1394.7228	-0.4	698.3684	2	12.53	1874	1	182	193	
L.EKSYELPDGQVIT.I	Y	34.60	1477.7300	-1.0	739.8715	2	12.16	1807	1	239	251	
E.KSYELPDGQ.V	Y	29.74	1035.4873	4.6	518.7533	2	10.72	1551	1	240	248	
L.DAGDGVTH.N	Y	29.15	770.3195	0.0	386.1670	2	8.66	1223	3	156	163	
E.KSYELPDGQVITIG.N	Y	29.00	1518.7930	-0.3	760.4036	2	13.49	2039	2	240	253	
E.KSYELPDGQVIT.I	Y	28.67	1348.6874	-0.9	675.3503	2	11.98	1776	1	240	251	
S.LEKSYELPDGQVI.T	Y	28.05	1489.7664	-1.6	745.8893	2	12.81	1923	1	238	250	
Y.VGDEAQSK.R	N	26.03	832.3926	0.0	417.2036	2	8.09	1115	1	56	63	
S.LEKSYELPDGQVITI.G	Y	22.10	1703.8981	1.1	852.9572	2	13.95	2115	1	238	252	
L.DLAGRDLTDYLM.K	Y	21.76	1381.6548	0.3	691.8349	2	14.01	2125	1	181	192	
T.MYPGIADRM.Q	Y	19.69	1052.4783	-1.2	527.2458	2	11.85	1751	1	307	315	
R.VAPEEHPTL.L	Y	19.35	991.4974	0.6	496.7563	2	10.69	1547	1	98	106	
G.IITNWDDMEK.I	Y	19.16	1263.5806	-1.2	632.7968	2	12.15	1805	1	77	86	
G.FAGDDAPRA.V	N	18.34	918.4195	0.1	460.2171	2	17.21	2654	7	23	31	
S.LEKSYELPDGQ.V	Y	16.48	1277.6139	-0.9	639.8137	2	11.17	1631	1	238	248	
L.DLAGRDLTDYLMK.I	Y	15.77	1509.7498	-1.3	755.8812	2	13.04	1962	1	181	193	
L.EKSYELPDGQVITI.G	Y	15.45	1590.8141	-0.6	796.4139	2	13.72	2078	1	239	252	

total 23 peptides

tr|A0A3Q1DE47|A0A3Q1DE47_AMPOC
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.LEKSYELPDGQVITIGNE.R	Y	62.40	2004.0051	-0.7	1003.0091	2	13.51	2043	1	238	255	
S.LEKSYELPDGQVITIG.N	Y	47.00	1760.9196	-0.2	881.4669	2	13.63	2063	2	238	253	
E.KSYELPDGQVITIGNE.R	Y	42.86	1761.8784	-1.3	881.9453	2	13.39	2022	2	240	255	
L.EKSYELPDGQVITIG.N	Y	40.62	1647.8356	-0.1	824.9250	2	13.49	2040	1	239	253	
G.IVLDAGDGVTH.N	Y	40.00	1095.5560	0.0	548.7853	2	11.28	1650	1	153	163	
A.GFAGDDAPRA.V	N	39.52	975.4410	-0.2	488.7277	2	10.22	1469	4	22	31	
D.LAGRDLTDYLMK.I	Y	35.48	1394.7228	-0.4	698.3684	2	12.53	1874	1	182	193	
L.EKSYELPDGQVIT.I	Y	34.60	1477.7300	-1.0	739.8715	2	12.16	1807	1	239	251	
E.KSYELPDGQ.V	Y	29.74	1035.4873	4.6	518.7533	2	10.72	1551	1	240	248	
L.DAGDGVTH.N	Y	29.15	770.3195	0.0	386.1670	2	8.66	1223	3	156	163	
E.KSYELPDGQVITIG.N	Y	29.00	1518.7930	-0.3	760.4036	2	13.49	2039	2	240	253	
E.KSYELPDGQVIT.I	Y	28.67	1348.6874	-0.9	675.3503	2	11.98	1776	1	240	251	
S.LEKSYELPDGQVI.T	Y	28.05	1489.7664	-1.6	745.8893	2	12.81	1923	1	238	250	
Y.VGDEAQSK.R	N	26.03	832.3926	0.0	417.2036	2	8.09	1115	1	56	63	
S.LEKSYELPDGQVITI.G	Y	22.10	1703.8981	1.1	852.9572	2	13.95	2115	1	238	252	
L.DLAGRDLTDYLM.K	Y	21.76	1381.6548	0.3	691.8349	2	14.01	2125	1	181	192	
T.MYPGIADRM.Q	Y	19.69	1052.4783	-1.2	527.2458	2	11.85	1751	1	307	315	
R.VAPEEHPTL.L	Y	19.35	991.4974	0.6	496.7563	2	10.69	1547	1	98	106	
G.IITNWDDMEK.I	Y	19.16	1263.5806	-1.2	632.7968	2	12.15	1805	1	77	86	
G.FAGDDAPRA.V	N	18.34	918.4195	0.1	460.2171	2	17.21	2654	7	23	31	

total 23 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.LEKSYELPDGQ.V	Y	16.48	1277.6139	-0.9	639.8137	2	11.17	1631	1	238	248	
L.DLAGRDLTDYLMK.I	Y	15.77	1509.7498	-1.3	755.8812	2	13.04	1962	1	181	193	
L.EKSYELPDGQVITI.G	Y	15.45	1590.8141	-0.6	796.4139	2	13.72	2078	1	239	252	

total 23 peptides

tr|A0A7J6C441|A0A7J6C441_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.LEKSYELPDGQVITIGNE.R	Y	62.40	2004.0051	-0.7	1003.0091	2	13.51	2043	1	238	255	
S.LEKSYELPDGQVITIG.N	Y	47.00	1760.9196	-0.2	881.4669	2	13.63	2063	2	238	253	
E.KSYELPDGQVITIGNE.R	Y	42.86	1761.8784	-1.3	881.9453	2	13.39	2022	2	240	255	
L.EKSYELPDGQVITIG.N	Y	40.62	1647.8356	-0.1	824.9250	2	13.49	2040	1	239	253	
G.IVLDAGDGVTH.N	Y	40.00	1095.5560	0.0	548.7853	2	11.28	1650	1	153	163	
A.GFAGDDAPRA.V	N	39.52	975.4410	-0.2	488.7277	2	10.22	1469	4	22	31	
D.LAGRDLTDYLMK.I	Y	35.48	1394.7228	-0.4	698.3684	2	12.53	1874	1	182	193	
L.EKSYELPDGQVIT.I	Y	34.60	1477.7300	-1.0	739.8715	2	12.16	1807	1	239	251	
E.KSYELPDGQ.V	Y	29.74	1035.4873	4.6	518.7533	2	10.72	1551	1	240	248	
L.DAGDGVTH.N	Y	29.15	770.3195	0.0	386.1670	2	8.66	1223	3	156	163	
E.KSYELPDGQVITIG.N	Y	29.00	1518.7930	-0.3	760.4036	2	13.49	2039	2	240	253	
E.KSYELPDGQVIT.I	Y	28.67	1348.6874	-0.9	675.3503	2	11.98	1776	1	240	251	
S.LEKSYELPDGQVI.T	Y	28.05	1489.7664	-1.6	745.8893	2	12.81	1923	1	238	250	
Y.VGDEAQSK.R	N	26.03	832.3926	0.0	417.2036	2	8.09	1115	1	56	63	
S.LEKSYELPDGQVITI.G	Y	22.10	1703.8981	1.1	852.9572	2	13.95	2115	1	238	252	
L.DLAGRDLTDYLM.K	Y	21.76	1381.6548	0.3	691.8349	2	14.01	2125	1	181	192	
T.MYPGIADRM.Q	Y	19.69	1052.4783	-1.2	527.2458	2	11.85	1751	1	307	315	
R.VAPEEHPTL.L	Y	19.35	991.4974	0.6	496.7563	2	10.69	1547	1	98	106	
G.IITNWDDMEK.I	Y	19.16	1263.5806	-1.2	632.7968	2	12.15	1805	1	77	86	
G.FAGDDAPRA.V	N	18.34	918.4195	0.1	460.2171	2	17.21	2654	7	23	31	
S.LEKSYELPDGQ.V	Y	16.48	1277.6139	-0.9	639.8137	2	11.17	1631	1	238	248	
L.DLAGRDLTDYLMK.I	Y	15.77	1509.7498	-1.3	755.8812	2	13.04	1962	1	181	193	
L.EKSYELPDGQVITI.G	Y	15.45	1590.8141	-0.6	796.4139	2	13.72	2078	1	239	252	

total 23 peptides

tr|A0A6P7M219|A0A6P7M219_BETSP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.LEKSYELPDGQVITIGNE.R	Y	62.40	2004.0051	-0.7	1003.0091	2	13.51	2043	1	238	255	
S.LEKSYELPDGQVITIG.N	Y	47.00	1760.9196	-0.2	881.4669	2	13.63	2063	2	238	253	
E.KSYELPDGQVITIGNE.R	Y	42.86	1761.8784	-1.3	881.9453	2	13.39	2022	2	240	255	
L.EKSYELPDGQVITIG.N	Y	40.62	1647.8356	-0.1	824.9250	2	13.49	2040	1	239	253	
G.IVLDAGDGVTH.N	Y	40.00	1095.5560	0.0	548.7853	2	11.28	1650	1	153	163	
A.GFAGDDAPRA.V	N	39.52	975.4410	-0.2	488.7277	2	10.22	1469	4	22	31	
D.LAGRDLTDYLMK.I	Y	35.48	1394.7228	-0.4	698.3684	2	12.53	1874	1	182	193	
L.EKSYELPDGQVIT.I	Y	34.60	1477.7300	-1.0	739.8715	2	12.16	1807	1	239	251	
E.KSYELPDGQ.V	Y	29.74	1035.4873	4.6	518.7533	2	10.72	1551	1	240	248	
L.DAGDGVTH.N	Y	29.15	770.3195	0.0	386.1670	2	8.66	1223	3	156	163	
E.KSYELPDGQVITIG.N	Y	29.00	1518.7930	-0.3	760.4036	2	13.49	2039	2	240	253	
E.KSYELPDGQVIT.I	Y	28.67	1348.6874	-0.9	675.3503	2	11.98	1776	1	240	251	
S.LEKSYELPDGQVI.T	Y	28.05	1489.7664	-1.6	745.8893	2	12.81	1923	1	238	250	
Y.VGDEAQSK.R	N	26.03	832.3926	0.0	417.2036	2	8.09	1115	1	56	63	
S.LEKSYELPDGQVITI.G	Y	22.10	1703.8981	1.1	852.9572	2	13.95	2115	1	238	252	
L.DLAGRDLTDYLM.K	Y	21.76	1381.6548	0.3	691.8349	2	14.01	2125	1	181	192	
T.MYPGIADRM.Q	Y	19.69	1052.4783	-1.2	527.2458	2	11.85	1751	1	307	315	
R.VAPEEHPTL.L	Y	19.35	991.4974	0.6	496.7563	2	10.69	1547	1	98	106	
G.IITNWDDMEK.I	Y	19.16	1263.5806	-1.2	632.7968	2	12.15	1805	1	77	86	
G.FAGDDAPRA.V	N	18.34	918.4195	0.1	460.2171	2	17.21	2654	7	23	31	
S.LEKSYELPDGQ.V	Y	16.48	1277.6139	-0.9	639.8137	2	11.17	1631	1	238	248	
L.DLAGRDLTDYLMK.I	Y	15.77	1509.7498	-1.3	755.8812	2	13.04	1962	1	181	193	
L.EKSYELPDGQVITI.G	Y	15.45	1590.8141	-0.6	796.4139	2	13.72	2078	1	239	252	

total 23 peptides

tr|A0A3Q2P9J5|A0A3Q2P9J5_FUNHE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.LEKSYELPDGQVITIGNE.R	Y	62.40	2004.0051	-0.7	1003.0091	2	13.51	2043	1	238	255	
S.LEKSYELPDGQVITIG.N	Y	47.00	1760.9196	-0.2	881.4669	2	13.63	2063	2	238	253	
E.KSYELPDGQVITIGNE.R	Y	42.86	1761.8784	-1.3	881.9453	2	13.39	2022	2	240	255	
L.EKSYELPDGQVITIG.N	Y	40.62	1647.8356	-0.1	824.9250	2	13.49	2040	1	239	253	
G.IVLDAGDGVTH.N	Y	40.00	1095.5560	0.0	548.7853	2	11.28	1650	1	153	163	
A.GFAGDDAPRA.V	N	39.52	975.4410	-0.2	488.7277	2	10.22	1469	4	22	31	
D.LAGRDLTDYLMK.I	Y	35.48	1394.7228	-0.4	698.3684	2	12.53	1874	1	182	193	
L.EKSYELPDGQVIT.I	Y	34.60	1477.7300	-1.0	739.8715	2	12.16	1807	1	239	251	
E.KSYELPDGQ.V	Y	29.74	1035.4873	4.6	518.7533	2	10.72	1551	1	240	248	
L.DAGDGVTH.N	Y	29.15	770.3195	0.0	386.1670	2	8.66	1223	3	156	163	
E.KSYELPDGQVITIG.N	Y	29.00	1518.7930	-0.3	760.4036	2	13.49	2039	2	240	253	
E.KSYELPDGQVIT.I	Y	28.67	1348.6874	-0.9	675.3503	2	11.98	1776	1	240	251	
S.LEKSYELPDGQVI.T	Y	28.05	1489.7664	-1.6	745.8893	2	12.81	1923	1	238	250	
Y.VGDEAQSK.R	N	26.03	832.3926	0.0	417.2036	2	8.09	1115	1	56	63	
S.LEKSYELPDGQVITI.G	Y	22.10	1703.8981	1.1	852.9572	2	13.95	2115	1	238	252	
L.DLAGRDLTDYLM.K	Y	21.76	1381.6548	0.3	691.8349	2	14.01	2125	1	181	192	
T.MYPGIADRM.Q	Y	19.69	1052.4783	-1.2	527.2458	2	11.85	1751	1	307	315	
R.VAPEEHPTL.L	Y	19.35	991.4974	0.6	496.7563	2	10.69	1547	1	98	106	
G.IITNWDDMEK.I	Y	19.16	1263.5806	-1.2	632.7968	2	12.15	1805	1	77	86	
G.FAGDDAPRA.V	N	18.34	918.4195	0.1	460.2171	2	17.21	2654	7	23	31	
S.LEKSYELPDGQ.V	Y	16.48	1277.6139	-0.9	639.8137	2	11.17	1631	1	238	248	
L.DLAGRDLTDYLMK.I	Y	15.77	1509.7498	-1.3	755.8812	2	13.04	1962	1	181	193	
L.EKSYELPDGQVITI.G	Y	15.45	1590.8141	-0.6	796.4139	2	13.72	2078	1	239	252	

total 23 peptides

tr|D4P4P1|D4P4P1_COBCH

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.LEKSYELPDGQVITIGNE.R	Y	62.40	2004.0051	-0.7	1003.0091	2	13.51	2043	1	238	255	
S.LEKSYELPDGQVITIG.N	Y	47.00	1760.9196	-0.2	881.4669	2	13.63	2063	2	238	253	
E.KSYELPDGQVITIGNE.R	Y	42.86	1761.8784	-1.3	881.9453	2	13.39	2022	2	240	255	
L.EKSYELPDGQVITIG.N	Y	40.62	1647.8356	-0.1	824.9250	2	13.49	2040	1	239	253	
G.IVLDAGDGVTH.N	Y	40.00	1095.5560	0.0	548.7853	2	11.28	1650	1	153	163	
A.GFAGDDAPRA.V	N	39.52	975.4410	-0.2	488.7277	2	10.22	1469	4	22	31	
D.LAGRDLTDYLMK.I	Y	35.48	1394.7228	-0.4	698.3684	2	12.53	1874	1	182	193	
L.EKSYELPDGQVIT.I	Y	34.60	1477.7300	-1.0	739.8715	2	12.16	1807	1	239	251	
E.KSYELPDGQ.V	Y	29.74	1035.4873	4.6	518.7533	2	10.72	1551	1	240	248	
L.DAGDGVTH.N	Y	29.15	770.3195	0.0	386.1670	2	8.66	1223	3	156	163	
E.KSYELPDGQVITIG.N	Y	29.00	1518.7930	-0.3	760.4036	2	13.49	2039	2	240	253	
E.KSYELPDGQVIT.I	Y	28.67	1348.6874	-0.9	675.3503	2	11.98	1776	1	240	251	
S.LEKSYELPDGQVI.T	Y	28.05	1489.7664	-1.6	745.8893	2	12.81	1923	1	238	250	
Y.VGDEAQSK.R	N	26.03	832.3926	0.0	417.2036	2	8.09	1115	1	56	63	
S.LEKSYELPDGQVITI.G	Y	22.10	1703.8981	1.1	852.9572	2	13.95	2115	1	238	252	
L.DLAGRDLTDYLM.K	Y	21.76	1381.6548	0.3	691.8349	2	14.01	2125	1	181	192	
T.MYPGIADRM.Q	Y	19.69	1052.4783	-1.2	527.2458	2	11.85	1751	1	307	315	
R.VAPEEHPTL.L	Y	19.35	991.4974	0.6	496.7563	2	10.69	1547	1	98	106	
G.IITNWDDMEK.I	Y	19.16	1263.5806	-1.2	632.7968	2	12.15	1805	1	77	86	
G.FAGDDAPRA.V	N	18.34	918.4195	0.1	460.2171	2	17.21	2654	7	23	31	
S.LEKSYELPDGQ.V	Y	16.48	1277.6139	-0.9	639.8137	2	11.17	1631	1	238	248	
L.DLAGRDLTDYLMK.I	Y	15.77	1509.7498	-1.3	755.8812	2	13.04	1962	1	181	193	
L.EKSYELPDGQVITI.G	Y	15.45	1590.8141	-0.6	796.4139	2	13.72	2078	1	239	252	

total 23 peptides

tr|A3F5V3|A3F5V3_ORENI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.LEKSYELPDGQVITIGNE.R	Y	62.40	2004.0051	-0.7	1003.0091	2	13.51	2043	1	233	250	
S.LEKSYELPDGQVITIG.N	Y	47.09	1760.9196	0.2	881.4669	2	13.63	2063	2	233	248	
E.KSYELPDGQVITIGNE.R	Y	42.86	1761.8784	-1.3	881.9453	2	13.39	2022	2	235	250	
L.EKSYELPDGQVITIG.N	Y	40.62	1647.8356	-0.1	824.9250	2	13.49	2040	1	234	248	
G.IVLDAGDGVTH.N	Y	40.00	1095.5560	0.0	548.7853	2	11.28	1650	1	148	158	
A.GFAGDDAPRA.V	N	39.52	975.4410	-0.2	488.7277	2	10.22	1469	4	17	26	
D.LAGRDLTDYLMK.I	Y	35.48	1394.7228	-0.4	698.3684	2	12.53	1874	1	177	188	
L.EKSYELPDGQVIT.I	Y	34.60	1477.7300	-1.0	739.8715	2	12.16	1807	1	234	246	
E.KSYELPDGQ.V	Y	29.74	1035.4873	4.6	518.7533	2	10.72	1551	1	235	243	
L.DAGDGVTH.N	Y	29.15	770.3195	0.0	386.1670	2	8.66	1223	3	151	158	
E.KSYELPDGQVITIG.N	Y	29.00	1518.7930	-0.3	760.4036	2	13.49	2039	2	235	248	
E.KSYELPDGQVIT.I	Y	28.67	1348.6874	-0.9	675.3503	2	11.98	1776	1	235	246	
S.LEKSYELPDGQVI.T	Y	28.05	1489.7664	-1.6	745.8893	2	12.81	1923	1	233	245	
Y.VGDEAQSK.R	N	26.03	832.3926	0.0	417.2036	2	8.09	1115	1	51	58	
S.LEKSYELPDGQVITI.G	Y	22.10	1703.8981	1.1	852.9572	2	13.95	2115	1	233	247	
L.DLAGRDLTDYLM.K	Y	21.76	1381.6548	0.3	691.8349	2	14.01	2125	1	176	187	
T.MYPGIADRM.H	Y	19.69	1052.4783	-1.2	527.2458	2	11.85	1751	1	302	310	
R.VAPEEHPTL.L	Y	19.35	991.4974	0.6	496.7563	2	10.69	1547	1	93	101	
G.IITNWDDMEK.I	Y	19.16	1263.5806	-1.2	632.7968	2	12.15	1805	1	72	81	
G.FAGDDAPRA.V	N	18.34	918.4195	0.1	460.2171	2	17.21	2654	7	18	26	
S.LEKSYELPDGQ.V	Y	16.48	1277.6139	-0.9	639.8137	2	11.17	1631	1	233	243	
L.DLAGRDLTDYLMK.I	Y	15.77	1509.7498	-1.3	755.8812	2	13.04	1962	1	176	188	
L.EKSYELPDGQVITI.G	Y	15.45	1590.8141	-0.6	796.4139	2	13.72	2078	1	234	247	

total 23 peptides

tr|A0A3P8QM38|A0A3P8QM38_ASTCA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	1026	1038	
W.LDKNKDPLNDSVVQ.L	N	41.51	1583.8154	-4.2	792.9117	2	15.56	2391	8	596	609	
E.NDKQQSDEKIKKK.D	N	41.47	1587.8580	-0.2	794.9362	2	7.54	1010	2	1070	1082	
T.VKEDDIHPM.N	N	31.40	1082.5066	-0.8	542.2601	2	10.15	1457	1	72	80	
S.VIPEGQF.I	N	30.48	788.4068	-0.7	395.2104	2	12.26	1825	2	729	735	
Q.IGETGKT.I	N	30.06	704.3705	-0.2	353.1924	2	8.67	1226	1	1515	1521	
E.YKKEGIEWEFIDF.G	N	29.33	1702.8242	-0.4	852.4191	2	14.27	2169	1	503	515	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1616	1624	
L.KAKNDENVRQ.L	N	26.18	1200.6211	-0.6	601.3174	2	7.67	1035	1	1259	1268	
Q.GEVDDAVQEAR.N	N	26.15	1187.5417	0.3	594.7783	2	10.44	1506	1	1738	1748	
K.SINDVEEF.I	N	23.98	951.4185	-0.5	476.7163	2	12.53	1873	1	324	331	
K.LHDQH.L	N	17.45	648.2980	0.3	325.1564	2	3.70	484	3	554	558	
E.LKKEQDTSAH.L	N	16.64	1155.5884	0.0	578.8015	2	7.73	1044	1	1768	1777	
N.VKNWPW.L	N	16.17	828.4282	-1.1	415.2209	2	12.79	1919	1	824	829	
K.FKQKQREEQAEPDGTEVADK.I	N	16.13	2332.1294	-0.3	778.3835	3	9.20	1310	1	366	385	
N.FTNEKLQQF.F	N	16.00	1153.5768	0.0	577.7957	2	11.46	1682	1	482	490	

total 16 peptides

tr|A0A6G0HED4|A0A6G0HED4_LARCR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	1029	1041	
W.LDKNKDPLNDSVVQ.L	N	41.51	1583.8154	-4.2	792.9117	2	15.56	2391	8	596	609	
E.NDKQQSDEKIKKK.D	N	41.47	1587.8580	-0.2	794.9362	2	7.54	1010	2	1073	1085	
S.VIPEGQF.I	N	30.48	788.4068	-0.7	395.2104	2	12.26	1825	2	731	737	
E.YKKEGIEWEFIDF.G	N	29.33	1702.8242	-0.4	852.4191	2	14.27	2169	1	503	515	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1619	1627	
L.SKIEDEQSL.G	N	26.50	1047.5084	-0.3	524.7614	2	10.37	1494	1	1094	1102	
L.KAKNDENVRQ.L	N	26.18	1200.6211	-0.6	601.3174	2	7.67	1035	1	1262	1271	
Q.GEVDDAVQEAR.N	N	26.15	1187.5417	0.3	594.7783	2	10.44	1506	1	1741	1751	
K.SINDVEEF.D	N	23.98	951.4185	-0.5	476.7163	2	12.53	1873	1	324	331	
L.SKIEDEQSLGAQ.L	N	20.57	1303.6255	-0.3	652.8198	2	10.23	1470	1	1094	1105	

total 17 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LHDQH.L	N	17.45	648.2980	0.3	325.1564	2	3.70	484	3	554	558	
E.LKKEQDTSAH.L	N	16.64	1155.5884	0.0	578.8015	2	7.73	1044	1	1771	1780	
N.VKNWPW.L	N	16.17	828.4282	-1.1	415.2209	2	12.79	1919	1	826	831	
K.FKQKQREEQAEPDGTEVADK.I	N	16.13	2332.1294	-0.3	778.3835	3	9.20	1310	1	366	385	
N.FTNEKLQQF.F	N	16.00	1153.5768	0.0	577.7957	2	11.46	1682	1	482	490	
A.EWKQKYEEGQAELE.G	N	15.02	1765.8158	-1.1	883.9142	2	10.99	1599	1	1457	1470	

total 17 peptides

tr|A0A665X5K8|A0A665X5K8_ECHNA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	1024	1036	
W.LDKNKDPLNDSVVQ.L	N	41.51	1583.8154	-4.2	792.9117	2	15.56	2391	8	596	609	
E.NDKQQSDEKIKKK.D	N	41.47	1587.8580	-0.2	794.9362	2	7.54	1010	2	1068	1080	
S.VIPEGQF.I	N	30.48	788.4068	-0.7	395.2104	2	12.26	1825	2	728	734	
E.YKKEGIEWEFIDF.G	N	29.33	1702.8242	-0.4	852.4191	2	14.27	2169	1	503	515	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1614	1622	
L.SKIEDEQSL.G	N	26.50	1047.5084	-0.3	524.7614	2	10.37	1494	1	1089	1097	
L.KAKNDENVRQ.L	N	26.18	1200.6211	-0.6	601.3174	2	7.67	1035	1	1257	1266	
Q.GEVDDAVQEAR.N	N	26.15	1187.5417	0.3	594.7783	2	10.44	1506	1	1736	1746	
K.SINDVEEF.I	N	23.98	951.4185	-0.5	476.7163	2	12.53	1873	1	324	331	
L.SKIEDEQSLGAQ.L	N	20.57	1303.6255	-0.3	652.8198	2	10.23	1470	1	1089	1100	
K.LHDQH.L	N	17.45	648.2980	0.3	325.1564	2	3.70	484	3	554	558	
E.LKKEQDTSAH.L	N	16.64	1155.5884	0.0	578.8015	2	7.73	1044	1	1766	1775	
N.VKNWPW.L	N	16.17	828.4282	-1.1	415.2209	2	12.79	1919	1	823	828	
K.FKQKQREEQAEPDGTEVADK.I	N	16.13	2332.1294	-0.3	778.3835	3	9.20	1310	1	366	385	
N.FTNEKLQQF.F	N	16.00	1153.5768	0.0	577.7957	2	11.46	1682	1	482	490	
A.EWKQKYEEGQAELE.G	N	15.02	1765.8158	-1.1	883.9142	2	10.99	1599	1	1452	1465	

total 17 peptides

tr|A0A6J2PN08|A0A6J2PN08_COTGO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	1041	1053	
W.LDKNKDPLNDSVVQ.L	N	41.51	1583.8154	-4.2	792.9117	2	15.56	2391	8	595	608	
E.NDKQQSDEKIKKK.D	N	41.47	1587.8580	-0.2	794.9362	2	7.54	1010	2	1085	1097	
P.MNPPKYDKIEDM.A	N	39.50	1479.6737	-0.8	740.8436	2	11.36	1664	1	79	90	
L.GFTADEKIGIY.K	N	39.36	1212.6027	-0.6	607.3082	2	12.49	1867	1	341	351	
S.VIPEGQF.I	N	30.48	788.4068	-0.7	395.2104	2	12.26	1825	2	743	749	
E.YKKEGIEWEFIDF.G	N	29.33	1702.8242	-0.4	852.4191	2	14.27	2169	1	502	514	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1631	1639	
M.NPPKYDKIEDM.A	N	26.69	1348.6333	-0.3	675.3237	2	10.87	1577	1	80	90	
L.SKIEDEQSL.G	N	26.50	1047.5084	-0.3	524.7614	2	10.37	1494	1	1106	1114	
K.FKQKQREEQAEPDGTEVADK.I	N	16.13	2332.1294	-0.3	778.3835	3	9.20	1310	1	365	384	
N.FTNEKLQQF.F	N	16.00	1153.5768	0.0	577.7957	2	11.46	1682	1	481	489	

total 12 peptides

tr|A0A6P7NC66|A0A6P7NC66_BETSP
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	1029	1041	
W.LDKNKDPLNDSVVQ.L	N	41.51	1583.8154	-4.2	792.9117	2	15.56	2391	8	595	608	
E.NDKQQSDEKIKKK.D	N	41.47	1587.8580	-0.2	794.9362	2	7.54	1010	2	1073	1085	
S.VIPEGQF.I	N	30.48	788.4068	-0.7	395.2104	2	12.26	1825	2	731	737	
Q.IGETGKT.I	N	30.06	704.3705	-0.2	353.1924	2	8.67	1226	1	1518	1524	
E.YKKEGIEWEFIDF.G	N	29.33	1702.8242	-0.4	852.4191	2	14.27	2169	1	502	514	

total 15 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1619	1627	
R.NPPKYDKIEDM.A	N	26.69	1348.6333	-0.3	675.3237	2	10.87	1577	1	80	90	
L.KAKNDENVRQ.L	N	26.18	1200.6211	-0.6	601.3174	2	7.67	1035	1	1262	1271	
K.SINDVEEF.I	N	23.98	951.4185	-0.5	476.7163	2	12.53	1873	1	323	330	
K.LHDQH.L	N	17.45	648.2980	0.3	325.1564	2	3.70	484	3	553	557	
E.LKKEQDTSAH.L	N	16.64	1155.5884	0.0	578.8015	2	7.73	1044	1	1771	1780	
N.VKNWPW.L	N	16.17	828.4282	-1.1	415.2209	2	12.79	1919	1	826	831	
K.FKQKQREEQAEPDGTEVADK.I	N	16.13	2332.1294	-0.3	778.3835	3	9.20	1310	1	365	384	
N.FTNEKLQQF.F	N	16.00	1153.5768	0.0	577.7957	2	11.46	1682	1	481	489	

total 15 peptides

tr|Q90YF6|Q90YF6_PARFO
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	1029	1041	
W.LDKNKDPLNDSVVQ.L	N	41.51	1583.8154	-4.2	792.9117	2	15.56	2391	8	596	609	
E.NDKQQSDEKIKKK.D	N	41.47	1587.8580	-0.2	794.9362	2	7.54	1010	2	1073	1085	
S.VIPEGQF.I	N	30.48	788.4068	-0.7	395.2104	2	12.26	1825	2	731	737	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1619	1627	
R.NPPKYDKIEDM.A	N	26.69	1348.6333	-0.3	675.3237	2	10.87	1577	1	81	91	
L.SKIEDEQSL.G	N	26.50	1047.5084	-0.3	524.7614	2	10.37	1494	1	1094	1102	
L.KAKNDENVRQ.L	N	26.18	1200.6211	-0.6	601.3174	2	7.67	1035	1	1262	1271	
K.SINDVEEF.I	N	23.98	951.4185	-0.5	476.7163	2	12.53	1873	1	324	331	
L.SKIEDEQSLGAQ.L	N	20.57	1303.6255	-0.3	652.8198	2	10.23	1470	1	1094	1105	
K.LHDQH.L	N	17.45	648.2980	0.3	325.1564	2	3.70	484	3	554	558	
E.LKKEQDTSAH.L	N	16.64	1155.5884	0.0	578.8015	2	7.73	1044	1	1771	1780	
N.VKNWPW.L	N	16.17	828.4282	-1.1	415.2209	2	12.79	1919	1	826	831	
K.FKQKQREEQAEPDGTEVADK.I	N	16.13	2332.1294	-0.3	778.3835	3	9.20	1310	1	366	385	
N.FTNEKLQQF.F	N	16.00	1153.5768	0.0	577.7957	2	11.46	1682	1	482	490	
A.EWKQKYEEGQAELE.G	N	15.02	1765.8158	-1.1	883.9142	2	10.99	1599	1	1457	1470	

total 16 peptides

tr|A0A665WXF0|A0A665WXF0_ECHNA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	1029	1041	
W.LDKNKDPLNDSVVQ.L	N	41.51	1583.8154	-4.2	792.9117	2	15.56	2391	8	594	607	
E.NDKQQSDEKIKKK.D	N	41.47	1587.8580	-0.2	794.9362	2	7.54	1010	2	1073	1085	
T.VKEDDIHPM.N	N	31.40	1082.5066	-0.8	542.2601	2	10.15	1457	1	72	80	
S.VIPEGQF.I	N	30.48	788.4068	-0.7	395.2104	2	12.26	1825	2	731	737	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1619	1627	
L.SKIEDEQSL.G	N	26.50	1047.5084	-0.3	524.7614	2	10.37	1494	1	1094	1102	
Q.GEVDDAVQEAR.N	N	26.15	1187.5417	0.3	594.7783	2	10.44	1506	1	1741	1751	
K.SINDVEEF.I	N	23.98	951.4185	-0.5	476.7163	2	12.53	1873	1	322	329	
L.SKIEDEQSLGAQ.L	N	20.57	1303.6255	-0.3	652.8198	2	10.23	1470	1	1094	1105	
K.LHDQH.L	N	17.45	648.2980	0.3	325.1564	2	3.70	484	3	552	556	
E.LKKEQDTSAH.L	N	16.64	1155.5884	0.0	578.8015	2	7.73	1044	1	1771	1780	
N.VKNWPW.M	N	16.17	828.4282	-1.1	415.2209	2	12.79	1919	1	826	831	
N.FTNEKLQQF.F	N	16.00	1153.5768	0.0	577.7957	2	11.46	1682	1	480	488	
A.EWKQKYEEGQAELE.G	N	15.02	1765.8158	-1.1	883.9142	2	10.99	1599	1	1457	1470	

total 15 peptides

tr|A0A7N8X0U0|A0A7N8X0U0_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	1018	1030	
W.LDKNKDPLNDSVVQ.L	N	41.51	1583.8154	-4.2	792.9117	2	15.56	2391	8	596	609	

total 17 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.VKEDDIHPM.N	N	31.40	1082.5066	-0.8	542.2601	2	10.15	1457	1	72	80	
S.VIPEGQF.I	N	30.48	788.4068	-0.7	395.2104	2	12.26	1825	2	729	735	
Q.IGETGKT.I	N	30.06	704.3705	-0.2	353.1924	2	8.67	1226	1	1507	1513	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1608	1616	
L.SKIEDEQSL.G	N	26.50	1047.5084	-0.3	524.7614	2	10.37	1494	1	1083	1091	
L.KAKNDENVRQ.L	N	26.18	1200.6211	-0.6	601.3174	2	7.67	1035	1	1251	1260	
Q.GEVDDAVQEAR.N	N	26.15	1187.5417	0.3	594.7783	2	10.44	1506	1	1730	1740	
K.SINDVEEF.I	N	23.98	951.4185	-0.5	476.7163	2	12.53	1873	1	324	331	
L.SKIEDEQSLGAQ.L	N	20.57	1303.6255	-0.3	652.8198	2	10.23	1470	1	1083	1094	
K.LHDQH.L	N	17.45	648.2980	0.3	325.1564	2	3.70	484	3	554	558	
E.LKKEQDTSAH.L	N	16.64	1155.5884	0.0	578.8015	2	7.73	1044	1	1760	1769	
N.VKNWPW.L	N	16.17	828.4282	-1.1	415.2209	2	12.79	1919	1	824	829	
K.FKQKQREEQAEPDGTEVADK.I	N	16.13	2332.1294	-0.3	778.3835	3	9.20	1310	1	366	385	
N.FTNEKLQQF.F	N	16.00	1153.5768	0.0	577.7957	2	11.46	1682	1	482	490	
A.EWKQKYEEGQAELE.G	N	15.02	1765.8158	-1.1	883.9142	2	10.99	1599	1	1446	1459	

total 17 peptides

tr|A0A7N8WLS2|A0A7N8WLS2_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	1026	1038	
W.LDKNKDPLNDSVVQ.L	N	41.51	1583.8154	-4.2	792.9117	2	15.56	2391	8	596	609	
T.VKEDDIHPM.N	N	31.40	1082.5066	-0.8	542.2601	2	10.15	1457	1	72	80	
S.VIPEGQF.I	N	30.48	788.4068	-0.7	395.2104	2	12.26	1825	2	728	734	
Q.IGETGKT.I	N	30.06	704.3705	-0.2	353.1924	2	8.67	1226	1	1515	1521	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1616	1624	
L.SKIEDEQSL.G	N	26.50	1047.5084	-0.3	524.7614	2	10.37	1494	1	1091	1099	
L.KAKNDENVRQ.L	N	26.18	1200.6211	-0.6	601.3174	2	7.67	1035	1	1259	1268	
Q.GEVDDAVQEAR.N	N	26.15	1187.5417	0.3	594.7783	2	10.44	1506	1	1738	1748	
K.SINDVEEF.I	N	23.98	951.4185	-0.5	476.7163	2	12.53	1873	1	324	331	
L.SKIEDEQSLGAQ.L	N	20.57	1303.6255	-0.3	652.8198	2	10.23	1470	1	1091	1102	
K.LHDQH.L	N	17.45	648.2980	0.3	325.1564	2	3.70	484	3	554	558	
E.LKKEQDTSAH.L	N	16.64	1155.5884	0.0	578.8015	2	7.73	1044	1	1768	1777	
N.VKNWPW.L	N	16.17	828.4282	-1.1	415.2209	2	12.79	1919	1	823	828	
K.FKQKQREEQAEPDGTEVADK.I	N	16.13	2332.1294	-0.3	778.3835	3	9.20	1310	1	366	385	
N.FTNEKLQQF.F	N	16.00	1153.5768	0.0	577.7957	2	11.46	1682	1	482	490	
A.EWKQKYEEGQAELE.G	N	15.02	1765.8158	-1.1	883.9142	2	10.99	1599	1	1454	1467	

total 17 peptides

tr|A0A6G0IP12|A0A6G0IP12_LARCR
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.FDMFDTDGGGDISTK.E	Y	62.48	1604.6664	-1.2	803.3395	2	12.80	1921	1	24	38	
E.VDEDGSGTIDFEEF.L	Y	46.93	1558.6311	0.5	780.3232	2	14.02	2127	1	63	76	
N.SDGMLDFDEFLKM.M	Y	35.92	1546.6683	-1.4	774.3404	2	15.29	2343	1	143	155	
D.EDGSGTIDFEEF.L	Y	24.63	1344.5356	0.3	673.2753	2	13.97	2119	1	65	76	
M.KDGDKNSDGMLDFDEFLK.M	Y	18.77	2072.9360	-0.2	691.9858	3	13.50	2041	1	137	154	
E.LMKDGDKNSDGMLDFDEFLK.M	Y	16.70	2317.0605	-0.1	773.3607	3	13.52	2045	1	135	154	

total 6 peptides

tr|A0A1A8Q0J1|A0A1A8Q0J1_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.FDMFDTDGGGDISTK.E	Y	62.48	1604.6664	-1.2	803.3395	2	12.80	1921	1	25	39	
E.VDEDGSGTIDFEEF.L	Y	46.93	1558.6311	0.5	780.3232	2	14.02	2127	1	64	77	
N.SDGMLDFDEFLKM.M	Y	35.92	1546.6683	-1.4	774.3404	2	15.29	2343	1	144	156	
D.EDGSGTIDFEEF.L	Y	24.63	1344.5356	0.3	673.2753	2	13.97	2119	1	66	77	

total 6 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.KDGDKNSDGMLDFDEFLK.M	Y	18.77	2072.9360	-0.2	691.9858	3	13.50	2041	1	138	155	
E.LMKDGDKNSDGMLDFDEFLK.M	Y	16.70	2317.0605	-0.1	773.3607	3	13.52	2045	1	136	155	

total 6 peptides

tr|A0A3P8SK70|A0A3P8SK70_AMPPE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	1027	1039	
W.LDKNKDPLNDSVVQ.L	N	41.51	1583.8154	-4.2	792.9117	2	15.56	2391	8	596	609	
S.VIPEGQF.I	N	30.48	788.4068	-0.7	395.2104	2	12.26	1825	2	729	735	
Q.IGETGKT.I	N	30.06	704.3705	-0.2	353.1924	2	8.67	1226	1	1516	1522	
E.YKKEGIEWEFIDF.G	N	29.33	1702.8242	-0.4	852.4191	2	14.27	2169	1	503	515	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1617	1625	
L.SKIEDEQSL.G	N	26.50	1047.5084	-0.3	524.7614	2	10.37	1494	1	1092	1100	
Q.GEVDDAVQEAR.N	N	26.15	1187.5417	0.3	594.7783	2	10.44	1506	1	1739	1749	
K.SINDVEEF.I	N	23.98	951.4185	-0.5	476.7163	2	12.53	1873	1	324	331	
L.SKIEDEQSLGAQ.L	N	20.57	1303.6255	-0.3	652.8198	2	10.23	1470	1	1092	1103	
K.LHDQH.L	N	17.45	648.2980	0.3	325.1564	2	3.70	484	3	554	558	
E.LKKEQDTSAH.L	N	16.64	1155.5884	0.0	578.8015	2	7.73	1044	1	1769	1778	
N.VKNWPW.L	N	16.17	828.4282	-1.1	415.2209	2	12.79	1919	1	824	829	
K.FKQKQREEQAEPDGTEVADK.I	N	16.13	2332.1294	-0.3	778.3835	3	9.20	1310	1	366	385	
N.FTNEKLQQF.F	N	16.00	1153.5768	0.0	577.7957	2	11.46	1682	1	482	490	
A.EWKQKYEEGQAELE.G	N	15.02	1765.8158	-1.1	883.9142	2	10.99	1599	1	1455	1468	

total 16 peptides

tr|A0A3P8SLP0|A0A3P8SLP0_AMPPE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	1031	1043	
W.LDKNKDPLNDSVVQ.L	N	41.51	1583.8154	-4.2	792.9117	2	15.56	2391	8	596	609	
S.VIPEGQF.I	N	30.48	788.4068	-0.7	395.2104	2	12.26	1825	2	733	739	
Q.IGETGKT.I	N	30.06	704.3705	-0.2	353.1924	2	8.67	1226	1	1520	1526	
E.YKKEGIEWEFIDF.G	N	29.33	1702.8242	-0.4	852.4191	2	14.27	2169	1	503	515	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1621	1629	
L.SKIEDEQSL.G	N	26.50	1047.5084	-0.3	524.7614	2	10.37	1494	1	1096	1104	
Q.GEVDDAVQEAR.N	N	26.15	1187.5417	0.3	594.7783	2	10.44	1506	1	1743	1753	
K.SINDVEEF.I	N	23.98	951.4185	-0.5	476.7163	2	12.53	1873	1	324	331	
L.SKIEDEQSLGAQ.L	N	20.57	1303.6255	-0.3	652.8198	2	10.23	1470	1	1096	1107	
K.LHDQH.L	N	17.45	648.2980	0.3	325.1564	2	3.70	484	3	554	558	
E.LKKEQDTSAH.L	N	16.64	1155.5884	0.0	578.8015	2	7.73	1044	1	1773	1782	
N.VKNWPW.L	N	16.17	828.4282	-1.1	415.2209	2	12.79	1919	1	828	833	
K.FKQKQREEQAEPDGTEVADK.I	N	16.13	2332.1294	-0.3	778.3835	3	9.20	1310	1	366	385	
N.FTNEKLQQF.F	N	16.00	1153.5768	0.0	577.7957	2	11.46	1682	1	482	490	
A.EWKQKYEEGQAELE.G	N	15.02	1765.8158	-1.1	883.9142	2	10.99	1599	1	1459	1472	

total 16 peptides

tr|A0A3Q3WZY2|A0A3Q3WZY2_MOLML
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	1001	1013	
W.LDKNKDPLNDSVVQ.L	N	41.51	1583.8154	-4.2	792.9117	2	15.56	2391	8	596	609	
T.VKEDDIHPM.N	N	31.40	1082.5066	-0.8	542.2601	2	10.15	1457	1	72	80	
S.VIPEGQF.I	N	30.48	788.4068	-0.7	395.2104	2	12.26	1825	2	730	736	
E.YKKEGIEWEFIDF.G	N	29.33	1702.8242	-0.4	852.4191	2	14.27	2169	1	503	515	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1473	1481	
L.SKIEDEQSL.G	N	26.50	1047.5084	-0.3	524.7614	2	10.37	1494	1	1066	1074	
K.SINDVEEF.D	N	23.98	951.4185	-0.5	476.7163	2	12.53	1873	1	324	331	

total 15 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SKIEDEQSLGAQ.L	N	20.57	1303.6255	-0.3	652.8198	2	10.23	1470	1	1066	1077	
K.LHDQH.L	N	17.45	648.2980	0.3	325.1564	2	3.70	484	3	554	558	
E.LKKEQDTSAH.L	N	16.64	1155.5884	0.0	578.8015	2	7.73	1044	1	1625	1634	
N.VKNWPW.M	N	16.17	828.4282	-1.1	415.2209	2	12.79	1919	1	825	830	
K.FKQKQREEQAEPDGTEVADK.I	N	16.13	2332.1294	-0.3	778.3835	3	9.20	1310	1	366	385	
N.FTNEKLQQF.F	N	16.00	1153.5768	0.0	577.7957	2	11.46	1682	1	482	490	
A.EWKQKYEEGQAELE.G	N	15.02	1765.8158	-1.1	883.9142	2	10.99	1599	1	1311	1324	

total 15 peptides

tr|A0A6P6KAZ0|A0A6P6KAZ0_CARAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	1027	1039	
W.LDKNKDPLNDSVVQ.L	N	41.51	1583.8154	-4.2	792.9117	2	15.56	2391	8	594	607	
L.GFTADEKIGIY.K	N	39.36	1212.6027	-0.6	607.3082	2	12.49	1867	1	340	350	
S.VIPEGQF.I	N	30.48	788.4068	-0.7	395.2104	2	12.26	1825	2	729	735	
Q.LGETGKT.I	N	30.06	704.3705	-0.2	353.1924	2	8.67	1226	1	1516	1522	
E.YKKEGIEWEFIDF.G	N	29.33	1702.8242	-0.4	852.4191	2	14.27	2169	1	501	513	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1617	1625	
K.SINDVEEF.V	N	23.98	951.4185	-0.5	476.7163	2	12.53	1873	1	322	329	
E.LKKEQDTSAH.L	N	16.64	1155.5884	0.0	578.8015	2	7.73	1044	1	1769	1778	
K.FKQKQREEQAEPDGTEVADK.I	N	16.13	2332.1294	-0.3	778.3835	3	9.20	1310	1	364	383	
N.FTNEKLQQF.F	N	16.00	1153.5768	0.0	577.7957	2	11.46	1682	1	480	488	

total 11 peptides

tr|A0A3Q3EJE1|A0A3Q3EJE1_9LABR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	1019	1031	
E.NDKQQSDEKIKKK.D	N	41.47	1587.8580	-0.2	794.9362	2	7.54	1010	2	1063	1075	
P.MNPPKYDKIEDM.A	N	39.50	1479.6737	-0.8	740.8436	2	11.36	1664	1	79	90	
S.VIPEGQF.I	N	30.48	788.4068	-0.7	395.2104	2	12.26	1825	2	721	727	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1609	1617	
M.NPPKYDKIEDM.A	N	26.69	1348.6333	-0.3	675.3237	2	10.87	1577	1	80	90	
L.SKIEDEQSL.G	N	26.50	1047.5084	-0.3	524.7614	2	10.37	1494	1	1084	1092	
L.SKIEDEQSLGAQ.L	N	20.57	1303.6255	-0.3	652.8198	2	10.23	1470	1	1084	1095	
E.LKKEQDTSAH.L	N	16.64	1155.5884	0.0	578.8015	2	7.73	1044	1	1761	1770	
N.FTNEKLQQF.F	N	16.00	1153.5768	0.0	577.7957	2	11.46	1682	1	476	484	
A.EWKQKYEEGQAELE.G	N	15.02	1765.8158	-1.1	883.9142	2	10.99	1599	1	1447	1460	

total 11 peptides

tr|A0A6P8GH29|A0A6P8GH29_CLUHA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	1026	1038	
E.NDKQQSDEKLKKK.D	N	41.47	1587.8580	-0.2	794.9362	2	7.54	1010	2	1070	1082	
P.MNPPKYDKIEDM.A	N	39.50	1479.6737	-0.8	740.8436	2	11.36	1664	1	80	91	
S.VIPEGQF.I	N	30.48	788.4068	-0.7	395.2104	2	12.26	1825	2	728	734	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1616	1624	
M.NPPKYDKIEDM.A	N	26.69	1348.6333	-0.3	675.3237	2	10.87	1577	1	81	91	
L.SKIEDEQSL.G	N	26.50	1047.5084	-0.3	524.7614	2	10.37	1494	1	1091	1099	
L.SKIEDEQSLGAQ.L	N	20.57	1303.6255	-0.3	652.8198	2	10.23	1470	1	1091	1102	
E.LKKEQDTSAH.L	N	16.64	1155.5884	0.0	578.8015	2	7.73	1044	1	1768	1777	
N.FTNEKLQQF.F	N	16.00	1153.5768	0.0	577.7957	2	11.46	1682	1	481	489	
A.EWKQKYEEGQAELE.G	N	15.02	1765.8158	-1.1	883.9142	2	10.99	1599	1	1454	1467	

total 11 peptides

tr|A0A7N8XS20|A0A7N8XS20_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	1030	1042	
S.VIPEGQF.I	N	30.48	788.4068	-0.7	395.2104	2	12.26	1825	2	732	738	
Q.IGETGKT.I	N	30.06	704.3705	-0.2	353.1924	2	8.67	1226	1	1519	1525	
E.YKKEGIEWEFIDF.G	N	29.33	1702.8242	-0.4	852.4191	2	14.27	2169	1	503	515	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1620	1628	
L.SKIEDEQSL.G	N	26.50	1047.5084	-0.3	524.7614	2	10.37	1494	1	1095	1103	
L.KAKNDENVRQ.V	N	26.18	1200.6211	-0.6	601.3174	2	7.67	1035	1	1263	1272	
Q.GEVDDAVQEAR.N	N	26.15	1187.5417	0.3	594.7783	2	10.44	1506	1	1742	1752	
K.SINDVEEF.I	N	23.98	951.4185	-0.5	476.7163	2	12.53	1873	1	324	331	
L.SKIEDEQSLGAQ.L	N	20.57	1303.6255	-0.3	652.8198	2	10.23	1470	1	1095	1106	
K.LHDQH.L	N	17.45	648.2980	0.3	325.1564	2	3.70	484	3	554	558	
E.LKKEQDTSAH.L	N	16.64	1155.5884	0.0	578.8015	2	7.73	1044	1	1772	1781	
N.VKNWPW.L	N	16.17	828.4282	-1.1	415.2209	2	12.79	1919	1	827	832	
K.FKQKQREEQAEPDGTEVADK.I	N	16.13	2332.1294	-0.3	778.3835	3	9.20	1310	1	366	385	
N.FTNEKLQQF.F	N	16.00	1153.5768	0.0	577.7957	2	11.46	1682	1	482	490	
A.EWKQKYEEGQAELE.G	N	15.02	1765.8158	-1.1	883.9142	2	10.99	1599	1	1458	1471	

total 16 peptides

tr|A0A6P8FM41|A0A6P8FM41_CLUHA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	1030	1042	
W.LDKNKDPLNDSVVQ.L	N	41.51	1583.8154	-4.2	792.9117	2	15.56	2391	8	598	611	
P.MNPPKYDKIEDM.A	N	39.50	1479.6737	-0.8	740.8436	2	11.36	1664	1	82	93	
T.VKEDDIHPM.N	N	31.40	1082.5066	-0.8	542.2601	2	10.15	1457	1	74	82	
Q.LGETGKT.I	N	30.06	704.3705	-0.2	353.1924	2	8.67	1226	1	1519	1525	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1620	1628	
M.NPPKYDKIEDM.A	N	26.69	1348.6333	-0.3	675.3237	2	10.87	1577	1	83	93	
E.LKKEQDTSAH.L	N	16.64	1155.5884	0.0	578.8015	2	7.73	1044	1	1772	1781	
N.FTNEKLQQF.F	N	16.00	1153.5768	0.0	577.7957	2	11.46	1682	1	484	492	

total 9 peptides

tr|A0A6P8G2F8|A0A6P8G2F8_CLUHA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	948	960	
W.LDKNKDPLNDSVVQ.L	N	41.51	1583.8154	-4.2	792.9117	2	15.56	2391	8	519	532	
MNPPKYDKIEDM.A	N	39.50	1479.6737	-0.8	740.8436	2	11.36	1664	1	1	12	
S.VIPEGQF.I	N	30.48	788.4068	-0.7	395.2104	2	12.26	1825	2	650	656	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1538	1546	
M.NPPKYDKIEDM.A	N	26.69	1348.6333	-0.3	675.3237	2	10.87	1577	1	2	12	
L.SKIEDEQSL.G	N	26.50	1047.5084	-0.3	524.7614	2	10.37	1494	1	1013	1021	
L.SKIEDEQSLGAQ.L	N	20.57	1303.6255	-0.3	652.8198	2	10.23	1470	1	1013	1024	
N.FTNEKLQQF.F	N	16.00	1153.5768	0.0	577.7957	2	11.46	1682	1	405	413	

total 9 peptides

tr|A0A6P8G1S8|A0A6P8G1S8_CLUHA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	949	961	
W.LDKNKDPLNDSVVQ.L	N	41.51	1583.8154	-4.2	792.9117	2	15.56	2391	8	520	533	
MNPPKYDKIEDM.A	N	39.50	1479.6737	-0.8	740.8436	2	11.36	1664	1	1	12	
S.VIPEGQF.I	N	30.48	788.4068	-0.7	395.2104	2	12.26	1825	2	651	657	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1539	1547	

total 9 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.NPPKYDKIEDM.A	N	26.69	1348.6333	-0.3	675.3237	2	10.87	1577	1	2	12	
L.SKIEDEQSL.G	N	26.50	1047.5084	-0.3	524.7614	2	10.37	1494	1	1014	1022	
L.SKIEDEQSLGAQ.L	N	20.57	1303.6255	-0.3	652.8198	2	10.23	1470	1	1014	1025	
N.FTNEKLQQF.F	N	16.00	1153.5768	0.0	577.7957	2	11.46	1682	1	406	414	

total 9 peptides

tr|A0A2U9CMP6|A0A2U9CMP6_SCOMX
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.VIDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
Y.VIDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	50	63	
Y.VIDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	50	65	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	
Y.VIDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	50	67	

total 5 peptides

tr|A0A6A4RT91|A0A6A4RT91_SCOMX
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.VIDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	214	224	
Y.VIDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	214	227	
Y.VIDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	214	229	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	223	231	
Y.VIDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	214	231	

total 5 peptides

tr|A0A3B3XMC4|A0A3B3XMC4_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.VLDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
S.VLDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	50	63	
S.VLDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	50	65	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	
S.VLDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	50	67	

total 5 peptides

tr|A0A3B5LQ20|A0A3B5LQ20_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.VLDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
T.VLDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	50	63	
T.VLDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	50	65	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	
T.VLDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	50	67	

total 5 peptides

tr|A0A3B3Z292|A0A3B3Z292_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.VLDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	48	58	
S.VLDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	48	61	
S.VLDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	48	63	

total 5 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	57	65	
S.VLDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	48	65	

total 5 peptides

tr|A0A671XKN2|A0A671XKN2_SPAAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.VIDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	48	58	
A.VIDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	48	61	
A.VIDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	48	63	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	57	65	
A.VIDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	48	65	

total 5 peptides

tr|A0A672Z6Y0|A0A672Z6Y0_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.VIDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
A.VIDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	50	63	
A.VIDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	50	65	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	
A.VIDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	50	67	

total 5 peptides

tr|D0VB96|D0VB96_SPAAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.VIDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	49	59	
A.VIDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	49	62	
A.VIDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	49	64	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	58	66	
A.VIDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	49	66	

total 5 peptides

tr|A0A087Y091|A0A087Y091_POEFO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.VLDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
T.VLDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	50	63	
T.VLDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	50	65	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	
T.VLDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	50	67	

total 5 peptides

tr|A0A5N5MFD7|A0A5N5MFD7_PANHP

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VLDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
K.VLDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	50	63	
K.VLDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	50	65	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	
K.VLDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	50	67	

total 5 peptides

tr|A0A087Y0W0|A0A087Y0W0_POEFO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.VLDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
T.VLDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	50	63	
T.VLDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	50	65	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	
T.VLDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	50	67	

total 5 peptides

tr|A0A668AEA1|A0A668AEA1_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.VIDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
Y.VIDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	50	63	
Y.VIDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	50	65	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	
Y.VIDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	50	67	

total 5 peptides

tr|C6GKU4|C6GKU4_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VIDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
K.VIDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	50	63	
K.VIDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	50	65	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	
K.VIDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	50	67	

total 5 peptides

tr|A0A087Y5E9|A0A087Y5E9_POEFO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.VIDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
A.VIDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	50	63	
A.VIDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	50	65	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	
A.VIDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	50	67	

total 5 peptides

tr|A0A1A8GBU0|A0A1A8GBU0_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.VIDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
A.VIDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	50	63	
A.VIDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	50	65	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	
A.VIDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	50	67	

total 5 peptides

tr|E0WD96|E0WD96_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VIDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
K.VIDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	50	63	
K.VIDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	50	65	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	
K.VIDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	50	67	

total 5 peptides

tr|A0A1A7WES6|A0A1A7WES6_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.VIDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
A.VIDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	50	63	
A.VIDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	50	65	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	
A.VIDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	50	67	

total 5 peptides

tr|A0A1A8EAV3|A0A1A8EAV3_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.VIDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
A.VIDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	50	63	
A.VIDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	50	65	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	
A.VIDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	50	67	

total 5 peptides

tr|A0A1A8PM62|A0A1A8PM62_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.VIDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
A.VIDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	50	63	
A.VIDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	50	65	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	
A.VIDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	50	67	

total 5 peptides

tr|A0A3B3TQ55|A0A3B3TQ55_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.VIDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
A.VIDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	50	63	
A.VIDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	50	65	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	
A.VIDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	50	67	

total 5 peptides

tr|A0A1A8JGR3|A0A1A8JGR3_NOTKU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.VIDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
A.VIDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	50	63	

total 5 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.VIDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	50	65	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	
A.VIDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	50	67	

total 5 peptides

tr|A0A3B3XME4|A0A3B3XME4_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.VLDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
S.VLDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	50	63	
S.VLDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	50	65	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	
S.VLDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	50	67	

total 5 peptides

tr|A0A668AEA6|A0A668AEA6_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.VIDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
Y.VIDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	50	63	
Y.VIDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	50	65	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	
Y.VIDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	50	67	

total 5 peptides

tr|A0A5N5MKE2|A0A5N5MKE2_PANHP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.VIDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	60	70	
Y.VIDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	60	73	
Y.VIDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	60	75	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	69	77	
Y.VIDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	60	77	

total 5 peptides

tr|A0A668ANA4|A0A668ANA4_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.VIDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
Y.VIDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	50	63	
Y.VIDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	50	65	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	
Y.VIDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	50	67	

total 5 peptides

tr|A0A3B3UHS0|A0A3B3UHS0_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.VLDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
T.VLDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	50	63	
T.VLDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	50	65	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	

total 5 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.VLDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	50	67	

total 5 peptides

tr|A0A556TIT9|A0A556TIT9_BAGYA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VIDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
F.VIDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	50	63	
F.VIDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	50	65	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	
F.VIDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	50	67	

total 5 peptides

tr|A0A7J6BCR9|A0A7J6BCR9_AMEME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VLDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
K.VLDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	50	63	
K.VLDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	50	65	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	
K.VLDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	50	67	

total 5 peptides

tr|A0A315V786|A0A315V786_GAMAF

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.VLDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	245	255	
T.VLDQDKSGFIEEEE.L	Y	43.10	1636.7467	-0.4	819.3803	2	11.51	1691	1	245	258	
T.VLDQDKSGFIEEEELK.L	Y	33.74	1877.9258	-1.1	939.9692	2	11.62	1710	2	245	260	
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	254	262	
T.VLDQDKSGFIEEEELKLF.L	Y	28.04	2138.0781	-1.0	1070.0453	2	13.82	2095	1	245	262	

total 5 peptides

tr|A0A1S3QJI3|A0A1S3QJI3_SALSA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	1031	1043	
E.MNPPKYDKIEDM.A	N	39.50	1479.6737	-0.8	740.8436	2	11.36	1664	1	85	96	
S.VIPEGQF.M	N	30.48	788.4068	-0.7	395.2104	2	12.26	1825	2	733	739	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1621	1629	
M.NPPKYDKIEDM.A	N	26.69	1348.6333	-0.3	675.3237	2	10.87	1577	1	86	96	
L.SKIEDEQSL.G	N	26.50	1047.5084	-0.3	524.7614	2	10.37	1494	1	1096	1104	
L.SKIEDEQSLGAQ.L	N	20.57	1303.6255	-0.3	652.8198	2	10.23	1470	1	1096	1107	
K.FKQKQREEQAEPDGTEVADK.I	N	16.13	2332.1294	-0.3	778.3835	3	9.20	1310	1	371	390	
N.FTNEKLQQF.F	N	16.00	1153.5768	0.0	577.7957	2	11.46	1682	1	487	495	
A.EWKQKYEEGQAELE.G	N	15.02	1765.8158	-1.1	883.9142	2	10.99	1599	1	1459	1472	

total 10 peptides

tr|A0A6J2PWE3|A0A6J2PWE3_COTGO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	1023	1035	

total 9 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.MNPPKYDKIEDM.A	N	39.50	1479.6737	-0.8	740.8436	2	11.36	1664	1	81	92	
G.VIPEGQF.I	N	30.48	788.4068	-0.7	395.2104	2	12.26	1825	2	725	731	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1613	1621	
M.NPPKYDKIEDM.A	N	26.69	1348.6333	-0.3	675.3237	2	10.87	1577	1	82	92	
L.SKIEDEQSL.G	N	26.50	1047.5084	-0.3	524.7614	2	10.37	1494	1	1088	1096	
L.SKIEDEQSLGAQ.L	N	20.57	1303.6255	-0.3	652.8198	2	10.23	1470	1	1088	1099	
K.LHDQH.L	N	17.45	648.2980	0.3	325.1564	2	3.70	484	3	550	554	
N.FTNEKLQQF.F	N	16.00	1153.5768	0.0	577.7957	2	11.46	1682	1	478	486	

total 9 peptides

tr|A0A3Q3WCX3|A0A3Q3WCX3_MOLML
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.FSVDEEFPDLSQH.N	Y	58.89	1548.6732	0.9	775.3446	2	13.11	1976	1	13	25	
S.VDEEFPDLSQH.N	Y	25.80	1314.5728	-0.7	658.2932	2	12.03	1784	1	15	25	
T.GVDNPGHPFIM.T	N	23.48	1182.5492	-0.7	592.2814	2	12.43	1855	1	59	69	
D.NLKGGDDLDPNY.V	N	18.44	1319.5994	-0.9	660.8063	2	11.14	1626	1	113	124	
L.LDPIISDR.H	N	18.39	927.5025	-0.8	464.7581	2	11.37	1667	1	88	95	
T.GVDNPGHPF.I	N	17.65	938.4246	-0.1	470.2195	2	10.83	1571	1	59	67	
L.VVDGVKL.M	N	15.93	728.4432	0.0	365.2289	2	11.27	1649	1	352	358	
F.DISNADRL.G	N	15.49	902.4457	-0.7	452.2298	2	10.97	1595	1	334	341	

total 8 peptides

tr|A0A0S7H3J1|A0A0S7H3J1_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.FSVDEEFPDLSQH.N	Y	58.89	1548.6732	0.9	775.3446	2	13.11	1976	1	15	27	
S.VDEEFPDLSQH.N	Y	25.80	1314.5728	-0.7	658.2932	2	12.03	1784	1	17	27	
T.GVDNPGHPFIM.T	N	23.48	1182.5492	-0.7	592.2814	2	12.43	1855	1	61	71	
E.NLKGGDDLDPNY.V	N	18.44	1319.5994	-0.9	660.8063	2	11.14	1626	1	115	126	
L.LDPIISDR.H	N	18.39	927.5025	-0.8	464.7581	2	11.37	1667	1	90	97	
T.GVDNPGHPF.I	N	17.65	938.4246	-0.1	470.2195	2	10.83	1571	1	61	69	
L.VVDGVKL.M	N	15.93	728.4432	0.0	365.2289	2	11.27	1649	1	354	360	
F.DISNADRL.G	N	15.49	902.4457	-0.7	452.2298	2	10.97	1595	1	336	343	

total 8 peptides

tr|A0A3B3XY74|A0A3B3XY74_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.FSVDEEFPDLSQH.N	Y	58.89	1548.6732	0.9	775.3446	2	13.11	1976	1	15	27	
S.VDEEFPDLSQH.N	Y	25.80	1314.5728	-0.7	658.2932	2	12.03	1784	1	17	27	
T.GVDNPGHPFIM.T	N	23.48	1182.5492	-0.7	592.2814	2	12.43	1855	1	61	71	
E.NLKGGDDLDPNY.V	N	18.44	1319.5994	-0.9	660.8063	2	11.14	1626	1	115	126	
L.LDPIISDR.H	N	18.39	927.5025	-0.8	464.7581	2	11.37	1667	1	90	97	
T.GVDNPGHPF.I	N	17.65	938.4246	-0.1	470.2195	2	10.83	1571	1	61	69	
L.VVDGVKL.M	N	15.93	728.4432	0.0	365.2289	2	11.27	1649	1	354	360	
F.DISNADRL.G	N	15.49	902.4457	-0.7	452.2298	2	10.97	1595	1	336	343	

total 8 peptides

tr|A0A3B3W291|A0A3B3W291_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.FSVDEEFPDLSQH.N	Y	58.89	1548.6732	0.9	775.3446	2	13.11	1976	1	15	27	
S.VDEEFPDLSQH.N	Y	25.80	1314.5728	-0.7	658.2932	2	12.03	1784	1	17	27	
T.GVDNPGHPFIM.T	N	23.48	1182.5492	-0.7	592.2814	2	12.43	1855	1	61	71	

total 8 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.NLKGGDDLDPNY.V	N	18.44	1319.5994	-0.9	660.8063	2	11.14	1626	1	115	126	
L.LDPIISDR.H	N	18.39	927.5025	-0.8	464.7581	2	11.37	1667	1	90	97	
T.GVDNPGHPF.I	N	17.65	938.4246	-0.1	470.2195	2	10.83	1571	1	61	69	
L.VVDGVKL.M	N	15.93	728.4432	0.0	365.2289	2	11.27	1649	1	354	360	
F.DISNADRL.G	N	15.49	902.4457	-0.7	452.2298	2	10.97	1595	1	336	343	

total 8 peptides

tr|A0A087YG46|A0A087YG46_POEFO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.FSVDEEFPDLSQH.N	Y	58.89	1548.6732	0.9	775.3446	2	13.11	1976	1	15	27	
S.VDEEFPDLSQH.N	Y	25.80	1314.5728	-0.7	658.2932	2	12.03	1784	1	17	27	
T.GVDNPGHPFIM.T	N	23.48	1182.5492	-0.7	592.2814	2	12.43	1855	1	61	71	
E.NLKGGDDLDPNY.V	N	18.44	1319.5994	-0.9	660.8063	2	11.14	1626	1	115	126	
L.LDPIISDR.H	N	18.39	927.5025	-0.8	464.7581	2	11.37	1667	1	90	97	
T.GVDNPGHPF.I	N	17.65	938.4246	-0.1	470.2195	2	10.83	1571	1	61	69	
L.VVDGVKL.M	N	15.93	728.4432	0.0	365.2289	2	11.27	1649	1	355	361	
F.DISNADRL.G	N	15.49	902.4457	-0.7	452.2298	2	10.97	1595	1	337	344	

total 8 peptides

tr|A0A3Q2D194|A0A3Q2D194_CYPVA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.GSSEVDQVQLVVDGVKLM.V	N	58.08	1901.9768	-0.1	951.9955	2	14.47	2202	1	344	361	
F.SVDEEFPDLSKH.N	Y	25.18	1401.6411	-26.7	701.8091	2	12.20	1814	1	16	27	
T.GVDNPGHPFIM.T	N	23.48	1182.5492	-0.7	592.2814	2	12.43	1855	1	61	71	
E.NLKGGDDLDPNY.V	N	18.44	1319.5994	-0.9	660.8063	2	11.14	1626	1	115	126	
T.GVDNPGHPF.I	N	17.65	938.4246	-0.1	470.2195	2	10.83	1571	1	61	69	
L.VVDGVKL.M	N	15.93	728.4432	0.0	365.2289	2	11.27	1649	1	354	360	
F.DISNADRL.G	N	15.49	902.4457	-0.7	452.2298	2	10.97	1595	1	336	343	

total 7 peptides

tr|A0A3Q2D1K7|A0A3Q2D1K7_CYPVA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.GSSEVDQVQLVVDGVKLM.V	N	58.08	1901.9768	-0.1	951.9955	2	14.47	2202	1	313	330	
F.SVDEEFPDLSKH.N	Y	25.18	1401.6411	-26.7	701.8091	2	12.20	1814	1	16	27	
T.GVDNPGHPFIM.T	N	23.48	1182.5492	-0.7	592.2814	2	12.43	1855	1	61	71	
E.NLKGGDDLDPNY.V	N	18.44	1319.5994	-0.9	660.8063	2	11.14	1626	1	115	126	
T.GVDNPGHPF.I	N	17.65	938.4246	-0.1	470.2195	2	10.83	1571	1	61	69	
L.VVDGVKL.M	N	15.93	728.4432	0.0	365.2289	2	11.27	1649	1	323	329	
F.DISNADRL.G	N	15.49	902.4457	-0.7	452.2298	2	10.97	1595	1	305	312	

total 7 peptides

tr|C7ASM1|C7ASM1_SINCH

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.GSSEVDQVQLVVDGVKLM.V	N	58.08	1901.9768	-0.1	951.9955	2	14.47	2202	1	343	360	
T.GVDNPGHPFIM.T	N	23.48	1182.5492	-0.7	592.2814	2	12.43	1855	1	60	70	
K.VEEEFPDLSKH.N	Y	18.63	1328.6248	-0.4	665.3194	2	11.41	1673	1	16	26	
E.NLKGGDDLDPNY.V	N	18.44	1319.5994	-0.9	660.8063	2	11.14	1626	1	114	125	
L.LDPIISDR.H	N	18.39	927.5025	-0.8	464.7581	2	11.37	1667	1	89	96	
T.GVDNPGHPF.I	N	17.65	938.4246	-0.1	470.2195	2	10.83	1571	1	60	68	
L.VVDGVKL.M	N	15.93	728.4432	0.0	365.2289	2	11.27	1649	1	353	359	
L.DISNADRL.G	N	15.49	902.4457	-0.7	452.2298	2	10.97	1595	1	335	342	

total 8 peptides

tr|M4AU26|M4AU26_XIPMA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.GSSEVDQVQLVVDGVKLM.V	N	58.08	1901.9768	-0.1	951.9955	2	14.47	2202	1	343	360	
T.GVDNPGHPFIM.T	N	23.48	1182.5492	-0.7	592.2814	2	12.43	1855	1	60	70	
K.VEEEFPDLSKH.N	Y	18.63	1328.6248	-0.4	665.3194	2	11.41	1673	1	16	26	
E.NLKGGDDLDPNY.V	N	18.44	1319.5994	-0.9	660.8063	2	11.14	1626	1	114	125	
L.LDPIISDR.H	N	18.39	927.5025	-0.8	464.7581	2	11.37	1667	1	89	96	
T.GVDNPGHPF.I	N	17.65	938.4246	-0.1	470.2195	2	10.83	1571	1	60	68	
L.VVDGVKL.M	N	15.93	728.4432	0.0	365.2289	2	11.27	1649	1	353	359	
F.DISNADRL.G	N	15.49	902.4457	-0.7	452.2298	2	10.97	1595	1	335	342	

total 8 peptides

tr|A0A3B5M9I5|A0A3B5M9I5_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.GSSEVDQVQLVVDGVKLM.V	N	58.08	1901.9768	-0.1	951.9955	2	14.47	2202	1	343	360	
T.GVDNPGHPFIM.T	N	23.48	1182.5492	-0.7	592.2814	2	12.43	1855	1	60	70	
K.VEEEFPDLSKH.N	Y	18.63	1328.6248	-0.4	665.3194	2	11.41	1673	1	16	26	
E.NLKGGDDLDPNY.V	N	18.44	1319.5994	-0.9	660.8063	2	11.14	1626	1	114	125	
L.LDPIISDR.H	N	18.39	927.5025	-0.8	464.7581	2	11.37	1667	1	89	96	
T.GVDNPGHPF.I	N	17.65	938.4246	-0.1	470.2195	2	10.83	1571	1	60	68	
L.VVDGVKL.M	N	15.93	728.4432	0.0	365.2289	2	11.27	1649	1	353	359	
F.DISNADRL.G	N	15.49	902.4457	-0.7	452.2298	2	10.97	1595	1	335	342	

total 8 peptides

tr|A0A6J2Q2L7|A0A6J2Q2L7_COTGO
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	1030	1042	
S.VIPEGQF.I	N	30.48	788.4068	-0.7	395.2104	2	12.26	1825	2	732	738	
E.YKKEGIEWEFIDF.G	N	29.33	1702.8242	-0.4	852.4191	2	14.27	2169	1	503	515	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1620	1628	
R.NPPKYDKIEDM.A	N	26.69	1348.6333	-0.3	675.3237	2	10.87	1577	1	81	91	
L.SKIEDEQSL.S	N	26.50	1047.5084	-0.3	524.7614	2	10.37	1494	1	1095	1103	
K.LHDQH.L	N	17.45	648.2980	0.3	325.1564	2	3.70	484	3	554	558	
N.VKNWPW.L	N	16.17	828.4282	-1.1	415.2209	2	12.79	1919	1	827	832	
N.FTNEKLQQF.F	N	16.00	1153.5768	0.0	577.7957	2	11.46	1682	1	482	490	

total 9 peptides

tr|A0A6P3WCZ7|A0A6P3WCZ7_CLUHA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	1034	1046	
P.MNPPKYDKIEDM.V	N	39.50	1479.6737	-0.8	740.8436	2	11.36	1664	1	80	91	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1624	1632	
M.NPPKYDKIEDM.V	N	26.69	1348.6333	-0.3	675.3237	2	10.87	1577	1	81	91	
N.VKNWPW.M	N	16.17	828.4282	-1.1	415.2209	2	12.79	1919	1	831	836	
K.FKQKQREEQAEPDGTEVADK.V	N	16.13	2332.1294	-0.3	778.3835	3	9.20	1310	1	366	385	
N.FTNEKLQQF.F	N	16.00	1153.5768	0.0	577.7957	2	11.46	1682	1	482	490	

total 7 peptides

tr|A0A4W4E3Q5|A0A4W4E3Q5_ELEEL
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	71	83	
E.NDKQQSDEKIKKK.D	N	41.47	1587.8580	-0.2	794.9362	2	7.54	1010	2	115	127	
Q.IGETGKT.I	N	30.06	704.3705	-0.2	353.1924	2	8.67	1226	1	560	566	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	661	669	
E.LKKEQDTSAH.L	N	16.64	1155.5884	0.0	578.8015	2	7.73	1044	1	807	816	
A.EWKQKYEEGQAELE.G	N	15.02	1765.8158	-1.1	883.9142	2	10.99	1599	1	499	512	

total 6 peptides

tr|A0A3B4FY50|A0A3B4FY50_9CICH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	1027	1039	
P.MNPPKYDKIEDM.A	N	39.50	1479.6737	-0.8	740.8436	2	11.36	1664	1	80	91	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1617	1625	
M.NPPKYDKIEDM.A	N	26.69	1348.6333	-0.3	675.3237	2	10.87	1577	1	81	91	
E.LKKEQDTSAH.L	N	16.64	1155.5884	0.0	578.8015	2	7.73	1044	1	1769	1778	
K.FKQKQREEQAEPDGTEVADK.V	N	16.13	2332.1294	-0.3	778.3835	3	9.20	1310	1	366	385	

total 6 peptides

tr|A0A3P9ART7|A0A3P9ART7_9CICH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEQQVDDLEGSLE.Q	N	41.80	1473.6835	-0.6	737.8486	2	12.66	1896	1	1027	1039	
P.MNPPKYDKIEDM.A	N	39.50	1479.6737	-0.8	740.8436	2	11.36	1664	1	80	91	
K.KMEGDLNEM.E	N	28.74	1065.4470	-0.5	533.7305	2	10.99	1598	1	1617	1625	
M.NPPKYDKIEDM.A	N	26.69	1348.6333	-0.3	675.3237	2	10.87	1577	1	81	91	
E.LKKEQDTSAH.L	N	16.64	1155.5884	0.0	578.8015	2	7.73	1044	1	1769	1778	
K.FKQKQREEQAEPDGTEVADK.V	N	16.13	2332.1294	-0.3	778.3835	3	9.20	1310	1	366	385	

total 6 peptides

tr|D2KQG3|D2KQG3_SINCH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VIDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
A.FEVIDQDKSGFIE.E	Y	45.26	1525.7300	-0.7	763.8717	2	12.66	1897	2	48	60	

total 2 peptides

tr|B9VJM3|B9VJM3_SINCH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VIDQDKSGFIE.E	N	52.45	1249.6190	-0.5	625.8165	2	11.38	1669	4	50	60	
A.FEVIDQDKSGFIE.E	Y	45.26	1525.7300	-0.7	763.8717	2	12.66	1897	2	48	60	

total 2 peptides

tr|A0A3Q0QYR9|A0A3Q0QYR9_AMPCI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	20	30	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	21	29	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	21	32	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	20	31	

total 4 peptides

P85280|NDKB_MERME
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	29	39	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	30	38	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	30	41	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	29	40	

total 4 peptides

P85284|NDKB_MERPA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	29	39	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	30	38	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	30	41	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	29	40	

total 4 peptides

P85292|NDKB_MACMG

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	29	39	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	30	38	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	30	41	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	29	40	

total 4 peptides

P85282|NDKB_MERSE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	29	39	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	30	38	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	30	41	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	29	40	

total 4 peptides

P85283|NDKB_MERPO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	29	39	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	30	38	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	30	41	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	29	40	

total 4 peptides

P85287|NDKB_MERAP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	31	41	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	32	40	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	32	43	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	31	42	

total 4 peptides

P85289|NDKB_MERPR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	31	41	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	32	40	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	32	43	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	31	42	

total 4 peptides

P85290|NDKB_MERBI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	31	41	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	32	40	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	32	43	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	31	42	

total 4 peptides

tr|A0A672Y4P6|A0A672Y4P6_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	49	59	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	50	58	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	50	61	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	49	60	

total 4 peptides

tr|A0A2I4CF45|A0A2I4CF45_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	49	59	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	50	58	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	50	61	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	49	60	

total 4 peptides

tr|A0A3Q1K2U7|A0A3Q1K2U7_ANATE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	49	59	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	50	58	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	50	61	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	49	60	

total 4 peptides

tr|A0A1A8C566|A0A1A8C566_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	49	59	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	50	58	

total 4 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	50	61	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	49	60	

total 4 peptides

tr|A0A6P7ISB4|A0A6P7ISB4_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	49	59	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	50	58	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	50	61	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	49	60	

total 4 peptides

tr|A0A3Q4I698|A0A3Q4I698_NEOBR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	49	59	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	50	58	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	50	61	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	49	60	

total 4 peptides

tr|A0A3Q3L2T8|A0A3Q3L2T8_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	49	59	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	50	58	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	50	61	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	49	60	

total 4 peptides

tr|A0A6P7NDJ7|A0A6P7NDJ7_BETSP
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	49	59	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	50	58	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	50	61	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	49	60	

total 4 peptides

tr|A0A3Q3A341|A0A3Q3A341_KRYMA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	49	59	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	50	58	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	50	61	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	49	60	

total 4 peptides

tr|A0A3Q4HQ85|A0A3Q4HQ85_NEOBR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	49	59	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	50	58	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	50	61	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	49	60	

total 4 peptides

tr|A0A3P8Q104|A0A3P8Q104_ASTCA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	51	61	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	52	60	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	52	63	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	51	62	

total 4 peptides

tr|A0A3Q3CUD8|A0A3Q3CUD8_HAPBU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	51	61	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	52	60	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	52	63	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	51	62	

total 4 peptides

tr|A0A3Q4I6B8|A0A3Q4I6B8_NEOBR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	51	61	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	52	60	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	52	63	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	51	62	

total 4 peptides

tr|A0A3Q0QSW6|A0A3Q0QSW6_AMPCI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	49	59	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	50	58	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	50	61	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	49	60	

total 4 peptides

tr|A0A3Q0QYR1|A0A3Q0QYR1_AMPCI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	52	62	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	53	61	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	53	64	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	52	63	

total 4 peptides

tr|A0A3Q3R7S1|A0A3Q3R7S1_MONAL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	52	62	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	53	61	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	53	64	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	52	63	

total 4 peptides

tr|A0A3Q0QXA4|A0A3Q0QXA4_AMPCI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	53	63	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	54	62	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	54	65	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	53	64	

total 4 peptides

tr|M4ADR4|M4ADR4_XIPMA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	62	72	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	63	71	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	63	74	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	62	73	

total 4 peptides

tr|A0A1A8J8K8|A0A1A8J8K8_NOTKU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	62	72	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	63	71	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	63	74	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	62	73	

total 4 peptides

tr|A0A1A7XFD3|A0A1A7XFD3_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	82	92	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	83	91	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	83	94	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	82	93	

total 4 peptides

tr|A0A0S7LYJ8|A0A0S7LYJ8_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.YLDLKDMPFYA.G	Y	45.04	1374.6530	-1.3	688.3329	2	14.23	2163	1	74	84	
Y.LDLKDMPFY.A	Y	30.13	1140.5525	0.0	571.2835	2	14.03	2129	1	75	83	
Y.LDLKDMPFYAGL.C	Y	25.91	1381.6951	0.1	691.8549	2	14.80	2258	1	75	86	
H.YLDLKDMPFYAG.L	Y	18.91	1431.6744	-0.4	716.8442	2	14.10	2141	1	74	85	

total 4 peptides

tr|H3CAK5|H3CAK5_TETNG

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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.SIEDPFDQDDWENWAK.F	Y	43.87	1993.8330	2.3	997.9260	2	14.25	2166	1	198	213	
K.YGKDATNVGDEGGFAPN.I	Y	32.36	1710.7485	-0.8	856.3809	2	11.09	1617	1	107	123	
Q.IVGDDLTVTNPKR.I	Y	20.07	1426.7780	0.0	476.5999	3	10.77	1559	2	222	234	
Q.SIEDPFDQDDWE.N	Y	19.74	1494.5786	-0.3	748.2963	2	14.19	2156	1	198	209	

total 4 peptides

tr|A0A3B3D6F1|A0A3B3D6F1_ORYME
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.SIEDPFDQDDWENWAK.F	Y	43.87	1993.8330	2.3	997.9260	2	14.25	2166	1	248	263	
K.YGKDATNVGDEGGFAPN.I	Y	32.36	1710.7485	-0.8	856.3809	2	11.09	1617	1	157	173	
Q.IVGDDLTVTNPKR.I	Y	20.07	1426.7780	0.0	476.5999	3	10.77	1559	2	272	284	
Q.SIEDPFDQDDWE.N	Y	19.74	1494.5786	-0.3	748.2963	2	14.19	2156	1	248	259	

total 4 peptides

tr|A0A3B3BLA1|A0A3B3BLA1_ORYME
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.SIEDPFDQDDWENWAK.F	Y	43.87	1993.8330	2.3	997.9260	2	14.25	2166	1	291	306	
K.YGKDATNVGDEGGFAPN.I	Y	32.36	1710.7485	-0.8	856.3809	2	11.09	1617	1	200	216	
Q.IVGDDLTVTNPKR.I	Y	20.07	1426.7780	0.0	476.5999	3	10.77	1559	2	315	327	
Q.SIEDPFDQDDWE.N	Y	19.74	1494.5786	-0.3	748.2963	2	14.19	2156	1	291	302	

total 4 peptides

tr|A0A3B4CPC9|A0A3B4CPC9_PYGNA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.SIEDPFDQDDWENWAK.F	Y	43.87	1993.8330	2.3	997.9260	2	14.25	2166	1	291	306	
K.YGKDATNVGDEGGFAPN.I	Y	32.36	1710.7485	-0.8	856.3809	2	11.09	1617	1	200	216	
Q.IVGDDLTVTNPKR.I	Y	20.07	1426.7780	0.0	476.5999	3	10.77	1559	2	315	327	
M.SIEDPFDQDDWE.N	Y	19.74	1494.5786	-0.3	748.2963	2	14.19	2156	1	291	302	

total 4 peptides

tr|A0A6M4C6H3|A0A6M4C6H3_DIOHY
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.SIEDPFDQDDWENWAK.F	Y	43.87	1993.8330	2.3	997.9260	2	14.25	2166	1	291	306	
K.YGKDATNVGDEGGFAPN.I	Y	32.36	1710.7485	-0.8	856.3809	2	11.09	1617	1	200	216	
Q.IVGDDLTVTNPKR.I	Y	20.07	1426.7780	0.0	476.5999	3	10.77	1559	2	315	327	
Q.SIEDPFDQDDWE.N	Y	19.74	1494.5786	-0.3	748.2963	2	14.19	2156	1	291	302	

total 4 peptides

tr|A0A0F8AN77|A0A0F8AN77_LARCR
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.SIEDPFDQDDWENWAK.F	Y	43.87	1993.8330	2.3	997.9260	2	14.25	2166	1	291	306	
K.YGKDATNVGDEGGFAPN.I	Y	32.36	1710.7485	-0.8	856.3809	2	11.09	1617	1	200	216	
Q.IVGDDLTVTNPKR.I	Y	20.07	1426.7780	0.0	476.5999	3	10.77	1559	2	315	327	
Q.SIEDPFDQDDWE.N	Y	19.74	1494.5786	-0.3	748.2963	2	14.19	2156	1	291	302	

total 4 peptides

tr|A0A437CFA6|A0A437CFA6_ORYJA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.SIEDPFDQDDWENWAK.F	Y	43.87	1993.8330	2.3	997.9260	2	14.25	2166	1	390	405	
K.YGKDATNVGDEGGFAPN.I	Y	32.36	1710.7485	-0.8	856.3809	2	11.09	1617	1	299	315	
Q.IVGDDLTVTNPKR.I	Y	20.07	1426.7780	0.0	476.5999	3	10.77	1559	2	414	426	
Q.SIEDPFDQDDWE.N	Y	19.74	1494.5786	-0.3	748.2963	2	14.19	2156	1	390	401	

total 4 peptides

tr|A0A671TWQ7|A0A671TWQ7_SPAAU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.SIEDPFDQDDWENWAK.F	Y	43.87	1993.8330	2.3	997.9260	2	14.25	2166	1	208	223	
K.YGKDATNVGDEGGFAPN.I	Y	32.36	1710.7485	-0.8	856.3809	2	11.09	1617	1	117	133	
Q.IVGDDLTVTNPKR.I	Y	20.07	1426.7780	0.0	476.5999	3	10.77	1559	2	232	244	
Q.SIEDPFDQDDWE.N	Y	19.74	1494.5786	-0.3	748.2963	2	14.19	2156	1	208	219	

total 4 peptides

tr|A0A671TWN1|A0A671TWN1_SPAAU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.SIEDPFDQDDWENWAK.F	Y	43.87	1993.8330	2.3	997.9260	2	14.25	2166	1	219	234	
K.YGKDATNVGDEGGFAPN.I	Y	32.36	1710.7485	-0.8	856.3809	2	11.09	1617	1	128	144	
Q.IVGDDLTVTNPKR.I	Y	20.07	1426.7780	0.0	476.5999	3	10.77	1559	2	243	255	
Q.SIEDPFDQDDWE.N	Y	19.74	1494.5786	-0.3	748.2963	2	14.19	2156	1	219	230	

total 4 peptides

tr|A0A671TZ14|A0A671TZ14_SPAAU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.SIEDPFDQDDWENWAK.F	Y	43.87	1993.8330	2.3	997.9260	2	14.25	2166	1	198	213	
K.YGKDATNVGDEGGFAPN.I	Y	32.36	1710.7485	-0.8	856.3809	2	11.09	1617	1	107	123	
Q.IVGDDLTVTNPKR.I	Y	20.07	1426.7780	0.0	476.5999	3	10.77	1559	2	222	234	
Q.SIEDPFDQDDWE.N	Y	19.74	1494.5786	-0.3	748.2963	2	14.19	2156	1	198	209	

total 4 peptides

tr|F5BZS7|F5BZS7_EPIBR
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.SIEDPFDQDDWENWAK.F	Y	43.87	1993.8330	2.3	997.9260	2	14.25	2166	1	291	306	
K.YGKDATNVGDEGGFAPN.I	Y	32.36	1710.7485	-0.8	856.3809	2	11.09	1617	1	200	216	
Q.IVGDDLTVTNPKR.I	Y	20.07	1426.7780	0.0	476.5999	3	10.77	1559	2	315	327	
Q.SIEDPFDQDDWE.N	Y	19.74	1494.5786	-0.3	748.2963	2	14.19	2156	1	291	302	

total 4 peptides

tr|Q4TBD1|Q4TBD1_TETNG
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.SIEDPFDQDDWENWAK.F	Y	43.87	1993.8330	2.3	997.9260	2	14.25	2166	1	291	306	
K.YGKDATNVGDEGGFAPN.I	Y	32.36	1710.7485	-0.8	856.3809	2	11.09	1617	1	200	216	

total 4 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.IVGDDLTVTNPKR.I	Y	20.07	1426.7780	0.0	476.5999	3	10.77	1559	2	315	327	
Q.SIEDPFDQDDWE.N	Y	19.74	1494.5786	-0.3	748.2963	2	14.19	2156	1	291	302	

total 4 peptides

tr|A0A2U9B0J8|A0A2U9B0J8_SCOMX
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.SIEDPFDQDDWENWAK.F	Y	43.87	1993.8330	2.3	997.9260	2	14.25	2166	1	291	306	
K.YGKDATNVGDEGGFAPN.I	Y	32.36	1710.7485	-0.8	856.3809	2	11.09	1617	1	200	216	
Q.IVGDDLTVTNPKR.I	Y	20.07	1426.7780	0.0	476.5999	3	10.77	1559	2	315	327	
Q.SIEDPFDQDDWE.N	Y	19.74	1494.5786	-0.3	748.2963	2	14.19	2156	1	291	302	

total 4 peptides

tr|A0A6J2P9G6|A0A6J2P9G6_COTGO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.SIEDPFDQDDWENWAK.F	Y	43.87	1993.8330	2.3	997.9260	2	14.25	2166	1	291	306	
K.YGKDATNVGDEGGFAPN.I	Y	32.36	1710.7485	-0.8	856.3809	2	11.09	1617	1	200	216	
Q.IVGDDLTVTNPKR.I	Y	20.07	1426.7780	0.0	476.5999	3	10.77	1559	2	315	327	
Q.SIEDPFDQDDWE.N	Y	19.74	1494.5786	-0.3	748.2963	2	14.19	2156	1	291	302	

total 4 peptides

tr|D6PVP1|D6PVP1_EPICO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.SIEDPFDQDDWENWAK.F	Y	43.87	1993.8330	2.3	997.9260	2	14.25	2166	1	291	306	
K.YGKDATNVGDEGGFAPN.I	Y	32.36	1710.7485	-0.8	856.3809	2	11.09	1617	1	200	216	
Q.IVGDDLTVTNPKR.I	Y	20.07	1426.7780	0.0	476.5999	3	10.77	1559	2	315	327	
Q.SIEDPFDQDDWE.N	Y	19.74	1494.5786	-0.3	748.2963	2	14.19	2156	1	291	302	

total 4 peptides

tr|A0A6A4S9A7|A0A6A4S9A7_SCOMX
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.SIEDPFDQDDWENWAK.F	Y	43.87	1993.8330	2.3	997.9260	2	14.25	2166	1	568	583	
K.YGKDATNVGDEGGFAPN.I	Y	32.36	1710.7485	-0.8	856.3809	2	11.09	1617	1	477	493	
Q.IVGDDLTVTNPKR.I	Y	20.07	1426.7780	0.0	476.5999	3	10.77	1559	2	592	604	
Q.SIEDPFDQDDWE.N	Y	19.74	1494.5786	-0.3	748.2963	2	14.19	2156	1	568	579	

total 4 peptides

tr|A0A6P7KDL5|A0A6P7KDL5_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEKTIDDLEDELY.A	Y	42.92	1594.7614	-1.6	798.3867	2	13.33	2012	1	249	261	
K.LEKTIDDLEDELYAQ.K	Y	35.49	1793.8571	-6.3	897.9302	2	13.28	2004	1	249	263	
K.LEKTIDDLEDE.L	Y	19.62	1318.6140	-0.6	660.3139	2	11.52	1693	1	249	259	
K.LKGTEDE.L	Y	17.70	790.3708	-0.3	396.1926	2	8.61	1214	1	50	56	

total 4 peptides

tr|A0A6P7MR93|A0A6P7MR93_BETSP
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEKTIDDLEDELY.A	Y	42.92	1594.7614	-1.6	798.3867	2	13.33	2012	1	249	261	
K.LEKTIDDLEDELYAQ.K	Y	35.49	1793.8571	-6.3	897.9302	2	13.28	2004	1	249	263	
K.LEKTIDDLEDE.L	Y	19.62	1318.6140	-0.6	660.3139	2	11.52	1693	1	249	259	
K.LKGTEDE.L	Y	17.70	790.3708	-0.3	396.1926	2	8.61	1214	1	50	56	

total 4 peptides

tr|A0A3P9D7I0|A0A3P9D7I0_9CICH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEKTIDDLEDELY.A	Y	42.92	1594.7614	-1.6	798.3867	2	13.33	2012	1	249	261	
K.LEKTIDDLEDELYAQ.K	Y	35.49	1793.8571	-6.3	897.9302	2	13.28	2004	1	249	263	
K.LEKTIDDLEDE.L	Y	19.62	1318.6140	-0.6	660.3139	2	11.52	1693	1	249	259	
K.LKGTEDE.L	Y	17.70	790.3708	-0.3	396.1926	2	8.61	1214	1	50	56	

total 4 peptides

tr|A0A665VR95|A0A665VR95_ECHNA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEKTIDDLEDELY.A	Y	42.92	1594.7614	-1.6	798.3867	2	13.33	2012	1	249	261	
K.LEKTIDDLEDELYAQ.K	Y	35.49	1793.8571	-6.3	897.9302	2	13.28	2004	1	249	263	
K.LEKTIDDLEDE.L	Y	19.62	1318.6140	-0.6	660.3139	2	11.52	1693	1	249	259	
K.LKGTEDE.L	Y	17.70	790.3708	-0.3	396.1926	2	8.61	1214	1	50	56	

total 4 peptides

tr|A0A3P8SLC6|A0A3P8SLC6_AMPPE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEKTIDDLEDELY.A	Y	42.92	1594.7614	-1.6	798.3867	2	13.33	2012	1	249	261	
K.LEKTIDDLEDELYAQ.K	Y	35.49	1793.8571	-6.3	897.9302	2	13.28	2004	1	249	263	
K.LEKTIDDLEDE.L	Y	19.62	1318.6140	-0.6	660.3139	2	11.52	1693	1	249	259	
K.LKGTEDE.L	Y	17.70	790.3708	-0.3	396.1926	2	8.61	1214	1	50	56	

total 4 peptides

tr|A0A668UDB6|A0A668UDB6_OREAU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEKTIDDLEDELY.A	Y	42.92	1594.7614	-1.6	798.3867	2	13.33	2012	1	300	312	
K.LEKTIDDLEDELYAQ.K	Y	35.49	1793.8571	-6.3	897.9302	2	13.28	2004	1	300	314	
K.LEKTIDDLEDE.L	Y	19.62	1318.6140	-0.6	660.3139	2	11.52	1693	1	300	310	
K.LKGTEDE.L	Y	17.70	790.3708	-0.3	396.1926	2	8.61	1214	1	101	107	

total 4 peptides

tr|X2J4M2|X2J4M2_PAROL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEKTIDDLEDELY.A	Y	42.92	1594.7614	-1.6	798.3867	2	13.33	2012	1	249	261	
K.LEKTIDDLEDELYAQ.K	Y	35.49	1793.8571	-6.3	897.9302	2	13.28	2004	1	249	263	
K.LEKTIDDLEDE.L	Y	19.62	1318.6140	-0.6	660.3139	2	11.52	1693	1	249	259	
K.LKGTEDE.L	Y	17.70	790.3708	-0.3	396.1926	2	8.61	1214	1	50	56	

total 4 peptides

tr|H2SQV9|H2SQV9_TAKRU
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEKTIDDLEDELY.A	Y	42.92	1594.7614	-1.6	798.3867	2	13.33	2012	1	236	248	
K.LEKTIDDLEDELYAQ.K	Y	35.49	1793.8571	-6.3	897.9302	2	13.28	2004	1	236	250	
K.LEKTIDDLEDE.L	Y	19.62	1318.6140	-0.6	660.3139	2	11.52	1693	1	236	246	
K.LKGTEDE.L	Y	17.70	790.3708	-0.3	396.1926	2	8.61	1214	1	50	56	

total 4 peptides

tr|A0A4U5UG20|A0A4U5UG20_COLLU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEKTIDDLEDELY.A	Y	42.92	1594.7614	-1.6	798.3867	2	13.33	2012	1	304	316	
K.LEKTIDDLEDELYAQ.K	Y	35.49	1793.8571	-6.3	897.9302	2	13.28	2004	1	304	318	
K.LEKTIDDLEDE.L	Y	19.62	1318.6140	-0.6	660.3139	2	11.52	1693	1	304	314	
K.LKGTEDE.L	Y	17.70	790.3708	-0.3	396.1926	2	8.61	1214	1	92	98	

total 4 peptides

tr|A0A6P3VQ87|A0A6P3VQ87_CLUHA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEKTIDDLEDELY.A	Y	42.92	1594.7614	-1.6	798.3867	2	13.33	2012	1	249	261	
K.LEKTIDDLEDELYAQ.K	Y	35.49	1793.8571	-6.3	897.9302	2	13.28	2004	1	249	263	
K.LEKTIDDLEDE.L	Y	19.62	1318.6140	-0.6	660.3139	2	11.52	1693	1	249	259	
K.LKGTEDE.L	Y	17.70	790.3708	-0.3	396.1926	2	8.61	1214	1	50	56	

total 4 peptides

tr|A0A4W4GLX2|A0A4W4GLX2_ELEEL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LEKTIDDLEDELY.A	Y	42.92	1594.7614	-1.6	798.3867	2	13.33	2012	1	244	256	
K.LEKTIDDLEDELYAQ.K	Y	35.49	1793.8571	-6.3	897.9302	2	13.28	2004	1	244	258	
K.LEKTIDDLEDE.L	Y	19.62	1318.6140	-0.6	660.3139	2	11.52	1693	1	244	254	
K.LKGTEDE.L	Y	17.70	790.3708	-0.3	396.1926	2	8.61	1214	1	50	56	

total 4 peptides

tr|A0A2I4D9D9|A0A2I4D9D9_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQG.P	N	37.56	1400.6796	-0.2	701.3469	2	9.77	1397	1	169	184	
R.GERGFPGLPGPS.G	N	28.43	1169.5829	-0.8	585.7983	2	12.09	1795	1	919	930	
G.FAGPPGADGQPGAK.G	N	22.00	1268.6149	-0.4	635.3145	2	10.23	1471	1	764	777	
S.GDRGETGSAGPA.G	Y	17.49	1073.4738	-0.3	537.7440	2	8.85	1256	1	1015	1026	

total 4 peptides

tr|A0A2I4D9D6|A0A2I4D9D6_9TELE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQG.P	N	37.56	1400.6796	-0.2	701.3469	2	9.77	1397	1	169	184	
R.GERGFPGLPGPS.G	N	28.43	1169.5829	-0.8	585.7983	2	12.09	1795	1	952	963	
G.FAGPPGADGQPGAK.G	N	22.00	1268.6149	-0.4	635.3145	2	10.23	1471	1	797	810	
S.GDRGETGSAGPA.G	Y	17.49	1073.4738	-0.3	537.7440	2	8.85	1256	1	1048	1059	

total 4 peptides

tr|A0A3P8WWA2|A0A3P8WWA2_CYNSE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.GFAGDDAPRA.L	N	39.52	975.4410	-0.2	488.7277	2	10.22	1469	4	22	31	
Y.VGDEAQSK.R	N	26.03	832.3926	0.0	417.2036	2	8.09	1115	1	56	63	
G.FAGDDAPRA.L	N	18.34	918.4195	0.1	460.2171	2	17.21	2654	7	23	31	
G.FAGDDAPRAL.F	Y	17.96	1031.5035	-0.9	516.7586	2	11.22	1639	1	23	32	

total 4 peptides

tr|A0A3P8X278|A0A3P8X278_CYNSE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.GFAGDDAPRA.L	N	39.52	975.4410	-0.2	488.7277	2	10.22	1469	4	19	28	
Y.VGDEAQSK.R	N	26.03	832.3926	0.0	417.2036	2	8.09	1115	1	53	60	
G.FAGDDAPRA.L	N	18.34	918.4195	0.1	460.2171	2	17.21	2654	7	20	28	
G.FAGDDAPRAL.F	Y	17.96	1031.5035	-0.9	516.7586	2	11.22	1639	1	20	29	

total 4 peptides

tr|A0A3P8X031|A0A3P8X031_CYNSE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.GFAGDDAPRA.L	N	39.52	975.4410	-0.2	488.7277	2	10.22	1469	4	22	31	
Y.VGDEAQSK.R	N	26.03	832.3926	0.0	417.2036	2	8.09	1115	1	56	63	
G.FAGDDAPRA.L	N	18.34	918.4195	0.1	460.2171	2	17.21	2654	7	23	31	
G.FAGDDAPRAL.F	Y	17.96	1031.5035	-0.9	516.7586	2	11.22	1639	1	23	32	

total 4 peptides

tr|A0A3P8WTX4|A0A3P8WTX4_CYNSE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.GFAGDDAPRA.L	N	39.52	975.4410	-0.2	488.7277	2	10.22	1469	4	22	31	
Y.VGDEAQSK.R	N	26.03	832.3926	0.0	417.2036	2	8.09	1115	1	56	63	
G.FAGDDAPRA.L	N	18.34	918.4195	0.1	460.2171	2	17.21	2654	7	23	31	
G.FAGDDAPRAL.F	Y	17.96	1031.5035	-0.9	516.7586	2	11.22	1639	1	23	32	

total 4 peptides

tr|A0A3P8WU36|A0A3P8WU36_CYNSE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.GFAGDDAPRA.L	N	39.52	975.4410	-0.2	488.7277	2	10.22	1469	4	19	28	
Y.VGDEAQSK.R	N	26.03	832.3926	0.0	417.2036	2	8.09	1115	1	53	60	
G.FAGDDAPRA.L	N	18.34	918.4195	0.1	460.2171	2	17.21	2654	7	20	28	
G.FAGDDAPRAL.F	Y	17.96	1031.5035	-0.9	516.7586	2	11.22	1639	1	20	29	

total 4 peptides

tr|A0A3P8WUR0|A0A3P8WUR0_CYNSE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.GFAGDDAPRA.L	N	39.52	975.4410	-0.2	488.7277	2	10.22	1469	4	22	31	
Y.VGDEAQSK.R	N	26.03	832.3926	0.0	417.2036	2	8.09	1115	1	56	63	
G.FAGDDAPRA.L	N	18.34	918.4195	0.1	460.2171	2	17.21	2654	7	23	31	
G.FAGDDAPRAL.F	Y	17.96	1031.5035	-0.9	516.7586	2	11.22	1639	1	23	32	

total 4 peptides

tr|A0A7N8WP58|A0A7N8WP58_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.FDDLPIHEQ.S	Y	35.62	1112.5138	-1.1	557.2635	2	11.85	1752	1	621	629	
Y.TGREFDDLPIHEQ.S	Y	24.24	1555.7267	1.3	778.8716	2	11.69	1722	2	617	629	
E.VSVGDKVPAD.I	Y	23.82	985.5080	-0.5	493.7610	2	10.19	1463	1	119	128	
L.GLPEALIPVQLL.W	Y	16.99	1261.7645	0.0	631.8895	2	15.85	2438	1	745	756	
E.IVPGDIVE.V	Y	15.52	840.4592	0.4	421.2371	2	12.27	1826	1	111	118	

total 5 peptides

tr|A0A668SKK1|A0A668SKK1_OREAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.FDDLPLHEQ.S	Y	35.62	1112.5138	-1.1	557.2635	2	11.85	1752	1	620	628	
Y.TGREFDDLPLHEQ.S	Y	24.24	1555.7267	1.3	778.8716	2	11.69	1722	2	616	628	
E.VSVGDKVPAD.I	Y	23.82	985.5080	-0.5	493.7610	2	10.19	1463	1	118	127	
L.GLPEALIPVQLL.W	Y	16.99	1261.7645	0.0	631.8895	2	15.85	2438	1	744	755	
E.IVPGDIVE.V	Y	15.52	840.4592	0.4	421.2371	2	12.27	1826	1	110	117	

total 5 peptides

tr|A0A3Q3BHF7|A0A3Q3BHF7_KRYMA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.FDDLPLHEQ.A	Y	35.62	1112.5138	-1.1	557.2635	2	11.85	1752	1	655	663	
Y.TGREFDDLPLHEQ.A	Y	24.24	1555.7267	1.3	778.8716	2	11.69	1722	2	651	663	
E.VSVGDKVPAD.I	Y	23.82	985.5080	-0.5	493.7610	2	10.19	1463	1	153	162	
L.GLPEALIPVQLL.W	Y	16.99	1261.7645	0.0	631.8895	2	15.85	2438	1	779	790	
E.IVPGDIVE.V	Y	15.52	840.4592	0.4	421.2371	2	12.27	1826	1	145	152	

total 5 peptides

tr|A0A3Q2WQG2|A0A3Q2WQG2_HAPBU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.FDDLPLHEQ.S	Y	35.62	1112.5138	-1.1	557.2635	2	11.85	1752	1	655	663	
Y.TGREFDDLPLHEQ.S	Y	24.24	1555.7267	1.3	778.8716	2	11.69	1722	2	651	663	
E.VSVGDKVPAD.I	Y	23.82	985.5080	-0.5	493.7610	2	10.19	1463	1	153	162	
L.GLPEALIPVQLL.W	Y	16.99	1261.7645	0.0	631.8895	2	15.85	2438	1	779	790	
E.IVPGDIVE.V	Y	15.52	840.4592	0.4	421.2371	2	12.27	1826	1	145	152	

total 5 peptides

tr|A0A3B3DXK1|A0A3B3DXK1_ORYME
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.FDDLPLHEQ.A	Y	35.62	1112.5138	-1.1	557.2635	2	11.85	1752	1	655	663	
Y.TGREFDDLPLHEQ.A	Y	24.24	1555.7267	1.3	778.8716	2	11.69	1722	2	651	663	
E.VSVGDKVPAD.I	Y	23.82	985.5080	-0.5	493.7610	2	10.19	1463	1	153	162	
L.GLPEALIPVQLL.W	Y	16.99	1261.7645	0.0	631.8895	2	15.85	2438	1	779	790	
E.IVPGDIVE.V	Y	15.52	840.4592	0.4	421.2371	2	12.27	1826	1	145	152	

total 5 peptides

tr|A0A3Q3BR63|A0A3Q3BR63_HAPBU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.FDDLPLHEQ.S	Y	35.62	1112.5138	-1.1	557.2635	2	11.85	1752	1	655	663	
Y.TGREFDDLPLHEQ.S	Y	24.24	1555.7267	1.3	778.8716	2	11.69	1722	2	651	663	
E.VSVGDKVPAD.I	Y	23.82	985.5080	-0.5	493.7610	2	10.19	1463	1	153	162	
L.GLPEALIPVQLL.W	Y	16.99	1261.7645	0.0	631.8895	2	15.85	2438	1	779	790	
E.IVPGDIVE.V	Y	15.52	840.4592	0.4	421.2371	2	12.27	1826	1	145	152	

total 5 peptides

tr|A0A3Q3H0F6|A0A3Q3H0F6_KRYMA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.FDDLPLHEQ.A	Y	35.62	1112.5138	-1.1	557.2635	2	11.85	1752	1	655	663	
Y.TGREFDDLPLHEQ.A	Y	24.24	1555.7267	1.3	778.8716	2	11.69	1722	2	651	663	
E.VSVGDKVPAD.I	Y	23.82	985.5080	-0.5	493.7610	2	10.19	1463	1	153	162	
L.GLPEALIPVQLL.W	Y	16.99	1261.7645	0.0	631.8895	2	15.85	2438	1	779	790	
E.IVPGDIVE.V	Y	15.52	840.4592	0.4	421.2371	2	12.27	1826	1	145	152	

total 5 peptides

tr|A0A3P9C9M1|A0A3P9C9M1_9CICH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.FDDLPLHEQ.S	Y	35.62	1112.5138	-1.1	557.2635	2	11.85	1752	1	655	663	
Y.TGREFDDLPLHEQ.S	Y	24.24	1555.7267	1.3	778.8716	2	11.69	1722	2	651	663	
E.VSVGDKVPAD.I	Y	23.82	985.5080	-0.5	493.7610	2	10.19	1463	1	153	162	
L.GLPEALIPVQLL.W	Y	16.99	1261.7645	0.0	631.8895	2	15.85	2438	1	779	790	
E.IVPGDIVE.V	Y	15.52	840.4592	0.4	421.2371	2	12.27	1826	1	145	152	

total 5 peptides

tr|A0A668SKH5|A0A668SKH5_OREAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.FDDLPLHEQ.S	Y	35.62	1112.5138	-1.1	557.2635	2	11.85	1752	1	655	663	
Y.TGREFDDLPLHEQ.S	Y	24.24	1555.7267	1.3	778.8716	2	11.69	1722	2	651	663	
E.VSVGDKVPAD.I	Y	23.82	985.5080	-0.5	493.7610	2	10.19	1463	1	153	162	
L.GLPEALIPVQLL.W	Y	16.99	1261.7645	0.0	631.8895	2	15.85	2438	1	779	790	
E.IVPGDIVE.V	Y	15.52	840.4592	0.4	421.2371	2	12.27	1826	1	145	152	

total 5 peptides

tr|A0A669D951|A0A669D951_ORENI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.FDDLPLHEQ.S	Y	35.62	1112.5138	-1.1	557.2635	2	11.85	1752	1	657	665	
Y.TGREFDDLPLHEQ.S	Y	24.24	1555.7267	1.3	778.8716	2	11.69	1722	2	653	665	
E.VSVGDKVPAD.I	Y	23.82	985.5080	-0.5	493.7610	2	10.19	1463	1	153	162	
L.GLPEALIPVQLL.W	Y	16.99	1261.7645	0.0	631.8895	2	15.85	2438	1	781	792	
E.IVPGDIVE.V	Y	15.52	840.4592	0.4	421.2371	2	12.27	1826	1	145	152	

total 5 peptides

tr|A0A674PDV8|A0A674PDV8_TAKRU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.FDDLPLHEQ.P	Y	35.62	1112.5138	-1.1	557.2635	2	11.85	1752	1	655	663	
Y.TGREFDDLPLHEQ.P	Y	24.24	1555.7267	1.3	778.8716	2	11.69	1722	2	651	663	

total 5 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VSVGDKVPAD.I	Y	23.82	985.5080	-0.5	493.7610	2	10.19	1463	1	153	162	
L.GLPEALIPVQLL.W	Y	16.99	1261.7645	0.0	631.8895	2	15.85	2438	1	779	790	
E.IVPGDIVE.V	Y	15.52	840.4592	0.4	421.2371	2	12.27	1826	1	145	152	

total 5 peptides

tr|A0A674P4B1|A0A674P4B1_TAKRU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.FDDLPLHEQ.P	Y	35.62	1112.5138	-1.1	557.2635	2	11.85	1752	1	655	663	
Y.TGREFDDLPLHEQ.P	Y	24.24	1555.7267	1.3	778.8716	2	11.69	1722	2	651	663	
E.VSVGDKVPAD.I	Y	23.82	985.5080	-0.5	493.7610	2	10.19	1463	1	153	162	
L.GLPEALIPVQLL.W	Y	16.99	1261.7645	0.0	631.8895	2	15.85	2438	1	779	790	
E.IVPGDIVE.V	Y	15.52	840.4592	0.4	421.2371	2	12.27	1826	1	145	152	

total 5 peptides

tr|A0A3Q1CVI2|A0A3Q1CVI2_AMPOC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.GEKLKGADPEDVILS.A	Y	39.52	1569.8250	-1.0	785.9189	2	11.73	1729	1	66	80	
V.LDPEGTGSIK.K	Y	24.55	1015.5186	-0.5	508.7663	2	10.19	1464	1	85	94	
K.LKGADPEDVIL.S	Y	19.66	1168.6339	-0.5	585.3239	2	12.52	1872	1	69	79	
A.AFPPDVAGN.V	Y	16.10	886.4185	-1.1	444.2160	2	11.80	1741	1	120	128	

total 4 peptides

tr|A0A4U5VU95|A0A4U5VU95_COLLU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.GEKLKGADPEDVILS.A	Y	39.52	1569.8250	-1.0	785.9189	2	11.73	1729	1	68	82	
V.LDPEGTGSIK.K	Y	24.55	1015.5186	-0.5	508.7663	2	10.19	1464	1	87	96	
K.LKGADPEDVIL.S	Y	19.66	1168.6339	-0.5	585.3239	2	12.52	1872	1	71	81	
A.AFPPDVAGN.V	Y	16.10	886.4185	-1.1	444.2160	2	11.80	1741	1	122	130	

total 4 peptides

tr|A0A6P7II88|A0A6P7II88_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.GEKLKGADPEDVILS.A	Y	39.52	1569.8250	-1.0	785.9189	2	11.73	1729	1	90	104	
V.LDPEGTGSIK.K	Y	24.55	1015.5186	-0.5	508.7663	2	10.19	1464	1	109	118	
K.LKGADPEDVIL.S	Y	19.66	1168.6339	-0.5	585.3239	2	12.52	1872	1	93	103	
A.AFPPDVAGN.V	Y	16.10	886.4185	-1.1	444.2160	2	11.80	1741	1	144	152	

total 4 peptides

tr|A0A3Q4GCJ7|A0A3Q4GCJ7_NEOBR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.GEKLKGADPEDVILS.A	Y	39.52	1569.8250	-1.0	785.9189	2	11.73	1729	1	90	104	
V.LDPEGTGSIK.K	Y	24.55	1015.5186	-0.5	508.7663	2	10.19	1464	1	109	118	
K.LKGADPEDVIL.S	Y	19.66	1168.6339	-0.5	585.3239	2	12.52	1872	1	93	103	
A.AFPPDVAGN.V	Y	16.10	886.4185	-1.1	444.2160	2	11.80	1741	1	144	152	

total 4 peptides

tr|A0A3P9IWY3|A0A3P9IWY3_ORYLA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.GEKLKGADPEDVILS.A	Y	39.52	1569.8250	-1.0	785.9189	2	11.73	1729	1	90	104	
V.LDPEGTGSIK.K	Y	24.55	1015.5186	-0.5	508.7663	2	10.19	1464	1	109	118	
K.LKGADPEDVIL.S	Y	19.66	1168.6339	-0.5	585.3239	2	12.52	1872	1	93	103	
A.AFPPDVAGN.V	Y	16.10	886.4185	-1.1	444.2160	2	11.80	1741	1	144	152	

total 4 peptides

tr|H3C4G7|H3C4G7_TETNG

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.GEKLKGADPEDVILS.A	Y	39.52	1569.8250	-1.0	785.9189	2	11.73	1729	1	90	104	
V.LDPEGTGSIK.K	Y	24.55	1015.5186	-0.5	508.7663	2	10.19	1464	1	109	118	
K.LKGADPEDVIL.S	Y	19.66	1168.6339	-0.5	585.3239	2	12.52	1872	1	93	103	
A.AFPPDVAGN.V	Y	16.10	886.4185	-1.1	444.2160	2	11.80	1741	1	144	152	

total 4 peptides

tr|A0A3B4VIC8|A0A3B4VIC8_SERDU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.GEKLKGADPEDVILS.S	Y	39.52	1569.8250	-1.0	785.9189	2	11.73	1729	1	90	104	
V.LDPEGTGSIK.K	Y	24.55	1015.5186	-0.5	508.7663	2	10.19	1464	1	109	118	
K.LKGADPEDVIL.S	Y	19.66	1168.6339	-0.5	585.3239	2	12.52	1872	1	93	103	
A.AFPPDVAGN.V	Y	16.10	886.4185	-1.1	444.2160	2	11.80	1741	1	144	152	

total 4 peptides

tr|I6U9W3|I6U9W3_ORYJA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.GEKLKGADPEDVILS.A	Y	39.52	1569.8250	-1.0	785.9189	2	11.73	1729	1	90	104	
V.LDPEGTGSIK.K	Y	24.55	1015.5186	-0.5	508.7663	2	10.19	1464	1	109	118	
K.LKGADPEDVIL.S	Y	19.66	1168.6339	-0.5	585.3239	2	12.52	1872	1	93	103	
S.AFPPDVAGN.V	Y	16.10	886.4185	-1.1	444.2160	2	11.80	1741	1	144	152	

total 4 peptides

tr|A0A3P9KRI4|A0A3P9KRI4_ORYLA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.GEKLKGADPEDVILS.A	Y	39.52	1569.8250	-1.0	785.9189	2	11.73	1729	1	112	126	
V.LDPEGTGSIK.K	Y	24.55	1015.5186	-0.5	508.7663	2	10.19	1464	1	131	140	
K.LKGADPEDVIL.S	Y	19.66	1168.6339	-0.5	585.3239	2	12.52	1872	1	115	125	
A.AFPPDVAGN.V	Y	16.10	886.4185	-1.1	444.2160	2	11.80	1741	1	166	174	

total 4 peptides

tr|A0A3B3HA26|A0A3B3HA26_ORYLA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.GEKLKGADPEDVILS.A	Y	39.52	1569.8250	-1.0	785.9189	2	11.73	1729	1	177	191	
V.LDPEGTGSIK.K	Y	24.55	1015.5186	-0.5	508.7663	2	10.19	1464	1	196	205	
K.LKGADPEDVIL.S	Y	19.66	1168.6339	-0.5	585.3239	2	12.52	1872	1	180	190	
A.AFPPDVAGN.V	Y	16.10	886.4185	-1.1	444.2160	2	11.80	1741	1	231	239	

total 4 peptides

tr|A0A7N8YD85|A0A7N8YD85_9TELE

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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.IFDVLEDPVEILDNSRE.L	N	44.53	2001.9894	-0.9	1002.0010	2	14.67	2236	1	142	158	
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	219	230	

total 2 peptides

tr|A0A7N8XIB6|A0A7N8XIB6_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.IFDVLEDPVEILDNSRE.L	N	44.53	2001.9894	-0.9	1002.0010	2	14.67	2236	1	139	155	
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	222	233	

total 2 peptides

tr|A0A7N8Y4P6|A0A7N8Y4P6_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.IFDVLEDPVEILDNSRE.L	N	44.53	2001.9894	-0.9	1002.0010	2	14.67	2236	1	139	155	
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	222	233	

total 2 peptides

tr|A0A7N8WMA4|A0A7N8WMA4_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.IFDVLEDPVEILDNSRE.L	N	44.53	2001.9894	-0.9	1002.0010	2	14.67	2236	1	142	158	
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	225	236	

total 2 peptides

tr|A0A7N8XJX7|A0A7N8XJX7_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.IFDVLEDPVEILDNSRE.L	N	44.53	2001.9894	-0.9	1002.0010	2	14.67	2236	1	142	158	
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	225	236	

total 2 peptides

tr|A0A3Q3SHA7|A0A3Q3SHA7_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.IFDVLEDPVEILDNSRE.L	N	44.53	2001.9894	-0.9	1002.0010	2	14.67	2236	1	154	170	
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	237	248	

total 2 peptides

tr|A0A7N8XSZ9|A0A7N8XSZ9_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.IFDVLEDPVEILDNSRE.L	N	44.53	2001.9894	-0.9	1002.0010	2	14.67	2236	1	154	170	
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	237	248	

total 2 peptides

tr|A0A7N8XRW1|A0A7N8XRW1_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.IFDVLEDPVEILDNSRE.L	N	44.53	2001.9894	-0.9	1002.0010	2	14.67	2236	1	155	171	
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	238	249	

total 2 peptides

tr|A0A7N8Y2R6|A0A7N8Y2R6_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.IFDVLEDPVEILDNSRE.L	N	44.53	2001.9894	-0.9	1002.0010	2	14.67	2236	1	155	171	
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	238	249	

total 2 peptides

tr|A0A7N8Y336|A0A7N8Y336_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.IFDVLEDPVEILDNSRE.L	N	44.53	2001.9894	-0.9	1002.0010	2	14.67	2236	1	158	174	
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	241	252	

total 2 peptides

tr|I3JGN1|I3JGN1_ORENI
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQG.F	N	37.56	1400.6796	-0.2	701.3469	2	9.77	1397	1	163	178	
G.LRGDKGETGEAGER.G	N	23.05	1473.7172	-0.3	492.2462	3	8.56	1206	1	900	913	
G.FAGPPGADGQPGAK.G	N	22.00	1268.6149	-0.4	635.3145	2	10.23	1471	1	677	690	

total 3 peptides

tr|G9M6I5|G9M6I5_ORENI
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQG.F	N	37.56	1400.6796	-0.2	701.3469	2	9.77	1397	1	169	184	
G.LRGDKGETGEAGER.G	N	23.05	1473.7172	-0.3	492.2462	3	8.56	1206	1	1076	1089	
G.FAGPPGADGQPGAK.G	N	22.00	1268.6149	-0.4	635.3145	2	10.23	1471	1	797	810	

total 3 peptides

tr|Q4RE90|Q4RE90_TETNG
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.AVDPVYPPGPPAFPK.V	Y	34.33	1550.8132	-1.1	776.4130	2	12.36	1842	1	7117	7131	
T.VVDRPQPPEGPVVF.N	Y	25.63	1534.8143	-1.2	768.4135	2	12.54	1875	1	4491	4504	
E.VVDVPGPVTDLKP.V	Y	25.28	1334.7445	-1.1	668.3788	2	12.39	1848	1	2931	2943	

total 3 peptides

tr|A0A484CUS5|A0A484CUS5_PERFV
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.VVDRPTPPVGPVVF.E	Y	45.69	1477.8292	-1.2	739.9210	2	13.05	1964	1	3654	3667	
A.ILPPGPPTPW.I	N	19.56	1073.5909	0.5	537.8030	2	13.74	2081	1	1746	1755	

total 2 peptides

tr|A0A6G0I8D2|A0A6G0I8D2_LARCR
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IGEDFIRD.L	Y	34.82	963.4661	-1.1	482.7398	2	11.83	1747	1	508	515	
F.ADYEDYIK.C	Y	26.24	1015.4498	-0.9	508.7317	2	11.59	1705	1	776	783	
E.RIGEDFIRDL.D	Y	17.59	1232.6512	-1.5	617.3320	2	12.88	1935	1	507	516	

total 3 peptides

tr|A0A669CG83|A0A669CG83_ORENI
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IGEDFIRD.L	Y	34.82	963.4661	-1.1	482.7398	2	11.83	1747	1	508	515	
F.ADYEDYIK.C	Y	26.24	1015.4498	-0.9	508.7317	2	11.59	1705	1	743	750	
E.RIGEDFIRDL.D	Y	17.59	1232.6512	-1.5	617.3320	2	12.88	1935	1	507	516	

total 3 peptides

tr|A0A3P8QJ74|A0A3P8QJ74_ASTCA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IGEDFIRD.L	Y	34.82	963.4661	-1.1	482.7398	2	11.83	1747	1	460	467	
F.ADYEDYIK.C	Y	26.24	1015.4498	-0.9	508.7317	2	11.59	1705	1	728	735	
E.RIGEDFIRDL.D	Y	17.59	1232.6512	-1.5	617.3320	2	12.88	1935	1	459	468	

total 3 peptides

tr|A0A669E543|A0A669E543_ORENI
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IGEDFIRD.L	Y	34.82	963.4661	-1.1	482.7398	2	11.83	1747	1	508	515	
F.ADYEDYIK.C	Y	26.24	1015.4498	-0.9	508.7317	2	11.59	1705	1	748	755	
E.RIGEDFIRDL.D	Y	17.59	1232.6512	-1.5	617.3320	2	12.88	1935	1	507	516	

total 3 peptides

tr|A0A3B4C8L5|A0A3B4C8L5_PYGNA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IGEDFIRD.L	Y	34.82	963.4661	-1.1	482.7398	2	11.83	1747	1	486	493	
F.ADYEDYIK.C	Y	26.24	1015.4498	-0.9	508.7317	2	11.59	1705	1	753	760	
E.RIGEDFIRDL.D	Y	17.59	1232.6512	-1.5	617.3320	2	12.88	1935	1	485	494	

total 3 peptides

tr|A0A669F5E7|A0A669F5E7_ORENI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IGEDFIRD.L	Y	34.82	963.4661	-1.1	482.7398	2	11.83	1747	1	508	515	
F.ADYEDYIK.C	Y	26.24	1015.4498	-0.9	508.7317	2	11.59	1705	1	743	750	
E.RIGEDFIRDL.D	Y	17.59	1232.6512	-1.5	617.3320	2	12.88	1935	1	507	516	

total 3 peptides

tr|A0A672GIA2|A0A672GIA2_SALFA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IGEDFIRD.L	Y	34.82	963.4661	-1.1	482.7398	2	11.83	1747	1	501	508	
F.ADYEDYIK.C	Y	26.24	1015.4498	-0.9	508.7317	2	11.59	1705	1	769	776	
E.RIGEDFIRDL.D	Y	17.59	1232.6512	-1.5	617.3320	2	12.88	1935	1	500	509	

total 3 peptides

tr|A0A3B4B6P0|A0A3B4B6P0_9GOBI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IGEDFIRD.L	Y	34.82	963.4661	-1.1	482.7398	2	11.83	1747	1	508	515	
F.ADYEDYIK.C	Y	26.24	1015.4498	-0.9	508.7317	2	11.59	1705	1	776	783	
E.RIGEDFIRDL.D	Y	17.59	1232.6512	-1.5	617.3320	2	12.88	1935	1	507	516	

total 3 peptides

tr|A0A6P7PB25|A0A6P7PB25_BETSP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IGEDFIRD.L	Y	34.82	963.4661	-1.1	482.7398	2	11.83	1747	1	508	515	
F.ADYEDYIK.C	Y	26.24	1015.4498	-0.9	508.7317	2	11.59	1705	1	776	783	
E.RIGEDFIRDL.D	Y	17.59	1232.6512	-1.5	617.3320	2	12.88	1935	1	507	516	

total 3 peptides

tr|M4A9F5|M4A9F5_XIPMA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IGEDFIRD.L	Y	34.82	963.4661	-1.1	482.7398	2	11.83	1747	1	508	515	
F.ADYEDYIK.C	Y	26.24	1015.4498	-0.9	508.7317	2	11.59	1705	1	776	783	
E.RIGEDFIRDL.D	Y	17.59	1232.6512	-1.5	617.3320	2	12.88	1935	1	507	516	

total 3 peptides

tr|A0A498LG69|A0A498LG69_LABRO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IGEDFIRD.L	Y	34.82	963.4661	-1.1	482.7398	2	11.83	1747	1	508	515	
F.ADYEDYIK.C	Y	26.24	1015.4498	-0.9	508.7317	2	11.59	1705	1	776	783	
E.RIGEDFIRDL.D	Y	17.59	1232.6512	-1.5	617.3320	2	12.88	1935	1	507	516	

total 3 peptides

tr|A0A0S7H0F8|A0A0S7H0F8_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IGEDFIRD.L	Y	34.82	963.4661	-1.1	482.7398	2	11.83	1747	1	508	515	
F.ADYEDYIK.C	Y	26.24	1015.4498	-0.9	508.7317	2	11.59	1705	1	776	783	
E.RIGEDFIRDL.D	Y	17.59	1232.6512	-1.5	617.3320	2	12.88	1935	1	507	516	

total 3 peptides

tr|A0A5J5D262|A0A5J5D262_9PERO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IGEDFIRD.L	Y	34.82	963.4661	-1.1	482.7398	2	11.83	1747	1	508	515	

total 3 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.ADYEDYIK.C	Y	26.24	1015.4498	-0.9	508.7317	2	11.59	1705	1	767	774	
E.RIGEDFIRDL.D	Y	17.59	1232.6512	-1.5	617.3320	2	12.88	1935	1	507	516	

total 3 peptides

tr|A0A6I9P2J6|A0A6I9P2J6_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.IFDVLEDPVEIIDNSRE.L	N	44.53	2001.9894	-0.9	1002.0010	2	14.67	2236	1	142	158	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	307	317	

total 2 peptides

tr|A0A2U9BKK8|A0A2U9BKK8_SCOMX
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.IFDVLEDPVEIIDNSRE.L	N	44.53	2001.9894	-0.9	1002.0010	2	14.67	2236	1	142	158	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	307	317	

total 2 peptides

tr|A0A6J2RKV3|A0A6J2RKV3_COTGO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.IFDVLEDPVEIIDNSRE.L	N	44.53	2001.9894	-0.9	1002.0010	2	14.67	2236	1	142	158	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	307	317	

total 2 peptides

tr|A0A6P8WKA1|A0A6P8WKA1_GYMAC
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.IFDVLEDPVEIIDNSRE.L	N	44.53	2001.9894	-0.9	1002.0010	2	14.67	2236	1	142	158	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	307	317	

total 2 peptides

tr|A0A6A4TIJ9|A0A6A4TIJ9_SCOMX
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.IFDVLEDPVEIIDNSRE.L	N	44.53	2001.9894	-0.9	1002.0010	2	14.67	2236	1	142	158	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	307	317	

total 2 peptides

tr|A0A3P8VNQ7|A0A3P8VNQ7_CYNSE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.IFDVLEDPVEIIDNSRE.L	N	44.53	2001.9894	-0.9	1002.0010	2	14.67	2236	1	142	158	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	307	317	

total 2 peptides

tr|A0A3P8VQY9|A0A3P8VQY9_CYNSE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.IFDVLEDPVEIIDNSRE.L	N	44.53	2001.9894	-0.9	1002.0010	2	14.67	2236	1	164	180	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	329	339	

Peptide Uniq -10lgP Mass ppm m/z z RT Scan #Spec Start End PTM

total 2 peptides

tr|A0A2I4B9K0|A0A2I4B9K0_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.IFDVLEDPVEIIDNSRE.L	N	44.53	2001.9894	-0.9	1002.0010	2	14.67	2236	1	142	158	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	307	317	

total 2 peptides

tr|A0A673A8U8|A0A673A8U8_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.GPRGPPGPPGSSGPQG.F	N	37.56	1400.6796	-0.2	701.3469	2	9.77	1397	1	78	93	
G.FSGLPGPSGEPGKQGPSG.V	Y	27.23	1654.7950	0.1	828.4049	2	11.29	1652	1	663	680	

total 2 peptides

tr|A0A671U7M6|A0A671U7M6_SPAAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	217	228	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	214	228	

total 2 peptides

tr|A0A3B3ZS88|A0A3B3ZS88_9GOBI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	157	168	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	154	168	

total 2 peptides

tr|A0A3Q1CJW7|A0A3Q1CJW7_AMPOC
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	157	168	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	154	168	

total 2 peptides

tr|A0A3Q3EFK1|A0A3Q3EFK1_9LABR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	162	173	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	159	173	

total 2 peptides

tr|A0A3Q3AF19|A0A3Q3AF19_KRYMA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	162	173	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	159	173	

Peptide Uniq -10lgP Mass ppm m/z z RT Scan #Spec Start End PTM

total 2 peptides

tr|A0A3Q3AF32|A0A3Q3AF32_KRYMA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	171	182	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	168	182	

total 2 peptides

tr|A0A3P8UNE3|A0A3P8UNE3_CYNSE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	168	179	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	165	179	

total 2 peptides

tr|A0SJB3|A0SJB3_SPAAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	168	179	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	165	179	

total 2 peptides

tr|A0A672Y3T4|A0A672Y3T4_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	168	179	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	165	179	

total 2 peptides

tr|A0SJB2|A0SJB2_SPAAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	171	182	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	168	182	

total 2 peptides

tr|A0A3P8UNF6|A0A3P8UNF6_CYNSE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	190	201	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	187	201	

total 2 peptides

tr|A0A3B4UYC0|A0A3B4UYC0_SERDU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	159	170	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	156	170	

total 2 peptides

tr|A0A3P8URR7|A0A3P8URR7_CYNSE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	169	180	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	166	180	

total 2 peptides

tr|A0A3P8URM3|A0A3P8URM3_CYNSE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	193	204	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	190	204	

total 2 peptides

tr|A0A3Q3XL97|A0A3Q3XL97_MOLML
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	204	215	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	201	215	

total 2 peptides

tr|A0A3P8ULW6|A0A3P8ULW6_CYNSE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	206	217	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	203	217	

total 2 peptides

tr|A0A5C6P7G2|A0A5C6P7G2_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	211	222	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	208	222	

total 2 peptides

tr|A0A3Q1CRB3|A0A3Q1CRB3_AMPOC
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	214	225	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	211	225	

total 2 peptides

tr|A0A665T7Y2|A0A665T7Y2_ECHNA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	220	231	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	217	231	

total 2 peptides

tr|A0A3Q1BEW8|A0A3Q1BEW8_AMPOC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	220	231	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	217	231	

total 2 peptides

tr|A0A3P8THB6|A0A3P8THB6_AMPPE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	229	240	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	226	240	

total 2 peptides

tr|A0A671U7Q2|A0A671U7Q2_SPAAU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	223	234	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	220	234	

total 2 peptides

tr|A0A672YCL7|A0A672YCL7_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	223	234	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	220	234	

total 2 peptides

tr|A0A672YCL2|A0A672YCL2_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	229	240	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	226	240	

total 2 peptides

tr|A0A6P7KCL6|A0A6P7KCL6_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	233	244	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	230	244	

total 2 peptides

tr|A0A6P7KCQ1|A0A6P7KCQ1_9TELE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	236	247	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	233	247	

Peptide Uniq -10lgP Mass ppm m/z z RT Scan #Spec Start End PTM

total 2 peptides

tr|A0A671UB90|A0A671UB90_SPAAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	202	213	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	199	213	

total 2 peptides

tr|A0A671U8G8|A0A671U8G8_SPAAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	205	216	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	202	216	

total 2 peptides

tr|A0A671U7M0|A0A671U7M0_SPAAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	184	195	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	181	195	

total 2 peptides

tr|A0A671UB76|A0A671UB76_SPAAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNEDKLKDKINE.L	Y	41.87	1457.7725	-0.2	729.8934	2	10.04	1439	1	204	215	
N.IDHLNEDKLKDKINE.L	Y	15.27	1822.9424	0.3	608.6549	3	10.49	1513	1	201	215	

total 2 peptides

tr|A0A6A5F2V4|A0A6A5F2V4_PERFL
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AIGNPLPDIVW.L	N	33.90	1193.6444	-0.2	597.8293	2	15.28	2342	1	622	632	
A.ILPPGPPTPW.I	N	19.56	1073.5909	0.5	537.8030	2	13.74	2081	1	7849	7858	
K.VVGRPMPDTYW.F	Y	15.12	1319.6332	-1.4	660.8229	2	12.61	1887	1	523	533	

total 3 peptides

tr|A0A0S7EPU5|A0A0S7EPU5_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AIGNPLPDIVW.L	N	33.90	1193.6444	-0.2	597.8293	2	15.28	2342	1	550	560	
L.IVEELPVKW.L	N	29.07	1111.6277	-0.4	556.8209	2	13.24	1997	1	3754	3762	

total 2 peptides

tr|A0A0S7ETZ8|A0A0S7ETZ8_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AIGNPLPDIVW.L	N	33.90	1193.6444	-0.2	597.8293	2	15.28	2342	1	550	560	
L.IVEELPVKW.L	N	29.07	1111.6277	-0.4	556.8209	2	13.24	1997	1	3754	3762	

total 2 peptides

tr|A0A0S7EQ56|A0A0S7EQ56_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AIGNPLPDIVW.L	N	33.90	1193.6444	-0.2	597.8293	2	15.28	2342	1	550	560	
L.IVEELPVKW.L	N	29.07	1111.6277	-0.4	556.8209	2	13.24	1997	1	3946	3954	

total 2 peptides

tr|A0A0S7F0D9|A0A0S7F0D9_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AIGNPLPDIVW.L	N	33.90	1193.6444	-0.2	597.8293	2	15.28	2342	1	550	560	
L.IVEELPVKW.L	N	29.07	1111.6277	-0.4	556.8209	2	13.24	1997	1	3946	3954	

total 2 peptides

tr|A0A146UF80|A0A146UF80_FUNHE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.ELNIPTGIPLVY.E	Y	33.55	1327.7388	0.0	664.8766	2	15.00	2292	1	219	230	
V.ELNIPTGIPLVYE.L	Y	27.50	1456.7812	-0.4	729.3976	2	14.71	2242	1	219	231	

total 2 peptides

tr|A0A671YMU3|A0A671YMU3_SPAAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GERGFPGLPGPS.G	N	28.43	1169.5829	-0.8	585.7983	2	12.09	1795	1	790	801	
G.LRGDKGETGEAGER.G	N	23.05	1473.7172	-0.3	492.2462	3	8.56	1206	1	860	873	
G.FAGPPGADGQPGAK.G	N	22.00	1268.6149	-0.4	635.3145	2	10.23	1471	1	647	660	

total 3 peptides

tr|A0A671YMZ1|A0A671YMZ1_SPAAU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GERGFPGLPGPS.G	N	28.43	1169.5829	-0.8	585.7983	2	12.09	1795	1	816	827	
G.LRGDKGETGEAGER.G	N	23.05	1473.7172	-0.3	492.2462	3	8.56	1206	1	886	899	
G.FAGPPGADGQPGAK.G	N	22.00	1268.6149	-0.4	635.3145	2	10.23	1471	1	661	674	

total 3 peptides

tr|A0A671YQ85|A0A671YQ85_SPAAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GERGFPGLPGPS.G	N	28.43	1169.5829	-0.8	585.7983	2	12.09	1795	1	816	827	
G.LRGDKGETGEAGER.G	N	23.05	1473.7172	-0.3	492.2462	3	8.56	1206	1	886	899	
G.FAGPPGADGQPGAK.G	N	22.00	1268.6149	-0.4	635.3145	2	10.23	1471	1	671	684	

total 3 peptides

tr|A0A671YMZ6|A0A671YMZ6_SPAAU
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GERGFPGLPGPS.G	N	28.43	1169.5829	-0.8	585.7983	2	12.09	1795	1	833	844	
G.LRGDKGETGEAGER.G	N	23.05	1473.7172	-0.3	492.2462	3	8.56	1206	1	903	916	
G.FAGPPGADGQPGAK.G	N	22.00	1268.6149	-0.4	635.3145	2	10.23	1471	1	690	703	

total 3 peptides

tr|A0A671YNQ4|A0A671YNQ4_SPAAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GERGFPGLPGPS.G	N	28.43	1169.5829	-0.8	585.7983	2	12.09	1795	1	833	844	
G.LRGDKGETGEAGER.G	N	23.05	1473.7172	-0.3	492.2462	3	8.56	1206	1	903	916	
G.FAGPPGADGQPGAK.G	N	22.00	1268.6149	-0.4	635.3145	2	10.23	1471	1	690	703	

total 3 peptides

tr|A0A671YN33|A0A671YN33_SPAAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GERGFPGLPGPS.G	N	28.43	1169.5829	-0.8	585.7983	2	12.09	1795	1	892	903	
G.LRGDKGETGEAGER.G	N	23.05	1473.7172	-0.3	492.2462	3	8.56	1206	1	962	975	
G.FAGPPGADGQPGAK.G	N	22.00	1268.6149	-0.4	635.3145	2	10.23	1471	1	747	760	

total 3 peptides

tr|A0A671YQA1|A0A671YQA1_SPAAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GERGFPGLPGPS.G	N	28.43	1169.5829	-0.8	585.7983	2	12.09	1795	1	900	911	
G.LRGDKGETGEAGER.G	N	23.05	1473.7172	-0.3	492.2462	3	8.56	1206	1	970	983	
G.FAGPPGADGQPGAK.G	N	22.00	1268.6149	-0.4	635.3145	2	10.23	1471	1	757	770	

total 3 peptides

tr|A0A671YNR4|A0A671YNR4_SPAAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GERGFPGLPGPS.G	N	28.43	1169.5829	-0.8	585.7983	2	12.09	1795	1	921	932	
G.LRGDKGETGEAGER.G	N	23.05	1473.7172	-0.3	492.2462	3	8.56	1206	1	991	1004	
G.FAGPPGADGQPGAK.G	N	22.00	1268.6149	-0.4	635.3145	2	10.23	1471	1	778	791	

total 3 peptides

tr|A0A671YPG6|A0A671YPG6_SPAAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GERGFPGLPGPS.G	N	28.43	1169.5829	-0.8	585.7983	2	12.09	1795	1	963	974	
G.LRGDKGETGEAGER.G	N	23.05	1473.7172	-0.3	492.2462	3	8.56	1206	1	1033	1046	
G.FAGPPGADGQPGAK.G	N	22.00	1268.6149	-0.4	635.3145	2	10.23	1471	1	817	830	

total 3 peptides

tr|A0A671YMN4|A0A671YMN4_SPAAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM

total 3 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GERGFPGLPGPS.G	N	28.43	1169.5829	-0.8	585.7983	2	12.09	1795	1	950	961	
G.LRGDKGETGEAGER.G	N	23.05	1473.7172	-0.3	492.2462	3	8.56	1206	1	1074	1087	
G.FAGPPGADGQPGAK.G	N	22.00	1268.6149	-0.4	635.3145	2	10.23	1471	1	795	808	

total 3 peptides

tr|A0A3Q3RR05|A0A3Q3RR05_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GERGFPGLPGPS.G	N	28.43	1169.5829	-0.8	585.7983	2	12.09	1795	1	752	763	
G.LRGDKGETGEAGER.G	N	23.05	1473.7172	-0.3	492.2462	3	8.56	1206	1	822	835	
G.FAGPPGADGQPGAK.G	N	22.00	1268.6149	-0.4	635.3145	2	10.23	1471	1	597	610	

total 3 peptides

tr|A0A0F8B7E5|A0A0F8B7E5_LARCR
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GERGFPGLPGPS.G	N	28.43	1169.5829	-0.8	585.7983	2	12.09	1795	1	916	927	
G.LRGDKGETGEAGER.G	N	23.05	1473.7172	-0.3	492.2462	3	8.56	1206	1	1040	1053	
G.FAGPPGADGQPGAK.G	N	22.00	1268.6149	-0.4	635.3145	2	10.23	1471	1	761	774	

total 3 peptides

tr|A0A6G0HX74|A0A6G0HX74_LARCR
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GERGFPGLPGPS.G	N	28.43	1169.5829	-0.8	585.7983	2	12.09	1795	1	952	963	
G.LRGDKGETGEAGER.G	N	23.05	1473.7172	-0.3	492.2462	3	8.56	1206	1	1076	1089	
G.FAGPPGADGQPGAK.G	N	22.00	1268.6149	-0.4	635.3145	2	10.23	1471	1	797	810	

total 3 peptides

tr|A0A5J6XWD3|A0A5J6XWD3_NIBCO
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GERGFPGLPGPS.G	N	28.43	1169.5829	-0.8	585.7983	2	12.09	1795	1	952	963	
G.LRGDKGETGEAGER.G	N	23.05	1473.7172	-0.3	492.2462	3	8.56	1206	1	1076	1089	
G.FAGPPGADGQPGAK.G	N	22.00	1268.6149	-0.4	635.3145	2	10.23	1471	1	797	810	

total 3 peptides

tr|A0A7N8XDE6|A0A7N8XDE6_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GERGFPGLPGPS.G	N	28.43	1169.5829	-0.8	585.7983	2	12.09	1795	1	754	765	
G.LRGDKGETGEAGER.G	N	23.05	1473.7172	-0.3	492.2462	3	8.56	1206	1	824	837	
G.FAGPPGADGQPGAK.G	N	22.00	1268.6149	-0.4	635.3145	2	10.23	1471	1	599	612	

total 3 peptides

tr|A0A7N8WW01|A0A7N8WW01_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GERGFPGLPGPS.G	N	28.43	1169.5829	-0.8	585.7983	2	12.09	1795	1	821	832	
G.LRGDKGETGEAGER.G	N	23.05	1473.7172	-0.3	492.2462	3	8.56	1206	1	891	904	

total 3 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.FAGPPGADGQPGAK.G	N	22.00	1268.6149	-0.4	635.3145	2	10.23	1471	1	666	679	

total 3 peptides

tr|A0A7N8XAN7|A0A7N8XAN7_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GERGFPGLPGPS.G	N	28.43	1169.5829	-0.8	585.7983	2	12.09	1795	1	862	873	
G.LRGDKGETGEAGER.G	N	23.05	1473.7172	-0.3	492.2462	3	8.56	1206	1	932	945	
G.FAGPPGADGQPGAK.G	N	22.00	1268.6149	-0.4	635.3145	2	10.23	1471	1	707	720	

total 3 peptides

tr|A0A4W4EA72|A0A4W4EA72_ELEEL
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	59	67	
T.VLDRDKSGFIEEEELK.L	Y	28.30	1905.9683	-20.3	953.9720	2	11.67	1719	2	50	65	

total 2 peptides

tr|A0A6F9CEX9|A0A6F9CEX9_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.LDPIDAPGKPDVIS.I	Y	29.78	1435.7559	-0.9	718.8846	2	11.96	1772	1	8748	8761	
L.IVEELPVKW.V	N	29.07	1111.6277	-0.4	556.8209	2	13.24	1997	1	577	585	

total 2 peptides

tr|A0A668V0Q0|A0A668V0Q0_OREAU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VIISAPSADAPMF.V	Y	36.31	1317.6638	0.4	659.8394	2	13.94	2114	1	126	138	
F.HERDPAN.I	N	15.89	837.3729	-0.2	419.6937	2	7.17	946	3	85	91	

total 2 peptides

tr|Q8AWX8|Q8AWX8_GADMO
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VIISAPSADAPMF.V	Y	36.31	1317.6638	0.4	659.8394	2	13.94	2114	1	117	129	
F.HERDPAN.I	N	15.89	837.3729	-0.2	419.6937	2	7.17	946	3	76	82	

total 2 peptides

tr|A0A6P7KWB3|A0A6P7KWB3_BETSP
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VIISAPSADAPMF.V	Y	36.31	1317.6638	0.4	659.8394	2	13.94	2114	1	117	129	
F.HERDPAN.I	N	15.89	837.3729	-0.2	419.6937	2	7.17	946	3	76	82	

total 2 peptides

tr|Q4VKA7|Q4VKA7_PARLE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VIISAPSADAPMF.V	Y	36.31	1317.6638	0.4	659.8394	2	13.94	2114	1	72	84	
F.HERDPAN.I	N	15.89	837.3729	-0.2	419.6937	2	7.17	946	3	31	37	

total 2 peptides

tr|A0A4W6CL45|A0A4W6CL45_LATCA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.S	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	225	236	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	307	317	

total 2 peptides

tr|A0A671XZM8|A0A671XZM8_SPAAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	225	236	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	307	317	

total 2 peptides

tr|A0A671Y6A5|A0A671Y6A5_SPAAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	211	222	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	284	294	

total 2 peptides

tr|A0A672HWD2|A0A672HWD2_SALFA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	211	222	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	293	303	

total 2 peptides

tr|A0A672HWL2|A0A672HWL2_SALFA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	218	229	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	300	310	

total 2 peptides

tr|A0A671XZM4|A0A671XZM4_SPAAU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	224	235	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	297	307	

total 2 peptides

tr|A0A672HWC2|A0A672HWC2_SALFA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	227	238	
Peptide	**Uniq**	**-10lgP**	**Mass**	**ppm**	**m/z**	**z**	**RT**	**Scan**	**#Spec**	**Start**	**End**	**PTM**
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	309	319	

total 2 peptides

tr|A0A672HXH8|A0A672HXH8_SALFA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	225	236	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	310	320	

total 2 peptides

tr|A0A672HWL0|A0A672HWL0_SALFA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	228	239	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	310	320	

total 2 peptides

tr|A0A672HXF4|A0A672HXF4_SALFA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	229	240	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	311	321	

total 2 peptides

tr|A0A671XZK3|A0A671XZK3_SPAAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	225	236	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	307	317	

total 2 peptides

tr|A0A672HWP0|A0A672HWP0_SALFA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	233	244	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	315	325	

total 2 peptides

tr|A0A4W6CL16|A0A4W6CL16_LATCA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.S	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	223	234	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	305	315	

total 2 peptides

tr|A0A4W6CL41|A0A4W6CL41_LATCA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.S	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	225	236	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	307	317	

total 2 peptides

tr|A0A672HXA9|A0A672HXA9_SALFA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	238	249	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	320	330	

total 2 peptides

tr|A0A672HW84|A0A672HW84_SALFA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	240	251	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	322	332	

total 2 peptides

tr|A0A671XZP8|A0A671XZP8_SPAAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	253	264	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	326	336	

total 2 peptides

tr|A0A4U5UZN8|A0A4U5UZN8_COLLU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.S	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	225	236	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	307	317	

total 2 peptides

tr|A0A3Q3JCJ6|A0A3Q3JCJ6_MONAL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	218	229	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	300	310	

total 2 peptides

tr|A0A3B4WCW4|A0A3B4WCW4_SERLL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	225	236	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	297	307	

total 2 peptides

tr|A0A3B4UFZ1|A0A3B4UFZ1_SERDU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	225	236	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	296	306	

total 2 peptides

tr|A0A3B4WCV3|A0A3B4WCV3_SERLL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.MDDPVVIPGKPY.T	N	35.25	1329.6638	-0.8	665.8386	2	12.28	1829	1	225	236	
S.IVWIDPDDFPL.L	N	15.72	1328.6652	-0.2	665.3397	2	16.16	2489	1	307	317	

total 2 peptides

tr|A0A484CIB2|A0A484CIB2_PERFV
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.LRGDKGETGEAGER.G	N	23.05	1473.7172	-0.3	492.2462	3	8.56	1206	1	1076	1089	
M.GPMGPRGPPGAP.G	N	22.19	1089.5389	-0.6	545.7764	2	10.30	1483	1	166	177	
G.FAGPPGADGQPGAK.G	N	22.00	1268.6149	-0.4	635.3145	2	10.23	1471	1	797	810	

total 3 peptides

tr|A0A6A4SNF9|A0A6A4SNF9_SCOMX
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.IEEEELKLF.L	N	30.75	1148.5964	-0.3	575.3053	2	13.44	2031	1	156	164	
A.FDIIDQDKSGFIE.E	Y	21.42	1525.7300	-2.3	763.8705	2	20.04	3125	1	226	238	

total 2 peptides

tr|A0A3B3CIU5|A0A3B3CIU5_ORYME
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GERGFPGLPGPS.G	N	28.43	1169.5829	-0.8	585.7983	2	12.09	1795	1	704	715	
M.GPMGPRGPPGAP.G	N	22.19	1089.5389	-0.6	545.7764	2	10.30	1483	1	44	55	

total 2 peptides

tr|A0A834FQR3|A0A834FQR3_ORYME
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GERGFPGLPGPS.G	N	28.43	1169.5829	-0.8	585.7983	2	12.09	1795	1	964	975	
S.GPMGPRGPPGAP.G	N	22.19	1089.5389	-0.6	545.7764	2	10.30	1483	1	253	264	

total 2 peptides

tr|A0A437DEJ9|A0A437DEJ9_ORYJA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GERGFPGLPGPS.G	N	28.43	1169.5829	-0.8	585.7983	2	12.09	1795	1	994	1005	
S.GPMGPRGPPGAP.G	N	22.19	1089.5389	-0.6	545.7764	2	10.30	1483	1	241	252	

total 2 peptides

tr|G3N515|G3N515_GASAC
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.IVEELPVKW.L	N	29.07	1111.6277	-0.4	556.8209	2	13.24	1997	1	130	138	
A.ILPPGPPTPW.I	N	19.56	1073.5909	0.5	537.8030	2	13.74	2081	1	3917	3926	

total 2 peptides

tr|Q4T444|Q4T444_TETNG
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.IVEELPVKW.V	N	29.07	1111.6277	-0.4	556.8209	2	13.24	1997	1	625	633	
A.ILPPGPPTPW.I	N	19.56	1073.5909	0.5	537.8030	2	13.74	2081	1	4399	4408	

total 2 peptides

tr|A0A6P7IXE2|A0A6P7IXE2_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.SLAPAPAPAPAPAPTTT.S	Y	37.39	1697.8988	-22.4	849.9377	2	11.95	1770	1	395	413	

total 1 peptides

tr|A0A3Q1HW42|A0A3Q1HW42_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.SELPVDDVFGQ.V	Y	24.56	1204.5612	0.1	603.2879	2	13.67	2069	1	175	185	
K.VDSELPVDDVFGQ.V	Y	23.48	1418.6565	-0.3	710.3353	2	13.85	2099	1	173	185	

total 2 peptides

tr|A0A3B5BIY5|A0A3B5BIY5_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.SELPVDDVFGQ.V	Y	24.56	1204.5612	0.1	603.2879	2	13.67	2069	1	175	185	
K.VDSELPVDDVFGQ.V	Y	23.48	1418.6565	-0.3	710.3353	2	13.85	2099	1	173	185	

total 2 peptides

tr|A0A3Q4GK85|A0A3Q4GK85_NEOBR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.SELPVDDVFGQ.V	Y	24.56	1204.5612	0.1	603.2879	2	13.67	2069	1	174	184	
K.VDSELPVDDVFGQ.V	Y	23.48	1418.6565	-0.3	710.3353	2	13.85	2099	1	172	184	

total 2 peptides

tr|A0A3Q4GS43|A0A3Q4GS43_NEOBR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.SELPVDDVFGQ.V	Y	24.56	1204.5612	0.1	603.2879	2	13.67	2069	1	175	185	
K.VDSELPVDDVFGQ.V	Y	23.48	1418.6565	-0.3	710.3353	2	13.85	2099	1	173	185	

total 2 peptides

tr|A0A3P8P8S3|A0A3P8P8S3_ASTCA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM

total 2 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.SELPVDDVFGQ.V	Y	24.56	1204.5612	0.1	603.2879	2	13.67	2069	1	175	185	
K.VDSELPVDDVFGQ.V	Y	23.48	1418.6565	-0.3	710.3353	2	13.85	2099	1	173	185	

total 2 peptides

tr|A0A3P9CWL7|A0A3P9CWL7_9CICH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.SELPVDDVFGQ.V	Y	24.56	1204.5612	0.1	603.2879	2	13.67	2069	1	175	185	
K.VDSELPVDDVFGQ.V	Y	23.48	1418.6565	-0.3	710.3353	2	13.85	2099	1	173	185	

total 2 peptides

tr|A0A3Q2VY92|A0A3Q2VY92_HAPBU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.SELPVDDVFGQ.V	Y	24.56	1204.5612	0.1	603.2879	2	13.67	2069	1	175	185	
K.VDSELPVDDVFGQ.V	Y	23.48	1418.6565	-0.3	710.3353	2	13.85	2099	1	173	185	

total 2 peptides

tr|A0A3B4FMK3|A0A3B4FMK3_9CICH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.SELPVDDVFGQ.V	Y	24.56	1204.5612	0.1	603.2879	2	13.67	2069	1	175	185	
K.VDSELPVDDVFGQ.V	Y	23.48	1418.6565	-0.3	710.3353	2	13.85	2099	1	173	185	

total 2 peptides

tr|A0A3Q3CWR9|A0A3Q3CWR9_HAPBU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.SELPVDDVFGQ.V	Y	24.56	1204.5612	0.1	603.2879	2	13.67	2069	1	193	203	
K.VDSELPVDDVFGQ.V	Y	23.48	1418.6565	-0.3	710.3353	2	13.85	2099	1	191	203	

total 2 peptides

tr|A0A3P8P8V3|A0A3P8P8V3_ASTCA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.SELPVDDVFGQ.V	Y	24.56	1204.5612	0.1	603.2879	2	13.67	2069	1	193	203	
K.VDSELPVDDVFGQ.V	Y	23.48	1418.6565	-0.3	710.3353	2	13.85	2099	1	191	203	

total 2 peptides

tr|A0A3Q3WSG6|A0A3Q3WSG6_MOLML
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.IKWGEAGAQ.Y	Y	25.43	958.4872	-0.5	480.2506	2	10.91	1584	1	83	91	
R.VVISAPSADAPMF.V	N	15.30	1303.6482	0.0	652.8314	2	13.76	2084	1	117	129	

total 2 peptides

tr|A0A6P7K206|A0A6P7K206_9TELE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.HERDPAN.I	N	15.89	837.3729	-0.2	419.6937	2	7.17	946	3	77	83	
R.VVISAPSADAPMF.V	N	15.30	1303.6482	0.0	652.8314	2	13.76	2084	1	114	126	

total 2 peptides

tr|F5BZT7|F5BZT7_EPIBR
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.HERDPAN.I	N	15.89	837.3729	-0.2	419.6937	2	7.17	946	3	77	83	
R.VVISAPSADAPMF.V	N	15.30	1303.6482	0.0	652.8314	2	13.76	2084	1	118	130	

total 2 peptides

tr|A0A076U5J2|A0A076U5J2_SALFO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.HERDPAN.I	N	15.89	837.3729	-0.2	419.6937	2	7.17	946	3	42	48	
R.VVISAPSADAPMF.V	N	15.30	1303.6482	0.0	652.8314	2	13.76	2084	1	83	95	

total 2 peptides

tr|A0A1A8SH28|A0A1A8SH28_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.VSGASGPLGPP.G	Y	23.48	937.4869	0.0	469.7507	2	10.51	1517	1	939	949	

total 1 peptides

tr|A0A1A8AFF3|A0A1A8AFF3_NOTFU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.VSGASGPLGPP.G	Y	23.48	937.4869	0.0	469.7507	2	10.51	1517	1	1328	1338	

total 1 peptides

tr|A0A6P6JF49|A0A6P6JF49_CARAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.VSGASGPLGPP.G	Y	23.48	937.4869	0.0	469.7507	2	10.51	1517	1	1373	1383	

total 1 peptides

tr|A0A1A7ZX47|A0A1A7ZX47_NOTFU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.VSGASGPLGPP.G	Y	23.48	937.4869	0.0	469.7507	2	10.51	1517	1	1397	1407	

total 1 peptides

tr|A0A6P6JAI8|A0A6P6JAI8_CARAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.VSGASGPLGPP.G	Y	23.48	937.4869	0.0	469.7507	2	10.51	1517	1	1402	1412	

total 1 peptides

tr|A0A1A8VA48|A0A1A8VA48_NOTFU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.VSGASGPLGPP.G	Y	23.48	937.4869	0.0	469.7507	2	10.51	1517	1	1488	1498	

total 1 peptides

tr|A0A6P6JA06|A0A6P6JA06_CARAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.VSGASGPLGPP.G	Y	23.48	937.4869	0.0	469.7507	2	10.51	1517	1	1422	1432	

total 1 peptides

tr|A0A6P6J9V5|A0A6P6J9V5_CARAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.VSGASGPLGPP.G	Y	23.48	937.4869	0.0	469.7507	2	10.51	1517	1	1474	1484	

total 1 peptides

tr|A0A1A8S1T5|A0A1A8S1T5_9TELE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.VSGASGPLGPP.G	Y	23.48	937.4869	0.0	469.7507	2	10.51	1517	1	1492	1502	

total 1 peptides

tr|A0A6P6JCL5|A0A6P6JCL5_CARAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.VSGASGPLGPP.G	Y	23.48	937.4869	0.0	469.7507	2	10.51	1517	1	1503	1513	

total 1 peptides

tr|A0A3P8TNL0|A0A3P8TNL0_AMPPE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.EVDAVRAL.P	Y	22.74	871.4763	-0.4	436.7452	2	11.50	1689	1	449	456	

total 1 peptides

tr|A0A6P6M1S2|A0A6P6M1S2_CARAU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.LENQQLAQIL.K	Y	22.02	1168.6451	-8.7	585.3248	2	13.10	1974	2	351	360	

total 1 peptides

tr|A0A315V5V2|A0A315V5V2_GAMAF
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.LNLDNVVSGLSI.H	Y	21.66	1242.6819	-10.1	622.3419	2	18.21	2815	4	844	855	

total 1 peptides

tr|A0A3P8PXL3|A0A3P8PXL3_ASTCA
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.SASPSPGPRMPM.P	Y	21.04	1213.5583	-22.2	607.7730	2	12.78	1917	1	109	120	

total 1 peptides

tr|A0A674A9W5|A0A674A9W5_SALTR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.IVPIVEPEILPD.G	Y	20.23	1332.7540	0.1	667.3843	2	14.32	2177	1	182	193	

total 1 peptides

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1. Notes

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)

Table 1. Statistics of data.

# of MS Scans	1020
# of MS/MS Scans	2347

Table 2. Result filtration parameters.

Peptide -10lgP	≥15
Protein -10lgP	≥20
Proteins unique peptides	≥0
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	104
Peptide Sequences	101
Protein Groups	32
Proteins	142
Proteins (#Unique Peptides)	18 (>2); 9 (=2); 91 (=1);
FDR (Peptide-Spectrum Matches)	28.8%
FDR (Peptide Sequences)	29.7%
FDR (Protein)	5.6%
De Novo Only Spectra	619

Table 4. PTM profile.

Name	ΔMass	#PSM	Position

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)

Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Orbi2222	0	0	0	0	101

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS 7.0
Parent Mass Error Tolerance: 0.03 Da
Fragment Mass Error Tolerance: 0.1 Da
Precursor Mass Search Type: monoisotopic
Enzyme: None
Max Missed Cleavages: 100
Non-specific Cleavage: both
Max variable PTM per peptide: 3
Database: Arthropoda
Taxon: All
Searched Entry: 6735671
FDR Estimation: Enabled
Merge Options: 0.1 min. 0.03 Da
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB_PIMENTA_HA_20220211_01.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID/ECD
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
1	53234	tr|A0A3R7M007|A0A3R7M007_PENVA	115.11	31	21	21	N	41323	Actin 1 OS=Penaeus vannamei OX=6689 GN=C7M84_012584 PE=3 SV=1
1	53235	tr|A0A2H4V3D7|A0A2H4V3D7_PENVA	115.11	31	21	21	N	41688	Actin 1 OS=Penaeus vannamei OX=6689 GN=C7M84_012586 PE=2 SV=1
1	53236	tr|H9B3Y9|H9B3Y9_SCYPA	115.11	31	21	21	N	41781	Beta-actin OS=Scylla paramamosain OX=85552 PE=2 SV=1
1	53237	tr|A0A6A0H005|A0A6A0H005_HYAAZ	115.11	31	21	21	N	41604	Uncharacterized protein OS=Hyalella azteca OX=294128 GN=HAZT_HAZT002759 PE=3 SV=1
1	53238	tr|A0A3R7NX50|A0A3R7NX50_PENVA	115.11	31	21	21	N	41716	Actin 1 OS=Penaeus vannamei OX=6689 GN=C7M84_012585 PE=3 SV=1
1	53239	tr|A0A482LUC2|A0A482LUC2_CANBE	115.11	31	21	21	N	41781	Actin 1 OS=Cancer borealis OX=39395 GN=ACT1 PE=2 SV=1
1	53240	tr|A0A0B5J9E4|A0A0B5J9E4_ERISI	115.11	31	21	21	N	41751	Skeletal muscle actin 1 OS=Eriocheir sinensis OX=95602 GN=ActSK1 PE=2 SV=1
1	53241	tr|A0A2H4V3D6|A0A2H4V3D6_PENVA	115.11	31	21	21	N	41801	Slow-type skeletal muscle actin 10 OS=Penaeus vannamei OX=6689 PE=2 SV=1
1	53242	tr|A0A2H4V3F0|A0A2H4V3F0_PENVA	115.11	31	21	21	N	41743	Slow-type skeletal muscle actin 7 OS=Penaeus vannamei OX=6689 PE=2 SV=1
1	53243	tr|U3M7F7|U3M7F7_PORTR	115.11	31	21	21	N	41793	Skeletal muscle actin 1 OS=Portunus trituberculatus OX=210409 PE=2 SV=1
10	53387	tr|A7BJ42|A7BJ42_PROCL	88.49	13	4	1	N	14275	Calcification associated soluble matrix protein 2 OS=Procambarus clarkii OX=6728 GN=casp-2 PE=2 SV=1
10	53388	tr|D7RVB0|D7RVB0_CALSI	88.49	12	4	1	N	15426	Early cuticle protein 3 OS=Callinectes sapidus OX=6763 PE=2 SV=1
10	53389	tr|D7RVB1|D7RVB1_CALSI	88.49	12	4	1	N	15460	Early cuticle protein 4 OS=Callinectes sapidus OX=6763 PE=2 SV=1
10	53390	tr|D7RVA8|D7RVA8_CALSI	88.49	12	4	1	N	15521	Early cuticle protein 1 OS=Callinectes sapidus OX=6763 PE=2 SV=1
10	53391	tr|D7RVA9|D7RVA9_CALSI	88.49	12	4	1	N	15462	Early cuticle protein 2 OS=Callinectes sapidus OX=6763 PE=2 SV=1
10	53392	tr|A0A5B7E6L1|A0A5B7E6L1_PORTR	88.49	11	4	1	N	17015	Endocuticle structural glycoprotein SgAbd-1 OS=Portunus trituberculatus OX=210409 GN=CUD1_1 PE=4 SV=1
10	53393	tr|A0A5B7E6X8|A0A5B7E6X8_PORTR	88.49	6	4	1	N	52804	Cuticle protein AM1199 OS=Portunus trituberculatus OX=210409 GN=CUPA3_11 PE=4 SV=1
11	53428	tr|A0A5B7E6A3|A0A5B7E6A3_PORTR	83.17	11	4	1	N	16545	Larval cuticle protein LCP-17 OS=Portunus trituberculatus OX=210409 GN=LCP17_3 PE=4 SV=1
4	53308	tr|A0A5B7IZE3|A0A5B7IZE3_PORTR	81.55	16	6	4	N	26459	Myosin heavy chain, muscle OS=Portunus trituberculatus OX=210409 GN=Mhc_24 PE=3 SV=1

total 142 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
8	53314	tr|F8WR03|F8WR03_PENJP	80.39	2	4	0	N	219503	Myosin heavy chain type a OS=Penaeus japonicus OX=27405 GN=MYHa PE=2 SV=1
8	53315	tr|K4Q111|K4Q111_PENVA	80.39	2	4	0	N	219712	Myosin heavy chain type 1 OS=Penaeus vannamei OX=6689 GN=MYH1 PE=2 SV=1
8	53316	tr|K4Q4N8|K4Q4N8_PENMO	80.39	2	4	0	N	219585	Myosin heavy chain type 1 OS=Penaeus monodon OX=6687 GN=MYH1 PE=2 SV=1
12	53411	tr|A0A2P1JJ59|A0A2P1JJ59_PROCL	75.46	3	4	4	N	97467	Alpha-1,4 glucan phosphorylase (Fragment) OS=Procambarus clarkii OX=6728 GN=Glyp PE=2 SV=1
7	53302	tr|A0A5B7DQZ0|A0A5B7DQZ0_PORTR	74.33	2	5	2	N	352200	Myosin heavy chain, muscle OS=Portunus trituberculatus OX=210409 GN=Mhc_1 PE=3 SV=1
6	53363	tr|A0A223G1B9|A0A223G1B9_SCYSE	71.99	4	5	5	N	79160	Cryptocyanin OS=Scylla serrata OX=6761 PE=2 SV=1
14	53398	tr|A0A7R8CX21|A0A7R8CX21_LEPSM	70.54	1	3	0	N	202190	MYH6_7 OS=Lepeophtheirus salmonis OX=72036 GN=LSAA_10697 PE=3 SV=1
14	53399	tr|A0A7T8HL88|A0A7T8HL88_CALRO	70.54	1	3	0	N	215000	Myosin heavy chain 1 OS=Caligus rogercresseyi OX=217165 GN=FKW44_003971 PE=3 SV=1
14	53400	tr|A0A7T8HL29|A0A7T8HL29_CALRO	70.54	1	3	0	N	214908	Myosin heavy chain 1 OS=Caligus rogercresseyi OX=217165 GN=FKW44_003975 PE=3 SV=1
14	53401	tr|A0A0K2V7Y7|A0A0K2V7Y7_LEPSM	70.54	1	3	0	N	218544	Myosin heavy chain 1 [Tribolium castaneum] OS=Lepeophtheirus salmonis OX=72036 GN=Mhc1 PE=3 SV=1
14	53402	tr|A0A7R8GZZ9|A0A7R8GZZ9_LEPSM	70.54	1	3	0	N	220303	MYH6_7 OS=Lepeophtheirus salmonis OX=72036 GN=LSAA_1562 PE=3 SV=1
14	53403	tr|A0A0K2T3U6|A0A0K2T3U6_LEPSM	70.54	1	3	0	N	220566	Myosin heavy chain 1 [Tribolium castaneum] OS=Lepeophtheirus salmonis OX=72036 GN=Mhc1 PE=3 SV=1
14	53404	tr|A0A0K2TSJ7|A0A0K2TSJ7_LEPSM	70.54	1	3	0	N	222210	Myosin heavy chain 1 [Tribolium castaneum] (Fragment) OS=Lepeophtheirus salmonis OX=72036 GN=Mhc1 PE=3 SV=1
3	53320	tr|A0A4Y7MKW9|A0A4Y7MKW9_9CRUS	67.38	5	6	0	N	97229	P-type Ca(2+) transporter (Fragment) OS=Daphnia magna OX=35525 GN=EOG090X00V6 PE=2 SV=1
3	53321	tr|A0A0P5KSW7|A0A0P5KSW7_9CRUS	67.38	4	6	0	N	110371	Calcium-transporting ATPase OS=Daphnia magna OX=35525 PE=3 SV=1
3	53322	tr|A0A4Y7MXF9|A0A4Y7MXF9_9CRUS	67.38	4	6	0	N	110591	Calcium-transporting ATPase OS=Daphnia pulicaria OX=35523 GN=EOG090X00V6 PE=2 SV=1
3	53323	tr|A0A0P4ZGF4|A0A0P4ZGF4_9CRUS	67.38	4	6	0	N	110708	Calcium-transporting ATPase OS=Daphnia magna OX=35525 GN=APZ42_012354 PE=3 SV=1
3	53324	tr|A0A4Y7MVM2|A0A4Y7MVM2_DAPPU	67.38	4	6	0	N	110862	Calcium-transporting ATPase OS=Daphnia pulex OX=6669 GN=EOG090X00V6 PE=2 SV=1
3	53325	tr|A0A4Y7M702|A0A4Y7M702_9CRUS	67.38	4	6	0	N	111071	Calcium-transporting ATPase OS=Daphnia hispanica OX=575233 GN=EOG090X00V6 PE=2 SV=1
3	53326	tr|A0A4Y7MHQ5|A0A4Y7MHQ5_9CRUS	67.38	4	6	0	N	111377	Calcium-transporting ATPase OS=Daphnia magna OX=35525 GN=EOG090X00V6 PE=2 SV=1
3	53327	tr|A0A4Y7ME47|A0A4Y7ME47_9CRUS	67.38	4	6	0	N	111392	Calcium-transporting ATPase OS=Daphnia magna OX=35525 GN=EOG090X00V6 PE=2 SV=1
3	53328	tr|A0A4Y7M4I0|A0A4Y7M4I0_9CRUS	67.38	4	6	0	N	111723	Calcium-transporting ATPase OS=Daphnia dolichocephala OX=2282166 GN=EOG090X00V6 PE=2 SV=1
3	53329	tr|A0A1D2MC18|A0A1D2MC18_ORCCI	67.38	4	6	0	N	112226	Calcium-transporting ATPase OS=Orchesella cincta OX=48709 GN=Ocin01_16136 PE=3 SV=1

total 142 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
3	53330	tr|E9HR84|E9HR84_DAPPU	67.38	4	6	0	N	113043	Calcium-transporting ATPase OS=Daphnia pulex OX=6669 GN=DAPPUDRAFT_65262 PE=3 SV=1
3	53331	tr|A0A0P5VJX3|A0A0P5VJX3_9CRUS	67.38	4	6	0	N	113098	Calcium-transporting ATPase OS=Daphnia magna OX=35525 PE=3 SV=1
3	53332	tr|A0A4Y7LYL4|A0A4Y7LYL4_9CRUS	67.38	4	6	0	N	113136	Calcium-transporting ATPase OS=Daphnia atkinsoni OX=342845 GN=EOG090X00V6 PE=2 SV=1
5	53318	tr|A0A0C5E1J4|A0A0C5E1J4_CHEDE	65.79	4	5	0	N	109565	Calcium-transporting ATPase OS=Cherax destructor OX=6723 PE=2 SV=1
9	53378	tr|A0A0N9EJJ5|A0A0N9EJJ5_ERIVE	61.23	4	4	4	N	77227	Hemocyanin OS=Eriphia verrucosa OX=483417 GN=H PE=2 SV=1
2	53418	tr|A0A2Z4I2U3|A0A2Z4I2U3_CALSI	58.61	4	7	1	N	111733	Calcium-transporting ATPase OS=Callinectes sapidus OX=6763 GN=SERCA PE=2 SV=1
16	53419	tr|A0A0P4W579|A0A0P4W579_SCYOL	58.49	4	2	2	N	54554	Uncharacterized protein OS=Scylla olivacea OX=85551 PE=4 SV=1
16	53420	tr|A0A0P4WKI4|A0A0P4WKI4_SCYOL	58.49	3	2	2	N	78230	Uncharacterized protein OS=Scylla olivacea OX=85551 PE=4 SV=1
16	53421	tr|A0A0P4WBU2|A0A0P4WBU2_SCYOL	58.49	3	2	2	N	94430	Uncharacterized protein OS=Scylla olivacea OX=85551 PE=4 SV=1
17	53427	tr|A0A3R7PTG0|A0A3R7PTG0_PENVA	49.31	8	2	2	N	18720	Myosin light chain 2 OS=Penaeus vannamei OX=6689 GN=C7M84_004824 PE=4 SV=1
15	53394	tr|A0A195D1T6|A0A195D1T6_9HYME	47.57	0	2	2	N	1073055	Titin OS=Cyphomyrmex costatus OX=456900 GN=ALC62_02215 PE=3 SV=1
15	53396	tr|A0A151I5T2|A0A151I5T2_9HYME	47.57	0	2	2	N	1059815	Titin OS=Atta colombica OX=520822 GN=ALC53_03162 PE=3 SV=1
15	53397	tr|A0A151J500|A0A151J500_9HYME	47.57	0	2	2	N	1075189	Titin OS=Trachymyrmex cornetzi OX=471704 GN=ALC57_09858 PE=3 SV=1
15	53469	tr|E2BUG0|E2BUG0_HARSA	47.57	0	2	2	N	660642	Titin OS=Harpegnathos saltator OX=610380 GN=EAI_13877 PE=3 SV=1
13	53379	tr|A0A5N5SKQ0|A0A5N5SKQ0_9CRUS	45.97	3	3	3	N	101132	Filamin-A OS=Armadillidium nasatum OX=96803 GN=cher PE=3 SV=1
13	53380	tr|A0A444SHR5|A0A444SHR5_ARMVU	45.97	3	3	3	N	88595	Filamin-A (Fragment) OS=Armadillidium vulgare OX=13347 GN=Avbf_11273 PE=3 SV=1
13	53381	tr|A0A3R7Q393|A0A3R7Q393_PENVA	45.97	3	3	3	N	99699	Putative filamin-A isoform X4 OS=Penaeus vannamei OX=6689 GN=C7M84_021889 PE=3 SV=1
13	53382	tr|A0A2P1JJ42|A0A2P1JJ42_PROCL	45.97	2	3	3	N	167860	Filamin-A isoform X5 (Fragment) OS=Procambarus clarkii OX=6728 GN=Flna PE=2 SV=1
42	53503	tr|A0A834J309|A0A834J309_RHYFE	39.43	0	1	1	N	981760	Uncharacterized protein OS=Rhynchophorus ferrugineus OX=354439 GN=GWI33_002833 PE=4 SV=1
18	53529	tr|A0A6M2D681|A0A6M2D681_RHIMP	31.83	11	1	1	N	13868	Putative conserved secreted protein OS=Rhipicephalus microplus OX=6941 PE=4 SV=1
18	53530	tr|A0A6G5A756|A0A6G5A756_RHIMP	31.83	11	1	1	N	13838	Putative conserved secreted protein OS=Rhipicephalus microplus OX=6941 PE=4 SV=1
43	53532	tr|A0A2J7R8E8|A0A2J7R8E8_9NEOP	28.61	1	1	1	N	110847	Uncharacterized protein OS=Cryptotermes secundus OX=105785 GN=B7P43_G07431 PE=4 SV=1
44	53533	tr|A0A423SLW8|A0A423SLW8_PENVA	28.36	4	1	1	N	24833	Malate dehydrogenase OS=Penaeus vannamei OX=6689 GN=C7M84_016800 PE=3 SV=1
44	53534	tr|A0A5B7CL07|A0A5B7CL07_PORTR	28.36	4	1	1	N	30579	Malate dehydrogenase OS=Portunus trituberculatus OX=210409 GN=MDH1 PE=3 SV=1
44	53535	tr|A0A0P4WLG3|A0A0P4WLG3_SCYOL	28.36	3	1	1	N	35829	Malate dehydrogenase OS=Scylla olivacea OX=85551 PE=3 SV=1

total 142 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
45	53537	tr|A0A1W4VNV5|A0A1W4VNV5_DROFC	26.84	1	1	1	N	111050	prominin-like protein isoform X4 OS=Drosophila ficusphila OX=30025 GN=LOC108099069 PE=3 SV=1
45	53538	tr|A0A1W4W0Y9|A0A1W4W0Y9_DROFC	26.84	1	1	1	N	113905	prominin-like protein isoform X3 OS=Drosophila ficusphila OX=30025 GN=LOC108099069 PE=3 SV=1
45	53539	tr|A0A1W4W054|A0A1W4W054_DROFC	26.84	1	1	1	N	116227	prominin-like protein isoform X2 OS=Drosophila ficusphila OX=30025 GN=LOC108099069 PE=3 SV=1
45	53540	tr|A0A1W4VNL1|A0A1W4VNL1_DROFC	26.84	1	1	1	N	116315	prominin-like protein isoform X1 OS=Drosophila ficusphila OX=30025 GN=LOC108099069 PE=3 SV=1
46	53541	tr|A0A146ME36|A0A146ME36_LYGHE	26.60	2	1	1	N	70072	AP-1 complex subunit gamma-1 (Fragment) OS=Lygus hesperus OX=30085 GN=Ap1g1 PE=3 SV=1
46	53542	tr|A0A0A9ZCU1|A0A0A9ZCU1_LYGHE	26.60	1	1	1	N	93178	AP-1 complex subunit gamma OS=Lygus hesperus OX=30085 GN=Ap1g1_2 PE=3 SV=1
46	53543	tr|A0A0A9Z559|A0A0A9Z559_LYGHE	26.60	1	1	1	N	94621	AP-1 complex subunit gamma OS=Lygus hesperus OX=30085 GN=Ap1g1_0 PE=3 SV=1
47	53551	tr|A0A553NSJ7|A0A553NSJ7_TIGCA	26.07	5	1	1	N	19175	H15 domain-containing protein OS=Tigriopus californicus OX=6832 GN=TCAL_13520 PE=3 SV=1
47	53552	tr|A0A553NV74|A0A553NV74_TIGCA	26.07	5	1	1	N	19189	H15 domain-containing protein OS=Tigriopus californicus OX=6832 GN=TCAL_17452 PE=3 SV=1
48	53553	tr|B4L6N9|B4L6N9_DROMO	25.98	1	1	1	N	99753	Uncharacterized protein, isoform A OS=Drosophila mojavensis OX=7230 GN=Dmoj\GI16404 PE=4 SV=2
48	53554	tr|A0A484AUC9|A0A484AUC9_DRONA	25.98	1	1	1	N	124075	Uncharacterized protein OS=Drosophila navojoa OX=7232 GN=AWZ03_014422 PE=4 SV=1
61	53716	tr|A0A182HNK7|A0A182HNK7_ANOAR	24.12	0	1	1	N	239313	RTTN_N domain-containing protein OS=Anopheles arabiensis OX=7173 PE=4 SV=1
24	53595	tr|A0A1B0CTB8|A0A1B0CTB8_LUTLO	23.80	0	1	1	N	466597	Uncharacterized protein OS=Lutzomyia longipalpis OX=7200 PE=3 SV=1
24	53604	tr|E9IDT0|E9IDT0_SOLIN	23.80	1	1	1	N	162100	Uncharacterized protein (Fragment) OS=Solenopsis invicta OX=13686 GN=SINV_15254 PE=4 SV=1
24	53606	tr|A0A6V7J2X2|A0A6V7J2X2_9HYME	23.80	13	1	1	N	7026	eRF1_3 domain-containing protein (Fragment) OS=Bracon brevicornis OX=1563983 GN=BBRV_LOCUS36952 PE=4 SV=1
24	53607	tr|A0A7R8V5M9|A0A7R8V5M9_HERIL	23.80	3	1	1	N	32248	N-acetylglucosaminylphosphatidylinositol deacetylase OS=Hermetia illucens OX=343691 GN=HERILL_LOCUS15608 PE=3 SV=1
24	53608	tr|A0A0K8TNK6|A0A0K8TNK6_TABBR	23.80	3	1	1	N	33165	N-acetylglucosaminylphosphatidylinositol deacetylase (Fragment) OS=Tabanus bromius OX=304241 PE=2 SV=1
24	53609	tr|B4NGC5|B4NGC5_DROWI	23.80	2	1	1	N	40030	N-acetylglucosaminylphosphatidylinositol deacetylase OS=Drosophila willistoni OX=7260 GN=Dwil\GK22798 PE=3 SV=1
24	53610	tr|B4M4U0|B4M4U0_DROVI	23.80	2	1	1	N	39814	N-acetylglucosaminylphosphatidylinositol deacetylase OS=Drosophila virilis OX=7244 GN=Dvir\GJ10171 PE=3 SV=1
24	53611	tr|A0A484BDS3|A0A484BDS3_DRONA	23.80	2	1	1	N	40350	N-acetylglucosaminylphosphatidylinositol deacetylase OS=Drosophila navojoa OX=7232 GN=AWZ03_006647 PE=3 SV=1

total 142 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
24	53612	tr|A0A6J1M8J1|A0A6J1M8J1_DROHY	23.80	2	1	1	N	40571	N-acetylglucosaminylphosphatidylinositol deacetylase OS=Drosophila hydei OX=7224 GN=LOC111602076 PE=3 SV=1
24	53613	tr|B4KE34|B4KE34_DROMO	23.80	2	1	1	N	40618	N-acetylglucosaminylphosphatidylinositol deacetylase OS=Drosophila mojavensis OX=7230 GN=Dmoj\GI10317 PE=3 SV=1
24	53614	tr|A0A0M4EG71|A0A0M4EG71_DROBS	23.80	2	1	1	N	39846	N-acetylglucosaminylphosphatidylinositol deacetylase OS=Drosophila busckii OX=30019 GN=Dbus_chr3Rg2066 PE=3 SV=1
24	53615	tr|A0A6P8XFN0|A0A6P8XFN0_DROAB	23.80	2	1	1	N	40056	N-acetylglucosaminylphosphatidylinositol deacetylase OS=Drosophila albomicans OX=7291 GN=LOC117575192 PE=3 SV=1
24	53616	tr|A0A6J2TAH7|A0A6J2TAH7_DROLE	23.80	2	1	1	N	41626	N-acetylglucosaminylphosphatidylinositol deacetylase OS=Drosophila lebanonensis OX=7225 GN=LOC115623577 PE=3 SV=1
24	53617	tr|A0A6J2TEK1|A0A6J2TEK1_DROLE	23.80	2	1	1	N	42257	N-acetylglucosaminylphosphatidylinositol deacetylase OS=Drosophila lebanonensis OX=7225 GN=LOC115623577 PE=3 SV=1
24	53618	tr|A0A7I0ZIP4|A0A7I0ZIP4_DANPL	23.80	1	1	1	N	62756	atlastin isoform X2 OS=Danaus plexippus plexippus OX=278856 GN=LOC116772859 PE=3 SV=1
24	53619	tr|A0A7I0ZK43|A0A7I0ZK43_DANPL	23.80	1	1	1	N	62815	atlastin isoform X1 OS=Danaus plexippus plexippus OX=278856 GN=LOC116772859 PE=3 SV=1
24	53620	tr|A0A7M6UVA6|A0A7M6UVA6_NASVI	23.80	1	1	1	N	82594	Vesicle-fusing ATPase OS=Nasonia vitripennis OX=7425 PE=3 SV=1
24	53621	tr|A0A7M7QVM7|A0A7M7QVM7_NASVI	23.80	1	1	1	N	82560	Vesicle-fusing ATPase OS=Nasonia vitripennis OX=7425 PE=3 SV=1
24	53622	tr|A0A232F624|A0A232F624_9HYME	23.80	1	1	1	N	83056	Vesicle-fusing ATPase (Fragment) OS=Trichomalopsis sarcophagae OX=543379 GN=TSAR_012849 PE=3 SV=1
51	53645	tr|F4WT59|F4WT59_ACREC	22.27	1	1	1	N	143072	Probable ATP-dependent RNA helicase spindle-E OS=Acromyrmex echinatior OX=103372 GN=G5I_09034 PE=3 SV=1
51	53646	tr|A0A836FB18|A0A836FB18_9HYME	22.27	1	1	1	N	154532	SPNE helicase (Fragment) OS=Acromyrmex heyeri OX=230685 GN=Spne_1 PE=4 SV=1
51	53647	tr|A0A0J7L582|A0A0J7L582_LASNI	22.27	1	1	1	N	156393	Probable ATP-dependent RNA helicase spindle-E OS=Lasius niger OX=67767 GN=RF55_1956 PE=3 SV=1
51	53648	tr|A0A151J597|A0A151J597_9HYME	22.27	1	1	1	N	160408	Probable ATP-dependent RNA helicase spindle-E OS=Trachymyrmex cornetzi OX=471704 GN=ALC57_09730 PE=3 SV=1
51	53649	tr|A0A836JUW8|A0A836JUW8_9HYME	22.27	1	1	1	N	161165	SPNE helicase (Fragment) OS=Pseudoatta argentina OX=621737 GN=Spne_1 PE=4 SV=1
51	53650	tr|A0A836JG75|A0A836JG75_9HYME	22.27	1	1	1	N	162126	SPNE helicase (Fragment) OS=Acromyrmex insinuator OX=230686 GN=Spne_0 PE=4 SV=1
25	53623	tr|A0A1L3IWM3|A0A1L3IWM3_RHOPD	20.57	1	1	1	N	77923	ABC transporter G family member 23 variant X1 OS=Rhopalosiphum padi OX=40932 GN=ABCG23-1 PE=2 SV=1
25	53656	tr|A0A2S2QP63|A0A2S2QP63_9HEMI	20.57	3	1	1	N	27832	ABC transporter G family member 20 OS=Sipha flava OX=143950 GN=abcG20_2 PE=4 SV=1

total 142 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
25	53688	tr|A0A2S2NYH2|A0A2S2NYH2_SCHGA	20.57	3	1	1	N	31666	ABC transporter G family member 20 OS=Schizaphis graminum OX=13262 GN=abcG20_6 PE=4 SV=1
25	53689	tr|A0A6G0YXF5|A0A6G0YXF5_APHCR	20.57	1	1	1	N	71048	ABC transporter G family member 23-like OS=Aphis craccivora OX=307492 GN=FWK35_00011512 PE=4 SV=1
25	53690	tr|A0A6G0UB83|A0A6G0UB83_APHGL	20.57	1	1	1	N	75345	ABC transporter domain-containing protein OS=Aphis glycines OX=307491 GN=AGLY_001125 PE=4 SV=1
53	53655	tr|A0A182VZF1|A0A182VZF1_9DIPT	20.54	6	1	1	N	21968	ZAD domain-containing protein OS=Anopheles minimus OX=112268 PE=4 SV=1
54	53657	tr|A0A023ERZ2|A0A023ERZ2_AEDAL	20.51	3	1	1	N	45728	Pyruvate kinase (Fragment) OS=Aedes albopictus OX=7160 PE=2 SV=1
54	53658	tr|A0A0P8Y097|A0A0P8Y097_DROAN	20.51	2	1	1	N	55184	Pyruvate kinase OS=Drosophila ananassae OX=7217 GN=Dana\GF18439 PE=3 SV=1
54	53659	tr|A0A6P8K875|A0A6P8K875_DROMA	20.51	2	1	1	N	55073	Pyruvate kinase OS=Drosophila mauritiana OX=7226 GN=LOC117143834 PE=3 SV=1
54	53660	tr|A0A6P4F4P4|A0A6P4F4P4_DRORH	20.51	2	1	1	N	55028	Pyruvate kinase OS=Drosophila rhopaloa OX=1041015 GN=LOC108048043 PE=3 SV=1
54	53661	tr|A0A1Y9GJY2|A0A1Y9GJY2_ANOAR	20.51	2	1	1	N	55698	Pyruvate kinase OS=Anopheles arabiensis OX=7173 PE=3 SV=1
54	53662	tr|A0A0Q9X1L7|A0A0Q9X1L7_DROMO	20.51	2	1	1	N	55236	Pyruvate kinase OS=Drosophila mojavensis OX=7230 GN=Dmoj\GI22374 PE=3 SV=1
54	53663	tr|A0A2M3ZFB9|A0A2M3ZFB9_9DIPT	20.51	2	1	1	N	56104	Pyruvate kinase (Fragment) OS=Anopheles braziliensis OX=58242 PE=3 SV=1
54	53664	tr|A0A2M3ZYS6|A0A2M3ZYS6_9DIPT	20.51	2	1	1	N	56023	Pyruvate kinase (Fragment) OS=Anopheles triannulatus OX=58253 PE=3 SV=1
54	53665	tr|A0A2M3ZYS8|A0A2M3ZYS8_9DIPT	20.51	2	1	1	N	56022	Pyruvate kinase (Fragment) OS=Anopheles triannulatus OX=58253 PE=3 SV=1
54	53666	tr|A0A1Y9GJK0|A0A1Y9GJK0_ANOAR	20.51	2	1	1	N	56271	Pyruvate kinase OS=Anopheles arabiensis OX=7173 PE=3 SV=1
54	53667	tr|A0A6A0H7S7|A0A6A0H7S7_HYAAZ	20.51	2	1	1	N	56703	Pyruvate kinase OS=Hyalella azteca OX=294128 GN=HAZT_HAZT006469 PE=3 SV=1
54	53668	tr|A0A1E1X8N4|A0A1E1X8N4_9ACAR	20.51	2	1	1	N	57708	Pyruvate kinase OS=Amblyomma aureolatum OX=187763 PE=2 SV=1
54	53669	tr|A0A6P4F9I4|A0A6P4F9I4_DRORH	20.51	2	1	1	N	57050	Pyruvate kinase OS=Drosophila rhopaloa OX=1041015 GN=LOC108048043 PE=3 SV=1
54	53670	tr|A0A182VPN6|A0A182VPN6_9DIPT	20.51	2	1	1	N	57977	Pyruvate kinase OS=Anopheles minimus OX=112268 PE=3 SV=1
54	53671	tr|A0A182MNQ6|A0A182MNQ6_9DIPT	20.51	2	1	1	N	57968	Pyruvate kinase OS=Anopheles culicifacies OX=139723 PE=3 SV=1
54	53672	tr|A0A6J2T5C5|A0A6J2T5C5_DROLE	20.51	2	1	1	N	57328	Pyruvate kinase OS=Drosophila lebanonensis OX=7225 GN=LOC115620839 PE=3 SV=1
54	53673	tr|A0A1W4W378|A0A1W4W378_DROFC	20.51	2	1	1	N	57395	Pyruvate kinase OS=Drosophila ficusphila OX=30025 GN=LOC108099555 PE=3 SV=1
54	53674	O62619|KPYK_DROME	20.51	2	1	1	N	57440	Pyruvate kinase OS=Drosophila melanogaster OX=7227 GN=PyK PE=2 SV=2
54	53675	tr|B4HE69|B4HE69_DROSE	20.51	2	1	1	N	57454	Pyruvate kinase OS=Drosophila sechellia OX=7238 GN=Dsec\GM26420 PE=3 SV=1
54	53676	tr|A0A6P4F0Q9|A0A6P4F0Q9_DRORH	20.51	2	1	1	N	57379	Pyruvate kinase OS=Drosophila rhopaloa OX=1041015 GN=LOC108048043 PE=3 SV=1
54	53677	tr|B3P7K4|B3P7K4_DROER	20.51	2	1	1	N	57539	Pyruvate kinase OS=Drosophila erecta OX=7220 GN=Dere\GG11123 PE=3 SV=1

total 142 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
54	53678	tr|B3M213|B3M213_DROAN	20.51	2	1	1	N	57565	Pyruvate kinase OS=Drosophila ananassae OX=7217 GN=Dana\GF18439 PE=3 SV=2
54	53679	tr|A0A6P8KMB4|A0A6P8KMB4_DROMA	20.51	2	1	1	N	57454	Pyruvate kinase OS=Drosophila mauritiana OX=7226 GN=LOC117143834 PE=3 SV=1
54	53680	tr|B4K5E3|B4K5E3_DROMO	20.51	2	1	1	N	57618	Pyruvate kinase OS=Drosophila mojavensis OX=7230 GN=Dmoj\GI22374 PE=3 SV=1
54	53681	tr|A0A484BWG4|A0A484BWG4_DRONA	20.51	2	1	1	N	57563	Pyruvate kinase OS=Drosophila navojoa OX=7232 GN=AWZ03_001260 PE=3 SV=1
54	53682	tr|A0A131XQM7|A0A131XQM7_9ACAR	20.51	2	1	1	N	59290	Pyruvate kinase OS=Hyalomma excavatum OX=257692 PE=2 SV=1
54	53683	tr|A0A0P9ARZ1|A0A0P9ARZ1_DROAN	20.51	2	1	1	N	59439	Pyruvate kinase OS=Drosophila ananassae OX=7217 GN=Dana\GF18439 PE=3 SV=1
54	53684	tr|G3MLC1|G3MLC1_AMBMU	20.51	2	1	1	N	61369	Pyruvate kinase OS=Amblyomma maculatum OX=34609 PE=2 SV=1
54	53685	tr|A0A023EVC5|A0A023EVC5_AEDAL	20.51	2	1	1	N	63958	Pyruvate kinase (Fragment) OS=Aedes albopictus OX=7160 PE=2 SV=1
54	53686	tr|B6RHH5|B6RHH5_PENVA	20.51	2	1	1	N	63782	Pyruvate kinase OS=Penaeus vannamei OX=6689 PE=2 SV=1
54	53687	tr|A0A5N5T493|A0A5N5T493_9CRUS	20.51	2	1	1	N	68944	Pyruvate kinase OS=Armadillidium nasatum OX=96803 GN=PyK PE=3 SV=1
21	53624	tr|A0A6P4EYV9|A0A6P4EYV9_DRORH	20.46	0	1	1	N	2391440	LOW QUALITY PROTEIN: uncharacterized protein LOC108047588 OS=Drosophila rhopaloa OX=1041015 GN=LOC108047588 PE=3 SV=1

total 142 proteins

tr|A0A3R7M007|A0A3R7M007_PENVA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYDESGPGIVH.R	Y	40.93	1201.5251	1.2	601.7706	2	10.52	1080	1	358	368	
E.KSYELPDGGQVITIG.N	Y	38.20	1518.7930	-0.7	760.4032	2	13.25	1584	1	235	248	
T.MYPGIADRM.Q	Y	32.95	1052.4783	0.0	527.2464	2	11.68	1301	1	302	310	
L.DTGDGVTH.T	Y	30.28	800.3301	-0.3	401.1722	2	7.91	634	3	151	158	
K.IIAPPERKYS.V	Y	30.21	1172.6553	2.8	587.3365	2	10.01	984	1	326	335	
A.GFAGDDAPR.A	Y	28.64	904.4039	0.1	453.2093	2	9.83	953	1	17	25	
G.FAGDDAPRA.V	Y	26.63	918.4195	-0.5	460.2168	2	9.87	959	1	18	26	
K.IIAPPERKY.S	Y	25.38	1085.6233	1.4	543.8197	2	10.17	1014	1	326	334	
E.KSYELPDGQVITIGNER.F	Y	24.35	1917.9795	1.3	640.3346	3	12.57	1461	1	235	251	
K.SYELPDGQ.V	Y	22.58	907.3923	0.0	454.7034	2	11.17	1205	1	236	243	
Y.DESGPGIVH.R	Y	21.74	909.4192	-0.6	455.7166	2	10.03	989	1	360	368	
T.NWDDMEKIWHH.S	Y	20.98	1509.6459	-0.3	755.8300	2	12.54	1455	1	75	85	
E.KSYELPDGQVITI.G	Y	20.38	1461.7715	-0.5	731.8926	2	13.39	1607	1	235	247	
Y.VGDEAQSK.R	Y	20.25	832.3926	0.0	417.2036	2	7.67	599	2	51	58	
L.GMESVGIH.E	Y	20.20	828.3800	2.3	415.1982	2	10.51	1077	1	265	272	
E.KSYELPDGQVITIGNE.R	Y	19.11	1761.8784	10.8	881.9560	2	13.18	1572	1	235	250	
L.TEAPLNPK.A	Y	17.45	868.4654	0.1	435.2400	2	9.61	912	1	103	110	
T.LKYPIE.H	Y	17.39	761.4323	1.0	381.7238	2	11.01	1175	1	64	69	
M.YPGIADRM.Q	Y	16.87	921.4378	-0.3	461.7260	2	11.25	1221	1	303	310	
L.RVAPEESPVLL.T	Y	16.76	1208.6764	0.0	605.3455	2	12.50	1451	1	92	102	
E.KSYELPDGQ.V	Y	15.82	1035.4873	2.6	518.7523	2	10.49	1073	1	235	243	

total 21 peptides

tr|A0A2H4V3D7|A0A2H4V3D7_PENVA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYDESGPGIVH.R	Y	40.93	1201.5251	1.2	601.7706	2	10.52	1080	1	362	372	
E.KSYELPDGQVITIG.N	Y	38.20	1518.7930	-0.7	760.4032	2	13.25	1584	1	239	252	
T.MYPGIADRM.Q	Y	32.95	1052.4783	0.0	527.2464	2	11.68	1301	1	306	314	
L.DTGDGVTH.T	Y	30.28	800.3301	-0.3	401.1722	2	7.91	634	3	155	162	
K.IIAPPERKYS.V	Y	30.21	1172.6553	2.8	587.3365	2	10.01	984	1	330	339	
A.GFAGDDAPR.A	Y	28.64	904.4039	0.1	453.2093	2	9.83	953	1	21	29	
G.FAGDDAPRA.V	Y	26.63	918.4195	-0.5	460.2168	2	9.87	959	1	22	30	
K.IIAPPERKY.S	Y	25.38	1085.6233	1.4	543.8197	2	10.17	1014	1	330	338	
E.KSYELPDGQVITIGNER.F	Y	24.35	1917.9795	1.3	640.3346	3	12.57	1461	1	239	255	
K.SYELPDGQ.V	Y	22.58	907.3923	0.0	454.7034	2	11.17	1205	1	240	247	
Y.DESGPGIVH.R	Y	21.74	909.4192	-0.6	455.7166	2	10.03	989	1	364	372	
T.NWDDMEKIWHH.S	Y	20.98	1509.6459	-0.3	755.8300	2	12.54	1455	1	79	89	
E.KSYELPDGQVITI.G	Y	20.38	1461.7715	-0.5	731.8926	2	13.39	1607	1	239	251	
Y.VGDEAQSK.R	Y	20.25	832.3926	0.0	417.2036	2	7.67	599	2	55	62	
L.GMESVGIH.E	Y	20.20	828.3800	2.3	415.1982	2	10.51	1077	1	269	276	
E.KSYELPDGQVITIGNE.R	Y	19.11	1761.8784	10.8	881.9560	2	13.18	1572	1	239	254	
L.TEAPLNPK.A	Y	17.45	868.4654	0.1	435.2400	2	9.61	912	1	107	114	
T.LKYPIE.H	Y	17.39	761.4323	1.0	381.7238	2	11.01	1175	1	68	73	
M.YPGIADRM.Q	Y	16.87	921.4378	-0.3	461.7260	2	11.25	1221	1	307	314	
L.RVAPEESPVLL.T	Y	16.76	1208.6764	0.0	605.3455	2	12.50	1451	1	96	106	
E.KSYELPDGQ.V	Y	15.82	1035.4873	2.6	518.7523	2	10.49	1073	1	239	247	

total 21 peptides

tr|H9B3Y9|H9B3Y9_SCYPA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYDESGPGIVH.R	Y	40.93	1201.5251	1.2	601.7706	2	10.52	1080	1	362	372	
E.KSYELPDGQVITIG.N	Y	38.20	1518.7930	-0.7	760.4032	2	13.25	1584	1	239	252	
T.MYPGIADRM.Q	Y	32.95	1052.4783	0.0	527.2464	2	11.68	1301	1	306	314	
L.DTGDGVTH.T	Y	30.28	800.3301	-0.3	401.1722	2	7.91	634	3	155	162	
K.IIAPPERKYS.V	Y	30.21	1172.6553	2.8	587.3365	2	10.01	984	1	330	339	
A.GFAGDDAPR.A	Y	28.64	904.4039	0.1	453.2093	2	9.83	953	1	21	29	
G.FAGDDAPRA.V	Y	26.63	918.4195	-0.5	460.2168	2	9.87	959	1	22	30	
K.IIAPPERKY.S	Y	25.38	1085.6233	1.4	543.8197	2	10.17	1014	1	330	338	
E.KSYELPDGQVITIGNER.F	Y	24.35	1917.9795	1.3	640.3346	3	12.57	1461	1	239	255	
K.SYELPDGQ.V	Y	22.58	907.3923	0.0	454.7034	2	11.17	1205	1	240	247	
Y.DESGPGIVH.R	Y	21.74	909.4192	-0.6	455.7166	2	10.03	989	1	364	372	
T.NWDDMEKIWHH.S	Y	20.98	1509.6459	-0.3	755.8300	2	12.54	1455	1	79	89	
E.KSYELPDGQVITI.G	Y	20.38	1461.7715	-0.5	731.8926	2	13.39	1607	1	239	251	
Y.VGDEAQSK.R	Y	20.25	832.3926	0.0	417.2036	2	7.67	599	2	55	62	
L.GMESVGIH.E	Y	20.20	828.3800	2.3	415.1982	2	10.51	1077	1	269	276	
E.KSYELPDGQVITIGNE.R	Y	19.11	1761.8784	10.8	881.9560	2	13.18	1572	1	239	254	
L.TEAPLNPK.A	Y	17.45	868.4654	0.1	435.2400	2	9.61	912	1	107	114	
T.LKYPIE.H	Y	17.39	761.4323	1.0	381.7238	2	11.01	1175	1	68	73	
M.YPGIADRM.Q	Y	16.87	921.4378	-0.3	461.7260	2	11.25	1221	1	307	314	
L.RVAPEESPVLL.T	Y	16.76	1208.6764	0.0	605.3455	2	12.50	1451	1	96	106	
E.KSYELPDGQ.V	Y	15.82	1035.4873	2.6	518.7523	2	10.49	1073	1	239	247	

total 21 peptides

tr|A0A6A0H005|A0A6A0H005_HYAAZ

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYDESGPGIVH.R	Y	40.93	1201.5251	1.2	601.7706	2	10.52	1080	1	362	372	
E.KSYELPDGQVITIG.N	Y	38.20	1518.7930	-0.7	760.4032	2	13.25	1584	1	239	252	
S.MYPGIADRM.Q	Y	32.95	1052.4783	0.0	527.2464	2	11.68	1301	1	306	314	
L.DTGDGVTH.T	Y	30.28	800.3301	-0.3	401.1722	2	7.91	634	3	155	162	
K.IIAPPERKYS.V	Y	30.21	1172.6553	2.8	587.3365	2	10.01	984	1	330	339	
A.GFAGDDAPR.A	Y	28.64	904.4039	0.1	453.2093	2	9.83	953	1	21	29	
G.FAGDDAPRA.V	Y	26.63	918.4195	-0.5	460.2168	2	9.87	959	1	22	30	
K.IIAPPERKY.S	Y	25.38	1085.6233	1.4	543.8197	2	10.17	1014	1	330	338	

total 21 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.KSYELPDGQVITIGNER.F	Y	24.35	1917.9795	1.3	640.3346	3	12.57	1461	1	239	255	
K.SYELPDGQ.V	Y	22.58	907.3923	0.0	454.7034	2	11.17	1205	1	240	247	
Y.DESGPGIVH.R	Y	21.74	909.4192	-0.6	455.7166	2	10.03	989	1	364	372	
T.NWDDMEKIWHH.T	Y	20.98	1509.6459	-0.3	755.8300	2	12.54	1455	1	79	89	
E.KSYELPDGQVITI.G	Y	20.38	1461.7715	-0.5	731.8926	2	13.39	1607	1	239	251	
Y.VGDEAQSK.R	Y	20.25	832.3926	0.0	417.2036	2	7.67	599	2	55	62	
L.GMESVGIH.E	Y	20.20	828.3800	2.3	415.1982	2	10.51	1077	1	269	276	
E.KSYELPDGQVITIGNE.R	Y	19.11	1761.8784	10.8	881.9560	2	13.18	1572	1	239	254	
L.TEAPLNPK.A	Y	17.45	868.4654	0.1	435.2400	2	9.61	912	1	107	114	
T.LKYPIE.H	Y	17.39	761.4323	1.0	381.7238	2	11.01	1175	1	68	73	
M.YPGIADRM.Q	Y	16.87	921.4378	-0.3	461.7260	2	11.25	1221	1	307	314	
L.RVAPEESPVLL.T	Y	16.76	1208.6764	0.0	605.3455	2	12.50	1451	1	96	106	
E.KSYELPDGQ.V	Y	15.82	1035.4873	2.6	518.7523	2	10.49	1073	1	239	247	

total 21 peptides

tr|A0A3R7NX50|A0A3R7NX50_PENVA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYDESGPGIVH.R	Y	40.93	1201.5251	1.2	601.7706	2	10.52	1080	1	362	372	
E.KSYELPDGQVITIG.N	Y	38.20	1518.7930	-0.7	760.4032	2	13.25	1584	1	239	252	
T.MYPGIADRM.Q	Y	32.95	1052.4783	0.0	527.2464	2	11.68	1301	1	306	314	
L.DTGDGVTH.T	Y	30.28	800.3301	-0.3	401.1722	2	7.91	634	3	155	162	
K.IIAPPERKYS.V	Y	30.21	1172.6553	2.8	587.3365	2	10.01	984	1	330	339	
A.GFAGDDAPR.A	Y	28.64	904.4039	0.1	453.2093	2	9.83	953	1	21	29	
G.FAGDDAPRA.V	Y	26.63	918.4195	-0.5	460.2168	2	9.87	959	1	22	30	
K.IIAPPERKY.S	Y	25.38	1085.6233	1.4	543.8197	2	10.17	1014	1	330	338	
E.KSYELPDGQVITIGNER.F	Y	24.35	1917.9795	1.3	640.3346	3	12.57	1461	1	239	255	
K.SYELPDGQ.V	Y	22.58	907.3923	0.0	454.7034	2	11.17	1205	1	240	247	
Y.DESGPGIVH.R	Y	21.74	909.4192	-0.6	455.7166	2	10.03	989	1	364	372	
T.NWDDMEKIWHH.S	Y	20.98	1509.6459	-0.3	755.8300	2	12.54	1455	1	79	89	
E.KSYELPDGQVITI.G	Y	20.38	1461.7715	-0.5	731.8926	2	13.39	1607	1	239	251	
Y.VGDEAQSK.R	Y	20.25	832.3926	0.0	417.2036	2	7.67	599	2	55	62	
L.GMESVGIH.E	Y	20.20	828.3800	2.3	415.1982	2	10.51	1077	1	269	276	
E.KSYELPDGQVITIGNE.R	Y	19.11	1761.8784	10.8	881.9560	2	13.18	1572	1	239	254	
L.TEAPLNPK.A	Y	17.45	868.4654	0.1	435.2400	2	9.61	912	1	107	114	
T.LKYPIE.H	Y	17.39	761.4323	1.0	381.7238	2	11.01	1175	1	68	73	
M.YPGIADRM.Q	Y	16.87	921.4378	-0.3	461.7260	2	11.25	1221	1	307	314	
L.RVAPEESPVLL.T	Y	16.76	1208.6764	0.0	605.3455	2	12.50	1451	1	96	106	
E.KSYELPDGQ.V	Y	15.82	1035.4873	2.6	518.7523	2	10.49	1073	1	239	247	

total 21 peptides

tr|A0A482LUC2|A0A482LUC2_CANBE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYDESGPGIVH.R	Y	40.93	1201.5251	1.2	601.7706	2	10.52	1080	1	362	372	
E.KSYELPDGQVITIG.N	Y	38.20	1518.7930	-0.7	760.4032	2	13.25	1584	1	239	252	
T.MYPGIADRM.Q	Y	32.95	1052.4783	0.0	527.2464	2	11.68	1301	1	306	314	
L.DTGDGVTH.T	Y	30.28	800.3301	-0.3	401.1722	2	7.91	634	3	155	162	
K.IIAPPERKYS.V	Y	30.21	1172.6553	2.8	587.3365	2	10.01	984	1	330	339	
A.GFAGDDAPR.A	Y	28.64	904.4039	0.1	453.2093	2	9.83	953	1	21	29	
G.FAGDDAPRA.V	Y	26.63	918.4195	-0.5	460.2168	2	9.87	959	1	22	30	
K.IIAPPERKY.S	Y	25.38	1085.6233	1.4	543.8197	2	10.17	1014	1	330	338	
E.KSYELPDGQVITIGNER.F	Y	24.35	1917.9795	1.3	640.3346	3	12.57	1461	1	239	255	
K.SYELPDGQ.V	Y	22.58	907.3923	0.0	454.7034	2	11.17	1205	1	240	247	
Y.DESGPGIVH.R	Y	21.74	909.4192	-0.6	455.7166	2	10.03	989	1	364	372	
T.NWDDMEKIWHH.S	Y	20.98	1509.6459	-0.3	755.8300	2	12.54	1455	1	79	89	
E.KSYELPDGQVITI.G	Y	20.38	1461.7715	-0.5	731.8926	2	13.39	1607	1	239	251	
Y.VGDEAQSK.R	Y	20.25	832.3926	0.0	417.2036	2	7.67	599	2	55	62	
L.GMESVGIH.E	Y	20.20	828.3800	2.3	415.1982	2	10.51	1077	1	269	276	

total 21 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.KSYELPDGQVITIGNE.R	Y	19.11	1761.8784	10.8	881.9560	2	13.18	1572	1	239	254	
L.TEAPLNPK.A	Y	17.45	868.4654	0.1	435.2400	2	9.61	912	1	107	114	
T.LKYPIE.H	Y	17.39	761.4323	1.0	381.7238	2	11.01	1175	1	68	73	
M.YPGIADRM.Q	Y	16.87	921.4378	-0.3	461.7260	2	11.25	1221	1	307	314	
L.RVAPEESPVLL.T	Y	16.76	1208.6764	0.0	605.3455	2	12.50	1451	1	96	106	
E.KSYELPDGQ.V	Y	15.82	1035.4873	2.6	518.7523	2	10.49	1073	1	239	247	

total 21 peptides

tr|A0A0B5J9E4|A0A0B5J9E4_ERISI
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYDESGPGIVH.R	Y	40.93	1201.5251	1.2	601.7706	2	10.52	1080	1	362	372	
E.KSYELPDGQVITIG.N	Y	38.20	1518.7930	-0.7	760.4032	2	13.25	1584	1	239	252	
A.MYPGIADRM.Q	Y	32.95	1052.4783	0.0	527.2464	2	11.68	1301	1	306	314	
L.DTGDGVTH.T	Y	30.28	800.3301	-0.3	401.1722	2	7.91	634	3	155	162	
K.IIAPPERKYS.V	Y	30.21	1172.6553	2.8	587.3365	2	10.01	984	1	330	339	
A.GFAGDDAPR.A	Y	28.64	904.4039	0.1	453.2093	2	9.83	953	1	21	29	
G.FAGDDAPRA.V	Y	26.63	918.4195	-0.5	460.2168	2	9.87	959	1	22	30	
K.IIAPPERKY.S	Y	25.38	1085.6233	1.4	543.8197	2	10.17	1014	1	330	338	
E.KSYELPDGQVITIGNER.F	Y	24.35	1917.9795	1.3	640.3346	3	12.57	1461	1	239	255	
K.SYELPDGQ.V	Y	22.58	907.3923	0.0	454.7034	2	11.17	1205	1	240	247	
Y.DESGPGIVH.R	Y	21.74	909.4192	-0.6	455.7166	2	10.03	989	1	364	372	
T.NWDDMEKIWHH.S	Y	20.98	1509.6459	-0.3	755.8300	2	12.54	1455	1	79	89	
E.KSYELPDGQVITI.G	Y	20.38	1461.7715	-0.5	731.8926	2	13.39	1607	1	239	251	
Y.VGDEAQSK.R	Y	20.25	832.3926	0.0	417.2036	2	7.67	599	2	55	62	
L.GMESVGIH.E	Y	20.20	828.3800	2.3	415.1982	2	10.51	1077	1	269	276	
E.KSYELPDGQVITIGNE.R	Y	19.11	1761.8784	10.8	881.9560	2	13.18	1572	1	239	254	
L.TEAPLNPK.A	Y	17.45	868.4654	0.1	435.2400	2	9.61	912	1	107	114	
T.LKYPIE.H	Y	17.39	761.4323	1.0	381.7238	2	11.01	1175	1	68	73	
M.YPGIADRM.Q	Y	16.87	921.4378	-0.3	461.7260	2	11.25	1221	1	307	314	
L.RVAPEESPVLL.T	Y	16.76	1208.6764	0.0	605.3455	2	12.50	1451	1	96	106	
E.KSYELPDGQ.V	Y	15.82	1035.4873	2.6	518.7523	2	10.49	1073	1	239	247	

total 21 peptides

tr|A0A2H4V3D6|A0A2H4V3D6_PENVA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYDESGPGIVH.R	Y	40.93	1201.5251	1.2	601.7706	2	10.52	1080	1	362	372	
E.KSYELPDGQVITIG.N	Y	38.20	1518.7930	-0.7	760.4032	2	13.25	1584	1	239	252	
T.MYPGIADRM.Q	Y	32.95	1052.4783	0.0	527.2464	2	11.68	1301	1	306	314	
L.DTGDGVTH.T	Y	30.28	800.3301	-0.3	401.1722	2	7.91	634	3	155	162	
K.IIAPPERKYS.V	Y	30.21	1172.6553	2.8	587.3365	2	10.01	984	1	330	339	
A.GFAGDDAPR.A	Y	28.64	904.4039	0.1	453.2093	2	9.83	953	1	21	29	
G.FAGDDAPRA.V	Y	26.63	918.4195	-0.5	460.2168	2	9.87	959	1	22	30	
K.IIAPPERKY.S	Y	25.38	1085.6233	1.4	543.8197	2	10.17	1014	1	330	338	
E.KSYELPDGQVITIGNER.F	Y	24.35	1917.9795	1.3	640.3346	3	12.57	1461	1	239	255	
K.SYELPDGQ.V	Y	22.58	907.3923	0.0	454.7034	2	11.17	1205	1	240	247	
Y.DESGPGIVH.R	Y	21.74	909.4192	-0.6	455.7166	2	10.03	989	1	364	372	
T.NWDDMEKIWHH.S	Y	20.98	1509.6459	-0.3	755.8300	2	12.54	1455	1	79	89	
E.KSYELPDGQVITI.G	Y	20.38	1461.7715	-0.5	731.8926	2	13.39	1607	1	239	251	
Y.VGDEAQSK.R	Y	20.25	832.3926	0.0	417.2036	2	7.67	599	2	55	62	
L.GMESVGIH.E	Y	20.20	828.3800	2.3	415.1982	2	10.51	1077	1	269	276	
E.KSYELPDGQVITIGNE.R	Y	19.11	1761.8784	10.8	881.9560	2	13.18	1572	1	239	254	
L.TEAPLNPK.A	Y	17.45	868.4654	0.1	435.2400	2	9.61	912	1	107	114	
T.LKYPIE.H	Y	17.39	761.4323	1.0	381.7238	2	11.01	1175	1	68	73	
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L.RVAPEESPVLL.T	Y	16.76	1208.6764	0.0	605.3455	2	12.50	1451	1	96	106	
E.KSYELPDGQ.V	Y	15.82	1035.4873	2.6	518.7523	2	10.49	1073	1	239	247	

total 21 peptides

tr|A0A2H4V3F0|A0A2H4V3F0_PENVA
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYDESGPGIVH.R	Y	40.93	1201.5251	1.2	601.7706	2	10.52	1080	1	362	372	
E.KSYELPDGQVITIG.N	Y	38.20	1518.7930	-0.7	760.4032	2	13.25	1584	1	239	252	
T.MYPGIADRM.Q	Y	32.95	1052.4783	0.0	527.2464	2	11.68	1301	1	306	314	
L.DTGDGVTH.T	Y	30.28	800.3301	-0.3	401.1722	2	7.91	634	3	155	162	
K.IIAPPERKYS.V	Y	30.21	1172.6553	2.8	587.3365	2	10.01	984	1	330	339	
A.GFAGDDAPR.A	Y	28.64	904.4039	0.1	453.2093	2	9.83	953	1	21	29	
G.FAGDDAPRA.V	Y	26.63	918.4195	-0.5	460.2168	2	9.87	959	1	22	30	
K.IIAPPERKY.S	Y	25.38	1085.6233	1.4	543.8197	2	10.17	1014	1	330	338	
E.KSYELPDGQVITIGNER.F	Y	24.35	1917.9795	1.3	640.3346	3	12.57	1461	1	239	255	
K.SYELPDGQ.V	Y	22.58	907.3923	0.0	454.7034	2	11.17	1205	1	240	247	
Y.DESGPGIVH.R	Y	21.74	909.4192	-0.6	455.7166	2	10.03	989	1	364	372	
T.NWDDMEKIWHH.S	Y	20.98	1509.6459	-0.3	755.8300	2	12.54	1455	1	79	89	
E.KSYELPDGQVITI.G	Y	20.38	1461.7715	-0.5	731.8926	2	13.39	1607	1	239	251	
Y.VGDEAQSK.R	Y	20.25	832.3926	0.0	417.2036	2	7.67	599	2	55	62	
L.GMESVGIH.E	Y	20.20	828.3800	2.3	415.1982	2	10.51	1077	1	269	276	
E.KSYELPDGQVITIGNE.R	Y	19.11	1761.8784	10.8	881.9560	2	13.18	1572	1	239	254	
L.TEAPLNPK.A	Y	17.45	868.4654	0.1	435.2400	2	9.61	912	1	107	114	
T.LKYPIE.H	Y	17.39	761.4323	1.0	381.7238	2	11.01	1175	1	68	73	
M.YPGIADRM.Q	Y	16.87	921.4378	-0.3	461.7260	2	11.25	1221	1	307	314	
L.RVAPEESPVLL.T	Y	16.76	1208.6764	0.0	605.3455	2	12.50	1451	1	96	106	
E.KSYELPDGQ.V	Y	15.82	1035.4873	2.6	518.7523	2	10.49	1073	1	239	247	

total 21 peptides

tr|U3M7F7|U3M7F7_PORTR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYDESGPGIVH.R	Y	40.93	1201.5251	1.2	601.7706	2	10.52	1080	1	362	372	
E.KSYELPDGQVITIG.N	Y	38.20	1518.7930	-0.7	760.4032	2	13.25	1584	1	239	252	
T.MYPGIADRM.Q	Y	32.95	1052.4783	0.0	527.2464	2	11.68	1301	1	306	314	
L.DTGDGVTH.T	Y	30.28	800.3301	-0.3	401.1722	2	7.91	634	3	155	162	
K.IIAPPERKYS.V	Y	30.21	1172.6553	2.8	587.3365	2	10.01	984	1	330	339	
A.GFAGDDAPR.A	Y	28.64	904.4039	0.1	453.2093	2	9.83	953	1	21	29	
G.FAGDDAPRA.V	Y	26.63	918.4195	-0.5	460.2168	2	9.87	959	1	22	30	
K.IIAPPERKY.S	Y	25.38	1085.6233	1.4	543.8197	2	10.17	1014	1	330	338	
E.KSYELPDGQVITIGNER.F	Y	24.35	1917.9795	1.3	640.3346	3	12.57	1461	1	239	255	
K.SYELPDGQ.V	Y	22.58	907.3923	0.0	454.7034	2	11.17	1205	1	240	247	
Y.DESGPGIVH.R	Y	21.74	909.4192	-0.6	455.7166	2	10.03	989	1	364	372	
T.NWDDMEKIWHH.S	Y	20.98	1509.6459	-0.3	755.8300	2	12.54	1455	1	79	89	
E.KSYELPDGQVITI.G	Y	20.38	1461.7715	-0.5	731.8926	2	13.39	1607	1	239	251	
Y.VGDEAQSK.R	Y	20.25	832.3926	0.0	417.2036	2	7.67	599	2	55	62	
L.GMESVGIH.E	Y	20.20	828.3800	2.3	415.1982	2	10.51	1077	1	269	276	
E.KSYELPDGQVITIGNE.R	Y	19.11	1761.8784	10.8	881.9560	2	13.18	1572	1	239	254	
L.TEAPLNPK.A	Y	17.45	868.4654	0.1	435.2400	2	9.61	912	1	107	114	
T.LKYPIE.H	Y	17.39	761.4323	1.0	381.7238	2	11.01	1175	1	68	73	
M.YPGIADRM.Q	Y	16.87	921.4378	-0.3	461.7260	2	11.25	1221	1	307	314	
L.RVAPEESPVLL.T	Y	16.76	1208.6764	0.0	605.3455	2	12.50	1451	1	96	106	
E.KSYELPDGQ.V	Y	15.82	1035.4873	2.6	518.7523	2	10.49	1073	1	239	247	

total 21 peptides

tr|A7BJ42|A7BJ42_PROCL

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.SDLLPVAPEFPHPIPQ.F	N	49.35	1755.9196	-0.5	878.9666	2	13.50	1627	1	96	111	
V.APEFPHPIPQF.V	Y	37.99	1278.6396	0.6	640.3275	2	13.08	1553	1	102	112	
P.VAPEFPHPIPQ.F	N	35.26	1230.6396	-0.1	616.3270	2	11.74	1313	1	101	111	
V.APEFPHPIPQ.F	N	33.54	1131.5713	-0.6	566.7926	2	11.56	1278	1	102	111	

total 4 peptides

tr|D7RVB0|D7RVB0_CALSI
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.SDLLPVAPEFPHPIPQ.F	N	49.35	1755.9196	-0.5	878.9666	2	13.50	1627	1	103	118	
V.APEFPHPIPQF.V	Y	37.99	1278.6396	0.6	640.3275	2	13.08	1553	1	109	119	
P.VAPEFPHPIPQ.F	N	35.26	1230.6396	-0.1	616.3270	2	11.74	1313	1	108	118	
V.APEFPHPIPQ.F	N	33.54	1131.5713	-0.6	566.7926	2	11.56	1278	1	109	118	

total 4 peptides

tr|D7RVB1|D7RVB1_CALSI
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.SDLLPVAPEFPHPIPQ.F	N	49.35	1755.9196	-0.5	878.9666	2	13.50	1627	1	103	118	
V.APEFPHPIPQF.V	Y	37.99	1278.6396	0.6	640.3275	2	13.08	1553	1	109	119	
P.VAPEFPHPIPQ.F	N	35.26	1230.6396	-0.1	616.3270	2	11.74	1313	1	108	118	
V.APEFPHPIPQ.F	N	33.54	1131.5713	-0.6	566.7926	2	11.56	1278	1	109	118	

total 4 peptides

tr|D7RVA8|D7RVA8_CALSI
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.SDLLPVAPEFPHPIPQ.F	N	49.35	1755.9196	-0.5	878.9666	2	13.50	1627	1	103	118	
V.APEFPHPIPQF.V	Y	37.99	1278.6396	0.6	640.3275	2	13.08	1553	1	109	119	
P.VAPEFPHPIPQ.F	N	35.26	1230.6396	-0.1	616.3270	2	11.74	1313	1	108	118	
V.APEFPHPIPQ.F	N	33.54	1131.5713	-0.6	566.7926	2	11.56	1278	1	109	118	

total 4 peptides

tr|D7RVA9|D7RVA9_CALSI
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.SDLLPVAPEFPHPIPQ.F	N	49.35	1755.9196	-0.5	878.9666	2	13.50	1627	1	103	118	
V.APEFPHPIPQF.V	Y	37.99	1278.6396	0.6	640.3275	2	13.08	1553	1	109	119	
P.VAPEFPHPIPQ.F	N	35.26	1230.6396	-0.1	616.3270	2	11.74	1313	1	108	118	
V.APEFPHPIPQ.F	N	33.54	1131.5713	-0.6	566.7926	2	11.56	1278	1	109	118	

total 4 peptides

tr|A0A5B7E6L1|A0A5B7E6L1_PORTR
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.SDLLPVAPEFPHPIPQ.F	N	49.35	1755.9196	-0.5	878.9666	2	13.50	1627	1	114	129	
V.APEFPHPIPQF.V	Y	37.99	1278.6396	0.6	640.3275	2	13.08	1553	1	120	130	
P.VAPEFPHPIPQ.F	N	35.26	1230.6396	-0.1	616.3270	2	11.74	1313	1	119	129	
V.APEFPHPIPQ.F	N	33.54	1131.5713	-0.6	566.7926	2	11.56	1278	1	120	129	

total 4 peptides

tr|A0A5B7E6X8|A0A5B7E6X8_PORTR
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.SDLLPVAPEFPHPIPQ.F	N	49.35	1755.9196	-0.5	878.9666	2	13.50	1627	1	444	459	
V.APEFPHPIPQF.V	Y	37.99	1278.6396	0.6	640.3275	2	13.08	1553	1	257	267	

total 4 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.VAPEFPHPIPQ.F	N	35.26	1230.6396	-0.1	616.3270	2	11.74	1313	1	256	266	
V.APEFPHPIPQ.F	N	33.54	1131.5713	-0.6	566.7926	2	11.56	1278	1	257	266	

total 4 peptides

tr|A0A5B7E6A3|A0A5B7E6A3_PORTR
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.SDLLPVAPEFPHPIPQ.Y	N	49.35	1755.9196	-0.5	878.9666	2	13.50	1627	1	109	124	
P.VAPEFPHPIPQ.Y	N	35.26	1230.6396	-0.1	616.3270	2	11.74	1313	1	114	124	
V.APEFPHPIPQ.Y	N	33.54	1131.5713	-0.6	566.7926	2	11.56	1278	1	115	124	
P.VAPEFPHPIPQY.V	Y	20.02	1393.7030	-0.5	697.8584	2	12.39	1430	1	114	125	

total 4 peptides

tr|A0A5B7IZE3|A0A5B7IZE3_PORTR
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SILEEESMFPK.A	N	38.15	1308.6271	-0.2	655.3207	2	12.66	1478	1	5	15	
E.KNKDPLNDTLVDLL.K	Y	33.35	1596.8722	0.6	799.4438	2	13.69	1659	1	70	83	
N.ETKSPGVIDAGLVM.H	Y	31.05	1415.7330	-0.3	708.8736	2	12.71	1487	1	152	165	
K.NKDPLNDTL.V	N	28.03	1028.5138	-0.3	515.2640	2	11.18	1207	1	71	79	
K.NKDPLNDTLVDLL.K	Y	27.68	1468.7773	-0.1	735.3959	2	14.30	1755	1	71	83	
E.KNKDPLNDTLVDL.L	Y	22.98	1483.7882	2.7	742.9034	2	12.42	1435	1	70	82	

total 6 peptides

tr|F8WR03|F8WR03_PENJP
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VTVPSIDDKEDMQF.T	N	49.33	1622.7498	-0.8	812.3815	2	12.56	1459	1	318	331	
L.SILEEESMFPK.A	N	38.15	1308.6271	-0.2	655.3207	2	12.66	1478	1	532	542	
K.VTVPSIDDKEDMQ.F	N	21.58	1475.6814	-0.3	738.8478	2	11.23	1217	1	318	330	
R.NEVPPHLF.A	N	19.14	951.4814	0.3	476.7481	2	12.21	1398	1	152	159	

total 4 peptides

tr|K4Q111|K4Q111_PENVA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VTVPSIDDKEDMQF.T	N	49.33	1622.7498	-0.8	812.3815	2	12.56	1459	1	318	331	
L.SILEEESMFPK.A	N	38.15	1308.6271	-0.2	655.3207	2	12.66	1478	1	532	542	
K.VTVPSIDDKEDMQ.F	N	21.58	1475.6814	-0.3	738.8478	2	11.23	1217	1	318	330	
R.NEVPPHLF.A	N	19.14	951.4814	0.3	476.7481	2	12.21	1398	1	152	159	

total 4 peptides

tr|K4Q4N8|K4Q4N8_PENMO
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VTVPSIDDKEDMQF.T	N	49.33	1622.7498	-0.8	812.3815	2	12.56	1459	1	318	331	
L.SILEEESMFPK.A	N	38.15	1308.6271	-0.2	655.3207	2	12.66	1478	1	532	542	
K.VTVPSIDDKEDMQ.F	N	21.58	1475.6814	-0.3	738.8478	2	11.23	1217	1	318	330	
R.NEVPPHLF.A	N	19.14	951.4814	0.3	476.7481	2	12.21	1398	1	152	159	

total 4 peptides

tr|A0A2P1JJ59|A0A2P1JJ59_PROCL
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.TSFDTFPDKVALQ.L	Y	50.35	1467.7245	0.3	734.8698	2	12.43	1436	1	325	337	
F.FSPNNPDQFKDL.V	Y	27.08	1420.6622	0.2	711.3386	2	11.99	1359	1	751	762	
R.TSFDTFPDKVA.L	Y	20.75	1226.5819	1.2	614.2990	2	11.95	1353	1	325	335	
T.SFDTFPDKVALQ.L	Y	18.60	1366.6769	0.6	684.3461	2	12.40	1431	1	326	337	

total 4 peptides

tr|A0A5B7DQZ0|A0A5B7DQZ0_PORTR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SILEEESMFPK.A	N	38.15	1308.6271	-0.2	655.3207	2	12.66	1478	1	403	413	
K.VTVPSIDDGEDM.Q	Y	37.10	1276.5493	-0.5	639.2816	2	12.32	1417	1	189	200	
K.NKDPLNDTL.V	N	28.03	1028.5138	-0.3	515.2640	2	11.18	1207	1	469	477	
R.NEVPPHLF.A	N	19.14	951.4814	0.3	476.7481	2	12.21	1398	1	150	157	
N.LNDEIKDL.V	Y	17.47	958.4971	0.4	480.2560	2	11.45	1259	1	1366	1373	

total 5 peptides

tr|A0A223G1B9|A0A223G1B9_SCYSE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LENPFWWKDTYGY.H	Y	38.09	1717.7776	-0.1	859.8960	2	14.01	1710	1	224	236	
H.LENPFWWKDTY.G	Y	31.27	1497.6929	-1.0	749.8530	2	13.93	1698	1	224	234	
R.GVQPDKRPF.G	Y	26.32	1042.5559	0.0	522.2852	2	10.12	1005	1	631	639	
L.ENPFWWKDTY.G	Y	23.30	1384.6088	0.4	693.3120	2	13.51	1629	1	225	234	
T.LPRDPAAW.K	Y	18.29	924.4817	0.0	463.2481	2	11.66	1297	1	399	406	

total 5 peptides

tr|A0A7R8CX21|A0A7R8CX21_LEPSM

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VTVPSIDDKEDMQF.A	N	49.33	1622.7498	-0.8	812.3815	2	12.56	1459	1	318	331	
K.NKDPLNDTI.V	N	28.03	1028.5138	-0.3	515.2640	2	11.18	1207	1	545	553	
K.VTVPSIDDKEDMQ.F	N	21.58	1475.6814	-0.3	738.8478	2	11.23	1217	1	318	330	

total 3 peptides

tr|A0A7T8HL88|A0A7T8HL88_CALRO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VTVPSIDDKEDMQF.A	N	49.33	1622.7498	-0.8	812.3815	2	12.56	1459	1	318	331	
K.NKDPLNDTI.V	N	28.03	1028.5138	-0.3	515.2640	2	11.18	1207	1	599	607	
K.VTVPSIDDKEDMQ.F	N	21.58	1475.6814	-0.3	738.8478	2	11.23	1217	1	318	330	

total 3 peptides

tr|A0A7T8HL29|A0A7T8HL29_CALRO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VTVPSIDDKEDMQF.A	N	49.33	1622.7498	-0.8	812.3815	2	12.56	1459	1	318	331	
K.NKDPLNDTI.V	N	28.03	1028.5138	-0.3	515.2640	2	11.18	1207	1	599	607	
K.VTVPSIDDKEDMQ.F	N	21.58	1475.6814	-0.3	738.8478	2	11.23	1217	1	318	330	

total 3 peptides

tr|A0A0K2V7Y7|A0A0K2V7Y7_LEPSM

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VTVPSIDDKEDMQF.A	N	49.33	1622.7498	-0.8	812.3815	2	12.56	1459	1	318	331	
K.NKDPLNDTI.V	N	28.03	1028.5138	-0.3	515.2640	2	11.18	1207	1	599	607	
K.VTVPSIDDKEDMQ.F	N	21.58	1475.6814	-0.3	738.8478	2	11.23	1217	1	318	330	

total 3 peptides

tr|A0A7R8GZZ9|A0A7R8GZZ9_LEPSM

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VTVPSIDDKEDMQF.A	N	49.33	1622.7498	-0.8	812.3815	2	12.56	1459	1	266	279	
K.NKDPLNDTI.V	N	28.03	1028.5138	-0.3	515.2640	2	11.18	1207	1	548	556	
K.VTVPSIDDKEDMQ.F	N	21.58	1475.6814	-0.3	738.8478	2	11.23	1217	1	266	278	

total 3 peptides

tr|A0A0K2T3U6|A0A0K2T3U6_LEPSM

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VTVPSIDDKEDMQF.A	N	49.33	1622.7498	-0.8	812.3815	2	12.56	1459	1	318	331	
K.NKDPLNDTI.V	N	28.03	1028.5138	-0.3	515.2640	2	11.18	1207	1	599	607	
K.VTVPSIDDKEDMQ.F	N	21.58	1475.6814	-0.3	738.8478	2	11.23	1217	1	318	330	

total 3 peptides

tr|A0A0K2TSJ7|A0A0K2TSJ7_LEPSM

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VTVPSIDDKEDMQF.A	N	49.33	1622.7498	-0.8	812.3815	2	12.56	1459	1	338	351	
K.NKDPLNDTI.V	N	28.03	1028.5138	-0.3	515.2640	2	11.18	1207	1	619	627	
K.VTVPSIDDKEDMQ.F	N	21.58	1475.6814	-0.3	738.8478	2	11.23	1217	1	338	350	

total 3 peptides

tr|A0A4Y7MKW9|A0A4Y7MKW9_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	35.45	1156.5724	3.0	579.2952	2	10.24	1027	1	594	605	
L.GFNPPDLDIM.N	N	24.56	1117.5114	0.1	559.7630	2	13.92	1697	2	701	710	
S.VGDKIPADI.R	N	23.26	926.5073	0.7	464.2612	2	11.32	1233	1	47	55	
E.VSVGDKIPADI.R	N	21.19	1112.6077	0.1	557.3112	2	11.82	1328	1	45	55	
V.KISLPVILL.D	N	19.28	994.6790	0.1	498.3468	2	14.71	1817	1	865	873	
V.KISLPVI.L	N	16.43	768.5109	0.2	385.2628	2	13.15	1567	1	865	871	

total 6 peptides

tr|A0A0P5KSW7|A0A0P5KSW7_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	35.45	1156.5724	3.0	579.2952	2	10.24	1027	1	705	716	
L.GFNPPDLDIM.N	N	24.56	1117.5114	0.1	559.7630	2	13.92	1697	2	812	821	
S.VGDKIPADI.R	N	23.26	926.5073	0.7	464.2612	2	11.32	1233	1	158	166	
E.VSVGDKIPADI.R	N	21.19	1112.6077	0.1	557.3112	2	11.82	1328	1	156	166	
V.KISLPVILL.D	N	19.28	994.6790	0.1	498.3468	2	14.71	1817	1	976	984	
V.KISLPVI.L	N	16.43	768.5109	0.2	385.2628	2	13.15	1567	1	976	982	

total 6 peptides

tr|A0A4Y7MXF9|A0A4Y7MXF9_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	35.45	1156.5724	3.0	579.2952	2	10.24	1027	1	705	716	
L.GFNPPDLDIM.N	N	24.56	1117.5114	0.1	559.7630	2	13.92	1697	2	812	821	
S.VGDKIPADI.R	N	23.26	926.5073	0.7	464.2612	2	11.32	1233	1	158	166	
E.VSVGDKIPADI.R	N	21.19	1112.6077	0.1	557.3112	2	11.82	1328	1	156	166	
I.KISLPVILL.D	N	19.28	994.6790	0.1	498.3468	2	14.71	1817	1	976	984	
I.KISLPVI.L	N	16.43	768.5109	0.2	385.2628	2	13.15	1567	1	976	982	

total 6 peptides

tr|A0A0P4ZGF4|A0A0P4ZGF4_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	35.45	1156.5724	3.0	579.2952	2	10.24	1027	1	705	716	
L.GFNPPDLDIM.N	N	24.56	1117.5114	0.1	559.7630	2	13.92	1697	2	812	821	
S.VGDKIPADI.R	N	23.26	926.5073	0.7	464.2612	2	11.32	1233	1	158	166	
E.VSVGDKIPADI.R	N	21.19	1112.6077	0.1	557.3112	2	11.82	1328	1	156	166	
V.KISLPVILL.D	N	19.28	994.6790	0.1	498.3468	2	14.71	1817	1	976	984	
V.KISLPVI.L	N	16.43	768.5109	0.2	385.2628	2	13.15	1567	1	976	982	

total 6 peptides

tr|A0A4Y7MVM2|A0A4Y7MVM2_DAPPU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	35.45	1156.5724	3.0	579.2952	2	10.24	1027	1	705	716	
L.GFNPPDLDIM.N	N	24.56	1117.5114	0.1	559.7630	2	13.92	1697	2	812	821	
S.VGDKIPADI.R	N	23.26	926.5073	0.7	464.2612	2	11.32	1233	1	158	166	
E.VSVGDKIPADI.R	N	21.19	1112.6077	0.1	557.3112	2	11.82	1328	1	156	166	
V.KISLPVILL.D	N	19.28	994.6790	0.1	498.3468	2	14.71	1817	1	976	984	
V.KISLPVI.L	N	16.43	768.5109	0.2	385.2628	2	13.15	1567	1	976	982	

total 6 peptides

tr|A0A4Y7M702|A0A4Y7M702_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	35.45	1156.5724	3.0	579.2952	2	10.24	1027	1	705	716	
L.GFNPPDLDIM.N	N	24.56	1117.5114	0.1	559.7630	2	13.92	1697	2	812	821	
S.VGDKIPADI.R	N	23.26	926.5073	0.7	464.2612	2	11.32	1233	1	158	166	
E.VSVGDKIPADI.R	N	21.19	1112.6077	0.1	557.3112	2	11.82	1328	1	156	166	
I.KISLPVILL.D	N	19.28	994.6790	0.1	498.3468	2	14.71	1817	1	976	984	
I.KISLPVI.L	N	16.43	768.5109	0.2	385.2628	2	13.15	1567	1	976	982	

total 6 peptides

tr|A0A4Y7MHQ5|A0A4Y7MHQ5_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	35.45	1156.5724	3.0	579.2952	2	10.24	1027	1	705	716	
L.GFNPPDLDIM.N	N	24.56	1117.5114	0.1	559.7630	2	13.92	1697	2	812	821	
S.VGDKIPADI.R	N	23.26	926.5073	0.7	464.2612	2	11.32	1233	1	158	166	
E.VSVGDKIPADI.R	N	21.19	1112.6077	0.1	557.3112	2	11.82	1328	1	156	166	
V.KISLPVILL.D	N	19.28	994.6790	0.1	498.3468	2	14.71	1817	1	976	984	
V.KISLPVI.L	N	16.43	768.5109	0.2	385.2628	2	13.15	1567	1	976	982	

total 6 peptides

tr|A0A4Y7ME47|A0A4Y7ME47_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	35.45	1156.5724	3.0	579.2952	2	10.24	1027	1	705	716	
L.GFNPPDLDIM.N	N	24.56	1117.5114	0.1	559.7630	2	13.92	1697	2	812	821	
S.VGDKIPADI.R	N	23.26	926.5073	0.7	464.2612	2	11.32	1233	1	158	166	
E.VSVGDKIPADI.R	N	21.19	1112.6077	0.1	557.3112	2	11.82	1328	1	156	166	
V.KISLPVILL.D	N	19.28	994.6790	0.1	498.3468	2	14.71	1817	1	976	984	
V.KISLPVI.L	N	16.43	768.5109	0.2	385.2628	2	13.15	1567	1	976	982	

total 6 peptides

tr|A0A4Y7M4I0|A0A4Y7M4I0_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	35.45	1156.5724	3.0	579.2952	2	10.24	1027	1	705	716	
L.GFNPPDLDIM.N	N	24.56	1117.5114	0.1	559.7630	2	13.92	1697	2	812	821	
S.VGDKIPADI.R	N	23.26	926.5073	0.7	464.2612	2	11.32	1233	1	158	166	
E.VSVGDKIPADI.R	N	21.19	1112.6077	0.1	557.3112	2	11.82	1328	1	156	166	
V.KISLPVILL.D	N	19.28	994.6790	0.1	498.3468	2	14.71	1817	1	976	984	
V.KISLPVI.L	N	16.43	768.5109	0.2	385.2628	2	13.15	1567	1	976	982	

total 6 peptides

tr|A0A1D2MC18|A0A1D2MC18_ORCCI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	35.45	1156.5724	3.0	579.2952	2	10.24	1027	1	702	713	
L.GFNPPDLDIM.T	N	24.56	1117.5114	0.1	559.7630	2	13.92	1697	2	809	818	
S.VGDKIPADI.R	N	23.26	926.5073	0.7	464.2612	2	11.32	1233	1	159	167	
E.VSVGDKIPADI.R	N	21.19	1112.6077	0.1	557.3112	2	11.82	1328	1	157	167	
M.KISLPVILL.D	N	19.28	994.6790	0.1	498.3468	2	14.71	1817	1	973	981	
M.KISLPVI.L	N	16.43	768.5109	0.2	385.2628	2	13.15	1567	1	973	979	

total 6 peptides

tr|E9HR84|E9HR84_DAPPU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	35.45	1156.5724	3.0	579.2952	2	10.24	1027	1	705	716	
L.GFNPPDLDIM.N	N	24.56	1117.5114	0.1	559.7630	2	13.92	1697	2	812	821	
S.VGDKIPADI.R	N	23.26	926.5073	0.7	464.2612	2	11.32	1233	1	158	166	
E.VSVGDKIPADI.R	N	21.19	1112.6077	0.1	557.3112	2	11.82	1328	1	156	166	
V.KISLPVILL.D	N	19.28	994.6790	0.1	498.3468	2	14.71	1817	1	976	984	
V.KISLPVI.L	N	16.43	768.5109	0.2	385.2628	2	13.15	1567	1	976	982	

total 6 peptides

tr|A0A0P5VJX3|A0A0P5VJX3_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	35.45	1156.5724	3.0	579.2952	2	10.24	1027	1	705	716	
L.GFNPPDLDIM.N	N	24.56	1117.5114	0.1	559.7630	2	13.92	1697	2	812	821	
S.VGDKIPADI.R	N	23.26	926.5073	0.7	464.2612	2	11.32	1233	1	158	166	
E.VSVGDKIPADI.R	N	21.19	1112.6077	0.1	557.3112	2	11.82	1328	1	156	166	
V.KISLPVILL.D	N	19.28	994.6790	0.1	498.3468	2	14.71	1817	1	976	984	
V.KISLPVI.L	N	16.43	768.5109	0.2	385.2628	2	13.15	1567	1	976	982	

total 6 peptides

tr|A0A4Y7LYL4|A0A4Y7LYL4_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	35.45	1156.5724	3.0	579.2952	2	10.24	1027	1	705	716	
L.GFNPPDLDIM.N	N	24.56	1117.5114	0.1	559.7630	2	13.92	1697	2	812	821	
S.VGDKIPADI.R	N	23.26	926.5073	0.7	464.2612	2	11.32	1233	1	158	166	
E.VSVGDKIPADI.R	N	21.19	1112.6077	0.1	557.3112	2	11.82	1328	1	156	166	
V.KISLPVILL.D	N	19.28	994.6790	0.1	498.3468	2	14.71	1817	1	976	984	
V.KISLPVI.L	N	16.43	768.5109	0.2	385.2628	2	13.15	1567	1	976	982	

total 6 peptides

tr|A0A0C5E1J4|A0A0C5E1J4_CHEDE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	35.45	1156.5724	3.0	579.2952	2	10.24	1027	1	701	712	
L.GFNPPDLDIM.D	N	24.56	1117.5114	0.1	559.7630	2	13.92	1697	2	808	817	
L.FSRVEPF.H	N	24.00	880.4443	0.0	441.2294	2	11.77	1319	1	676	682	
S.VGDKIPADI.R	N	23.26	926.5073	0.7	464.2612	2	11.32	1233	1	155	163	
E.VSVGDKIPADI.R	N	21.19	1112.6077	0.1	557.3112	2	11.82	1328	1	153	163	

total 5 peptides

tr|A0A0N9EJJ5|A0A0N9EJJ5_ERIVE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.VVLPPLYEVTPH.L	Y	34.71	1362.7546	0.3	682.3848	2	13.33	1598	1	153	164	
N.VHFEDVDGVAR.V	Y	27.30	1242.5992	0.8	622.3074	2	10.75	1125	1	297	307	
H.VVLPPLYE.V	Y	25.66	928.5269	0.0	465.2707	2	13.61	1646	1	153	160	
A.TRDPAFF.R	Y	17.22	852.4130	0.2	427.2138	2	12.10	1379	1	397	403	

total 4 peptides

tr|A0A2Z4I2U3|A0A2Z4I2U3_CALSI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.GFNPPDLDIM.E	N	24.56	1117.5114	0.1	559.7630	2	13.92	1697	2	808	817	
L.FSRVEPF.H	N	24.00	880.4443	0.0	441.2294	2	11.77	1319	1	676	682	
S.VGDKIPADL.R	N	23.26	926.5073	0.7	464.2612	2	11.32	1233	1	155	163	
E.VSVGDKIPADL.R	N	21.19	1112.6077	0.1	557.3112	2	11.82	1328	1	153	163	
L.KISLPVLLL.D	N	19.28	994.6790	0.1	498.3468	2	14.71	1817	1	972	980	
L.DESLKFL.A	Y	16.75	850.4436	0.2	426.2292	2	12.91	1523	1	981	987	
L.KISLPVL.L	N	16.43	768.5109	0.2	385.2628	2	13.15	1567	1	972	978	

total 7 peptides

tr|A0A0P4W579|A0A0P4W579_SCYOL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.GPAPVLPKPTPLPN.L	Y	42.82	1396.8077	0.6	699.4116	2	11.62	1290	1	294	307	
N.MDPIIVKPG.A	Y	31.34	968.5364	0.2	485.2756	2	11.44	1256	1	109	117	

total 2 peptides

tr|A0A0P4WKI4|A0A0P4WKI4_SCYOL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.GPAPVLPKPTPLPN.L	Y	42.82	1396.8077	0.6	699.4116	2	11.62	1290	1	668	681	
N.MDPIIVKPG.A	Y	31.34	968.5364	0.2	485.2756	2	11.44	1256	1	483	491	

Peptide Uniq -10lgP Mass ppm m/z z RT Scan #Spec Start End PTM

total 2 peptides

tr|A0A0P4WBU2|A0A0P4WBU2_SCYOL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.GPAPVLPKPTPLPN.L	Y	42.82	1396.8077	0.6	699.4116	2	11.62	1290	1	668	681	
N.MDPIIVKPG.A	Y	31.34	968.5364	0.2	485.2756	2	11.44	1256	1	483	491	

total 2 peptides

tr|A0A3R7PTG0|A0A3R7PTG0_PENVA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.DAPGPINF.T	Y	35.72	829.3970	0.2	415.7058	2	12.89	1518	1	73	80	
A.FGDKFT.N	Y	27.18	713.3384	-0.3	357.6764	2	10.67	1109	1	127	132	

total 2 peptides

tr|A0A195D1T6|A0A195D1T6_9HYME
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VIVVDKPGPPQGPL.Q	Y	38.18	1414.8184	-0.2	708.4163	2	11.78	1320	1	6879	6892	
K.NWDKDFVDL.E	Y	18.76	1150.5294	0.7	576.2724	2	13.28	1589	1	4336	4344	

total 2 peptides

tr|A0A151I5T2|A0A151I5T2_9HYME
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VIVVDKPGPPQGPL.Q	Y	38.18	1414.8184	-0.2	708.4163	2	11.78	1320	1	6775	6788	
K.NWDKDFVDL.E	Y	18.76	1150.5294	0.7	576.2724	2	13.28	1589	1	4232	4240	

total 2 peptides

tr|A0A151J500|A0A151J500_9HYME
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VIVVDKPGPPQGPL.Q	Y	38.18	1414.8184	-0.2	708.4163	2	11.78	1320	1	6901	6914	
K.NWDKDFVDL.E	Y	18.76	1150.5294	0.7	576.2724	2	13.28	1589	1	4358	4366	

total 2 peptides

tr|E2BUG0|E2BUG0_HARSA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VIVVDKPGPPQGPL.Q	Y	38.18	1414.8184	-0.2	708.4163	2	11.78	1320	1	3242	3255	
K.NWDKDFVDL.E	Y	18.76	1150.5294	0.7	576.2724	2	13.28	1589	1	1187	1195	

total 2 peptides

tr|A0A5N5SKQ0|A0A5N5SKQ0_9CRUS
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.GIHIPGSPF.R	Y	27.98	923.4865	0.1	462.7505	2	12.99	1537	1	696	704	
G.YKPTEPGYY.I	Y	21.97	1116.5127	1.3	559.2643	2	10.73	1121	1	390	398	
E.MHIPGSPF.Q	Y	21.02	884.4214	0.1	443.2180	2	12.65	1476	1	505	512	

total 3 peptides

tr|A0A444SHR5|A0A444SHR5_ARMVU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.GIHIPGSPF.R	Y	27.98	923.4865	0.1	462.7505	2	12.99	1537	1	735	743	
G.YKPTEPGYY.I	Y	21.97	1116.5127	1.3	559.2643	2	10.73	1121	1	429	437	
E.MHIPGSPF.Q	Y	21.02	884.4214	0.1	443.2180	2	12.65	1476	1	544	551	

total 3 peptides

tr|A0A3R7Q393|A0A3R7Q393_PENVA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.GIHIPGSPF.R	Y	27.98	923.4865	0.1	462.7505	2	12.99	1537	1	685	693	
G.YKPTEPGYY.I	Y	21.97	1116.5127	1.3	559.2643	2	10.73	1121	1	377	385	
D.MHIPGSPF.Q	Y	21.02	884.4214	0.1	443.2180	2	12.65	1476	1	492	499	

total 3 peptides

tr|A0A2P1JJ42|A0A2P1JJ42_PROCL
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.GIHIPGSPF.R	Y	27.98	923.4865	0.1	462.7505	2	12.99	1537	1	1330	1338	
G.YKPTEPGYY.I	Y	21.97	1116.5127	1.3	559.2643	2	10.73	1121	1	1026	1034	
E.MHIPGSPF.Q	Y	21.02	884.4214	0.1	443.2180	2	12.65	1476	1	1141	1148	

total 3 peptides

tr|A0A834J309|A0A834J309_RHYFE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.AWRPPLDDGGSPITNY.I	Y	39.43	1757.8373	0.3	879.9261	2	12.74	1491	1	6856	6871	

total 1 peptides

tr|A0A6M2D681|A0A6M2D681_RHIMP
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.LVLALVVLMAVAQ.S	Y	31.83	1338.8308	-13.7	670.4135	2	13.49	1626	2	6	18	

total 1 peptides

tr|A0A6G5A756|A0A6G5A756_RHIMP
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.LVLALVVLMAVAQ.S	Y	31.83	1338.8308	-13.7	670.4135	2	13.49	1626	2	6	18	

total 1 peptides

tr|A0A2J7R8E8|A0A2J7R8E8_9NEOP
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.MQQLMKSGLPPEPK.R	Y	28.61	1582.8210	-7.1	792.4122	2	12.31	1415	1	85	98	

total 1 peptides

tr|A0A423SLW8|A0A423SLW8_PENVA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.IVKDLPIDDF.A	Y	28.36	1173.6281	0.3	587.8215	2	13.13	1562	1	194	203	

total 1 peptides

tr|A0A5B7CL07|A0A5B7CL07_PORTR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.IVKDLPIDDF.A	Y	28.36	1173.6281	0.3	587.8215	2	13.13	1562	1	247	256	

total 1 peptides

tr|A0A0P4WLG3|A0A0P4WLG3_SCYOL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.IVKDLPIDDF.A	Y	28.36	1173.6281	0.3	587.8215	2	13.13	1562	1	298	307	

total 1 peptides

tr|A0A1W4VNV5|A0A1W4VNV5_DROFC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.EDLSGVVLL.T	Y	26.84	943.5226	11.7	472.7741	2	13.85	1685	1	673	681	

total 1 peptides

tr|A0A1W4W0Y9|A0A1W4W0Y9_DROFC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.EDLSGVVLL.T	Y	26.84	943.5226	11.7	472.7741	2	13.85	1685	1	673	681	

total 1 peptides

tr|A0A1W4W054|A0A1W4W054_DROFC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.EDLSGVVLL.T	Y	26.84	943.5226	11.7	472.7741	2	13.85	1685	1	673	681	

total 1 peptides

tr|A0A1W4VNL1|A0A1W4VNL1_DROFC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.EDLSGVVLL.T	Y	26.84	943.5226	11.7	472.7741	2	13.85	1685	1	673	681	

total 1 peptides

tr|A0A146ME36|A0A146ME36_LYGHE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.EKPIDLKLNN.E	Y	26.60	1182.6608	-24.2	592.3234	2	13.16	1568	1	479	488	

total 1 peptides

tr|A0A0A9ZCU1|A0A0A9ZCU1_LYGHE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.EKPIDLKLNN.E	Y	26.60	1182.6608	-24.2	592.3234	2	13.16	1568	1	682	691	

total 1 peptides

tr|A0A0A9Z559|A0A0A9Z559_LYGHE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.EKPIDLKLNN.E	Y	26.60	1182.6608	-24.2	592.3234	2	13.16	1568	1	695	704	

total 1 peptides

tr|A0A553NSJ7|A0A553NSJ7_TIGCA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VVAKKPAGE.K	Y	26.07	897.5283	19.8	449.7803	2	10.02	986	1	117	125	

total 1 peptides

tr|A0A553NV74|A0A553NV74_TIGCA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VVAKKPAGE.K	Y	26.07	897.5283	19.8	449.7803	2	10.02	986	1	117	125	

total 1 peptides

tr|B4L6N9|B4L6N9_DROMO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.AGGAGGSPGA.G	Y	25.98	700.3140	0.1	351.1643	2	8.34	695	1	703	712	

total 1 peptides

tr|A0A484AUC9|A0A484AUC9_DRONA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.AGGAGGSPGA.G	Y	25.98	700.3140	0.1	351.1643	2	8.34	695	1	797	806	

total 1 peptides

tr|A0A182HNK7|A0A182HNK7_ANOAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
C.FGYTSK.N	Y	24.12	701.3384	8.1	351.6793	2	16.26	2033	1	634	639	

total 1 peptides

tr|A0A1B0CTB8|A0A1B0CTB8_LUTLO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.EALEHLII.I	Y	23.80	936.5280	-0.4	469.2711	2	13.10	1557	1	2360	2367	
				total 1 peptides								

tr|E9IDT0|E9IDT0_SOLIN
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.EALEHLIL.C	Y	23.80	936.5280	-0.4	469.2711	2	13.10	1557	1	530	537	
				total 1 peptides								

tr|A0A6V7J2X2|A0A6V7J2X2_9HYME
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.EAIEHLLI.S	Y	23.80	936.5280	-0.4	469.2711	2	13.10	1557	1	51	58	
				total 1 peptides								

tr|A0A7R8V5M9|A0A7R8V5M9_HERIL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.EALEHIII.V	Y	23.80	936.5280	-0.4	469.2711	2	13.10	1557	1	30	37	
				total 1 peptides								

tr|A0A0K8TNK6|A0A0K8TNK6_TABBR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.EALEHILI.V	Y	23.80	936.5280	-0.4	469.2711	2	13.10	1557	1	17	24	
				total 1 peptides								

tr|B4NGC5|B4NGC5_DROWI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.EALEHILI.A	Y	23.80	936.5280	-0.4	469.2711	2	13.10	1557	1	47	54	
				total 1 peptides								

tr|B4M4U0|B4M4U0_DROVI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.EALEHLLI.A	Y	23.80	936.5280	-0.4	469.2711	2	13.10	1557	1	50	57	
				total 1 peptides								

tr|A0A484BDS3|A0A484BDS3_DRONA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.EALEHILI.A	Y	23.80	936.5280	-0.4	469.2711	2	13.10	1557	1	50	57	
				total 1 peptides								

tr|A0A6J1M8J1|A0A6J1M8J1_DROHY
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.EALEHILI.A	Y	23.80	936.5280	-0.4	469.2711	2	13.10	1557	1	50	57	

total 1 peptides

tr|B4KE34|B4KE34_DROMO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.EALEHILI.A	Y	23.80	936.5280	-0.4	469.2711	2	13.10	1557	1	50	57	

total 1 peptides

tr|A0A0M4EG71|A0A0M4EG71_DROBS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.EALEHILI.A	Y	23.80	936.5280	-0.4	469.2711	2	13.10	1557	1	49	56	

total 1 peptides

tr|A0A6P8XFN0|A0A6P8XFN0_DROAB

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.EALEHILI.A	Y	23.80	936.5280	-0.4	469.2711	2	13.10	1557	1	49	56	

total 1 peptides

tr|A0A6J2TAH7|A0A6J2TAH7_DROLE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.EALEHILI.V	Y	23.80	936.5280	-0.4	469.2711	2	13.10	1557	1	58	65	

total 1 peptides

tr|A0A6J2TEK1|A0A6J2TEK1_DROLE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.EALEHILI.V	Y	23.80	936.5280	-0.4	469.2711	2	13.10	1557	1	58	65	

total 1 peptides

tr|A0A7I0ZIP4|A0A7I0ZIP4_DANPL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EALEHLLL.Q	Y	23.80	936.5280	-0.4	469.2711	2	13.10	1557	1	50	57	

total 1 peptides

tr|A0A7I0ZK43|A0A7I0ZK43_DANPL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EALEHLLL.Q	Y	23.80	936.5280	-0.4	469.2711	2	13.10	1557	1	52	59	

total 1 peptides

tr|A0A7M6UVA6|A0A7M6UVA6_NASVI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.EALEHLLI.R	Y	23.80	936.5280	-0.4	469.2711	2	13.10	1557	1	501	508	

total 1 peptides

tr|A0A7M7QVM7|A0A7M7QVM7_NASVI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.EALEHLLI.R	Y	23.80	936.5280	-0.4	469.2711	2	13.10	1557	1	501	508	

total 1 peptides

tr|A0A232F624|A0A232F624_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.EALEHLLI.R	Y	23.80	936.5280	-0.4	469.2711	2	13.10	1557	1	505	512	

total 1 peptides

tr|F4WT59|F4WT59_ACREC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.AESSITVPDVKYVI.D	Y	22.27	1519.8134	-24.0	760.8957	2	12.27	1409	1	309	322	

total 1 peptides

tr|A0A836FB18|A0A836FB18_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.AESSITVPDVKYVI.D	Y	22.27	1519.8134	-24.0	760.8957	2	12.27	1409	1	382	395	

total 1 peptides

tr|A0A0J7L582|A0A0J7L582_LASNI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.AESSITVPDVKYVI.D	Y	22.27	1519.8134	-24.0	760.8957	2	12.27	1409	1	382	395	

total 1 peptides

tr|A0A151J597|A0A151J597_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.AESSITVPDVKYVI.D	Y	22.27	1519.8134	-24.0	760.8957	2	12.27	1409	1	382	395	

total 1 peptides

tr|A0A836JUW8|A0A836JUW8_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.AESSITVPDVKYVI.D	Y	22.27	1519.8134	-24.0	760.8957	2	12.27	1409	1	407	420	

total 1 peptides

tr|A0A836JG75|A0A836JG75_9HYME

back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.AESSITVPDVKYVI.D	Y	22.27	1519.8134	-24.0	760.8957	2	12.27	1409	1	398	411	

total 1 peptides

tr|A0A1L3IWM3|A0A1L3IWM3_RHOPD
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VLVSTVIM.Q	Y	20.57	860.5042	11.8	431.2644	2	11.34	1236	1	537	544	

total 1 peptides

tr|A0A2S2QP63|A0A2S2QP63_9HEMI
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VLVSTVIM.Q	Y	20.57	860.5042	11.8	431.2644	2	11.34	1236	1	93	100	

total 1 peptides

tr|A0A2S2NYH2|A0A2S2NYH2_SCHGA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VLVSTVIM.Q	Y	20.57	860.5042	11.8	431.2644	2	11.34	1236	1	127	134	

total 1 peptides

tr|A0A6G0YXF5|A0A6G0YXF5_APHCR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VLVSTVIM.Q	Y	20.57	860.5042	11.8	431.2644	2	11.34	1236	1	489	496	

total 1 peptides

tr|A0A6G0UB83|A0A6G0UB83_APHGL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VLVSTVIM.Q	Y	20.57	860.5042	11.8	431.2644	2	11.34	1236	1	511	518	

total 1 peptides

tr|A0A182VZF1|A0A182VZF1_9DIPT
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DRTKRKPKKALT.Q	Y	20.54	1440.8888	11.5	721.4600	2	22.62	3041	1	178	189	

total 1 peptides

tr|A0A023ERZ2|A0A023ERZ2_AEDAL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	281	291	

total 1 peptides

tr|A0A0P8Y097|A0A0P8Y097_DROAN
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	277	287	

total 1 peptides

tr|A0A6P8K875|A0A6P8K875_DROMA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	277	287	

total 1 peptides

tr|A0A6P4F4P4|A0A6P4F4P4_DRORH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	277	287	

total 1 peptides

tr|A0A1Y9GJY2|A0A1Y9GJY2_ANOAR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	277	287	

total 1 peptides

tr|A0A0Q9X1L7|A0A0Q9X1L7_DROMO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	277	287	

total 1 peptides

tr|A0A2M3ZFB9|A0A2M3ZFB9_9DIPT
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	281	291	

total 1 peptides

tr|A0A2M3ZYS6|A0A2M3ZYS6_9DIPT
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	281	291	

total 1 peptides

tr|A0A2M3ZYS8|A0A2M3ZYS8_9DIPT
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM

total 1 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	281	291	

total 1 peptides

tr|A0A1Y9GJK0|A0A1Y9GJK0_ANOAR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	282	292	

total 1 peptides

tr|A0A6A0H7S7|A0A6A0H7S7_HYAAZ

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	286	296	

total 1 peptides

tr|A0A1E1X8N4|A0A1E1X8N4_9ACAR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	290	300	

total 1 peptides

tr|A0A6P4F9I4|A0A6P4F9I4_DRORH

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	298	308	

total 1 peptides

tr|A0A182VPN6|A0A182VPN6_9DIPT

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	293	303	

total 1 peptides

tr|A0A182MNQ6|A0A182MNQ6_9DIPT

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	293	303	

total 1 peptides

tr|A0A6J2T5C5|A0A6J2T5C5_DROLE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	298	308	

total 1 peptides

tr|A0A1W4W378|A0A1W4W378_DROFC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	298	308	

total 1 peptides

O62619|KPYK_DROME
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	298	308	

total 1 peptides

tr|B4HE69|B4HE69_DROSE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	298	308	

total 1 peptides

tr|A0A6P4F0Q9|A0A6P4F0Q9_DRORH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	298	308	

total 1 peptides

tr|B3P7K4|B3P7K4_DROER
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	298	308	

total 1 peptides

tr|B3M213|B3M213_DROAN
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	298	308	

total 1 peptides

tr|A0A6P8KMB4|A0A6P8KMB4_DROMA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	298	308	

total 1 peptides

tr|B4K5E3|B4K5E3_DROMO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	298	308	

total 1 peptides

tr|A0A484BWG4|A0A484BWG4_DRONA
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	298	308	

total 1 peptides

tr|A0A131XQM7|A0A131XQM7_9ACAR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	290	300	

total 1 peptides

tr|A0A0P9ARZ1|A0A0P9ARZ1_DROAN

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	312	322	

total 1 peptides

tr|G3MLC1|G3MLC1_AMBMU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	290	300	

total 1 peptides

tr|A0A023EVC5|A0A023EVC5_AEDAL

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	350	360	

total 1 peptides

tr|B6RHH5|B6RHH5_PENVA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	286	296	

total 1 peptides

tr|A0A5N5T493|A0A5N5T493_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.51	1140.6025	0.0	571.3085	2	11.94	1350	1	390	400	

total 1 peptides

tr|A0A6P4EYV9|A0A6P4EYV9_DRORH

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.IVETSIITQSVE.P	Y	20.46	1317.7028	-4.3	659.8558	2	14.85	1838	1	9452	9463	

total 1 peptides

1. Notes

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)

Table 1. Statistics of data.

# of MS Scans	1027
# of MS/MS Scans	2900

Table 2. Result filtration parameters.

Peptide -10lgP	≥15
Protein -10lgP	≥20
Proteins unique peptides	≥0
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	96
Peptide Sequences	96
Protein Groups	29
Proteins	144
Proteins (#Unique Peptides)	39 (>2); 4 (=2); 74 (=1);
FDR (Peptide-Spectrum Matches)	20.8%
FDR (Peptide Sequences)	20.8%
FDR (Protein)	2.8%
De Novo Only Spectra	1110

Table 4. PTM profile.

Name	ΔMass	#PSM	Position

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)

Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Orbi2222	0	0	0	0	96

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS 7.0
Parent Mass Error Tolerance: 0.03 Da
Fragment Mass Error Tolerance: 0.1 Da
Precursor Mass Search Type: monoisotopic
Enzyme: None
Max Missed Cleavages: 100
Non-specific Cleavage: both
Max variable PTM per peptide: 3
Database: Arthropoda
Taxon: All
Searched Entry: 6735671
FDR Estimation: Enabled
Merge Options: 0.1 min. 0.03 Da
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB_PIMENTA_HP_20220211_04.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID/ECD
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
1	53234	tr|A0A3R7M007|A0A3R7M007_PENVA	121.02	23	17	17	N	41323	Actin 1 OS=Penaeus vannamei OX=6689 GN=C7M84_012584 PE=3 SV=1
1	53236	tr|H9B3Y9|H9B3Y9_SCYPA	121.02	23	17	17	N	41781	Beta-actin OS=Scylla paramamosain OX=85552 PE=2 SV=1
1	53237	tr|A0A6A0H005|A0A6A0H005_HYAAZ	121.02	23	17	17	N	41604	Uncharacterized protein OS=Hyalella azteca OX=294128 GN=HAZT_HAZT002759 PE=3 SV=1
1	53239	tr|A0A482LUC2|A0A482LUC2_CANBE	121.02	23	17	17	N	41781	Actin 1 OS=Cancer borealis OX=39395 GN=ACT1 PE=2 SV=1
1	53241	tr|A0A2H4V3D6|A0A2H4V3D6_PENVA	121.02	23	17	17	N	41801	Slow-type skeletal muscle actin 10 OS=Penaeus vannamei OX=6689 PE=2 SV=1
5	53308	tr|A0A5B7IZE3|A0A5B7IZE3_PORTR	78.60	17	5	1	N	26459	Myosin heavy chain, muscle OS=Portunus trituberculatus OX=210409 GN=Mhc_24 PE=3 SV=1
6	53314	tr|F8WR03|F8WR03_PENJP	74.27	2	5	0	N	219503	Myosin heavy chain type a OS=Penaeus japonicus OX=27405 GN=MYHa PE=2 SV=1
6	53315	tr|K4Q111|K4Q111_PENVA	74.27	2	5	0	N	219712	Myosin heavy chain type 1 OS=Penaeus vannamei OX=6689 GN=MYH1 PE=2 SV=1
6	53316	tr|K4Q4N8|K4Q4N8_PENMO	74.27	2	5	0	N	219585	Myosin heavy chain type 1 OS=Penaeus monodon OX=6687 GN=MYH1 PE=2 SV=1
4	53320	tr|A0A4Y7MKW9|A0A4Y7MKW9_9CRUS	74.24	5	6	0	N	97229	P-type Ca(2+) transporter (Fragment) OS=Daphnia magna OX=35525 GN=EOG090X00V6 PE=2 SV=1
4	53321	tr|A0A0P5KSW7|A0A0P5KSW7_9CRUS	74.24	4	6	0	N	110371	Calcium-transporting ATPase OS=Daphnia magna OX=35525 PE=3 SV=1
4	53322	tr|A0A4Y7MXF9|A0A4Y7MXF9_9CRUS	74.24	4	6	0	N	110591	Calcium-transporting ATPase OS=Daphnia pulicaria OX=35523 GN=EOG090X00V6 PE=2 SV=1

total 144 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
4	53323	tr|A0A0P4ZGF4|A0A0P4ZGF4_9CRUS	74.24	4	6	0	N	110708	Calcium-transporting ATPase OS=Daphnia magna OX=35525 GN=APZ42_012354 PE=3 SV=1
4	53324	tr|A0A4Y7MVM2|A0A4Y7MVM2_DAPPU	74.24	4	6	0	N	110862	Calcium-transporting ATPase OS=Daphnia pulex OX=6669 GN=EOG090X00V6 PE=2 SV=1
4	53325	tr|A0A4Y7M702|A0A4Y7M702_9CRUS	74.24	4	6	0	N	111071	Calcium-transporting ATPase OS=Daphnia hispanica OX=575233 GN=EOG090X00V6 PE=2 SV=1
4	53326	tr|A0A4Y7MHQ5|A0A4Y7MHQ5_9CRUS	74.24	4	6	0	N	111377	Calcium-transporting ATPase OS=Daphnia magna OX=35525 GN=EOG090X00V6 PE=2 SV=1
4	53327	tr|A0A4Y7ME47|A0A4Y7ME47_9CRUS	74.24	4	6	0	N	111392	Calcium-transporting ATPase OS=Daphnia magna OX=35525 GN=EOG090X00V6 PE=2 SV=1
4	53328	tr|A0A4Y7M4I0|A0A4Y7M4I0_9CRUS	74.24	4	6	0	N	111723	Calcium-transporting ATPase OS=Daphnia dolichocephala OX=2282166 GN=EOG090X00V6 PE=2 SV=1
4	53329	tr|A0A1D2MC18|A0A1D2MC18_ORCCI	74.24	4	6	0	N	112226	Calcium-transporting ATPase OS=Orchesella cincta OX=48709 GN=Ocin01_16136 PE=3 SV=1
4	53330	tr|E9HR84|E9HR84_DAPPU	74.24	4	6	0	N	113043	Calcium-transporting ATPase OS=Daphnia pulex OX=6669 GN=DAPPUDRAFT_65262 PE=3 SV=1
4	53331	tr|A0A0P5VJX3|A0A0P5VJX3_9CRUS	74.24	4	6	0	N	113098	Calcium-transporting ATPase OS=Daphnia magna OX=35525 PE=3 SV=1
4	53332	tr|A0A4Y7LYL4|A0A4Y7LYL4_9CRUS	74.24	4	6	0	N	113136	Calcium-transporting ATPase OS=Daphnia atkinsoni OX=342845 GN=EOG090X00V6 PE=2 SV=1
2	53318	tr|A0A0C5E1J4|A0A0C5E1J4_CHEDE	74.06	4	6	0	N	109565	Calcium-transporting ATPase OS=Cherax destructor OX=6723 PE=2 SV=1
11	55331	tr|Q86GD6|Q86GD6_PROCL	73.88	0	3	1	N	962665	Projectin OS=Procambarus clarkii OX=6728 GN=proj PE=2 SV=1
10	53406	tr|A0A444TVR3|A0A444TVR3_ARMVU	71.61	12	4	4	N	14352	Cuticle protein AMP1A (Fragment) OS=Armadillidium vulgare OX=13347 GN=Avbf_10288 PE=4 SV=1
9	53398	tr|A0A7R8CX21|A0A7R8CX21_LEPSM	69.38	2	4	0	N	202190	MYH6_7 OS=Lepeophtheirus salmonis OX=72036 GN=LSAA_10697 PE=3 SV=1
9	53401	tr|A0A0K2V7Y7|A0A0K2V7Y7_LEPSM	69.38	2	4	0	N	218544	Myosin heavy chain 1 [Tribolium castaneum] OS=Lepeophtheirus salmonis OX=72036 GN=Mhc1 PE=3 SV=1

total 144 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
9	53399	tr|A0A7T8HL88|A0A7T8HL88_CALRO	69.38	2	4	0	N	215000	Myosin heavy chain 1 OS=Caligus rogercresseyi OX=217165 GN=FKW44_003971 PE=3 SV=1
9	53400	tr|A0A7T8HL29|A0A7T8HL29_CALRO	69.38	2	4	0	N	214908	Myosin heavy chain 1 OS=Caligus rogercresseyi OX=217165 GN=FKW44_003975 PE=3 SV=1
9	53403	tr|A0A0K2T3U6|A0A0K2T3U6_LEPSM	69.38	2	4	0	N	220566	Myosin heavy chain 1 [Tribolium castaneum] OS=Lepeophtheirus salmonis OX=72036 GN=Mhc1 PE=3 SV=1
9	53404	tr|A0A0K2TSJ7|A0A0K2TSJ7_LEPSM	69.38	2	4	0	N	222210	Myosin heavy chain 1 [Tribolium castaneum] (Fragment) OS=Lepeophtheirus salmonis OX=72036 GN=Mhc1 PE=3 SV=1
14	55341	tr|A0A0P4WFG0|A0A0P4WFG0_SCYOL	62.37	4	3	3	N	64765	Uncharacterized protein OS=Scylla olivacea OX=85551 PE=3 SV=1
14	55342	tr|A0A5B7GFK1|A0A5B7GFK1_PORTR	62.37	4	3	3	N	64777	Sodium/calcium exchanger 3 OS=Portunus trituberculatus OX=210409 GN=Slc8a3 PE=3 SV=1
14	55343	tr|A0A110A0P3|A0A110A0P3_ASTLP	62.37	2	3	3	N	100282	Sodium-calcium exchanger OS=Astacus leptodactylus OX=6717 PE=2 SV=1
12	55333	tr|A0A5B7EE36|A0A5B7EE36_PORTR	58.38	2	3	0	N	161842	Myosin heavy chain, muscle OS=Portunus trituberculatus OX=210409 GN=Mhc_15 PE=3 SV=1
3	53418	tr|A0A2Z4I2U3|A0A2Z4I2U3_CALSI	58.27	4	6	0	N	111733	Calcium-transporting ATPase OS=Callinectes sapidus OX=6763 GN=SERCA PE=2 SV=1
16	55332	tr|Q95YM2|Q95YM2_PROCL	52.84	0	2	2	N	1962327	I-connectin OS=Procambarus clarkii OX=6728 GN=I-con PE=2 SV=1
8	55348	tr|A0A6P7F415|A0A6P7F415_DIAVI	50.86	2	5	0	N	224155	myosin heavy chain, muscle isoform X15 OS=Diabrotica virgifera virgifera OX=50390 GN=LOC114326036 PE=3 SV=1
13	53782	tr|A0A5E4QJ96|A0A5E4QJ96_9NEOP	50.28	9	3	3	N	14403	Fructose-bisphosphate aldolase OS=Leptidea sinapis OX=189913 GN=LSINAPIS_LOCUS8982 PE=3 SV=1
13	53783	tr|A0A0A7BYS9|A0A0A7BYS9_OSTFU	50.28	6	3	3	N	22770	Fructose-bisphosphate aldolase (Fragment) OS=Ostrinia furnacalis OX=93504 PE=2 SV=1
13	53784	tr|A0A2H1WAZ2|A0A2H1WAZ2_SPOFR	50.28	5	3	3	N	25625	Fructose-bisphosphate aldolase (Fragment) OS=Spodoptera frugiperda OX=7108 GN=SFRICE_035466 PE=3 SV=1
13	53785	tr|A0A6J3BVA9|A0A6J3BVA9_GALME	50.28	5	3	3	N	26581	Fructose-bisphosphate aldolase OS=Galleria mellonella OX=7137 GN=LOC113515179 PE=3 SV=1

total 144 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
13	53786	tr|A0A6J1WK99|A0A6J1WK99_GALME	50.28	5	3	3	N	26425	Fructose-bisphosphate aldolase OS=Galleria mellonella OX=7137 GN=LOC113515179 PE=3 SV=1
13	54142	tr|A0A444T6K9|A0A444T6K9_ARMVU	50.28	4	3	3	N	34837	Fructose-bisphosphate aldolase OS=Armadillidium vulgare OX=13347 GN=Avbf_05003 PE=3 SV=1
13	53787	tr|A0A222AJC5|A0A222AJC5_SPOLI	50.28	4	3	3	N	36607	Fructose-bisphosphate aldolase (Fragment) OS=Spodoptera littoralis OX=7109 PE=3 SV=1
13	53788	tr|A0A0Q9WRY5|A0A0Q9WRY5_DROVI	50.28	3	3	3	N	38982	Fructose-bisphosphate aldolase OS=Drosophila virilis OX=7244 GN=Dvir\GJ23350 PE=3 SV=1
13	53789	tr|B4NKQ7|B4NKQ7_DROWI	50.28	3	3	3	N	38856	Fructose-bisphosphate aldolase OS=Drosophila willistoni OX=7260 GN=Dwil\GK13316 PE=3 SV=2
13	53790	tr|B4LYD3|B4LYD3_DROVI	50.28	3	3	3	N	39331	Fructose-bisphosphate aldolase OS=Drosophila virilis OX=7244 GN=Dvir\GJ23350 PE=3 SV=1
13	53791	tr|A0A0Q9WWZ4|A0A0Q9WWZ4_DROWI	50.28	3	3	3	N	39342	Fructose-bisphosphate aldolase OS=Drosophila willistoni OX=7260 GN=Dwil\GK13316 PE=3 SV=1
13	53792	tr|A0A0Q9WQB4|A0A0Q9WQB4_DROVI	50.28	3	3	3	N	39454	Fructose-bisphosphate aldolase OS=Drosophila virilis OX=7244 GN=Dvir\GJ23350 PE=3 SV=1
13	53793	tr|A0A2A4K0C6|A0A2A4K0C6_HELVI	50.28	3	3	3	N	39578	Fructose-bisphosphate aldolase OS=Heliothis virescens OX=7102 GN=B5V51_7176 PE=3 SV=1
13	53794	tr|A0A6J1NBL3|A0A6J1NBL3_BICAN	50.28	3	3	3	N	39565	Fructose-bisphosphate aldolase OS=Bicyclus anynana OX=110368 GN=LOC112048916 PE=3 SV=1
13	53795	tr|A0A6J2KNU6|A0A6J2KNU6_BOMMA	50.28	3	3	3	N	39653	Fructose-bisphosphate aldolase OS=Bombyx mandarina OX=7092 GN=LOC114252770 PE=3 SV=1
13	53796	tr|A0A6J2KQG2|A0A6J2KQG2_BOMMA	50.28	3	3	3	N	39554	Fructose-bisphosphate aldolase OS=Bombyx mandarina OX=7092 GN=LOC114252770 PE=3 SV=1
13	53797	tr|Q1HPN7|Q1HPN7_BOMMO	50.28	3	3	3	N	39653	Fructose-bisphosphate aldolase OS=Bombyx mori OX=7091 GN=ALD PE=2 SV=1
13	53798	tr|S4PKR2|S4PKR2_9NEOP	50.28	3	3	3	N	39565	Fructose-bisphosphate aldolase OS=Pararge aegeria OX=116150 PE=3 SV=1
13	53799	tr|A0A7S5LJX7|A0A7S5LJX7_BEMTA	50.28	3	3	3	N	39474	Fructose-bisphosphate aldolase OS=Bemisia tabaci OX=7038 PE=2 SV=1

total 144 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
13	53800	tr|A0A7R9X220|A0A7R9X220_9CRUS	50.28	3	3	3	N	39795	Fructose-bisphosphate aldolase (Fragment) OS=Argulus foliaceus OX=509924 GN=AFOL1_LOCUS42511 PE=3 SV=1
13	53801	tr|A0A7R9A8N4|A0A7R9A8N4_9CRUS	50.28	3	3	3	N	40451	Fructose-bisphosphate aldolase OS=Darwinula stevensoni OX=69355 GN=DSTB1V02_LOCUS9328 PE=3 SV=1
13	53802	tr|A0A7R9A8M7|A0A7R9A8M7_9CRUS	50.28	3	3	3	N	40361	Fructose-bisphosphate aldolase OS=Darwinula stevensoni OX=69355 GN=DSTB1V02_LOCUS9328 PE=3 SV=1
13	53803	tr|A0A4C1UD71|A0A4C1UD71_EUMVA	50.28	3	3	3	N	41921	Fructose-bisphosphate aldolase OS=Eumeta variegata OX=151549 GN=Ald PE=3 SV=1
13	53804	tr|A0A6J2KM35|A0A6J2KM35_BOMMA	50.28	3	3	3	N	41930	Fructose-bisphosphate aldolase OS=Bombyx mandarina OX=7092 GN=LOC114252770 PE=3 SV=1
13	53805	tr|A0A821PCJ9|A0A821PCJ9_9NEOP	50.28	3	3	3	N	42283	Hypothetical protein OS=Pieris macdunnoughi OX=345717 GN=PMACD_LOCUS3545 PE=4 SV=1
13	53806	tr|A0A7E5VF38|A0A7E5VF38_TRINI	50.28	3	3	3	N	42482	Fructose-bisphosphate aldolase OS=Trichoplusia ni OX=7111 GN=LOC113493218 PE=3 SV=1
13	53807	tr|A0A7I1A027|A0A7I1A027_DANPL	50.28	3	3	3	N	44674	Fructose-bisphosphate aldolase OS=Danaus plexippus plexippus OX=278856 GN=LOC116777233 PE=3 SV=1
13	53808	tr|A0A821PCK8|A0A821PCK8_9NEOP	50.28	3	3	3	N	44744	Hypothetical protein OS=Pieris macdunnoughi OX=345717 GN=PMACD_LOCUS3545 PE=4 SV=1
13	53809	tr|A0A811X398|A0A811X398_PLUXY	50.28	3	3	3	N	45068	(diamondback moth) hypothetical protein OS=Plutella xylostella OX=51655 GN=PLXY1_LOCUS14297 PE=4 SV=1
13	53810	tr|A0A2P8YG29|A0A2P8YG29_BLAGE	50.28	2	3	3	N	66209	Fructose-bisphosphate aldolase (Fragment) OS=Blattella germanica OX=6973 GN=C0J52_17262 PE=3 SV=1
7	53302	tr|A0A5B7DQZ0|A0A5B7DQZ0_PORTR	49.27	1	5	0	N	352200	Myosin heavy chain, muscle OS=Portunus trituberculatus OX=210409 GN=Mhc_1 PE=3 SV=1
19	53698	tr|A0A821V8C5|A0A821V8C5_9NEOP	47.29	0	2	1	N	829790	Hypothetical protein OS=Pieris macdunnoughi OX=345717 GN=PMACD_LOCUS11411 PE=4 SV=1

total 144 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
20	55356	tr|A0A7J7AR02|A0A7J7AR02_9COLE	42.81	2	2	2	N	56047	DNA topoisomerase 2 OS=Lamprigera yunnana OX=370605 GN=FQA39_LY13024 PE=3 SV=1
17	55347	tr|A0A444T9K0|A0A444T9K0_ARMVU	38.42	0	2	1	N	677780	Twitchin OS=Armadillidium vulgare OX=13347 GN=Avbf_03670 PE=3 SV=1
18	53382	tr|A0A2P1JJ42|A0A2P1JJ42_PROCL	33.62	1	2	2	N	167860	Filamin-A isoform X5 (Fragment) OS=Procambarus clarkii OX=6728 GN=Flna PE=2 SV=1
15	53378	tr|A0A0N9EJJ5|A0A0N9EJJ5_ERIVE	30.04	2	2	2	N	77227	Hemocyanin OS=Eriphia verrucosa OX=483417 GN=H PE=2 SV=1
29	55367	tr|A0A1J1IN48|A0A1J1IN48_9DIPT	25.85	0	1	1	N	464835	HECT-type E3 ubiquitin transferase OS=Clunio marinus OX=568069 GN=CLUMA_CG014451 PE=4 SV=1
29	55370	tr|A0A1E1XMV5|A0A1E1XMV5_9ACAR	25.85	2	1	1	N	48988	F-box domain-containing protein (Fragment) OS=Amblyomma sculptum OX=1581419 PE=2 SV=1
39	55371	tr|B4J4N0|B4J4N0_DROGR	25.31	6	1	1	N	14634	GH22151 OS=Drosophila grimshawi OX=7222 GN=Dgri\GH22151 PE=4 SV=1
23	55369	tr|A0A4S2KBN7|A0A4S2KBN7_9HYME	25.31	0	1	1	N	276373	Uncharacterized protein (Fragment) OS=Temnothorax longispinosus OX=300112 GN=DBV15_11441 PE=4 SV=1
40	55404	tr|A0A2P8XAH3|A0A2P8XAH3_BLAGE	23.47	9	1	1	N	9271	Uncharacterized protein (Fragment) OS=Blattella germanica OX=6973 GN=C0J52_27736 PE=4 SV=1
22	55372	tr|R9YY56|R9YY56_9EUCA	21.53	6	1	1	N	22569	Arginine kinase (Fragment) OS=Kiwa sp. n. East Scotia Ridge OX=1335429 GN=AK PE=3 SV=1
22	55373	tr|R9YY47|R9YY47_9EUCA	21.53	6	1	1	N	22701	Arginine kinase (Fragment) OS=Eumunida picta OX=497012 GN=AK PE=3 SV=1
22	55374	tr|G3C6J8|G3C6J8_9EUCA	21.53	5	1	1	N	25125	Arginine kinase (Fragment) OS=Eumunida funambulus OX=497008 GN=AK PE=3 SV=1
22	55375	tr|G3C6I8|G3C6I8_AEGAL	21.53	5	1	1	N	25111	Arginine kinase (Fragment) OS=Aegla alacalufi OX=172761 GN=AK PE=3 SV=1
22	55376	tr|G3C6N2|G3C6N2_9EUCA	21.53	5	1	1	N	25296	Arginine kinase (Fragment) OS=Conchoecetes artificiosus OX=516906 GN=AK PE=3 SV=1
22	43554	P86699|KARG_CHIOP	21.53	5	1	1	N	25324	Arginine kinase (Fragments) OS=Chionoecetes opilio OX=41210 PE=1 SV=1
22	55377	tr|G3D680|G3D680_PORTR	21.53	4	1	1	N	35589	Arginine kinase OS=Portunus trituberculatus OX=210409 PE=3 SV=1
22	55378	tr|I1TMM2|I1TMM2_SCYPA	21.53	3	1	1	N	39899	Arginine kinase (Fragment) OS=Scylla paramamosain OX=85552 PE=2 SV=1

total 144 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
22	53723	tr|K7PD48|K7PD48_SCYPA	21.53	3	1	1	N	40187	Arginine kinase OS=Scylla paramamosain OX=85552 PE=2 SV=1
22	43542	C9EIP1|KARG_SCYSE	21.53	3	1	1	N	40189	Arginine kinase Scy s 2 OS=Scylla serrata OX=6761 PE=1 SV=1
22	55379	tr|G3D692|G3D692_PORTR	21.53	3	1	1	N	40315	Arginine kinase OS=Portunus trituberculatus OX=210409 GN=KARG PE=3 SV=1
22	55380	tr|H6AC60|H6AC60_PORTR	21.53	3	1	1	N	40291	Arginine kinase OS=Portunus trituberculatus OX=210409 PE=3 SV=1
22	55381	tr|A0A8A8ZWC2|A0A8A8ZWC2_CALBE	21.53	3	1	1	N	40243	Arginine kinase OS=Callinectes bellicosus OX=257890 GN=AK PE=4 SV=1
22	55382	tr|G3D676|G3D676_PORTR	21.53	3	1	1	N	40299	Arginine kinase OS=Portunus trituberculatus OX=210409 PE=3 SV=1
22	43545	Q9GYX1|KARG_PACMR	21.53	3	1	1	N	40243	Arginine kinase OS=Pachygrapsus marmoratus OX=135190 PE=2 SV=1
22	43546	H6VGI2|KARG_PROCL	21.53	3	1	1	N	40120	Arginine kinase Pro c 2.0101 OS=Procambarus clarkii OX=6728 PE=1 SV=1
22	55383	tr|G3D677|G3D677_PORTR	21.53	3	1	1	N	40287	Arginine kinase OS=Portunus trituberculatus OX=210409 PE=3 SV=1
22	55384	tr|H6AC58|H6AC58_PORTR	21.53	3	1	1	N	40373	Arginine kinase OS=Portunus trituberculatus OX=210409 PE=3 SV=1
22	55385	tr|A0A068EFU4|A0A068EFU4_9EUCA	21.53	3	1	1	N	40328	Arginine kinase OS=Macrophthalmus japonicus OX=138195 PE=2 SV=1
22	55386	tr|G3D691|G3D691_PORTR	21.53	3	1	1	N	40287	Arginine kinase OS=Portunus trituberculatus OX=210409 PE=3 SV=1
22	43543	Q9NH49|KARG_CALSI	21.53	3	1	1	N	40315	Arginine kinase OS=Callinectes sapidus OX=6763 PE=2 SV=1
22	43544	Q9U9J4|KARG_CARMA	21.53	3	1	1	N	40237	Arginine kinase OS=Carcinus maenas OX=6759 PE=2 SV=1
22	55387	tr|H6UKS0|H6UKS0_SCYPA	21.53	3	1	1	N	40244	Arginine kinase OS=Scylla paramamosain OX=85552 PE=3 SV=1
22	43548	Q9NH48|KARG_ERISI	21.53	3	1	1	N	40339	Arginine kinase OS=Eriocheir sinensis OX=95602 PE=2 SV=1
22	55388	tr|G3D675|G3D675_PORTR	21.53	3	1	1	N	40244	Arginine kinase OS=Portunus trituberculatus OX=210409 PE=3 SV=1
22	43549	H6VGI3|KARG0_SCYPA	21.53	3	1	1	N	40299	Arginine kinase Scy p 2.0101 OS=Scylla paramamosain OX=85552 PE=1 SV=1
22	55405	tr|A0A1C6ZZL8|A0A1C6ZZL8_PROCL	21.53	4	1	1	N	31849	Arginine kinase (Fragment) OS=Procambarus clarkii OX=6728 PE=2 SV=1
22	55406	tr|A0A0C5DEY3|A0A0C5DEY3_CHEDE	21.53	3	1	1	N	40205	Arginine kinase OS=Cherax destructor OX=6723 PE=2 SV=1
22	55464	tr|D2DSQ8|D2DSQ8_SCYPA	21.53	12	1	1	N	10580	Arginine kinase (AK) (Fragment) OS=Scylla paramamosain OX=85552 PE=2 SV=1

total 144 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
22	55465	tr|F5A6C6|F5A6C6_PROCL	21.53	5	1	1	N	27566	Arginine kinase OS=Procambarus clarkii OX=6728 PE=2 SV=1
42	55470	tr|J9K049|J9K049_ACYPI	21.41	0	1	1	N	224673	Uncharacterized protein OS=Acyrthosiphon pisum OX=7029 PE=4 SV=2
43	55473	tr|A0A0R3NUC8|A0A0R3NUC8_DROPS	20.28	9	1	1	N	12839	Uncharacterized protein, isoform B OS=Drosophila pseudoobscura pseudoobscura OX=46245 GN=Dpse\GA28972 PE=4 SV=1
43	55474	tr|B4GX09|B4GX09_DROPE	20.28	3	1	1	N	37162	GL21085 OS=Drosophila persimilis OX=7234 GN=Dper\GL21085 PE=4 SV=1
27	55477	tr|A0A821UPU7|A0A821UPU7_9NEOP	20.24	0	1	1	N	1690556	Hypothetical protein OS=Pieris macdunnoughi OX=345717 GN=PMACD_LOCUS10683 PE=4 SV=1
44	53657	tr|A0A023ERZ2|A0A023ERZ2_AEDAL	20.21	3	1	1	N	45728	Pyruvate kinase (Fragment) OS=Aedes albopictus OX=7160 PE=2 SV=1
44	53658	tr|A0A0P8Y097|A0A0P8Y097_DROAN	20.21	2	1	1	N	55184	Pyruvate kinase OS=Drosophila ananassae OX=7217 GN=Dana\GF18439 PE=3 SV=1
44	53659	tr|A0A6P8K875|A0A6P8K875_DROMA	20.21	2	1	1	N	55073	Pyruvate kinase OS=Drosophila mauritiana OX=7226 GN=LOC117143834 PE=3 SV=1
44	53660	tr|A0A6P4F4P4|A0A6P4F4P4_DRORH	20.21	2	1	1	N	55028	Pyruvate kinase OS=Drosophila rhopaloa OX=1041015 GN=LOC108048043 PE=3 SV=1
44	53661	tr|A0A1Y9GJY2|A0A1Y9GJY2_ANOAR	20.21	2	1	1	N	55698	Pyruvate kinase OS=Anopheles arabiensis OX=7173 PE=3 SV=1
44	53662	tr|A0A0Q9X1L7|A0A0Q9X1L7_DROMO	20.21	2	1	1	N	55236	Pyruvate kinase OS=Drosophila mojavensis OX=7230 GN=Dmoj\GI22374 PE=3 SV=1
44	55475	tr|A0A182UE55|A0A182UE55_9DIPT	20.21	2	1	1	N	56051	Pyruvate kinase OS=Anopheles melas OX=34690 PE=3 SV=2
44	53663	tr|A0A2M3ZFB9|A0A2M3ZFB9_9DIPT	20.21	2	1	1	N	56104	Pyruvate kinase (Fragment) OS=Anopheles braziliensis OX=58242 PE=3 SV=1
44	53664	tr|A0A2M3ZYS6|A0A2M3ZYS6_9DIPT	20.21	2	1	1	N	56023	Pyruvate kinase (Fragment) OS=Anopheles triannulatus OX=58253 PE=3 SV=1
44	53665	tr|A0A2M3ZYS8|A0A2M3ZYS8_9DIPT	20.21	2	1	1	N	56022	Pyruvate kinase (Fragment) OS=Anopheles triannulatus OX=58253 PE=3 SV=1
44	53666	tr|A0A1Y9GJK0|A0A1Y9GJK0_ANOAR	20.21	2	1	1	N	56271	Pyruvate kinase OS=Anopheles arabiensis OX=7173 PE=3 SV=1
44	53667	tr|A0A6A0H7S7|A0A6A0H7S7_HYAAZ	20.21	2	1	1	N	56703	Pyruvate kinase OS=Hyalella azteca OX=294128 GN=HAZT_HAZT006469 PE=3 SV=1
44	53668	tr|A0A1E1X8N4|A0A1E1X8N4_9ACAR	20.21	2	1	1	N	57708	Pyruvate kinase OS=Amblyomma aureolatum OX=187763 PE=2 SV=1

total 144 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
44	53669	tr|A0A6P4F9I4|A0A6P4F9I4_DRORH	20.21	2	1	1	N	57050	Pyruvate kinase OS=Drosophila rhopaloa OX=1041015 GN=LOC108048043 PE=3 SV=1
44	53670	tr|A0A182VPN6|A0A182VPN6_9DIPT	20.21	2	1	1	N	57977	Pyruvate kinase OS=Anopheles minimus OX=112268 PE=3 SV=1
44	53671	tr|A0A182MNQ6|A0A182MNQ6_9DIPT	20.21	2	1	1	N	57968	Pyruvate kinase OS=Anopheles culicifacies OX=139723 PE=3 SV=1
44	53672	tr|A0A6J2T5C5|A0A6J2T5C5_DROLE	20.21	2	1	1	N	57328	Pyruvate kinase OS=Drosophila lebanonensis OX=7225 GN=LOC115620839 PE=3 SV=1
44	53673	tr|A0A1W4W378|A0A1W4W378_DROFC	20.21	2	1	1	N	57395	Pyruvate kinase OS=Drosophila ficusphila OX=30025 GN=LOC108099555 PE=3 SV=1
44	53674	O62619|KPYK_DROME	20.21	2	1	1	N	57440	Pyruvate kinase OS=Drosophila melanogaster OX=7227 GN=PyK PE=2 SV=2
44	53675	tr|B4HE69|B4HE69_DROSE	20.21	2	1	1	N	57454	Pyruvate kinase OS=Drosophila sechellia OX=7238 GN=Dsec\GM26420 PE=3 SV=1
44	53676	tr|A0A6P4F0Q9|A0A6P4F0Q9_DRORH	20.21	2	1	1	N	57379	Pyruvate kinase OS=Drosophila rhopaloa OX=1041015 GN=LOC108048043 PE=3 SV=1
44	53677	tr|B3P7K4|B3P7K4_DROER	20.21	2	1	1	N	57539	Pyruvate kinase OS=Drosophila erecta OX=7220 GN=Dere\GG11123 PE=3 SV=1
44	53678	tr|B3M213|B3M213_DROAN	20.21	2	1	1	N	57565	Pyruvate kinase OS=Drosophila ananassae OX=7217 GN=Dana\GF18439 PE=3 SV=2
44	53679	tr|A0A6P8KMB4|A0A6P8KMB4_DROMA	20.21	2	1	1	N	57454	Pyruvate kinase OS=Drosophila mauritiana OX=7226 GN=LOC117143834 PE=3 SV=1
44	53680	tr|B4K5E3|B4K5E3_DROMO	20.21	2	1	1	N	57618	Pyruvate kinase OS=Drosophila mojavensis OX=7230 GN=Dmoj\GI22374 PE=3 SV=1
44	53681	tr|A0A484BWG4|A0A484BWG4_DRONA	20.21	2	1	1	N	57563	Pyruvate kinase OS=Drosophila navojoa OX=7232 GN=AWZ03_001260 PE=3 SV=1
44	53682	tr|A0A131XQM7|A0A131XQM7_9ACAR	20.21	2	1	1	N	59290	Pyruvate kinase OS=Hyalomma excavatum OX=257692 PE=2 SV=1
44	53683	tr|A0A0P9ARZ1|A0A0P9ARZ1_DROAN	20.21	2	1	1	N	59439	Pyruvate kinase OS=Drosophila ananassae OX=7217 GN=Dana\GF18439 PE=3 SV=1

total 144 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
44	53684	tr|G3MLC1|G3MLC1_AMBMU	20.21	2	1	1	N	61369	Pyruvate kinase OS=Amblyomma maculatum OX=34609 PE=2 SV=1
44	53685	tr|A0A023EVC5|A0A023EVC5_AEDAL	20.21	2	1	1	N	63958	Pyruvate kinase (Fragment) OS=Aedes albopictus OX=7160 PE=2 SV=1
44	53687	tr|A0A5N5T493|A0A5N5T493_9CRUS	20.21	2	1	1	N	68944	Pyruvate kinase OS=Armadillidium nasatum OX=96803 GN=PyK PE=3 SV=1

total 144 proteins

tr|A0A3R7M007|A0A3R7M007_PENVA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.KEEYDESGPGIVHR.K	Y	49.90	1614.7638	-1.3	539.2612	3	10.08	1349	2	356	369	
K.SYELPDGQVITI.G	Y	39.95	1333.6765	-0.3	667.8453	2	14.58	2163	1	236	247	
T.NWDDMEKIWHH.S	Y	36.38	1509.6459	0.3	755.8304	2	12.78	1846	1	75	85	
G.FAGDDAPRA.V	Y	34.08	918.4195	-1.0	460.2166	2	10.01	1336	1	18	26	
E.EYDESGPGIVH.R	Y	32.14	1201.5251	-0.1	601.7698	2	10.85	1492	1	358	368	
K.IIAPPERKYS.V	Y	26.54	1172.6553	-0.6	587.3345	2	10.19	1367	1	326	335	
E.KSYELPDGQVITI.G	Y	23.84	1461.7715	-0.3	731.8928	2	13.76	2020	1	235	247	
L.DTGDGVTH.T	Y	22.68	800.3301	0.0	401.1723	2	8.83	1133	2	151	158	
E.EYDESGPGIVHR.K	Y	22.68	1357.6262	-0.8	679.8198	2	10.41	1408	1	358	369	
K.AGFAGDDAPR.A	Y	19.76	975.4410	-1.8	488.7269	2	10.25	1378	1	16	25	
T.MYPGIADRM.Q	Y	19.04	1052.4783	-0.3	527.2463	2	11.98	1702	1	302	310	
L.LTEAPLNPK.A	Y	18.48	981.5494	-1.0	491.7815	2	10.51	1426	1	102	110	
E.KSYELPDGQVIT.I	Y	17.94	1348.6874	-0.7	675.3505	2	12.15	1733	1	235	246	
L.TEAPLNPK.A	Y	17.21	868.4654	-0.5	435.2397	2	9.70	1282	2	103	110	
E.SGPGIVH.R	Y	16.57	665.3497	-0.5	333.6819	2	9.75	1291	1	362	368	
K.SYELPDGQVI.T	Y	16.19	1119.5448	-0.3	560.7795	2	13.65	2001	1	236	245	
F.AGDDAPR.A	Y	15.34	700.3140	-5.0	351.1625	2	15.31	2292	2	19	25	

total 17 peptides

tr|H9B3Y9|H9B3Y9_SCYPA
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.KEEYDESGPGIVHR.K	Y	49.90	1614.7638	-1.3	539.2612	3	10.08	1349	2	360	373	
K.SYELPDGQVITI.G	Y	39.95	1333.6765	-0.3	667.8453	2	14.58	2163	1	240	251	
T.NWDDMEKIWHH.S	Y	36.38	1509.6459	0.3	755.8304	2	12.78	1846	1	79	89	
G.FAGDDAPRA.V	Y	34.08	918.4195	-1.0	460.2166	2	10.01	1336	1	22	30	
E.EYDESGPGIVH.R	Y	32.14	1201.5251	-0.1	601.7698	2	10.85	1492	1	362	372	
K.IIAPPERKYS.V	Y	26.54	1172.6553	-0.6	587.3345	2	10.19	1367	1	330	339	
E.KSYELPDGQVITI.G	Y	23.84	1461.7715	-0.3	731.8928	2	13.76	2020	1	239	251	
L.DTGDGVTH.T	Y	22.68	800.3301	0.0	401.1723	2	8.83	1133	2	155	162	
E.EYDESGPGIVHR.K	Y	22.68	1357.6262	-0.8	679.8198	2	10.41	1408	1	362	373	
K.AGFAGDDAPR.A	Y	19.76	975.4410	-1.8	488.7269	2	10.25	1378	1	20	29	
T.MYPGIADRM.Q	Y	19.04	1052.4783	-0.3	527.2463	2	11.98	1702	1	306	314	
L.LTEAPLNPK.A	Y	18.48	981.5494	-1.0	491.7815	2	10.51	1426	1	106	114	
E.KSYELPDGQVIT.I	Y	17.94	1348.6874	-0.7	675.3505	2	12.15	1733	1	239	250	
L.TEAPLNPK.A	Y	17.21	868.4654	-0.5	435.2397	2	9.70	1282	2	107	114	
E.SGPGIVH.R	Y	16.57	665.3497	-0.5	333.6819	2	9.75	1291	1	366	372	
K.SYELPDGQVI.T	Y	16.19	1119.5448	-0.3	560.7795	2	13.65	2001	1	240	249	
F.AGDDAPR.A	Y	15.34	700.3140	-5.0	351.1625	2	15.31	2292	2	23	29	

total 17 peptides

tr|A0A6A0H005|A0A6A0H005_HYAAZ
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.KEEYDESGPGIVHR.K	Y	49.90	1614.7638	-1.3	539.2612	3	10.08	1349	2	360	373	
K.SYELPDGQVITI.G	Y	39.95	1333.6765	-0.3	667.8453	2	14.58	2163	1	240	251	
T.NWDDMEKIWHH.T	Y	36.38	1509.6459	0.3	755.8304	2	12.78	1846	1	79	89	
G.FAGDDAPRA.V	Y	34.08	918.4195	-1.0	460.2166	2	10.01	1336	1	22	30	
E.EYDESGPGIVH.R	Y	32.14	1201.5251	-0.1	601.7698	2	10.85	1492	1	362	372	
K.IIAPPERKYS.V	Y	26.54	1172.6553	-0.6	587.3345	2	10.19	1367	1	330	339	
E.KSYELPDGQVITI.G	Y	23.84	1461.7715	-0.3	731.8928	2	13.76	2020	1	239	251	
L.DTGDGVTH.T	Y	22.68	800.3301	0.0	401.1723	2	8.83	1133	2	155	162	
E.EYDESGPGIVHR.K	Y	22.68	1357.6262	-0.8	679.8198	2	10.41	1408	1	362	373	
K.AGFAGDDAPR.A	Y	19.76	975.4410	-1.8	488.7269	2	10.25	1378	1	20	29	
S.MYPGIADRM.Q	Y	19.04	1052.4783	-0.3	527.2463	2	11.98	1702	1	306	314	
L.LTEAPLNPK.A	Y	18.48	981.5494	-1.0	491.7815	2	10.51	1426	1	106	114	
E.KSYELPDGQVIT.I	Y	17.94	1348.6874	-0.7	675.3505	2	12.15	1733	1	239	250	
L.TEAPLNPK.A	Y	17.21	868.4654	-0.5	435.2397	2	9.70	1282	2	107	114	
E.SGPGIVH.R	Y	16.57	665.3497	-0.5	333.6819	2	9.75	1291	1	366	372	
K.SYELPDGQVI.T	Y	16.19	1119.5448	-0.3	560.7795	2	13.65	2001	1	240	249	
F.AGDDAPR.A	Y	15.34	700.3140	-5.0	351.1625	2	15.31	2292	2	23	29	

total 17 peptides

tr|A0A482LUC2|A0A482LUC2_CANBE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.KEEYDESGPGIVHR.K	Y	49.90	1614.7638	-1.3	539.2612	3	10.08	1349	2	360	373	
K.SYELPDGQVITI.G	Y	39.95	1333.6765	-0.3	667.8453	2	14.58	2163	1	240	251	
T.NWDDMEKIWHH.S	Y	36.38	1509.6459	0.3	755.8304	2	12.78	1846	1	79	89	
G.FAGDDAPRA.V	Y	34.08	918.4195	-1.0	460.2166	2	10.01	1336	1	22	30	
E.EYDESGPGIVH.R	Y	32.14	1201.5251	-0.1	601.7698	2	10.85	1492	1	362	372	
K.IIAPPERKYS.V	Y	26.54	1172.6553	-0.6	587.3345	2	10.19	1367	1	330	339	
E.KSYELPDGQVITI.G	Y	23.84	1461.7715	-0.3	731.8928	2	13.76	2020	1	239	251	
L.DTGDGVTH.T	Y	22.68	800.3301	0.0	401.1723	2	8.83	1133	2	155	162	
E.EYDESGPGIVHR.K	Y	22.68	1357.6262	-0.8	679.8198	2	10.41	1408	1	362	373	
K.AGFAGDDAPR.A	Y	19.76	975.4410	-1.8	488.7269	2	10.25	1378	1	20	29	
T.MYPGIADRM.Q	Y	19.04	1052.4783	-0.3	527.2463	2	11.98	1702	1	306	314	
L.LTEAPLNPK.A	Y	18.48	981.5494	-1.0	491.7815	2	10.51	1426	1	106	114	
E.KSYELPDGQVIT.I	Y	17.94	1348.6874	-0.7	675.3505	2	12.15	1733	1	239	250	
L.TEAPLNPK.A	Y	17.21	868.4654	-0.5	435.2397	2	9.70	1282	2	107	114	
E.SGPGIVH.R	Y	16.57	665.3497	-0.5	333.6819	2	9.75	1291	1	366	372	
K.SYELPDGQVI.T	Y	16.19	1119.5448	-0.3	560.7795	2	13.65	2001	1	240	249	
F.AGDDAPR.A	Y	15.34	700.3140	-5.0	351.1625	2	15.31	2292	2	23	29	

total 17 peptides

tr|A0A2H4V3D6|A0A2H4V3D6_PENVA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.KEEYDESGPGIVHR.K	Y	49.90	1614.7638	-1.3	539.2612	3	10.08	1349	2	360	373	
K.SYELPDGQVITI.G	Y	39.95	1333.6765	-0.3	667.8453	2	14.58	2163	1	240	251	
T.NWDDMEKIWHH.S	Y	36.38	1509.6459	0.3	755.8304	2	12.78	1846	1	79	89	
G.FAGDDAPRA.V	Y	34.08	918.4195	-1.0	460.2166	2	10.01	1336	1	22	30	
E.EYDESGPGIVH.R	Y	32.14	1201.5251	-0.1	601.7698	2	10.85	1492	1	362	372	
K.IIAPPERKYS.V	Y	26.54	1172.6553	-0.6	587.3345	2	10.19	1367	1	330	339	
E.KSYELPDGQVITI.G	Y	23.84	1461.7715	-0.3	731.8928	2	13.76	2020	1	239	251	
L.DTGDGVTH.T	Y	22.68	800.3301	0.0	401.1723	2	8.83	1133	2	155	162	

total 17 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYDESGPGIVHR.K	Y	22.68	1357.6262	-0.8	679.8198	2	10.41	1408	1	362	373	
K.AGFAGDDAPR.A	Y	19.76	975.4410	-1.8	488.7269	2	10.25	1378	1	20	29	
T.MYPGIADRM.Q	Y	19.04	1052.4783	-0.3	527.2463	2	11.98	1702	1	306	314	
L.LTEAPLNPK.A	Y	18.48	981.5494	-1.0	491.7815	2	10.51	1426	1	106	114	
E.KSYELPDGQVIT.I	Y	17.94	1348.6874	-0.7	675.3505	2	12.15	1733	1	239	250	
L.TEAPLNPK.A	Y	17.21	868.4654	-0.5	435.2397	2	9.70	1282	2	107	114	
E.SGPGIVH.R	Y	16.57	665.3497	-0.5	333.6819	2	9.75	1291	1	366	372	
K.SYELPDGQVI.T	Y	16.19	1119.5448	-0.3	560.7795	2	13.65	2001	1	240	249	
F.AGDDAPR.A	Y	15.34	700.3140	-5.0	351.1625	2	15.31	2292	2	23	29	

total 17 peptides

tr|A0A5B7IZE3|A0A5B7IZE3_PORTR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.SPGVIDAGLVMH.Q	N	44.78	1194.6067	-0.9	598.3101	2	12.56	1806	1	155	166	
W.LEKNKDPLNDTLVDLL.K	Y	33.09	1838.9989	0.3	920.5070	2	14.28	2111	1	68	83	
L.SILEEESMFPK.A	N	26.45	1308.6271	-0.7	655.3204	2	12.91	1869	1	5	15	
K.NKDPLNDTL.V	N	20.74	1028.5138	-0.9	515.2637	2	11.46	1603	1	71	79	
N.ETKSPGVIDAGLVM.H	N	16.36	1415.7330	-0.4	708.8735	2	12.98	1882	1	152	165	

total 5 peptides

tr|F8WR03|F8WR03_PENJP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VTVPSIDDKEDMQF.T	N	40.27	1622.7498	-0.4	812.3818	2	12.86	1860	1	318	331	
K.VTVPSIDDKEDMQ.F	N	31.89	1475.6814	-0.1	738.8479	2	11.58	1627	1	318	330	
L.SILEEESMFPK.A	N	26.45	1308.6271	-0.7	655.3204	2	12.91	1869	1	532	542	
L.ITGESGAGK.T	N	23.91	818.4134	-0.2	410.2139	2	8.67	1104	1	180	188	
R.NEVPPHLF.A	N	16.25	951.4814	-0.3	476.7478	2	13.07	1899	1	152	159	

total 5 peptides

tr|K4Q111|K4Q111_PENVA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VTVPSIDDKEDMQF.T	N	40.27	1622.7498	-0.4	812.3818	2	12.86	1860	1	318	331	
K.VTVPSIDDKEDMQ.F	N	31.89	1475.6814	-0.1	738.8479	2	11.58	1627	1	318	330	
L.SILEEESMFPK.A	N	26.45	1308.6271	-0.7	655.3204	2	12.91	1869	1	532	542	
L.ITGESGAGK.T	N	23.91	818.4134	-0.2	410.2139	2	8.67	1104	1	180	188	
R.NEVPPHLF.A	N	16.25	951.4814	-0.3	476.7478	2	13.07	1899	1	152	159	

total 5 peptides

tr|K4Q4N8|K4Q4N8_PENMO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VTVPSIDDKEDMQF.T	N	40.27	1622.7498	-0.4	812.3818	2	12.86	1860	1	318	331	
K.VTVPSIDDKEDMQ.F	N	31.89	1475.6814	-0.1	738.8479	2	11.58	1627	1	318	330	
L.SILEEESMFPK.A	N	26.45	1308.6271	-0.7	655.3204	2	12.91	1869	1	532	542	
L.ITGESGAGK.T	N	23.91	818.4134	-0.2	410.2139	2	8.67	1104	1	180	188	
R.NEVPPHLF.A	N	16.25	951.4814	-0.3	476.7478	2	13.07	1899	1	152	159	

total 5 peptides

tr|A0A4Y7MKW9|A0A4Y7MKW9_9CRUS

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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	40.51	1156.5724	-0.4	579.2932	2	10.50	1423	1	594	605	
V.SVGDKIPAD.I	N	30.16	900.4552	-0.6	451.2346	2	10.20	1370	1	46	54	
L.GFNPPDLDIM.N	N	23.83	1117.5114	-0.4	559.7628	2	14.97	2231	1	701	710	
E.VSVGDKIPAD.I	N	18.74	999.5236	-0.1	500.7690	2	10.76	1472	1	45	54	
V.KISLPVILL.D	N	16.43	994.6790	-0.3	498.3466	2	15.13	2259	1	865	873	
S.VGDKIPADI.R	N	16.36	926.5073	-0.4	464.2607	2	11.57	1624	1	47	55	

total 6 peptides

tr|A0A0P5KSW7|A0A0P5KSW7_9CRUS
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	40.51	1156.5724	-0.4	579.2932	2	10.50	1423	1	705	716	
V.SVGDKIPAD.I	N	30.16	900.4552	-0.6	451.2346	2	10.20	1370	1	157	165	
L.GFNPPDLDIM.N	N	23.83	1117.5114	-0.4	559.7628	2	14.97	2231	1	812	821	
E.VSVGDKIPAD.I	N	18.74	999.5236	-0.1	500.7690	2	10.76	1472	1	156	165	
V.KISLPVILL.D	N	16.43	994.6790	-0.3	498.3466	2	15.13	2259	1	976	984	
S.VGDKIPADI.R	N	16.36	926.5073	-0.4	464.2607	2	11.57	1624	1	158	166	

total 6 peptides

tr|A0A4Y7MXF9|A0A4Y7MXF9_9CRUS
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	40.51	1156.5724	-0.4	579.2932	2	10.50	1423	1	705	716	
V.SVGDKIPAD.I	N	30.16	900.4552	-0.6	451.2346	2	10.20	1370	1	157	165	
L.GFNPPDLDIM.N	N	23.83	1117.5114	-0.4	559.7628	2	14.97	2231	1	812	821	
E.VSVGDKIPAD.I	N	18.74	999.5236	-0.1	500.7690	2	10.76	1472	1	156	165	
I.KISLPVILL.D	N	16.43	994.6790	-0.3	498.3466	2	15.13	2259	1	976	984	
S.VGDKIPADI.R	N	16.36	926.5073	-0.4	464.2607	2	11.57	1624	1	158	166	

total 6 peptides

tr|A0A0P4ZGF4|A0A0P4ZGF4_9CRUS
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	40.51	1156.5724	-0.4	579.2932	2	10.50	1423	1	705	716	
V.SVGDKIPAD.I	N	30.16	900.4552	-0.6	451.2346	2	10.20	1370	1	157	165	
L.GFNPPDLDIM.N	N	23.83	1117.5114	-0.4	559.7628	2	14.97	2231	1	812	821	
E.VSVGDKIPAD.I	N	18.74	999.5236	-0.1	500.7690	2	10.76	1472	1	156	165	
V.KISLPVILL.D	N	16.43	994.6790	-0.3	498.3466	2	15.13	2259	1	976	984	
S.VGDKIPADI.R	N	16.36	926.5073	-0.4	464.2607	2	11.57	1624	1	158	166	

total 6 peptides

tr|A0A4Y7MVM2|A0A4Y7MVM2_DAPPU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	40.51	1156.5724	-0.4	579.2932	2	10.50	1423	1	705	716	
V.SVGDKIPAD.I	N	30.16	900.4552	-0.6	451.2346	2	10.20	1370	1	157	165	
L.GFNPPDLDIM.N	N	23.83	1117.5114	-0.4	559.7628	2	14.97	2231	1	812	821	
E.VSVGDKIPAD.I	N	18.74	999.5236	-0.1	500.7690	2	10.76	1472	1	156	165	
V.KISLPVILL.D	N	16.43	994.6790	-0.3	498.3466	2	15.13	2259	1	976	984	

total 6 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.VGDKIPADI.R	N	16.36	926.5073	-0.4	464.2607	2	11.57	1624	1	158	166	

total 6 peptides

tr|A0A4Y7M702|A0A4Y7M702_9CRUS
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	40.51	1156.5724	-0.4	579.2932	2	10.50	1423	1	705	716	
V.SVGDKIPAD.I	N	30.16	900.4552	-0.6	451.2346	2	10.20	1370	1	157	165	
L.GFNPPDLDIM.N	N	23.83	1117.5114	-0.4	559.7628	2	14.97	2231	1	812	821	
E.VSVGDKIPAD.I	N	18.74	999.5236	-0.1	500.7690	2	10.76	1472	1	156	165	
I.KISLPVILL.D	N	16.43	994.6790	-0.3	498.3466	2	15.13	2259	1	976	984	
S.VGDKIPADI.R	N	16.36	926.5073	-0.4	464.2607	2	11.57	1624	1	158	166	

total 6 peptides

tr|A0A4Y7MHQ5|A0A4Y7MHQ5_9CRUS
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	40.51	1156.5724	-0.4	579.2932	2	10.50	1423	1	705	716	
V.SVGDKIPAD.I	N	30.16	900.4552	-0.6	451.2346	2	10.20	1370	1	157	165	
L.GFNPPDLDIM.N	N	23.83	1117.5114	-0.4	559.7628	2	14.97	2231	1	812	821	
E.VSVGDKIPAD.I	N	18.74	999.5236	-0.1	500.7690	2	10.76	1472	1	156	165	
V.KISLPVILL.D	N	16.43	994.6790	-0.3	498.3466	2	15.13	2259	1	976	984	
S.VGDKIPADI.R	N	16.36	926.5073	-0.4	464.2607	2	11.57	1624	1	158	166	

total 6 peptides

tr|A0A4Y7ME47|A0A4Y7ME47_9CRUS
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	40.51	1156.5724	-0.4	579.2932	2	10.50	1423	1	705	716	
V.SVGDKIPAD.I	N	30.16	900.4552	-0.6	451.2346	2	10.20	1370	1	157	165	
L.GFNPPDLDIM.N	N	23.83	1117.5114	-0.4	559.7628	2	14.97	2231	1	812	821	
E.VSVGDKIPAD.I	N	18.74	999.5236	-0.1	500.7690	2	10.76	1472	1	156	165	
V.KISLPVILL.D	N	16.43	994.6790	-0.3	498.3466	2	15.13	2259	1	976	984	
S.VGDKIPADI.R	N	16.36	926.5073	-0.4	464.2607	2	11.57	1624	1	158	166	

total 6 peptides

tr|A0A4Y7M4I0|A0A4Y7M4I0_9CRUS
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	40.51	1156.5724	-0.4	579.2932	2	10.50	1423	1	705	716	
V.SVGDKIPAD.I	N	30.16	900.4552	-0.6	451.2346	2	10.20	1370	1	157	165	
L.GFNPPDLDIM.N	N	23.83	1117.5114	-0.4	559.7628	2	14.97	2231	1	812	821	
E.VSVGDKIPAD.I	N	18.74	999.5236	-0.1	500.7690	2	10.76	1472	1	156	165	
V.KISLPVILL.D	N	16.43	994.6790	-0.3	498.3466	2	15.13	2259	1	976	984	
S.VGDKIPADI.R	N	16.36	926.5073	-0.4	464.2607	2	11.57	1624	1	158	166	

total 6 peptides

tr|A0A1D2MC18|A0A1D2MC18_ORCCI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	40.51	1156.5724	-0.4	579.2932	2	10.50	1423	1	702	713	
V.SVGDKIPAD.I	N	30.16	900.4552	-0.6	451.2346	2	10.20	1370	1	158	166	
L.GFNPPDLDIM.T	N	23.83	1117.5114	-0.4	559.7628	2	14.97	2231	1	809	818	
E.VSVGDKIPAD.I	N	18.74	999.5236	-0.1	500.7690	2	10.76	1472	1	157	166	
M.KISLPVILL.D	N	16.43	994.6790	-0.3	498.3466	2	15.13	2259	1	973	981	
S.VGDKIPADI.R	N	16.36	926.5073	-0.4	464.2607	2	11.57	1624	1	159	167	

total 6 peptides

tr|E9HR84|E9HR84_DAPPU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	40.51	1156.5724	-0.4	579.2932	2	10.50	1423	1	705	716	
V.SVGDKIPAD.I	N	30.16	900.4552	-0.6	451.2346	2	10.20	1370	1	157	165	
L.GFNPPDLDIM.N	N	23.83	1117.5114	-0.4	559.7628	2	14.97	2231	1	812	821	
E.VSVGDKIPAD.I	N	18.74	999.5236	-0.1	500.7690	2	10.76	1472	1	156	165	
V.KISLPVILL.D	N	16.43	994.6790	-0.3	498.3466	2	15.13	2259	1	976	984	
S.VGDKIPADI.R	N	16.36	926.5073	-0.4	464.2607	2	11.57	1624	1	158	166	

total 6 peptides

tr|A0A0P5VJX3|A0A0P5VJX3_9CRUS
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	40.51	1156.5724	-0.4	579.2932	2	10.50	1423	1	705	716	
V.SVGDKIPAD.I	N	30.16	900.4552	-0.6	451.2346	2	10.20	1370	1	157	165	
L.GFNPPDLDIM.N	N	23.83	1117.5114	-0.4	559.7628	2	14.97	2231	1	812	821	
E.VSVGDKIPAD.I	N	18.74	999.5236	-0.1	500.7690	2	10.76	1472	1	156	165	
V.KISLPVILL.D	N	16.43	994.6790	-0.3	498.3466	2	15.13	2259	1	976	984	
S.VGDKIPADI.R	N	16.36	926.5073	-0.4	464.2607	2	11.57	1624	1	158	166	

total 6 peptides

tr|A0A4Y7LYL4|A0A4Y7LYL4_9CRUS
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	40.51	1156.5724	-0.4	579.2932	2	10.50	1423	1	705	716	
V.SVGDKIPAD.I	N	30.16	900.4552	-0.6	451.2346	2	10.20	1370	1	157	165	
L.GFNPPDLDIM.N	N	23.83	1117.5114	-0.4	559.7628	2	14.97	2231	1	812	821	
E.VSVGDKIPAD.I	N	18.74	999.5236	-0.1	500.7690	2	10.76	1472	1	156	165	
V.KISLPVILL.D	N	16.43	994.6790	-0.3	498.3466	2	15.13	2259	1	976	984	
S.VGDKIPADI.R	N	16.36	926.5073	-0.4	464.2607	2	11.57	1624	1	158	166	

total 6 peptides

tr|A0A0C5E1J4|A0A0C5E1J4_CHEDE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.TGDGVNDAPALK.K	N	40.51	1156.5724	-0.4	579.2932	2	10.50	1423	1	701	712	
V.SVGDKIPAD.I	N	30.16	900.4552	-0.6	451.2346	2	10.20	1370	1	154	162	
L.GFNPPDLDIM.D	N	23.83	1117.5114	-0.4	559.7628	2	14.97	2231	1	808	817	
E.VSVGDKIPAD.I	N	18.74	999.5236	-0.1	500.7690	2	10.76	1472	1	153	162	
S.VGDKIPADI.R	N	16.36	926.5073	-0.4	464.2607	2	11.57	1624	1	155	163	
K.HTDAIPDPKA.V	N	15.37	1063.5298	-0.3	532.7720	2	10.00	1334	1	190	199	

total 6 peptides

tr|Q86GD6|Q86GD6_PROCL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.LNLPVPVVGEPPATK.Q	Y	59.77	1529.8817	-1.6	765.9469	2	13.13	1909	1	4993	5007	
A.VIKIPF.I	N	17.57	715.4632	0.5	358.7390	2	13.33	1944	1	7458	7463	
R.IKDPNAATPPEII.T	N	15.97	1377.7504	-1.0	689.8818	2	12.19	1742	1	7335	7347	

total 3 peptides

tr|A0A444TVR3|A0A444TVR3_ARMVU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.KWLPVAPEFPHPIPQ.F	Y	44.03	1754.9507	-8.3	878.4753	2	13.73	2015	1	94	108	
V.APEFPHPIPQ.F	Y	29.02	1131.5713	-0.9	566.7924	2	11.82	1672	1	99	108	
W.LPVAPEFPHPIPQ.F	Y	25.73	1440.7765	-0.8	721.3950	2	12.95	1877	1	96	108	
P.VAPEFPHPIPQ.F	Y	17.95	1230.6396	-0.4	616.3268	2	12.02	1709	1	98	108	

total 4 peptides

tr|A0A7R8CX21|A0A7R8CX21_LEPSM
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VTVPSIDDKEDMQF.A	N	40.27	1622.7498	-0.4	812.3818	2	12.86	1860	1	318	331	
K.VTVPSIDDKEDMQ.F	N	31.89	1475.6814	-0.1	738.8479	2	11.58	1627	1	318	330	
L.ITGESGAGK.T	N	23.91	818.4134	-0.2	410.2139	2	8.67	1104	1	181	189	
K.NKDPLNDTI.V	N	20.74	1028.5138	-0.9	515.2637	2	11.46	1603	1	545	553	

total 4 peptides

tr|A0A0K2V7Y7|A0A0K2V7Y7_LEPSM
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VTVPSIDDKEDMQF.A	N	40.27	1622.7498	-0.4	812.3818	2	12.86	1860	1	318	331	
K.VTVPSIDDKEDMQ.F	N	31.89	1475.6814	-0.1	738.8479	2	11.58	1627	1	318	330	
L.ITGESGAGK.T	N	23.91	818.4134	-0.2	410.2139	2	8.67	1104	1	181	189	
K.NKDPLNDTI.V	N	20.74	1028.5138	-0.9	515.2637	2	11.46	1603	1	599	607	

total 4 peptides

tr|A0A7T8HL88|A0A7T8HL88_CALRO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VTVPSIDDKEDMQF.A	N	40.27	1622.7498	-0.4	812.3818	2	12.86	1860	1	318	331	
K.VTVPSIDDKEDMQ.F	N	31.89	1475.6814	-0.1	738.8479	2	11.58	1627	1	318	330	
L.ITGESGAGK.T	N	23.91	818.4134	-0.2	410.2139	2	8.67	1104	1	181	189	
K.NKDPLNDTI.V	N	20.74	1028.5138	-0.9	515.2637	2	11.46	1603	1	599	607	

total 4 peptides

tr|A0A7T8HL29|A0A7T8HL29_CALRO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VTVPSIDDKEDMQF.A	N	40.27	1622.7498	-0.4	812.3818	2	12.86	1860	1	318	331	

total 4 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VTVPSIDDKEDMQ.F	N	31.89	1475.6814	-0.1	738.8479	2	11.58	1627	1	318	330	
L.ITGESGAGK.T	N	23.91	818.4134	-0.2	410.2139	2	8.67	1104	1	181	189	
K.NKDPLNDTI.V	N	20.74	1028.5138	-0.9	515.2637	2	11.46	1603	1	599	607	

total 4 peptides

tr|A0A0K2T3U6|A0A0K2T3U6_LEPSM
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VTVPSIDDKEDMQF.A	N	40.27	1622.7498	-0.4	812.3818	2	12.86	1860	1	318	331	
K.VTVPSIDDKEDMQ.F	N	31.89	1475.6814	-0.1	738.8479	2	11.58	1627	1	318	330	
L.ITGESGAGK.T	N	23.91	818.4134	-0.2	410.2139	2	8.67	1104	1	181	189	
K.NKDPLNDTI.V	N	20.74	1028.5138	-0.9	515.2637	2	11.46	1603	1	599	607	

total 4 peptides

tr|A0A0K2TSJ7|A0A0K2TSJ7_LEPSM
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VTVPSIDDKEDMQF.A	N	40.27	1622.7498	-0.4	812.3818	2	12.86	1860	1	338	351	
K.VTVPSIDDKEDMQ.F	N	31.89	1475.6814	-0.1	738.8479	2	11.58	1627	1	338	350	
L.ITGESGAGK.T	N	23.91	818.4134	-0.2	410.2139	2	8.67	1104	1	201	209	
K.NKDPLNDTI.V	N	20.74	1028.5138	-0.9	515.2637	2	11.46	1603	1	619	627	

total 4 peptides

tr|A0A0P4WFG0|A0A0P4WFG0_SCYOL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.ELAAPYVATIMILDDDHGGIF.N	Y	39.77	2260.1084	-1.0	1131.0603	2	15.95	2403	1	497	517	
E.LAAPYVATIMILDDDHGGIF.N	Y	28.96	2131.0659	-0.4	1066.5398	2	15.73	2367	1	498	517	
L.AAPYVATIMILDDDHGGIF.N	Y	24.35	2017.9818	-0.3	1009.9979	2	15.31	2291	1	499	517	

total 3 peptides

tr|A0A5B7GFK1|A0A5B7GFK1_PORTR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.ELAAPYVATIMILDDDHGGIF.N	Y	39.77	2260.1084	-1.0	1131.0603	2	15.95	2403	1	497	517	
E.LAAPYVATIMILDDDHGGIF.N	Y	28.96	2131.0659	-0.4	1066.5398	2	15.73	2367	1	498	517	
L.AAPYVATIMILDDDHGGIF.N	Y	24.35	2017.9818	-0.3	1009.9979	2	15.31	2291	1	499	517	

total 3 peptides

tr|A0A110A0P3|A0A110A0P3_ASTLP
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.ELAAPYVATIMILDDDHGGIF.N	Y	39.77	2260.1084	-1.0	1131.0603	2	15.95	2403	1	498	518	
E.LAAPYVATIMILDDDHGGIF.N	Y	28.96	2131.0659	-0.4	1066.5398	2	15.73	2367	1	499	518	
L.AAPYVATIMILDDDHGGIF.N	Y	24.35	2017.9818	-0.3	1009.9979	2	15.31	2291	1	500	518	

total 3 peptides

tr|A0A5B7EE36|A0A5B7EE36_PORTR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.SPGVIDAGLVMH.Q	N	44.78	1194.6067	-0.9	598.3101	2	12.56	1806	1	205	216	
N.ETKSPGVIDAGLVM.H	N	16.36	1415.7330	-0.4	708.8735	2	12.98	1882	1	202	215	
R.NEVPPHLF.A	N	16.25	951.4814	-0.3	476.7478	2	13.07	1899	1	150	157	

total 3 peptides

tr|A0A2Z4I2U3|A0A2Z4I2U3_CALSI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.SVGDKIPAD.L	N	30.16	900.4552	-0.6	451.2346	2	10.20	1370	1	154	162	
L.GFNPPDLDIM.E	N	23.83	1117.5114	-0.4	559.7628	2	14.97	2231	1	808	817	
E.VSVGDKIPAD.L	N	18.74	999.5236	-0.1	500.7690	2	10.76	1472	1	153	162	
L.KISLPVLLL.D	N	16.43	994.6790	-0.3	498.3466	2	15.13	2259	1	972	980	
S.VGDKIPADL.R	N	16.36	926.5073	-0.4	464.2607	2	11.57	1624	1	155	163	
K.HTDAIPDPKA.V	N	15.37	1063.5298	-0.3	532.7720	2	10.00	1334	1	190	199	

total 6 peptides

tr|Q95YM2|Q95YM2_PROCL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.SPFDKPGPPIGPF.D	Y	41.08	1354.6920	1.2	678.3541	2	13.50	1974	1	16981	16993	
L.IPVGDPDLK.V	Y	23.50	952.5229	-0.4	477.2685	2	11.07	1530	1	1731	1739	

total 2 peptides

tr|A0A6P7F415|A0A6P7F415_DIAVI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SILEEESMFPK.A	N	26.45	1308.6271	-0.7	655.3204	2	12.91	1869	1	533	543	
L.ITGESGAGK.T	N	23.91	818.4134	-0.2	410.2139	2	8.67	1104	1	178	186	
R.NEVPPHIF.A	N	16.25	951.4814	-0.3	476.7478	2	13.07	1899	1	150	157	
M.FDRVF.K	N	15.90	682.3438	-0.9	342.1789	2	11.93	1692	1	433	437	
M.FDRVFKF.L	N	15.27	957.5072	-1.0	479.7604	2	12.36	1771	1	433	439	

total 5 peptides

tr|A0A5E4QJ96|A0A5E4QJ96_9NEOP
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	97	106	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	97	107	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	96	107	

total 3 peptides

tr|A0A0A7BYS9|A0A0A7BYS9_OSTFU
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	192	201	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	192	202	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	191	202	

total 3 peptides

tr|A0A2H1WAZ2|A0A2H1WAZ2_SPOFR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	65	74	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	65	75	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	64	75	

total 3 peptides

tr|A0A6J3BVA9|A0A6J3BVA9_GALME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	73	82	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	73	83	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	72	83	

total 3 peptides

tr|A0A6J1WK99|A0A6J1WK99_GALME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	73	82	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	73	83	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	72	83	

total 3 peptides

tr|A0A444T6K9|A0A444T6K9_ARMVU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	148	157	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	148	158	
I.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	147	158	

total 3 peptides

tr|A0A222AJC5|A0A222AJC5_SPOLI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	192	201	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	192	202	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	191	202	

total 3 peptides

tr|A0A0Q9WRY5|A0A0Q9WRY5_DROVI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	192	201	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	192	202	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	191	202	

total 3 peptides

tr|B4NKQ7|B4NKQ7_DROWI

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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	192	201	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	192	202	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	191	202	

total 3 peptides

tr|B4LYD3|B4LYD3_DROVI
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	192	201	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	192	202	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	191	202	

total 3 peptides

tr|A0A0Q9WWZ4|A0A0Q9WWZ4_DROWI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	192	201	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	192	202	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	191	202	

total 3 peptides

tr|A0A0Q9WQB4|A0A0Q9WQB4_DROVI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	192	201	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	192	202	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	191	202	

total 3 peptides

tr|A0A2A4K0C6|A0A2A4K0C6_HELVI
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	192	201	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	192	202	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	191	202	

total 3 peptides

tr|A0A6J1NBL3|A0A6J1NBL3_BICAN
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	192	201	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	192	202	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	191	202	

total 3 peptides

tr|A0A6J2KNU6|A0A6J2KNU6_BOMMA
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	192	201	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	192	202	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	191	202	

total 3 peptides

tr|A0A6J2KQG2|A0A6J2KQG2_BOMMA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	192	201	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	192	202	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	191	202	

total 3 peptides

tr|Q1HPN7|Q1HPN7_BOMMO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	192	201	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	192	202	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	191	202	

total 3 peptides

tr|S4PKR2|S4PKR2_9NEOP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	192	201	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	192	202	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	191	202	

total 3 peptides

tr|A0A7S5LJX7|A0A7S5LJX7_BEMTA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	192	201	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	192	202	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	191	202	

total 3 peptides

tr|A0A7R9X220|A0A7R9X220_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	195	204	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	195	205	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	194	205	

total 3 peptides

tr|A0A7R9A8N4|A0A7R9A8N4_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	199	208	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	199	209	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	198	209	

total 3 peptides

tr|A0A7R9A8M7|A0A7R9A8M7_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	199	208	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	199	209	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	198	209	

total 3 peptides

tr|A0A4C1UD71|A0A4C1UD71_EUMVA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	212	221	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	212	222	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	211	222	

total 3 peptides

tr|A0A6J2KM35|A0A6J2KM35_BOMMA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	192	201	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	192	202	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	191	202	

total 3 peptides

tr|A0A821PCJ9|A0A821PCJ9_9NEOP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	218	227	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	218	228	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	217	228	

total 3 peptides

tr|A0A7E5VF38|A0A7E5VF38_TRINI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	220	229	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	220	230	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	219	230	

total 3 peptides

tr|A0A7I1A027|A0A7I1A027_DANPL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	218	227	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	218	228	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	217	228	

total 3 peptides

tr|A0A821PCK8|A0A821PCK8_9NEOP
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	218	227	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	218	228	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	217	228	

total 3 peptides

tr|A0A811X398|A0A811X398_PLUXY
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	221	230	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	221	231	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	220	231	

total 3 peptides

tr|A0A2P8YG29|A0A2P8YG29_BLAGE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LPDGEHDLDR.A	Y	33.64	1165.5364	-0.2	583.7753	2	10.20	1369	1	65	74	
V.LPDGEHDLDRA.Q	Y	22.49	1236.5735	-0.7	619.2936	2	10.49	1422	2	65	75	
E.VLPDGEHDLDRA.Q	Y	16.15	1335.6418	-0.7	668.8277	2	10.73	1466	1	64	75	

total 3 peptides

tr|A0A5B7DQZ0|A0A5B7DQZ0_PORTR
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SILEEESMFPK.A	N	26.45	1308.6271	-0.7	655.3204	2	12.91	1869	1	403	413	
K.NKDPLNDTL.V	N	20.74	1028.5138	-0.9	515.2637	2	11.46	1603	1	469	477	
R.NEVPPHLF.A	N	16.25	951.4814	-0.3	476.7478	2	13.07	1899	1	150	157	
L.FDRVF.K	N	15.90	682.3438	-0.9	342.1789	2	11.93	1692	1	303	307	
L.FDRVFKF.I	N	15.27	957.5072	-1.0	479.7604	2	12.36	1771	1	303	309	

total 5 peptides

tr|A0A821V8C5|A0A821V8C5_9NEOP
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VIVVDKPGPPKGPL.S	Y	38.50	1414.8547	-26.0	708.4163	2	12.03	1712	1	4803	4816	
V.VIKIPF.T	N	17.57	715.4632	0.5	358.7390	2	13.33	1944	1	6310	6315	

total 2 peptides

tr|A0A7J7AR02|A0A7J7AR02_9COLE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.DTFSLPGK.L	Y	29.05	863.4388	-0.6	432.7264	2	11.48	1607	1	290	297	
L.DTFSLPGKLS.D	Y	27.50	1063.5549	-0.1	532.7847	2	11.99	1704	1	290	299	

total 2 peptides

tr|A0A444T9K0|A0A444T9K0_ARMVU
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.APYDPPSPPGIPK.V	Y	30.43	1334.6870	-0.5	668.3505	2	11.62	1633	1	4704	4716	
K.IKDPNAATPPEII.S	N	15.97	1377.7504	-1.0	689.8818	2	12.19	1742	1	4803	4815	

total 2 peptides

tr|A0A2P1JJ42|A0A2P1JJ42_PROCL
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.IHIPGSPF.R	Y	25.89	866.4650	-1.2	434.2393	2	13.11	1905	1	1331	1338	
F.KLPGISPF.D	Y	15.46	857.5010	-0.2	429.7577	2	13.01	1888	1	1087	1094	

total 2 peptides

tr|A0A0N9EJJ5|A0A0N9EJJ5_ERIVE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VFAWPK.Y	Y	21.14	746.4115	-0.8	374.2127	2	12.32	1763	1	502	507	
H.VVLPPLYE.V	Y	17.78	928.5269	0.0	465.2708	2	13.82	2031	1	153	160	

total 2 peptides

tr|A0A1J1IN48|A0A1J1IN48_9DIPT
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.KVPCANAL.K	Y	25.85	814.4371	-3.7	408.2243	2	11.33	1580	1	1614	1621	

total 1 peptides

tr|A0A1E1XMV5|A0A1E1XMV5_9ACAR
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.KVPCANAI.N	Y	25.85	814.4371	-3.7	408.2243	2	11.33	1580	1	2	9	

total 1 peptides

tr|B4J4N0|B4J4N0_DROGR
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.RVKVPVVP.H	Y	25.31	892.5858	1.2	447.3007	2	15.88	2392	1	70	77	

total 1 peptides

tr|A0A4S2KBN7|A0A4S2KBN7_9HYME
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.EDSIKFI.V	Y	25.31	850.4436	0.0	426.2291	2	13.21	1923	1	1873	1879	

total 1 peptides

tr|A0A2P8XAH3|A0A2P8XAH3_BLAGE
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| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.AELHKNIL.V	Y	23.47	936.5392	-12.2	469.2712	2	13.35	1948	1	39	46	

total 1 peptides

tr|R9YY56|R9YY56_9EUCA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	7	18	

total 1 peptides

tr|R9YY47|R9YY47_9EUCA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	8	19	

total 1 peptides

tr|G3C6J8|G3C6J8_9EUCA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	19	30	

total 1 peptides

tr|G3C6I8|G3C6I8_AEGAL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	19	30	

total 1 peptides

tr|G3C6N2|G3C6N2_9EUCA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	19	30	

total 1 peptides

P86699|KARG_CHIOP
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	48	59	

total 1 peptides

tr|G3D680|G3D680_PORTR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	111	122	

total 1 peptides

tr|I1TMM2|I1TMM2_SCYPA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	107	118	

total 1 peptides

tr|K7PD48|K7PD48_SCYPA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	110	121	

total 1 peptides

C9EIP1|KARG_SCYSE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	111	122	

total 1 peptides

tr|G3D692|G3D692_PORTR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	111	122	

total 1 peptides

tr|H6AC60|H6AC60_PORTR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	111	122	

total 1 peptides

tr|A0A8A8ZWC2|A0A8A8ZWC2_CALBE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	111	122	

total 1 peptides

tr|G3D676|G3D676_PORTR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	111	122	

total 1 peptides

Q9GYX1|KARG_PACMR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	111	122	

total 1 peptides

H6VGI2|KARG_PROCL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	111	122	

total 1 peptides

tr|G3D677|G3D677_PORTR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	111	122	

total 1 peptides

tr|H6AC58|H6AC58_PORTR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	111	122	

total 1 peptides

tr|A0A068EFU4|A0A068EFU4_9EUCA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	111	122	

total 1 peptides

tr|G3D691|G3D691_PORTR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	111	122	

total 1 peptides

Q9NH49|KARG_CALSI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	111	122	

total 1 peptides

Q9U9J4|KARG_CARMA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	111	122	

total 1 peptides

tr|H6UKS0|H6UKS0_SCYPA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	111	122	

total 1 peptides

Q9NH48|KARG_ERISI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	111	122	

total 1 peptides

tr|G3D675|G3D675_PORTR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	111	122	

total 1 peptides

H6VGI3|KARG0_SCYPA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	111	122	

total 1 peptides

tr|A0A1C6ZZL8|A0A1C6ZZL8_PROCL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	111	122	

total 1 peptides

tr|A0A0C5DEY3|A0A0C5DEY3_CHEDE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	111	122	

total 1 peptides

tr|D2DSQ8|D2DSQ8_SCYPA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	82	93	

total 1 peptides

tr|F5A6C6|F5A6C6_PROCL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VNVDPDGKFVIS.T	Y	21.53	1288.6663	-0.6	645.3400	2	12.28	1756	1	111	122	

total 1 peptides

tr|J9K049|J9K049_ACYPI
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.ETQVINAV.G	Y	21.41	872.4603	0.1	437.2375	2	11.26	1566	1	559	566	

total 1 peptides

tr|A0A0R3NUC8|A0A0R3NUC8_DROPS
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.EDADKGVLVAL.V	Y	20.28	1128.6027	-22.2	565.2961	2	12.43	1783	1	70	80	

total 1 peptides

tr|B4GX09|B4GX09_DROPE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.EDADKGVLVAL.V	Y	20.28	1128.6027	-22.2	565.2961	2	12.43	1783	1	48	58	

total 1 peptides

tr|A0A821UPU7|A0A821UPU7_9NEOP
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.LKNKTLLQEI.S	Y	20.24	1198.7285	0.3	600.3717	2	14.24	2104	1	3604	3613	

total 1 peptides

tr|A0A023ERZ2|A0A023ERZ2_AEDAL
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	281	291	

total 1 peptides

tr|A0A0P8Y097|A0A0P8Y097_DROAN
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	277	287	

total 1 peptides

tr|A0A6P8K875|A0A6P8K875_DROMA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	277	287	

total 1 peptides

tr|A0A6P4F4P4|A0A6P4F4P4_DRORH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	277	287	

total 1 peptides

tr|A0A1Y9GJY2|A0A1Y9GJY2_ANOAR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	277	287	

total 1 peptides

tr|A0A0Q9X1L7|A0A0Q9X1L7_DROMO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	277	287	

total 1 peptides

tr|A0A182UE55|A0A182UE55_9DIPT
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	277	287	

total 1 peptides

tr|A0A2M3ZFB9|A0A2M3ZFB9_9DIPT
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	281	291	

total 1 peptides

tr|A0A2M3ZYS6|A0A2M3ZYS6_9DIPT
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	281	291	

total 1 peptides

tr|A0A2M3ZYS8|A0A2M3ZYS8_9DIPT
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	281	291	

total 1 peptides

tr|A0A1Y9GJK0|A0A1Y9GJK0_ANOAR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	282	292	

total 1 peptides

tr|A0A6A0H7S7|A0A6A0H7S7_HYAAZ
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	286	296	

total 1 peptides

tr|A0A1E1X8N4|A0A1E1X8N4_9ACAR
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	290	300	

total 1 peptides

tr|A0A6P4F9I4|A0A6P4F9I4_DRORH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	298	308	

total 1 peptides

tr|A0A182VPN6|A0A182VPN6_9DIPT
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	293	303	

total 1 peptides

tr|A0A182MNQ6|A0A182MNQ6_9DIPT
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	293	303	

total 1 peptides

tr|A0A6J2T5C5|A0A6J2T5C5_DROLE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:
Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	298	308	

total 1 peptides

tr|A0A1W4W378|A0A1W4W378_DROFC
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	298	308	

total 1 peptides

O62619|KPYK_DROME
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	298	308	

total 1 peptides

tr|B4HE69|B4HE69_DROSE
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	298	308	

total 1 peptides

tr|A0A6P4F0Q9|A0A6P4F0Q9_DRORH
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	298	308	

total 1 peptides

tr|B3P7K4|B3P7K4_DROER
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	298	308	

total 1 peptides

tr|B3M213|B3M213_DROAN
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	298	308	

total 1 peptides

tr|A0A6P8KMB4|A0A6P8KMB4_DROMA
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	298	308	

total 1 peptides

tr|B4K5E3|B4K5E3_DROMO
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	298	308	

total 1 peptides

tr|A0A484BWG4|A0A484BWG4_DRONA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	298	308	

total 1 peptides

tr|A0A131XQM7|A0A131XQM7_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	290	300	

total 1 peptides

tr|A0A0P9ARZ1|A0A0P9ARZ1_DROAN

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	312	322	

total 1 peptides

tr|G3MLC1|G3MLC1_AMBMU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	290	300	

total 1 peptides

tr|A0A023EVC5|A0A023EVC5_AEDAL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	350	360	

total 1 peptides

tr|A0A5N5T493|A0A5N5T493_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GDLGIEIPAEK.V	Y	20.21	1140.6025	-0.7	571.3082	2	12.21	1745	1	390	400	

total 1 peptides

Scan	Peptide	Tag length	ALC (%)	m/z	z	RT	Mass	ppm	PTM
1308	LTKLL	5	97	2,942,098	2	11.72	5,864,054	-0.5	
1128	LPTKF	5	95	3,031,871	2	10.77	6,043,584	2.1	
986	VVAKKPQE	8	95	4,497,803	2	10.02	8,975,283	19.8	
762	KLHWH	5	94	3,607,007	2	8.76	7,193,867	0.1	
993	VHLKLPK	7	94	4,177,813	2	10.05	8,335,486	-0.7	
1523	MLSLKEM	7	93	4,262,292	2	12.91	8,504,293	17.1	
1518	WPGPLNF	7	92	4,157,058	2	12.89	8,294,122	-18.2	
1109	FGDKFT	6	92	3,576,764	2	10.67	7,133,384	-0.4	
899	LDAPSQPEDF	10	91	5,597,551	2	9.53	11,174,927	2.6	
1646	VVLPKNME	8	91	4,652,707	2	13.61	9,285,052	23.4	
1697	DFDLSLMFM	9	91	5,597,630	2	13.92	11,174,824	26.0	
1026	ELLPNTDAGDY	11	90	6,042,846	2	10.23	12,065,405	11.7	
599	VGDEAKTN	8	90	4,172,036	2	7.67	8,323,926	0.0	
1221	YPGLADTW	8	90	4,617,260	2	11.25	9,214,232	15.5	
1328	VSVGDKLPAMP	11	90	5,573,112	2	11.82	11,125,898	16.1	
560	VGDEAQSK	8	90	4,172,036	2	7.39	8,323,926	0.0	
953	GFAGDDAPR	9	89	4,532,093	2	9.83	9,044,039	0.1	
1247	DDRLSL	6	89	3,596,901	2	11.39	7,173,657	0.1	
1275	LDRADF	6	89	3,686,973	2	11.54	7,353,551	33.8	
1087	MVAYFAH	7	89	4,197,014	2	10.56	8,373,843	4.6	
1002	DPVDNYPR	8	89	4,882,300	2	10.10	9,744,457	-0.3	
1553	APEFPHPLPQF	11	89	6,403,275	2	13.08	12,786,396	0.6	
614	KKPKF	5	89	3,242,155	2	7.78	6,464,166	-0.3	
1071	NYTDVPPVPK	10	89	5,652,995	2	10.47	11,285,815	2.6	
1157	VTVPSLDPQF	10	89	5,517,860	2	10.92	11,015,706	-11.9	
786	AGACPL	6	89	2,661,479	2	8.89	5,302,523	54.9	
1003	LDGANEDNLRE	11	89	6,232,885	2	10.11	12,445,632	-0.6	
1805	DVFLGTFLYEYSR	13	89	8,053,983	2	14.62	16,087,825	-0.2	
1626	LAVLLVVEEGVAK	13	89	6,704,135	2	13.49	13,388,123	0.2	
1165	VNVDDPGKF	9	88	4,957,486	2	10.96	9,894,818	0.9	
1009	LTEEVAAALH	10	88	5,272,699	2	10.14	10,525,503	-23.8	
1119	SKLPKW	6	88	3,797,321	2	10.72	7,574,486	1.3	
1557	EALEHLLL	8	88	4,692,711	2	13.10	9,365,280	-0.4	
1163	SLEDELR	7	88	4,312,197	2	10.95	8,604,240	1.0	
1286	VLDLLK	6	88	3,507,338	2	11.60	6,994,531	-0.1	
1027	TGDGVNDAPALK	12	87	5,792,952	2	10.24	11,565,723	3.1	
1175	LKYPLE	6	87	3,817,238	2	11.01	7,614,323	1.0	
1152	NPLDKL	6	87	3,502,057	2	10.89	6,983,962	0.9	
1301	MYPGLADRM	9	87	5,272,464	2	11.68	10,524,783	0.0	
1065	LDAPSKPEDM	10	87	5,517,589	2	10.44	11,015,012	1.9	
1261	KLLEDVHQN	9	87	5,483,057	2	11.46	10,945,720	22.7	
1335	FGPST	5	87	2,546,370	2	11.86	5,072,329	52.2	
1333	VSKEVLDEM	9	87	5,252,688	2	11.85	10,485,110	11.5	
3160	LVRGPR	6	87	3,492,269	2	23.43	6,964,395	-0.4	
1548	FSEWPGPW	8	87	5,032,325	2	13.05	10,044,392	11.2	
1127	FGDKF	5	86	3,071,532	2	10.77	6,122,907	1.8	

1362	VLRLL	5	86	3,072,234	2	12.01	6,124,323	0.1
1256	MDPLLVGPK	9	86	4,852,756	2	11.44	9,685,364	0.2
1161	NYTDVPRHK	9	86	5,652,990	2	10.94	11,285,676	14.0
1131	SDELKDL	7	86	4,102,223	2	10.78	8,184,022	34.1
1321	DSQLPELKDL	10	86	5,792,969	2	11.78	11,565,974	-15.6
1590	ALEMDLFVK	9	86	5,332,861	2	13.28	10,645,576	0.1
1205	FCELPDGQ	8	86	4,547,034	2	11.17	9,073,746	19.5
1615	NFDPTFVEDVKDF	13	86	7,868,641	2	13.43	15,717,144	-0.4
1655	VENPFWWKDTY	11	85	7,428,453	2	13.66	14,836,772	-0.8
1371	LWKVY	5	85	3,547,076	2	12.06	7,074,006	-0.1
1459	VTVPSLDDKEDMQF	14	85	8,123,815	2	12.56	16,227,498	-0.8
1376	LDLPRM	6	85	3,727,072	2	12.09	7,434,000	0.0
1579	APEEPHALL	9	85	4,887,516	2	13.22	9,755,025	-14.1
1005	RQPDKRLM	8	85	5,222,852	2	10.12	10,425,706	-14.1
1206	VKLPKL	6	85	3,492,520	2	11.18	6,964,897	-0.4
926	WGSKGPHEW	9	85	5,422,462	2	9.68	10,824,934	-14.3
1023	LPDWHDLDQV	10	85	6,192,948	2	10.22	12,365,774	-1.9
1596	TVEDELKVL	9	85	5,232,798	2	13.32	10,445,703	-24.2

local confidence (%)	tag (>=0%)	mode
96 95 97 99 99	LTKLL	CID
97 94 94 95 98	LPTKF	CID
98 99 99 99 94 88 89 96	VVAKKPQE	CID
98 100 88 88 98	KLHWH	CID
92 96 98 90 96 94 94	VHLKLPK	CID
91 97 97 97 96 92 83	MLSLKEM	CID
86 87 82 97 99 96 98	WPGPLNF	CID
93 88 86 88 97 99	FGDKFT	CID
89 94 97 98 90 95 90 92 89 80	LDAPSQPEDF	CID
83 91 98 95 82 84 98 99	VVLPKNME	CID
68 74 96 99 97 96 92 97 97	DFDLSLMFM	CID
71 65 88 95 95 99 99 99 98 96 90	ELLPNTDAGDY	CID
91 91 98 99 99 88 81 73	VGDEAKTN	CID
94 95 97 99 96 92 79 69	YPGLADTW	CID
89 92 92 94 98 98 99 92 91 83 65	VSVGDKLPAMP	CID
92 92 97 99 94 84 84 77	VGDEAQSK	CID
70 89 96 98 98 95 98 85 79	GFAGDDAPR	CID
91 86 73 92 97 99	DDRLSL	CID
89 91 81 94 93 89	LDRADF	CID
93 96 98 98 95 72 74	MVAYFAH	CID
84 91 97 99 92 96 83 74	DPVDNYPR	CID
67 76 97 99 95 95 92 96 96 86 83	APEFPHPLPQF	CID
96 94 79 88 90	KKPKF	CID
69 77 98 99 100 99 94 89 84 85	NYTDVPPVPK	CID
82 87 96 98 97 97 96 82 83 75	VTVPSLDPQF	CID
85 85 86 86 96 97	AGACPL	CID
77 86 92 95 97 99 95 97 98 52 91	LDGANEDNLRE	CID
52 55 88 100 100 100 100 100 100 100 94 92 78	DVFLGTFLYEYSR	CID
54 51 91 100 100 100 100 100 100 98 96 89 79	LAVLLVVEEGVAK	CID
92 92 94 97 88 73 69 97 94	VNVDDPGKF	CID
86 82 99 99 96 87 62 79 98 94	LTEEVAAALH	CID
82 86 97 93 88 83	SKLPKW	CID
84 68 92 98 86 85 97 96	EALEHLLL	CID
79 85 99 94 99 86 73	SLEDELR	CID
96 97 79 86 82 88	VLDLLK	CID
61 69 91 94 99 99 99 92 86 89 89 83	TGDGVNDAPALK	CID
95 92 79 73 89 99	LKYPLE	CID
83 83 91 94 84 90	NPLDKL	CID
92 92 93 96 98 98 80 60 81	MYPGLADRM	CID
69 77 93 97 95 89 73 96 95 92	LDAPSKPEDM	CID
86 96 95 99 95 97 88 72 61	KLLEDVHQN	CID
96 93 71 86 92	FGPST	CID
92 95 95 90 48 79 98 98 89	VSKEVLDEM	CID
96 96 85 82 85 79	LVRGPR	CID
71 78 98 94 98 95 80 79	FSEWPGPW	CID
97 91 73 83 88	FGDKF	CID

91 93 65 85 98	VLRLL	CID
94 95 95 99 98 96 51 63 84	MDPLLVGPK	CID
59 78 93 99 99 94 79 89 83	NYTDVPRHK	CID
85 87 97 99 80 72 82	SDELKDL	CID
68 71 79 98 97 99 95 94 77 81	DSQLPELKDL	CID
71 77 97 93 78 79 90 95 92	ALEMDLFVK	CID
77 82 97 99 96 78 77 80	FCELPDGQ	CID
45 50 98 97 97 98 99 100 98 99 96 78 62	NFDPTFVEDVKDF	CID
50 90 79 91 95 97 96 84 90 88 82	VENPFWWKDTY	CID
88 77 78 89 96	LWKVY	CID
61 67 82 91 99 99 98 93 82 96 89 89 74 74	VTVPSLDDKEDMQF	CID
89 89 95 84 70 84	LDLPRM	CID
69 78 99 95 74 79 89 93 91	APEEPHALL	CID
86 85 89 97 91 65 89 79	RQPDKRLM	CID
66 84 90 85 86 98	VKLPKL	CID
79 91 97 89 72 60 96 97 82	WGSKGPHEW	CID
84 86 94 89 96 97 81 73 76 72	LPDWHDLDQV	CID
41 63 98 99 100 99 81 90 91	TVEDELKVL	CID

Scan	Peptide	Tag length	ALC (%)	m/z	z	RT	Mass	ppm	PTM
1571	LKYPLE	6	95	3,817,234	2	11.29	7,614,323	0.0	
1565	VNVDPDGKF	9	94	4,957,480	2	11.26	9,894,818	-0.2	
1369	LPDWHPMDR	9	93	5,837,753	2	10.20	11,655,339	1.9	
1354	VHLKLPK	7	93	4,177,815	2	10.11	8,335,486	-0.2	
2016	LDKFF	5	91	3,351,840	2	13.73	6,683,533	0.2	
1923	MLSLQFL	7	91	4,262,291	2	13.21	8,504,622	-21.8	
2247	VDFLGTFLYEYSR	13	90	8,053,986	2	15.06	16,087,825	0.1	
1570	LKMPL	5	90	3,011,995	2	11.28	6,003,669	29.2	
1464	LDAPSKPEDM	10	90	5,517,578	2	10.72	11,015,012	-0.1	
1881	LHLML	5	89	3,136,866	2	12.98	6,253,621	-5.6	
1691	TLKLL	5	89	2,942,096	2	11.93	5,864,054	-1.2	
1367	LLAPPERQHL	10	89	5,873,345	2	10.19	11,726,665	-10.2	
1482	APNELLAMK	9	88	4,937,794	2	10.82	9,855,266	18.0	
2004	VFAALVT	7	88	3,607,132	2	13.67	7,194,218	-13.8	
1608	YPGLADWT	8	88	4,617,259	2	11.49	9,214,232	15.1	
1806	SPGVLDAGLVMH	12	88	5,983,101	2	12.56	11,946,067	-0.9	
1402	LLAPLLVGQY	10	88	5,438,184	2	10.38	10,856,484	-24.2	
1518	AKLPKW	6	88	3,717,338	2	11.01	7,414,537	-0.9	
1668	**LDNLFR**	**6**	**88**	**3,892,162**	**2**	**11.80**	**7,764,180**	**-0.3**	
1554	KLLP	4	87	2,356,703	2	11.20	4,693,264	-0.5	
1909	VKLPVPVVGEQHTK	14	87	7,659,469	2	13.13	15,298,928	-8.9	
1721	FGKFL	5	87	3,061,811	2	12.08	6,103,478	-0.3	
2023	FNDPTFVEDVQYV	13	87	7,868,642	2	13.77	15,717,144	-0.3	
1918	APEESFALL	9	86	4,887,516	2	13.18	9,754,913	-2.8	
1307	KLPKL	5	86	2,997,178	2	9.84	5,974,213	-0.3	
1718	EKPLW	5	86	3,366,948	2	12.07	6,713,643	16.1	
908	EARE	4	86	2,526,244	2	7.59	5,032,339	0.6	
1667	APEESSML	8	86	4,322,091	2	11.80	8,623,742	34.1	
1648	MDPLLVKGP	9	86	4,852,751	2	11.70	9,685,364	-0.9	
1024	TEMEQ	5	85	3,191,284	2	8.26	6,362,425	-0.3	
1588	APEESPVLLK	10	85	5,418,079	2	11.38	10,816,018	-0.6	
1422	LPDGEHDLDRA	11	85	6,192,936	2	10.49	12,365,735	-0.7	
309	FHTDSQ	6	85	3,676,695	2	2.60	7,333,031	29.2	
1468	NYTDVPPPVK	10	85	5,652,980	2	10.74	11,285,815	-0.1	
1152	KLHEGH	6	85	3,607,008	2	8.93	7,193,715	21.6	
1905	FCLQLPF	7	85	4,342,393	2	13.11	8,664,360	32.2	
2097	LQWFDLLDKDKSGFNQ	16	85	9,774,758	2	14.20	19,529,631	-13.3	
1686	LKPLKL	6	85	3,562,597	2	11.90	7,105,054	-0.8	

local confidence (%)	tag (>=0%)	mode
98 96 92 94 94 99	LKYPLE	CID
92 94 98 99 91 96 91 96 94	VNVDPDGKF	CID
97 97 98 98 99 91 82 90 91	LPDWHPMDR	CID
86 94 98 99 95 87 92	VHLKLPK	CID
85 83 95 96 96	LDKFF	CID
93 99 91 91 90 88 86	MLSLQFL	CID
60 63 81 97 99 100 100 100 100 100 99 95 80	VDFLGTFLYEYSR	CID
96 83 80 94 98	LKMPL	CID
90 92 95 97 92 97 63 94 92 86	LDAPSKPEDM	CID
83 82 89 95 98	LHLML	CID
82 88 79 97 98	TLKLL	CID
98 99 99 95 76 95 74 90 81 82	LLAPPERQHL	CID
86 89 92 99 95 85 82 86 85	APNELLAMK	CID
96 97 94 94 84 74 81	VFAALVT	CID
95 95 91 99 96 79 81 72	YPGLADWT	CID
68 77 85 96 100 98 96 90 97 90 86 79	SPGVLDAGLVMH	CID
97 98 98 98 97 92 74 67 82 80	LLAPLLVGQY	CID
82 92 96 97 75 87	AKLPKW	CID
92 94 92 97 77 75	**LDNLFR**	**CID**
90 88 90 81	KLLP	CID
75 82 94 86 90 90 94 98 85 98 86 87 80 77	VKLPVPVVGEQHTK	CID
94 87 79 82 95	FGKFL	CID
57 60 93 98 99 99 100 100 98 97 85 77 69	FNDPTFVEDVQYV	CID
92 93 99 98 85 67 65 90 90	APEESFALL	CID
98 97 65 86 86	KLPKL	CID
85 82 85 89 89	EKPLW	CID
95 95 56 98	EARE	CID
89 90 97 79 62 85 92 93	APEESSML	CID
90 91 91 99 100 99 92 56 55	MDPLLVKGP	CID
84 98 82 95 67	TEMEQ	CID
76 81 98 99 98 60 65 95 95 88	APEESPVLLK	CID
92 92 96 73 98 97 98 78 73 73 68	LPDGEHDLDRA	CID
91 96 89 78 79 79	FHTDSQ	CID
70 79 96 99 99 96 89 57 78 86	NYTDVPPPVK	CID
90 96 86 93 55 91	KLHEGH	CID
81 83 93 88 90 76 84	FCLQLPF	CID
57 52 88 99 100 100 100 100 99 98 88 86 85 82 68 56	LQWFDLLDKDKSGFNQ	CID
93 92 85 79 69 91	LKPLKL	CID

Scan	Peptide	Tag length	ALC (%)	m/z	z	RT	Mass	ppm	PTM
2094	LDEVLKFF	8	95	5,057,813	2	14.37	10,095,484	-0.4	
1054	LEHEE	5	95	3,286,490	2	8.51	6,552,813	3.2	
1619	LNNLL	5	93	2,936,705	2	11.73	5,853,486	-37.8	
1395	TKTPGLME	8	93	4,387,279	2	10.50	8,754,423	-1.2	
114	KLKKK	5	93	3,227,447	2	0.94	6,434,744	0.5	
2002	MKFLW	5	92	3,626,955	2	13.84	7,233,778	-1.8	
1528	LKYPLE	6	92	3,817,229	2	11.25	7,614,323	-1.5	
1610	APPHLF	6	91	3,411,891	2	11.68	6,803,646	-1.5	
1311	LLAPPEVGKY	10	91	5,438,178	2	10.01	10,856,121	8.3	
1526	VVDGVKL	7	91	3,652,283	2	11.24	7,284,432	-1.5	
2265	WLDPDDFPLLLFS	13	91	7,894,025	2	15.34	15,767,812	5.8	
1550	FLFGSKDKDPP	11	90	6,258,155	2	11.36	12,496,343	-14.3	
1137	AGDDAPVK	8	90	3,866,826	2	8.96	7,713,762	-33.0	
2185	LLVYPW	6	90	3,957,285	2	14.89	7,894,425	0.0	
147	KKTSPAE	7	90	3,807,189	2	1.29	7,594,127	14.0	
1493	FDDLQVR	7	90	4,467,291	2	11.05	8,914,450	-1.5	
1737	KDLLMVLTHSK	11	90	6,428,607	2	12.36	12,837,271	-15.7	
1907	KFLVLADLW	9	90	5,528,275	2	13.30	11,036,379	2.2	
1300	LLAPLLHFYS	10	89	5,873,343	2	9.95	11,726,594	-4.6	
1128	TERGY	5	89	3,131,508	2	8.90	6,242,867	0.4	
1701	LDLLEKDL	8	89	4,797,668	2	12.17	9,575,382	-19.9	
330	KCVHR	5	89	3,216,878	2	2.82	6,413,431	28.0	
1224	KDGCPGPPGLPGEH	14	89	6,808,327	2	9.50	13,596,240	19.7	
1546	NVLRL	5	88	3,077,021	2	11.34	6,133,911	-2.2	
1587	ADDWLR	6	88	3,881,899	2	11.56	7,743,660	-1.1	
1148	MENVAK	6	88	3,461,756	2	9.03	6,903,370	-0.7	
561	EARE	4	88	2,526,244	2	5.06	5,032,339	0.4	
2215	MDLFAHNE	8	88	4,887,139	2	15.06	9,754,120	1.2	
23	EKKK	4	88	2,666,763	2	0.15	5,313,380	0.0	
1509	VGDKLNL	7	88	3,797,235	2	11.14	7,574,334	-1.2	
1426	LDYVPR	6	87	3,817,104	2	10.67	7,614,072	-1.1	
1926	FKLPF	5	87	3,261,964	2	13.40	6,503,792	-1.4	
14	FHET	4	87	2,671,338	2	0.10	5,322,281	46.6	
711	LVHR	4	87	2,626,689	2	6.34	5,233,231	0.2	
1640	MYPGLADRM	9	87	5,272,455	2	11.84	10,524,783	-1.8	
720	EARE	4	87	2,526,244	2	6.40	5,032,339	0.4	
974	QDGVTH	6	87	3,286,536	2	8.10	6,552,925	0.2	
1352	NTLEDEKSL	9	87	5,247,610	2	10.24	10,475,083	-0.7	
243	AERE	4	87	2,526,244	2	2.14	5,032,339	0.6	
869	RKMHE	5	86	3,506,961	2	7.54	6,993,486	41.6	
1532	NGRHLL	6	86	3,551,971	2	11.27	7,084,031	-33.0	
1510	FDARL	5	86	3,111,836	2	11.15	6,203,282	39.3	
1617	KDLVDQL	7	86	4,157,338	2	11.72	8,294,545	-1.7	
1503	LLAGHE	6	86	3,201,888	2	11.11	6,383,387	38.2	
1538	FKLKPL	6	86	3,732,514	2	11.30	7,444,897	-1.9	
1322	APKLDPGE	8	86	4,137,180	2	10.07	8,254,232	-2.0	

2125	MAGMLDFDEFLQ	12	86	7,088,210	2	14.54	14,156,101	12.3
1394	VAPMKAY	7	86	3,902,181	2	10.49	7,784,047	21.7
1484	SVGASGLPGNH	11	85	4,982,604	2	11.00	9,944,832	23.2
2394	FDVALQPL	8	85	4,517,526	2	16.09	9,014,909	-0.4
2051	LVLLPEVPKVL	11	85	6,104,048	2	14.12	12,187,952	-0.1
1496	VNPYVE	6	85	3,606,814	2	11.07	7,193,490	-1.1
1479	YLKVE	5	85	3,261,888	2	10.97	6,503,639	-1.4
454	KKTPA	5	85	2,726,821	2	3.99	5,433,380	21.5
1346	LLPYMMNLK	9	85	5,617,925	2	10.21	11,215,977	-24.3
1466	TSLDWFQ	7	85	4,487,210	2	10.90	8,954,076	22.3
1622	LFDKF	5	85	3,351,834	2	11.75	6,683,533	-1.5
1702	MKKNEL	6	85	3,817,231	2	12.17	7,614,105	27.6
2067	MDLLRW	6	85	4,172,057	2	14.21	8,324,265	-35.7

local confidence (%)	tag (>=0%)	mode
90 95 99 99 100 95 97 91	LDEVLKFF	CID
89 96 97 98 97	LEHEE	CID
92 90 90 98 99	LNNLL	CID
95 96 97 86 85 94 97 98	TKTPGLME	CID
90 92 90 96 98	KLKKK	CID
86 91 97 97 91	MKFLW	CID
97 96 97 74 90 98	LKYPLE	CID
95 95 86 87 91 96	APPHLF	CID
98 99 99 99 92 99 81 70 90 89	LLAPPEVGKY	CID
99 99 99 88 86 81 89	VVDGVKL	CID
74 84 95 96 98 98 98 90 96 100 99 82 75	WLDPDDFPLLLFS	CID
96 98 96 91 97 98 98 96 98 70 59	FLFGSKDKDPP	CID
88 87 99 99 99 79 86 87	AGDDAPVK	CID
92 94 94 95 83 85	LLVYPW	CID
98 96 91 88 86 82 93	KKTSPAE	CID
90 97 99 98 94 81 75	FDDLQVR	CID
90 94 99 99 95 95 99 95 76 77 72	KDLLMVLTHSK	CID
92 96 99 99 99 94 67 88 75	KFLVLADLW	CID
92 97 95 96 82 89 89 93 87 77	LLAPLLHFYS	CID
87 96 72 93 98	TERGY	CID
82 88 96 100 99 84 80 82	LDLLEKDL	CID
92 90 91 93 78	KCVHR	CID
48 80 93 99 100 99 99 97 94 98 94 95 87 61	KDGCPGPPGLPGEH	CID
85 91 92 82 93	NVLRL	CID
79 90 95 96 93 79	ADDWLR	CID
85 95 81 85 91 95	MENVAK	CID
98 95 70 91	EARE	CID
91 93 93 90 76 77 90 95	MDLFAHNE	CID
92 82 87 92	EKKK	CID
93 88 92 85 91 80 86	VGDKLNL	CID
95 97 99 98 66 70	LDYVPR	CID
91 95 97 77 78	FKLPF	CID
93 82 93 81	FHET	CID
95 91 91 72	LVHR	CID
93 94 97 82 90 97 79 79 73	MYPGLADRM	CID
99 95 62 92	EARE	CID
72 90 79 89 96 94	QDGVTH	CID
41 67 97 100 100 100 96 93 90	NTLEDEKSL	CID
86 95 77 89	AERE	CID
70 94 95 83 91	RKMHE	CID
81 77 73 90 99 100	NGRHLL	CID
94 95 83 63 97	FDARL	CID
81 79 88 94 92 78 90	KDLVDQL	CID
97 97 94 54 75 99	LLAGHE	CID
84 90 95 86 70 90	FKLKPL	CID
97 95 88 86 82 71 76 92	APKLDPGE	CID

57 57 75 80 98 100 99 95 99 97 91 81	MAGMLDFDEFLQ	CID
97 96 62 70 78 99 99	VAPMKAY	CID
61 69 83 86 95 92 99 98 98 83 78	SVGASGLPGNH	CID
85 90 94 95 89 74 76 79	FDVALQPL	CID
63 82 98 99 77 91 79 72 93 91 91	LVLLPEVPKVL	CID
54 69 94 97 98 100	VNPYVE	CID
86 90 82 72 95	YLKVE	CID
98 92 73 81 82	KKTPA	CID
98 99 95 85 79 55 78 93 86	LLPYMMNLK	CID
94 96 98 90 77 70 69	TSLDWFQ	CID
78 72 96 87 92	LFDKF	CID
71 75 90 90 96 89	MKKNEL	CID
98 99 100 91 43 79	MDLLRW	CID

Scan	Peptide	Tag length	ALC (%)	m/z	z	RT	Mass	ppm	PTM
2031	LEEEELKLF	9	97	5,753,053	2	13.44	11,485,964	-0.3	
1897	FLDLDQDKKFEE	12	94	7,638,717	2	12.66	15,257,300	-0.7	
1892	LVLHL	5	93	2,977,020	2	12.64	5,933,901	-1.2	
1669	VLDQDKSGFLE	11	93	6,258,165	2	11.38	12,496,189	-0.4	
1676	LEKERL	6	93	3,942,227	2	11.42	7,864,599	-37.0	
1650	LVLDAGDRTH	10	92	5,487,853	2	11.28	10,955,671	-10.2	
1997	LVEELPARW	9	92	5,568,209	2	13.24	11,116,025	22.3	
484	LHDQH	5	92	3,251,564	2	3.70	6,482,980	0.3	
1115	VGDEAQSK	8	92	4,172,036	2	8.09	8,323,926	0.0	
710	VMLKQ	5	91	3,096,761	2	5.47	6,173,571	-31.3	
1976	FSVDEEFPDLSQH	13	91	7,753,446	2	13.11	15,486,731	1.0	
1572	LEDQYSELK	9	91	5,627,770	2	10.84	11,235,398	-0.3	
1784	DVEEFPDLSHQ	11	90	6,582,932	2	12.03	13,145,728	-0.7	
1639	FAGDDAPRAL	10	90	5,167,586	2	11.22	10,315,035	-0.9	
1171	LKEAETR	7	90	4,237,376	2	8.38	8,454,606	0.1	
1649	VVDRQL	6	89	3,652,289	2	11.27	7,284,181	34.5	
2060	LDTVLDLKM	9	89	5,242,910	2	13.62	10,465,681	-0.7	
1841	LLDPLLSRD	9	89	5,213,002	2	12.35	10,405,865	-0.6	
2832	FAGDDAVKP	9	89	4,602,170	2	18.30	9,184,446	-27.4	
1682	FTNEKLQQF	9	88	5,777,957	2	11.46	11,535,767	0.1	
1565	LLWDPQY	7	88	4,677,477	2	10.80	9,334,596	22.7	
1506	WVDDAVQELN	10	88	5,947,783	2	10.44	11,875,459	-3.2	
199	WDEAKKK	7	88	4,527,402	2	1.52	9,034,814	-17.1	
1745	FGLEEEELK	9	88	5,472,736	2	11.82	10,925,339	-1.3	
311	AGGERK	6	88	3,091,719	2	2.39	6,163,292	0.0	
3236	KTKLLL	6	88	3,582,678	2	20.70	7,145,003	28.9	
1747	LGEDFLRD	8	88	4,827,398	2	11.83	9,634,661	-1.1	
2301	FAGDSFYL	8	88	4,602,206	2	15.05	9,184,123	15.6	
1517	WGASGLPGPP	10	87	4,697,507	2	10.51	9,374,658	22.5	
1181	NDENVRQ	7	87	4,377,042	2	8.43	8,733,940	-0.2	
650	LHDQH	5	87	3,251,563	2	5.03	6,482,980	0.1	
124	TKEKKA	6	87	3,527,191	2	0.96	7,034,228	1.1	
1675	LFKYP	5	87	3,341,942	2	11.42	6,663,741	-0.2	
3760	WGGHEW	6	87	3,861,671	2	23.76	7,703,136	7.9	
1691	FEEELFGSKDKDGH	14	87	8,193,803	2	11.51	16,367,368	5.7	
2163	YLDLKDMPFYA	11	87	6,883,329	2	14.23	13,746,528	-1.2	
441	AAEDTQAAK	9	87	4,527,276	2	3.36	9,034,297	12.0	
1689	LDDAVRAL	8	86	4,367,452	2	11.50	8,714,763	-0.4	
770	KTLQQ	5	86	3,091,719	2	5.93	6,163,544	-40.7	
443	VTRE	4	86	2,526,308	2	3.32	5,032,704	-46.2	
1706	LTDVLHVT	8	86	4,492,552	2	11.60	8,964,967	-1.0	
1705	ADYEDLYK	8	86	5,087,317	2	11.59	10,154,498	-0.9	
1596	FDELDDNLP	9	86	5,392,504	2	10.98	10,764,661	18.8	
3023	FAGDDAPVK	9	86	4,602,169	2	19.43	9,184,446	-27.6	
1791	MEPKSHHM	8	86	4,987,296	2	12.07	9,954,317	13.0	
1867	GFTADEKLGLY	11	86	6,073,082	2	12.49	12,126,025	-0.5	

3805	DAGAAETH	8	86	3,861,668	2	24.04	7,703,195	-0.4
1748	LLFK	4	86	2,606,780	2	11.83	5,193,420	-1.2
1439	LNEDKLQDKLDK	12	86	7,298,934	2	10.04	14,577,725	-0.2
183	VDKR	4	86	2,591,583	2	1.40	5,163,020	0.2
1800	WEQVKLW	7	86	4,947,582	2	12.12	9,875,178	-16.2
2129	VELKDMPFY	9	86	5,712,835	2	14.03	11,405,525	0.0
2166	VTEDPFDQTEDAENQEK	17	85	9,979,260	2	14.25	19,938,389	-0.7
3821	LVNR	4	85	2,511,590	2	24.14	5,003,071	-7.3
2699	LETAQL	6	85	3,376,803	2	17.49	6,733,646	-27.5
1124	VLEVGR	6	85	3,367,112	2	8.14	6,713,966	16.8
1693	NQKTLDDLEDE	11	85	6,603,139	2	11.52	13,185,889	18.5
1542	LDKVDEDRYDME	12	85	7,643,349	2	10.66	15,266,558	-0.3

local confidence (%)	tag (>=0%)	mode
92 98 99 100 100 99 98 98 93	LEEEELKLF	CID
79 92 99 99 99 98 99 97 89 90 96 91	FLDLDQDKKFEE	CID
85 95 99 93 96	LVLHL	CID
86 90 97 96 99 97 92 85 94 95 97	VLDQDKSGFLE	CID
94 98 91 97 85 94	LEKERL	CID
79 86 95 98 99 96 97 94 93 90	LVLDAGDRTH	CID
97 97 100 99 96 92 79 84 89	LVEELPARW	CID
89 86 93 97 99	LHDQH	CID
94 94 98 99 96 88 90 78	VGDEAQSK	CID
90 91 98 90 90	VMLKQ	CID
65 68 91 97 100 100 100 99 98 98 93 88 86	FSVDEEFPDLSQH	CID
95 99 92 95 93 75 94 91 84	LEDQYSELK	CID
78 79 97 100 100 99 98 97 90 85 77	DVEEFPDLSHQ	CID
94 96 93 100 99 99 70 79 89 88	FAGDDAPRAL	CID
87 89 98 95 99 82 79	LKEAETR	CID
97 97 93 72 88 90	VVDRQL	CID
90 88 94 99 99 83 85 83 82	LDTVLDLKM	CID
97 96 97 98 98 97 76 72 71	LLDPLLSRD	CID
90 97 92 99 95 97 81 83 65	FAGDDAVKP	CID
78 86 92 99 90 93 94 88 80	FTNEKLQQF	CID
99 99 92 97 70 77 88	LLWDPQY	CID
70 98 97 98 91 90 93 98 82 68	WVDDAVQELN	CID
62 85 96 86 93 98 98	WDEAKKK	CID
69 60 95 99 94 93 93 97 94	FGLEEEELK	CID
85 82 91 97 80 95	AGGERK	CID
75 76 85 97 97 98	KTKLLL	CID
94 86 98 100 99 93 54 79	LGEDFLRD	CID
88 90 78 93 95 89 88 81	FAGDSFYL	CID
66 90 97 100 99 100 99 95 70 62	WGASGLPGPP	CID
81 95 98 81 92 85 81	NDENVRQ	CID
79 81 92 90 95	LHDQH	CID
81 88 96 95 82 81	TKEKKA	CID
85 78 90 94 88	LFKYP	CID
95 94 87 78 90 79	WGGHEW	CID
74 96 99 100 100 100 98 99 99 97 96 90 32 40	FEEELFGSKDKDGH	CID
79 86 95 96 95 93 95 79 88 80 70	YLDLKDMPFYA	CID
85 91 97 92 91 79 74 86 86	AAEDTQAAK	CID
86 91 99 99 96 61 77 85	LDDAVRAL	CID
97 88 83 77 88	KTLQQ	CID
90 95 66 96	VTRE	CID
89 90 91 86 96 82 80 78	LTDVLHVT	CID
84 92 99 99 76 82 79 80	ADYEDLYK	CID
92 96 99 98 96 97 62 80 55	FDELDDNLP	CID
94 95 91 98 99 94 68 74 62	FAGDDAPVK	CID
93 98 91 89 88 73 81 75	MEPKSHHM	CID
46 70 85 96 97 99 94 90 83 94 93	GFTADEKLGLY	CID

74 86 85 90 96 95 81 82	DAGAAETH	CID
89 86 90 79	LLFK	CID
55 78 92 98 93 95 95 99 93 91 78 66	LNEDKLQDKLDK	CID
89 91 85 79	VDKR	CID
75 98 97 97 82 76 76	WEQVKLW	CID
62 85 90 85 84 96 82 93 95	VELKDMPFY	CID
54 78 97 99 98 99 95 87 76 92 88 98 99 85 66 86 56	VTEDPFDQTEDAENQEK	CID
92 85 84 80	LVNR	CID
88 96 86 91 66 86	LETAQL	CID
72 94 94 78 84 89	VLEVGR	CID
29 32 89 99 99 99 99 99 98 95 96	NQKTLDDLEDE	CID
55 75 72 95 99 98 93 75 90 84 87 95	LDKVDEDRYDME	CID

Scan	Peptide	Tag length	ALC (%)	m/z	z	RT	Mass	ppm	PTM
1584	LLAPPE	6	97	3,201,890	2	11.09	6,383,639	-0.8	
90	YEKK	4	96	2,841,605	2	0.69	5,663,064	0.1	
2104	LVYPSV	6	94	3,391,865	2	13.97	6,763,796	-31.2	
1612	VKLPKL	6	94	3,492,519	2	11.25	6,964,897	-0.6	
1606	LKYPLE	6	94	3,817,231	2	11.22	7,614,323	-0.8	
2257	LDFDEFLMK	9	94	5,792,814	2	14.85	11,565,474	0.7	
1678	LLDQDKSGFLE	11	93	6,328,278	2	11.60	12,636,345	5.2	
1667	SERRLL	6	93	3,872,292	2	11.54	7,724,555	-15.0	
874	EYKK	4	92	2,841,605	2	7.02	5,663,064	0.0	
2266	LLVYPW	6	91	3,957,284	2	14.90	7,894,425	-0.4	
1639	TGPLKF	6	91	3,316,970	2	11.39	6,613,799	-0.8	
1961	VDLVSFK	7	91	4,042,233	2	13.15	8,064,538	-26.9	
1053	QDDKLKDK	8	91	4,952,665	2	8.10	9,885,189	-0.5	
257	VGADKK	6	90	3,091,841	2	2.03	6,163,544	-1.3	
1600	VVDRLK	6	90	3,652,286	2	11.18	7,284,545	-16.1	
1984	LDLPKLM	7	89	4,152,462	2	13.28	8,284,779	-0.2	
1204	TDALQR	6	89	3,521,902	2	8.91	7,023,660	-0.3	
1547	TSLDWFQ	7	89	4,487,218	2	10.88	8,954,076	23.9	
2568	WGDRTH	6	89	3,861,669	2	16.69	7,703,460	-34.8	
1572	VNPYVE	6	88	3,606,816	2	11.02	7,193,490	-0.5	
1400	APKLPDGDKV	10	88	5,202,917	2	10.03	10,385,709	-1.9	
1552	FDELDDPNL	9	88	5,392,508	2	10.91	10,764,661	19.5	
467	DPWLR	5	88	3,436,884	2	3.69	6,853,547	10.9	
1495	EVDLR	5	88	3,161,739	2	10.59	6,303,337	-0.6	
2262	FVLLAHPL	8	88	4,552,682	2	14.88	9,085,483	-29.3	
274	AERE	4	87	2,526,244	2	2.16	5,032,339	0.6	
1705	YFKLKPL	7	87	4,547,835	2	11.75	9,075,531	-0.8	
1271	KDGSSGLPGLPGEY	14	87	6,888,306	2	9.27	13,756,619	-11.0	
8	KLLT	4	87	2,376,737	2	0.07	4,733,213	24.3	
2051	VAKVLQVL	8	86	4,352,942	2	13.66	8,685,746	-0.9	
1908	FGLRT	5	86	2,971,756	2	12.85	5,923,333	5.8	
1577	FDDLQVR	7	86	4,467,296	2	11.05	8,914,450	-0.4	
1601	FDEMDPPLKD	10	86	6,037,719	2	11.19	12,055,273	1.6	
1963	MMVGLL	6	86	3,321,945	2	13.16	6,623,495	37.6	
1658	WQLDNL	6	86	3,946,929	2	11.49	7,873,864	-19.2	
759	KDDLR	5	86	3,236,853	2	6.12	6,453,445	17.8	
1780	LGPLKVL	7	85	3,702,574	2	12.15	7,385,003	-0.1	
1644	YPGLADSAE	9	85	4,617,257	2	11.42	9,214,080	31.4	
2068	AFLPM	5	85	2,896,538	2	13.76	5,772,934	-0.7	
2130	ADLFPM	6	85	3,471,674	2	14.12	6,923,203	0.1	
1679	QDDLLEKL	8	85	4,872,719	2	11.61	9,725,128	17.0	
1804	LKWL	4	85	2,801,835	2	12.28	5,583,530	-1.0	

local confidence (%)	tag (>=0%)	mode
95 95 96 99 99 100	LLAPPE	CID
90 97 99 99	YEKK	CID
95 95 98 93 93 94	LVYPSV	CID
94 96 97 86 95 96	VKLPKL	CID
97 96 97 84 93 99	LKYPLE	CID
89 93 98 98 100 98 96 90 85	LDFDEFLMK	CID
99 99 98 97 99 96 89 76 90 93 95	LLDQDKSGFLE	CID
79 93 93 94 99 99	SERRLL	CID
96 90 87 96	EYKK	CID
83 90 92 97 95 93	LLVYPW	CID
87 85 90 94 96 96	TGPLKF	CID
93 95 97 89 85 90 92	VDLVSFK	CID
82 93 92 95 94 89 97 89	QDDKLKDK	CID
91 88 87 88 93 93	VGADKK	CID
97 96 94 74 90 88	VVDRLK	CID
95 94 96 93 79 82 86	LDLPKLM	CID
88 93 97 99 76 82	TDALQR	CID
93 96 97 88 91 78 80	TSLDWFQ	CID
86 95 94 87 82 90	WGDRTH	CID
65 79 93 96 98 99	VNPYVE	CID
71 82 92 100 99 99 76 92 89 83	APKLPDGDKV	CID
92 96 99 99 99 95 57 78 77	FDELDDPNL	CID
84 94 91 96 75	DPWLR	CID
90 76 91 95 88	EVDLR	CID
77 89 95 99 86 75 92 91	FVLLAHPL	CID
83 92 82 92	AERE	CID
90 94 97 99 98 59 76	YFKLKPL	CID
39 75 84 99 98 92 98 99 99 100 99 97 85 55	KDGSSGLPGLPGEY	CID
94 86 90 78	KLLT	CID
62 70 89 95 89 92 98 98	VAKVLQVL	CID
97 94 96 75 70	FGLRT	CID
80 97 89 93 88 85 71	FDDLQVR	CID
85 94 99 92 89 83 93 95 70 61	FDEMDPPLKD	CID
77 86 93 70 96 94	MMVGLL	CID
84 85 93 79 82 92	WQLDNL	CID
90 76 79 91 93	KDDLR	CID
95 87 82 86 68 87 95	LGPLKVL	CID
84 88 90 99 97 77 65 81 89	YPGLADSAE	CID
74 79 89 89 95	AFLPM	CID
79 85 85 79 92 90	ADLFPM	CID
74 93 94 94 86 82 75 81	QDDLLEKL	CID
93 88 78 80	LKWL	CID

Scan	Peptide	Tag length	ALC (%)	m/z	z	RT	Mass	ppm	PTM
1927	LEEEELKLF	9	97	5,753,052	2	13.44	11,485,964	-0.4	
324	EYKK	4	95	2,841,604	2	2.46	5,663,064	-0.3	
1879	VDLWFK	6	95	4,042,233	2	13.17	8,064,327	-0.9	
1961	LKLFL	5	94	3,172,202	2	13.64	6,324,261	-0.4	
1696	LEDDLVALK	9	92	5,082,898	2	12.13	10,145,597	5.3	
1124	VGDEAKSQ	8	91	4,172,036	2	8.15	8,323,926	0.1	
1915	VDLWFKA	7	90	4,397,417	2	13.37	8,774,698	-1.1	
1551	TVDDKVELE	9	90	5,242,637	2	11.30	10,465,132	-0.4	
1832	LVVDRKL	7	90	4,217,705	2	12.90	8,415,385	-14.4	
1392	LLDKNRDGLLSQ	12	90	6,863,862	2	10.32	13,707,517	4.4	
542	EARE	4	90	2,526,242	2	4.23	5,032,339	-0.1	
635	QGREK	5	90	3,091,719	2	4.94	6,163,292	0.1	
1897	LVEELPVKW	9	89	5,568,206	2	13.27	11,116,277	-1.0	
1374	KSLEDEQSLGAQ	12	89	6,528,231	2	10.20	13,036,255	4.7	
28	AKTK	4	89	2,241,501	2	0.18	4,462,853	0.8	
1786	ALLDQDNSGFLEEEELK	17	89	9,754,704	2	12.63	19,489,265	-0.1	
3687	WGDHEQ	6	89	3,861,672	2	23.87	7,702,983	27.9	
143	KGREQ	5	89	3,091,719	2	1.06	6,163,292	0.1	
1815	KEFLEEL	7	89	4,542,419	2	12.80	9,064,698	-0.5	
1959	LGEDFLTGLL	10	89	5,392,854	2	13.63	10,765,754	-17.8	
1993	FDMDKLPL	8	89	4,897,516	2	13.83	9,774,892	-0.7	
1190	NDENVRQ	7	89	4,377,041	2	8.49	8,733,940	-0.4	
791	FCDKH	5	89	3,251,561	2	6.10	6,482,690	44.2	
1596	FAGDDAPRAF	10	89	5,337,512	2	11.54	10,654,878	0.0	
1522	VFCGNGEKLET	11	88	5,987,839	2	11.12	11,955,542	-0.8	
1756	FEEELFGSKDKDHW	14	88	8,839,014	2	12.46	17,657,947	-3.7	
1588	FDELDDLTKSH	11	88	6,603,140	2	11.50	13,186,040	7.2	
1080	LVKER	5	88	3,227,081	2	7.92	6,434,017	0.1	
315	NDQQKSDEK	9	88	5,462,517	2	2.39	10,904,890	-0.1	
1664	LELLEKRE	8	88	5,152,857	2	11.93	10,285,865	-28.9	
1641	GFLEEEEKL	9	88	5,472,741	2	11.80	10,925,339	-0.2	
7	VGDEAQSK	8	87	4,172,018	2	0.04	8,323,926	-4.4	
145	KLKKK	5	87	3,227,447	2	1.08	6,434,744	0.7	
1995	NFLLDFADQLEPQ	13	87	7,753,726	2	13.84	15,487,458	-9.8	
2094	VETVLDMLKW	10	87	6,173,229	2	14.44	12,326,475	-13.2	
95	AERE	4	87	2,526,244	2	0.73	5,032,339	0.7	
1005	LHDQH	5	87	3,251,563	2	7.53	6,482,980	0.1	
598	QGKER	5	87	3,091,720	2	4.68	6,163,292	0.5	
1850	QLDAFDLLDKDTN	13	86	7,543,659	2	13.00	15,067,202	-2.0	
281	QGERK	5	86	3,091,720	2	2.12	6,163,292	0.5	
1809	FEVPKSGSPP	10	86	5,227,839	2	12.77	10,435,288	23.5	
399	LVHKR	5	86	3,267,162	2	3.07	6,514,180	-0.3	
1760	NNLDQDKSGFLE	12	86	6,903,375	2	12.49	13,786,365	17.3	
1354	MNEPKLKDKLNE	12	86	7,298,974	2	10.03	14,577,549	17.4	
1469	LLADRM	6	86	3,596,982	2	10.82	7,173,843	-3.5	
1548	LALASF	6	86	3,111,858	2	11.28	6,203,533	6.1	

1732	FAPPDVQN	8	86	4,442,165	2	12.33	8,864,185	0.0
1605	FLFGSKDKDHA	11	86	6,328,243	2	11.60	12,636,248	7.3
1529	LFDRVGDSQ	9	85	5,187,564	2	11.16	10,354,985	-0.3
2582	LQDFADLLDKDKSGFNQ	17	85	9,774,777	2	17.33	19,529,480	-3.7
1614	LLDKVDEDRFML	12	85	7,473,760	2	11.65	14,927,595	-14.8
1724	LLDQDNSGFLEEENQK	16	85	9,399,510	2	12.28	18,778,643	12.4
1847	CCLLKLLVAM	10	85	5,537,985	2	12.99	11,056,062	-21.4
1928	VDLWFK	6	85	4,042,235	2	13.45	8,064,327	-0.3
1479	RDNPGHPF	8	85	4,702,193	2	10.88	9,384,359	-12.6
1898	MMLLDQDKSGFNK	13	85	7,638,712	2	13.28	15,257,268	0.7
1599	FEEELFGSRDSRPP	14	85	8,333,835	2	11.56	16,647,793	-16.1
2191	FLTLGTFLYECFR	13	85	8,053,986	2	15.01	16,088,010	-11.5
1814	VKNWPW	6	85	4,152,213	2	12.80	8,284,282	-0.3
698	KEQK	4	85	2,666,582	2	5.44	5,313,016	0.4
697	AERE	4	85	2,526,244	2	5.43	5,032,339	0.4
96	KAKT	4	85	2,241,500	2	0.73	4,462,853	0.6
2668	FLFGTTQRSHW	11	85	6,903,382	2	17.85	13,786,782	-11.9
1533	LEKSYELPDGQ	11	85	6,398,138	2	11.19	12,776,140	-0.7
2038	VLLLPEPVKVL	11	85	6,104,048	2	14.11	12,187,952	0.0
1186	LVRD	4	85	2,516,529	2	8.47	5,012,911	0.4
1730	LLDPLLSRD	9	85	5,213,004	2	12.32	10,405,865	-0.3
2145	LNHQGTWL	8	85	4,847,383	2	14.74	9,674,875	-26.4

local confidence (%)	tag (>=0%)	mode
89 98 99 99 99 98 97 99 95	LEEEELKLF	CID
99 95 91 98	EYKK	CID
96 97 98 95 93 92	VDLWFK	CID
90 94 93 95 98	LKLFL	CID
88 96 92 96 94 95 93 94 87	LEDDLVALK	CID
90 90 97 99 96 91 87 77	VGDEAKSQ	CID
92 95 99 86 90 84 89	VDLWFKA	CID
79 82 94 96 92 82 93 97 97	TVDDKVELE	CID
95 94 95 83 71 97 96	LVVDRKL	CID
86 93 88 93 85 85 98 89 98 98 92 79	LLDKNRDGLLSQ	CID
95 93 76 96	EARE	CID
90 80 84 98 96	QGREK	CID
89 88 100 100 99 80 75 93 85	LVEELPVKW	CID
59 79 91 100 100 100 98 99 99 84 92 78	KSLEDEQSLGAQ	CID
86 94 90 89	AKTK	CID
41 86 89 92 95 98 94 97 91 96 100 100 99 99 90 83 75	ALLDQDNSGFLEEEELK	CID
93 90 93 82 92 86	WGDHEQ	CID
92 84 82 96 94	KGREQ	CID
57 89 89 97 99 99 98	KEFLEEL	CID
89 78 96 99 99 99 82 78 89 86	LGEDFLTGLL	CID
85 89 91 91 94 98 80 86	FDMDKLPL	CID
72 90 99 95 97 86 84	NDENVRQ	CID
90 86 91 92 86	FCDKH	CID
93 96 90 99 99 99 92 81 68 71	FAGDDAPRAF	CID
85 93 91 78 92 95 98 96 99 88 62	VFCGNGEKLET	CID
92 99 100 100 98 92 79 95 98 99 95 94 56 44	FEEELFGSKDKDHW	CID
82 94 100 99 99 100 99 98 97 59 49	FDELDDLTKSH	CID
84 83 88 95 91	LVKER	CID
62 80 85 96 94 95 95 97 86	NDQQKSDEK	CID
87 97 98 99 98 93 57 75	LELLEKRE	CID
46 82 97 99 99 96 97 88 88	GFLEEEEKL	CID
82 82 95 99 96 82 89 78	VGDEAQSK	CID
68 85 91 95 98	KLKKK	CID
54 60 99 99 99 99 98 98 90 95 95 79 73	NFLLDFADQLEPQ	CID
55 82 85 98 99 98 91 97 87 81	VETVLDMLKW	CID
85 95 76 92	AERE	CID
82 85 93 79 95	LHDQH	CID
93 93 72 92 85	QGKER	CID
57 88 91 98 100 100 100 100 99 99 86 65 44	QLDAFDLLDKDTN	CID
71 89 95 85 93	QGERK	CID
88 97 98 90 84 88 91 92 72 66	FEVPKSGSPP	CID
94 95 98 88 56	LVHKR	CID
57 79 98 97 98 99 98 81 63 75 94 93	NNLDQDKSGFLE	CID
48 49 95 97 100 99 97 99 90 88 85 90	MNEPKLKDKLNE	CID
99 99 88 89 61 80	LLADRM	CID
96 96 96 73 80 74	LALASF	CID

69 74 85 96 97 94 92 80	FAPPDVQN	CID
91 93 86 89 96 88 90 94 88 68 60	FLFGSKDKDHA	CID
91 93 95 92 95 61 78 92 72	LFDRVGDSQ	CID
52 75 79 82 90 99 100 100 100 99 99 99 95 82 77 76 51	LQDFADLLDKDKSGFNQ	CID
94 95 92 97 100 99 92 79 74 68 62 75	LLDKVDEDRFML	CID
70 69 90 96 99 98 99 98 99 99 100 100 96 43 45 67	LLDQDNSGFLEEENQK	CID
85 85 98 99 81 66 89 85 85 79	CCLLKLLVAM	CID
90 93 95 69 85 81	VDLWFK	CID
66 92 96 88 92 95 80 73	RDNPGHPF	CID
55 62 87 99 100 98 98 95 91 89 95 72 68	MMLLDQDKSGFNK	CID
68 95 99 99 100 99 96 98 76 86 78 62 72 66	FEEELFGSRDSRPP	CID
52 67 84 98 97 99 100 100 100 100 80 71 61	FLTLGTFLYECFR	CID
91 88 80 79 84 88	VKNWPW	CID
71 95 85 89	KEQK	CID
74 92 79 95	AERE	CID
85 86 84 85	KAKT	CID
86 95 95 82 92 85 88 87 94 70 61	FLFGTTQRSHW	CID
66 84 87 91 95 99 99 85 86 69 73	LEKSYELPDGQ	CID
60 76 98 99 93 97 67 77 91 89 88	VLLLPEPVKVL	CID
89 82 81 88	LVRD	CID
98 97 97 92 99 98 72 55 56	LLDPLLSRD	CID
90 91 94 81 65 90 83 84	LNHQGTWL	CID