

**UNIVERSIDADE ESTADUAL PAULISTA UNESP
CÂMPUS DE JABOTICABAL**

**CARACTERIZAÇÃO DO PROTEOMA DE *Genlisea violacea*
A.St.-Hil. (LENTIBULARIACEAE)**

Néstor Darío Franco Marulanda
Engenheiro de Produção Biotecnológica

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(LENTIBULARIACEAE)

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CARACTERIZAÇÃO DO PROTEOMA DE *Genlisea violacea* A.St.-Hil. (LENTIBULARIACEAE)

RESUMO - A família Lentibulariaceae, da ordem Lamiales, é a maior entre as famílias de plantas carnívoras e está composta pelos gêneros *Pinguicula*, *Genlisea* e *Utricularia*. Filogeneticamente o gênero *Pinguicula* é o grupo irmão do clado *Genlisea-Utricularia*. Cada gênero exibe especializações morfológicas em suas armadilhas que permitem a captura e digestão de pequenos organismos. O gênero *Pinguicula* apresenta diferentes características pleiomórficas, sendo o único gênero da família com raízes e com folhas pegajosas modificadas em armadilhas, por sua vez, o gênero *Utricularia* apresenta armadilhas em forma de vesículas, chamadas de utrículos, e o gênero *Genlisea* apresenta folhas utriculíferas submersas com forma de “Y” invertido como armadilhas. As proteínas expressas nos tipos foliares de *Genlisea*, folhas e armadilhas, são pouco conhecidas, e análise diferencial das proteínas expressas nos dois tipos foliares podem auxiliar no entendimento dos seus processos biológicos. Deste modo, neste trabalho foi realizado o estudo proteômico dos tipos foliares de dois morfotipos de *Genlisea violacea*, de flor roxa e flor branca. Para tal, amostras de folhas e armadilhas dos dois morfotipos foram empregadas para extração das proteínas totais, realizado o sequenciamento *de novo* dos peptídeos e criado um inventário de proteínas presentes nos tipos foliares de cada morfotipo. Além disso, foram realizadas quantificações das proteínas compartilhadas por folhas e armadilhas dos dois morfotipos. Assim, foram identificadas um total de 482 proteínas exclusivas para folhas fotossintéticas e 14 para as armadilhas e 65 proteínas foram compartilhadas pelos dois tipos foliares. A análise comparativa mostrou que oito proteínas foram expressas diferentemente entre os dois tipos de folhas. As análises funcionais e a quantificação indicaram que as proteínas das folhas fotossintéticas estão envolvidas principalmente na fotossíntese e respostas aos estímulos e as proteínas das armadilhas estão relacionadas à respiração, transporte e digestão. A identificação em larga escala das proteínas de *Genlisea violacea* permite esclarecer algumas diferenças e similitudes funcionais entre folhas fotossintetizantes e as armadilhas, aumentando nossa compreensão da biologia deste gênero de plantas carnívoras.

Palavras chave: Plantas carnívoras, armadilhas, proteômica, sequenciamento *de novo*, LC-MS/MS.

**CHARACTERIZATION OF THE PROTEOM OF *Genlisea violacea* A.St.-Hil.
(LENTIBULARIACEAE)**

ABSTRACT – The family Lentibulariaceae, of the order Lamiales, is the largest among the families of carnivorous plants and is composed of the genera *Pinguicula*, *Genlisea* and *Utricularia*. Phylogenetically the genus *Pinguicula* is the sister group of the *Genlisea-Utricularia* clade. Each genus exhibits morphological specializations in its traps that allow the capture and digestion of small organisms. The genus *Pinguicula* present different pleisomorphic characteristics, being the only genus of the family with roots and sticky leaves modified in traps, in turn, the genus *Utricularia* presents traps in the form of vesicles, called utricles, and the genus *Genlisea* presents submerged utriculiferous leaves. inverted “Y” shape like traps. The proteins expressed in the leaf types of *Genlisea*, leaves and traps, are little known, and differential analysis of the proteins expressed in the two leaf types can help in the understanding of their biological processes. Thus, in this work, the proteomic study of the leaf types of two morphotypes of *Genlisea violacea*, of purple and white flowers, was carried out. For this, samples of leaves and traps of the two morphotypes were used to extract the total proteins, after that a *de novo* peptide sequencing was carried out and an inventory of proteins present in the leaf types of each morphotype was generated. In addition, quantifications of the proteins shared by leaves and traps of the two morphotypes were performed. Thus, a total of 482 exclusive proteins for photosynthetic leaves and 14 for traps were identified and 65 proteins were shared by the two leaves types. Comparative analysis showed that eight proteins were expressed differently between the two types of leaves. Functional analysis and quantification indicated that photosynthetic leaf proteins are mainly involved in photosynthesis and responses to stimuli and trap proteins are related to respiration, transport and digestion. The large-scale identification of *Genlisea violacea* proteins allows to clarify some differences and functional similarities between photosynthetic leaves and traps, increasing our compression of the biology of this genus of carnivorous plants.

Keywords: Carnivorous plants, traps, proteomics, *de novo* sequencing, LC-MS/MS.

CAPÍTULO 1 - Considerações gerais

Introdução

As plantas carnívoras apresentam diferentes adaptações para atrair, capturar e digerir presas (JUNIPER; ROBINS; JOEL, 1989; ELLISON, 2006; ELLISON; ADAMEC, 2018). Na história evolutiva das angiospermas, a síndrome da carnívoría surgiu em momentos diferentes, agrupando 10 famílias de cinco ordens (GIVNISH, 2015; WHEELER; CARSTENS, 2018). Dentro da ordem Lamiales, no clado das Asterídeas, encontra-se a família Lentibulariaceae Rich. (APG IV, 2016), a maior família de plantas carnívoras, agrupando cerca de 350 espécies nos gêneros *Pinguicula* L, *Genlisea* A. St.-Hil. e *Utricularia* L. (FLEISCHMANN, 2012; FLEISCHMANN; STAATSSAMMLUNG; MENZINGER, 2015). No Brasil, centro de diversidade da família (TAYLOR, 1991; MCPHERSON, 2010), até o momento, foram descritas 86 espécies dos gêneros *Genlisea* e *Utricularia*, dos quais 30 são endêmicas (MIRANDA et al., 2015.; FLORA DO BRASIL 2020, em construção). Além disso, nesta família encontram-se os menores genomas de plantas conhecidos, particularmente em espécies dos gêneros *Genlisea* e *Utricularia*, com genomas de aproximadamente de 60 Mpb (ALBERT et al., 2010). Cada gênero da família apresenta especializações morfológicas, com adaptações à captura e digestão de artrópodes e outros pequenos organismos (JUNIPER et al., 1989). O gênero *Pinguicula* apresenta estados de carácter pleiosomórficos para as características raízes (presença) e armadilhas (folhas adesivas), enquanto os gêneros *Genlisea* e *Utricularia* apresentam estados de carácter apomórficos para esses caracteres, não apresentando raízes e com armadilhas complexas (JUNIPER; ROBINS; JOEL, 1989; TAYLOR, 1989; MÜLLER et al., 2006).

O gênero *Genlisea* está composto por 31 espécies de ervas rosetadas (FLEISCHMANN, 2012; SILVA et al., 2020a), com folhas aéreas fotossintéticas e folhas subterrâneas não-fotossintéticas modificadas em armadilhas, com aparência de raiz, chamadas folhas utriculíferas (FLEISCHMANN, 2012). Dentre as presas de

Genlisea encontram-se bactérias, protozoários, algas e integrantes da microfauna, como nematoides, rotíferos, anelídeos e pequenos artrópodes (BARTHLOTT et al., 1998; STUDNICKA, 2003; PŁACHNO; FABER; JANKUN, 2005; PŁACHNO et al., 2006; CARAVIERI et al., 2014; KOLLER-PEROUTKA et al 2014). Dentro das armadilhas, os tricomas permitem capturar e digerir as presas (PŁACHNO; KOZIERADZKA-KISZKURNO; SWIATEK, 2007). Pouco se sabe sobre a produção de enzimas hidrolíticas e mecanismos de digestão nos gêneros de Lentibulariaceae. Entretanto, em *Genlisea*, por meio de testes enzimáticos, já foi detectada atividade da fosfatase nas células terminais dos tricomas no interior das armadilhas (PŁACHNO et al., 2006).

A disponibilidade de sequências genômicas tem contribuído para a descoberta de enzimas e para o melhor entendimento dos mecanismos e evolução da carnivoría em diferentes famílias de plantas (RAVEE et al., 2018). Entretanto, poucos estudos com enfoque proteômico têm sido desenvolvidos em plantas carnívoras (HATANO; HAMADA, 2008; 2012; SCHULZE et al., 2012; BITEAU et al. 2013; LEE et al., 2016; ZAKARIA et al., 2019). Entre os estudos proteômicos, as abordagens mais comuns usadas para identificar proteínas com dados de espectrometria de massa em tandem (MS / MS) dependem de banco de dados disponível para comparação com dados experimentais (MA et al., 2003). Assim, no sequenciamento de peptídeos *de novo*, a identidade dos peptídeos originada pela digestão de proteínas pode ser inferida diretamente a partir dos espectros de massa adquiridos, permitindo a identificação de proteínas sem a existência de um genoma de referência (MA, 2015).

No gênero *Genlisea* há proteoma disponível apenas para *Genlisea aurea* (LEUSHKIN et al., 2013), mas não para a espécie-tipo do subgênero *Tayloria*, *Genlisea violacea*. Essa espécie, endêmica do Brasil, encontrada em São Paulo e Minas Gerais (FLEISHMANN et al, 2011; BFG, 2015; FLORA DO BRASIL 2020, em construção; MIRANDA et al., 2015), e exibe uma alta variação na morfologia, incluindo variações no tamanho da planta, dos tricomas e cor e tamanho da corola, apresentando plantas com flores violetas/lilás, ou brancas (FLEISCHMANN et al., 2010, 2011; FLEISCHMANN, 2012).

Nesse contexto, o presente trabalho visa caracterizar e comparar os proteomas das folhas fotossintetizantes e utriculíferas (armadilhas) dos morfotipos de flores roxas e brancas de *Genlisea violacea* e como objetivos específicos: (i) identificar as proteínas das folhas fotossintetizantes e armadilhas dos morfotipos de flor roxa e branca de *Genlisea violacea*; (ii) verificar a variação da produção de proteínas compartilhadas nos diferentes tipos foliares de cada morfotipo, (iii) comparar a produção de proteínas relacionadas à carnivoría nos diferentes tecidos da espécie estudada.

Revisão de literatura

Síndrome de carnivoría em plantas

A síndrome da carnivoría é pouco comum em plantas, sendo exibida em menos de 0,3% das espécies vegetais conhecidas (MCPHERSON, 2010; ELLISON; ADAMEC, 2018; CROSS 2019). As plantas carnívoras geralmente se desenvolvem em ambientes úmidos, ensolarados com solos ácidos e deficientes em nutrientes (GIVNISH et al., 1984; ELLISON; GOTELLI, 2001). Para se estabelecer neste tipo de ambiente, essas plantas possuem um conjunto de adaptações que permitem atrair, capturar, matar, digerir e absorver nutrientes a partir de presas (DARWIN, 1875; GIVNISH et al. 1984; JUNIPER; ROBINS; JOEL, 1989; ELLISON, 2006; ELLISON; ADAMEC, 2018). Na história evolutiva das plantas, a síndrome de carnivoría surgiu em processos homoplásticos, sendo que hoje são reconhecidas aproximadamente 800 espécies de 20 gêneros de 12 famílias representando cinco ordens (Caryophyllales, Ericales, Lamiales, Oxalidales e Poales). Nesses casos, são observadas adaptações funcionais significativas na morfologia e fisiologia das espécies (JUNIPER; ROBINS; JOEL, 1989; ALBERT; WILLIAMS; CHASE, 1992; MÜLLER et al., 2004; MCPHERSON, 2010; KRÓL et al., 2011; GIVNISH, 2015; ELLISON; ADAMEC, 2018). Segundo o mecanismo de captura da presa, as armadilhas podem ser classificadas em ativas ou passivas, *i.e.*, se realizam ou não movimento para capturar a presa (BAUER et al., 2015). Morfologicamente, há diferentes tipos, como folha adesiva, apanha-moscas, tipo jarra ou em um nível mais complexo as armadilhas dos gêneros *Genlisea* e *Utricularia* (JUNIPER; ROBINS; JOEL, 1989; MCPHERSON, 2010; RAVEE et al., 2018).

Família Lentibulariaceae

A família Lentibulariaceae (Lamiales), no clado das Asterídeas (APG IV, 2016; LI et al. 2020) é a maior dentre as famílias de plantas carnívoras (FLEISCHMANN, 2012; FLEISCHMANN; STAATSSAMMLUNG; MENZINGER, 2015), ocorrendo em todo o planeta exceto na Antártica, regiões muito áridas, regiões polares e algumas

ilhas oceânicas (TAYLOR, 1989; MCPHERSON, 2010). A família agrupa cerca de 350 espécies distribuídas nos gêneros *Pinguicula*, *Genlisea* e *Utricularia* (FLEISCHMANN, 2012; FLEISCHMANN; STAATSSAMMLUNG; MENZINGER, 2015). O Brasil é o centro de diversidade dos gêneros *Genlisea* e *Utricularia* (MCPHERSON, 2010), onde é possível encontrar 86 espécies desses dois gêneros, das quais 30 espécies são endêmicas (BFG, 2015; FLORA DO BRASIL 2020, em construção; MIRANDA et al., 2015).

O gênero *Pinguicula* é o grupo irmão do clado constituído por *Utricularia* e *Genlisea* (JOBSON; ALBERT, 2002; MÜLLER et al., 2000, 2004, 2006). Cada gênero da família apresenta diversas especializações morfológicas, com adaptações à captura e digestão de artrópodes e outros pequenos organismos (JUNIPER et al., 1989). Essas adaptações estão também na forma de tricomas glandulares que segregam mucilagem e enzimas digestivas (METCALFE; CHALK, 1972; KRÓL et al., 2011) (Figura 1). *Pinguicula* tem características pleisomórficas, como raízes, e folhas adesivas como mecanismo de captura de presas, enquanto os gêneros *Genlisea* e *Utricularia* são desprovidas de raízes e apresentam armadilhas complexas (JUNIPER; ROBINS; JOEL, 1989; TAYLOR, 1989; MÜLLER et al., 2006). Além disso, a reconstrução da história evolutiva de caracteres morfológicos na família indica que as armadilhas de *Genlisea* e *Utricularia* evoluíram pelo dobramento das folhas homólogas às folhas adesivas de *Pinguicula* do ancestral do clado *Genlisea-Utricularia* (JUNIPER; ROBINS; JOEL, 1989; TAYLOR, 1989; MÜLLER et al., 2004; WHITEWOODS et al., 2017, 2020).

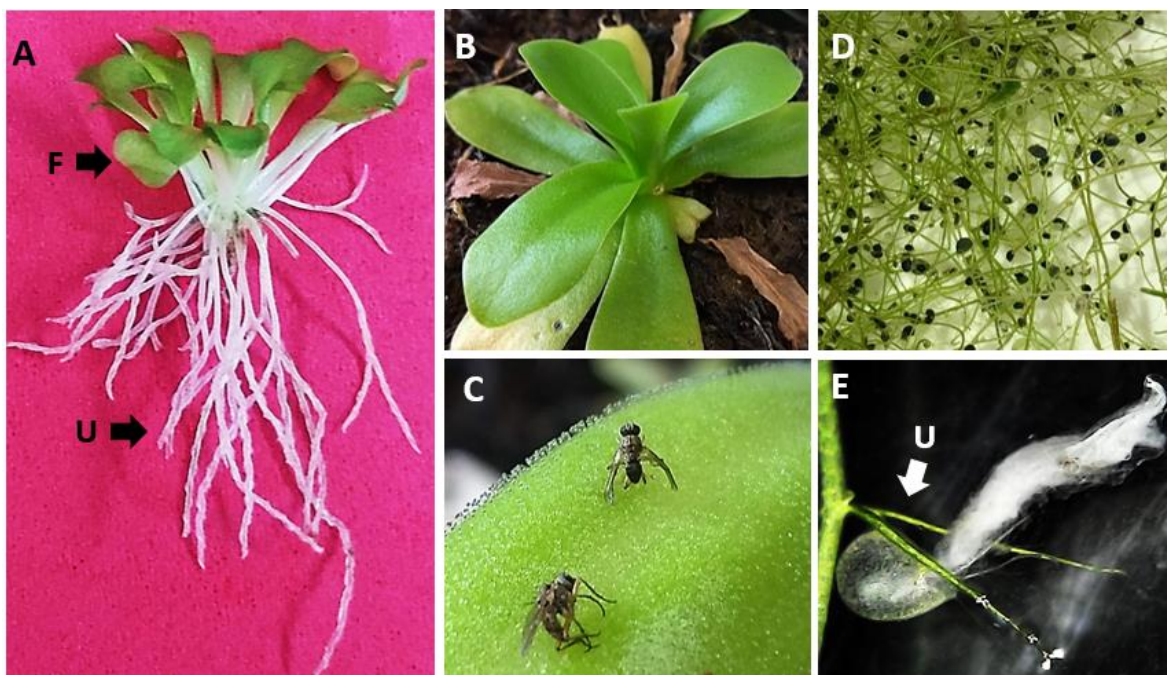


Figura 1. Representantes da família Lentibulariaceae. A- *Genlisea violacea*, folhas fotossintetizantes (F) e utriculíferas (U). B- *Pinguicula gigantea*. C- Folha pegajosa de *Pinguicula gigantea* com presas. D- *Utricularia gibba* (notar utrículos enegrescidos). E- Detalhe do utrículo (U) de *Utricularia gibba* com presa – larva de inseto. (Créditos: Equipe Laboratório Sistemática Vegetal, LSV. UNESP-Jaboticabal.)

O gênero *Pinguicula* (Figura 1B,1C) é composto por aproximadamente 95 espécies (STEIGER, 1998; LEGENDRE, 2000; LUSTOFIN et al., 2020), encontra-se distribuído na Europa, Ásia, América do Norte, América Central, inclusive no Caribe e nos Andes (CASPER, 1966; FLEISCHMANN; ROCCIA, 2018), sendo o centro de diversidade a região Centro-Americana e o Caribe (CASPER; STIMPER, 2009). As plantas de *Pinguicula* apresentam raízes adventícias fibrosas (LEGENDRE, 2000) e geralmente pouco desenvolvidas (ADLASSNIG et al., 2005). As folhas em roseta capturam e digerem insetos graças à ação de tricomas glandulares (Figura 1C), encontrados na parte adaxial das folhas para a maioria das espécies (CIESLAK et al., 2005). As glândulas que produzem mucilagem que auxiliam a captura de presas apenas são encontradas no gênero *Pinguicula*, enquanto que as glândulas sésseis, secretoras de enzimas digestivas, são uma sinapomorfia da família (LEGENDRE, 2000; CIESLAK et al, 2005).

O gênero *Utricularia* (Figura 1D, 1E) agrupa aproximadamente 35% de todas as espécies de plantas carnívoras, mas ainda a biologia do gênero é pouco compreendida (GUISANDE, 2007). A maioria das espécies é encontrada em regiões tropicais e subtropicais da Venezuela, Guianas e Brasil e apresentam hábitos diversos, como terrícolas, aquáticas livres, aquáticas fixadas, reofíticas, epifíticas e litofíticas (TAYLOR, 1989; JOBSON et al., 2018; SILVA et al., 2018a).

Assim como em *Genlisea* (Figura 1A), as plantas de *Utricularia* apresentam dois tipos folhares, as folhas fotossintetizantes e as utriculíferas, sendo as armadilhas do gênero formadas por folhas modificadas em forma de vesícula especializadas em capturar a presa por sucção (Figura 1E). As armadilhas, apresentam alta diversidade morfológica e têm sido empregadas em estudos para sistemática do grupo (JUNIPER; ROBINS; JOEL, 1989; TAYLOR, 1989, POPPINGA et al., 2016). Além disso, as plantas de gênero *Utricularia* não possuem raiz, nem radícula no estado embrionário (TAYLOR, 1989; PŁACHNO; ŚWIĄTEK, 2010).

Genlisea e *Utricularia* apresentam extrema variação no tamanho genômico e altas taxas de substituição nucleotídica nos seus DNA nucleares e plastidiais (JOBSON et al., 2004; MÜLLER et al., 2004, 2006; GREILHUBER et al., 2006; MÜLLER; BORSCH, 2005). Enquanto, o tamanho dos genomas das espécies do gênero *Genlisea* variam entre os ~63 e ~1.700 Mpb (GREILHUBER et al., 2006; VELEBA et al., 2014; FLEISCHMANN et al., 2014). Entretanto, os menores genomas foram encontrados em *G. aurea* e *G. tuberosa* com aproximadamente ~63 Mpb e ~61 Mpb, respectivamente, sendo o último o menor genoma de plantas conhecido (ALBERT et al., 2010; LEUSHKIN et al., 2013; FLEISCHMANN et al., 2014). No gênero *Utricularia* também foi descrito o genoma reduzido de *Utricularia gibba*, com ~80-101 Mpb (GREILHUBER et al., 2006; IBARRA-LACLETTE et al., 2011, 2013; LAN et al., 2017).

O gênero *Genlisea* A.St.-Hil.

O gênero *Genlisea* é composto por 31 espécies (FLEISCHMANN, 2018; SILVA et al., 2020) divididas em dois subgêneros, *Tayloria* e *Genlisea*. O subgênero *Tayloria* é endêmico do Brasil, enquanto o subgênero *Genlisea* se distribui nas Américas do Sul e Central, África e Madagascar (FLEISCHMANN, 2012). Os subgêneros são diferenciados pelo tipo de deiscência dos frutos, sendo longitudinal em *Tayloria* e circuncisa em *Genlisea* (FROMM-TRINTA, 1979; TAYLOR, 1989; FISCHER et al., 2000), e pela morfologia floral, com flores lilases, lavandas ou brancas, com cálcio geralmente pequeno e divergente a partir do lábio inferior e paralelo ao pedicelo em *Tayloria* e flores amarelas, lilás ou brancas e calcar paralelo ao lábio inferior da corola em *Genlisea* (FLEISCHMANN et al., 2010, 2011).

As espécies do gênero *Genlisea* são ervas rosetadas sem raízes, anuais ou perenes que produzem folhas espatuladas fotossintetizantes epiterrestres e folhas utriculíferas subterrâneas como armadilhas, essas últimas compostas por um pecíolo basal e uma vesícula seguida por um pecíolo bifurcado dicotomicamente no ápice em dois braços fistulados helicoidais (Figura 1A) (FROMM-TRINTA, 1979; JUNIPER; ROBINS; JOEL, 1989; REUT, 1993; BARTHLOTT et al., 1998; PŁACHNO; KOZIERADZKA-KISZKURNO; SWIATEK, 2007; FLEISCHMANN, 2014). Observações em campo e em condições de laboratório sugerem que existe uma variedade de presas incluindo bactérias, protozoários, algas e microfauna, como nematoides, rotíferos, anelídeos e pequenos artrópodes (BARTHLOTT et al., 1998; STUDNICKA, 2003; PŁACHNO; FABER; JANKUN, 2005; PŁACHNO et al., 2006; CARAVIERI et al., 2014; FLEISCHMANN, 2012; KOLLER-PEROUTKA et al 2014).

A espécie objeto do estudo: *Genlisea violacea* A.St.-Hil.

Genlisea violacea (Figura 2) é uma espécie endêmica do Brasil, ocorrendo nos Estados de São Paulo e Minas Gerais (FLEISHMANN et al, 2011; BFG, 2015; FLORA

DO BRASIL 2020, em construção; MIRANDA et al., 2015) e apresenta uma alta variação na morfologia floral (FLEISCHMANN et al, 2010, 2011). Encontra-se em elevações entre 680-1950 m, em locais sazonalmente úmidos como solos quartizíticos arenosos, em camadas de matéria orgânicas sobre rochas, *Sphagnum*, musgos ou paredões úmidos (FLEISCHMANN, 2012).

As plantas de *Genlisea violacea* são anuais de tamanho pequeno a médio com inflorescências que podem atingir até 25 cm e com até seis flores (FLEISCHMANN, 2012). As inflorescências são racemosas com flores zigomorfas e corolas bilabiadas, compostas por cinco pétalas fundidas, duas no lábio superior e três no inferior, e um cálcio (FROMM-TRINTA 1979, 1981; FLEISCHMANN et al. 2011; FLEISCHMANN, 2012). A corola é geralmente violeta ou lilás, raramente branca; folhas espatuladas de 3-12 mm de comprimento e 1,5-7 mm de largura, rizófilos com pedúnculo curto, seguido pela vesícula e os braços da armadilha de 0,2-0,5 largura e 30 mm de comprimento (FLEISCHMANN, 2012). *G. violacea* é alógama e autocompatível, tendo como polinizadores abelhas dos gêneros *Lasioglossum* e *Ceratina*, sendo que moscas da família Syrphidae também podem ser polinizadores ocasionais (ARANGUREN et al., 2018). *G. violacea* é altamente heterogênea em tamanho da planta, tricomas, e tamanho e cor de corola (FLEISCHMANN, 2012) (Figura 2). Além disso, Greilhuber et al. (2006) reportaram o genoma de *Genlisea violacea* com um tamanho de 1.005 Mpb e, por sua vez, FLEISHMANN et al. (2014) reportaram 1.609 Mbp. Devido às variações morfológicas *G. violacea* tem sido dividida em diferentes espécies (FLEISCHMANN et al., 2011; FLEISCHMANN, 2012).

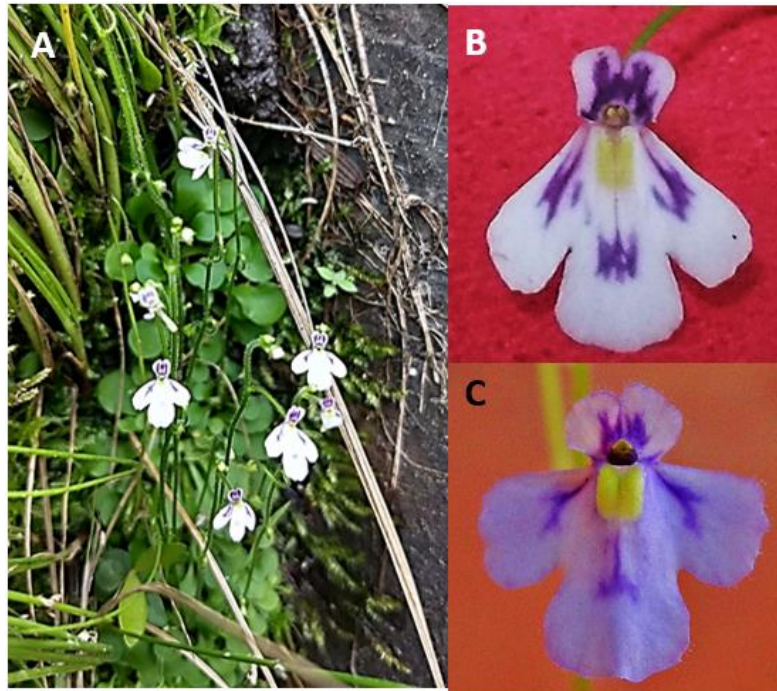


Figura 2. *Genlisea violacea*. A- Planta com flor, B- Morfotipo flor branca, C- Morfotipo flor roxa. (Créditos: Equipe Laboratório Sistemática Vegetal, LSV. UNESP-Jaboticabal.)

Proteômica e sequenciamento *de novo* de peptídeos

A proteômica analisa de forma sistemática o proteoma, o qual é o complemento expresso de um genoma ou todas as proteínas codificadas por um genoma (WILKINS et al., 1995; PANDEY; MANN, 2000). Assim, a proteômica permite o estudo em larga escala do proteoma, em especial a expressão, função, estrutura e mudanças em diferentes condições (MALLICK; KUSTER, 2010). Desta forma, é possível realizar mensurações qualitativas e quantitativas de um grande número de proteínas que podem afetar a bioquímica celular, gerando informações precisas do estado celular ou mudanças do sistema durante diferentes fases do desenvolvimento ou em respostas a mudanças ambientais dos organismos. Por essas razões, a proteômica é uma ferramenta importante para a compreensão de sistemas biológicos dinâmicos e complexos, podendo trazer informações que não seriam preditas por

outras técnicas (CHEN; HARMON, 2006). Como exemplo, os estudos de expressão gênica por análise transcriptômica, que podem trazer informações importantes sobre a atividade gênica, porém é importante ressaltar que a abundância de mRNAs nem sempre está associada com a quantidade de proteínas expressas (GYGI et al., 1999, IDEKER; GALITSKI; HOOD, 2001; DE SOUSA ABREU et al., 2009). Isso pode ser explicado uma vez que um gene pode produzir diferentes proteínas por *splicing* alternativo, processamento de mRNA, proteólises e modificações pós-traducionais (PANDEY; MANN, 2000; SERVICE, 2001; CHEN et al, 2012; ULE; BLENCOWE, 2019; SONG et al., 2019).

As abordagens comumente usadas na identificação de proteínas precisam de uma base de dados disponíveis, dificultando a identificação de proteínas de organismos sem genomas publicados. Para contornar essa situação, têm sido desenvolvidas novas metodologias e *softwares* capazes de inferir a sequência de aminoácidos a partir dos espectros de massas adquiridos (MA et al., 2003, MA, 2015). Assim sendo, o sequenciamento *de novo* tem sido utilizado principalmente para sequenciar peptídeos endógenos (ALHAIDER et al, 2013; VIALA et al., 2014), análises proteômicas de organismos sem genomas conhecidos ou com genomas incompletos (HATANO; HAMADA, 2008; CATUSSE et al., 2008; NOVO et al., 2015) e em casos que existe um genoma de referência do organismo, mas se precisa aumentar a sensibilidade e acurácia dos resultados (MA, 2015).

Proteômica de plantas carnívoras

A disponibilidade de sequências genômicas tem contribuído grandemente para a descoberta de enzimas e para melhorar o entendimento dos mecanismos de carnivorismo e evolução em diferentes famílias de plantas carnívoras (RAVEE et al., 2018). Até o momento, há poucas espécies de plantas carnívoras com seus genomas disponíveis, entre elas *Cephalotus follicularis* (FUKUSHIMA et al., 2017), *Drosera capensis* (BUTTS et al., 2016), *Genlisea aurea* (LEUSHKIN et al., 2013), *G. hispidula* e *G. nigrocaulis* (Vu et al., 2015) e *Utricularia gibba* (IBARRA-LACLETTE et al., 2013). Recentemente, foi publicado o genoma de *Utricularia reniformis* que apresenta

tamanho de genoma de 304 MB e número cromossômico $2n=40$, e quando comparado com o genoma de *U.gibba*, foi mostrado que o genoma de *U. reniformis* é altamente repetitivo (aproximadamente 60% do genoma), resultado de rearranjos e fraccionamentos após duplicações genômicas e proliferação de LTR-retrotransposons. Ademais, o genoma de *U. reniformis* exibe padrões únicos de genes associados à carnivoría, desenvolvimento e adaptação ao ambiente terrestre (SILVA et al., 2020).

Poucos estudos com abordagem proteômica têm sido realizados para espécies de plantas carnívoras. Entre eles, estudos do fluido digestivo das armadilhas de espécies de *Nepenthes* detalharam que as proteínas mais abundantes no fluido são proteases, nucleases, peroxidases, quitinases, fosfatases e glucanases (HATANO; HAMADA, 2008; 2012; LEE et al., 2016). Outro exemplo, da abordagem proteômica, foi descrito por Biteau et al. (2013) que, baseados nos perfis de expressão de proteínas do jarro de diferentes espécies de *Nepenthes*, desenvolveram um método para a distinção de espécies. Além disso, outros estudos baseados em dados transcriptômicos têm servido como referência em análises proteômicas de plantas carnívoras, como em *Dionaea* (SCHULZE et al., 2012) e *Nepenthes* (ZAKARIA et al., 2019).

Estudos ômicos na família Lentibulariaceae

Poucos trabalhos identificando os mecanismos de digestão ou a produção de enzimas hidrolíticas têm sido desenvolvidos para a família Lentibulariaceae (IBARRA-LACLETTE et al., 2011; CAO et al., 2015; WHEELER; CARSTENS, 2018), sendo que os dados disponíveis de sequências de proteínas para a família são resultados de estudos genômicos, transcriptômicos, metagenômicos e testes enzimáticos. Desta forma, empregando substratos de fosfatase, foi possível detectar a atividade específica da enzima, produzidas em diferentes locais dos três gêneros: pelas glândulas quadrífidas em *Utricularia*, nas células terminais de tricomas das folhas

utriculíferas, pescoço, braços em *Genlisea* e nas glândulas sésseis das folhas e inflorescências em *Pinguicula* (PŁACHNO et al., 2006). Além desses, diferentes estudos com enfoque transcritômico têm sido desenvolvidos para espécies da família. Bárta et al. (2015), comparando o transcrito de *Utricularia vulgaris* com dois transcritos de *Utricularia gibba*, observaram uma forte correspondência na presença ou ausência de genes associados às raízes entre as duas espécies, sugerindo que a perda de alguns genes específicos das raízes ocorreu na linhagem ancestral do clado *Genlisea-Utricularia*. Por sua vez, Cao et al. (2015) comparando o transcrito de folhas e armadilhas de *Genlisea nigrocaulis* e *G. hispidula* constataram que as armadilhas apresentaram transcritos altamente expressos de NADH oxidases e ácido fosfatases, importantes para a digestão das presas, indicando que a carnivoría provê fósforo inorgânico e diferentes formas de compostos nitrogenados para as plantas. Além disso, em estudo do metagenoma dos utrículos de *Utricularia gibba*, também se destaca a importância do microbioma das armadilhas com uma comunidade com alta diversidade bacteriana (ALCARAZ et al., 2016). Além desse estudos, para a montagem do genoma de *Genlisea aurea* por Leushkin et al. (2013) foram empregados sequências do transcrito de *Utricularia intermedia* e *Pinguicula vulgaris* para melhorar a anotação do genoma o qual apresentou um número reduzido de genes, regiões intergênicas e *introns* curtos, sendo que no total foram identificadas aproximadamente 18.000 sequências de proteínas.

Igualmente têm sido realizados diferentes estudos moleculares plastidiais para espécies da família, como os genomas cloroplastidiais de *Utricularia gibba* (IBARRA-LACLETTE et al., 2013), *Genlisea margaretae*, *Pinguicula ehlersiae*, *U. macrorhiza*, (WICKE et al., 2013), *U. foliosa* (SILVA et al., 2016a), *G. aurea*, *G. filiformis*, *G. pygmaea*, *G. repens*, *G. tuberosa* e *G. violacea* (SILVA et al., 2018b) e para *U. reniformis* o genoma e transcrito cloroplastidial (SILVA et al., 2016b) e mitocondrial (SILVA et al., 2017). Além disso, a comparação dos genomas cloroplastidiais de três morfotipos de *U. amethystina* (SILVA et al., 2019). Estudos como estes têm contribuído na identificação de proteínas associadas à carnivoría e melhorado a compreensão dos processos moleculares de espécies da família Lentibulariaceae.

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CAPÍTULO 2 - Label-free shotgun proteomics reveals different functions and protein profiles in dimorphic leaves of two morphotypes of the carnivorous plant *Genlisea violacea* A.St.-Hil. (Lentibulariaceae)¹

Highlights:

- Characterization of photosynthetic leaves and traps proteomes.
- Functional analysis of shared proteins between leaves and traps reveals basic cellular functions.
- Functional analysis and quantification indicated distinct leaves and traps functions.
- Proteome analysis reveals single amino acid substitutions between close related species and between *G. violacea* morphotypes.
- New insights into the mechanisms related to carnivory in *Genlisea*.

¹ Este capítulo corresponde ao manuscrito a ser submetido à revista *Journal of Proteomics*.

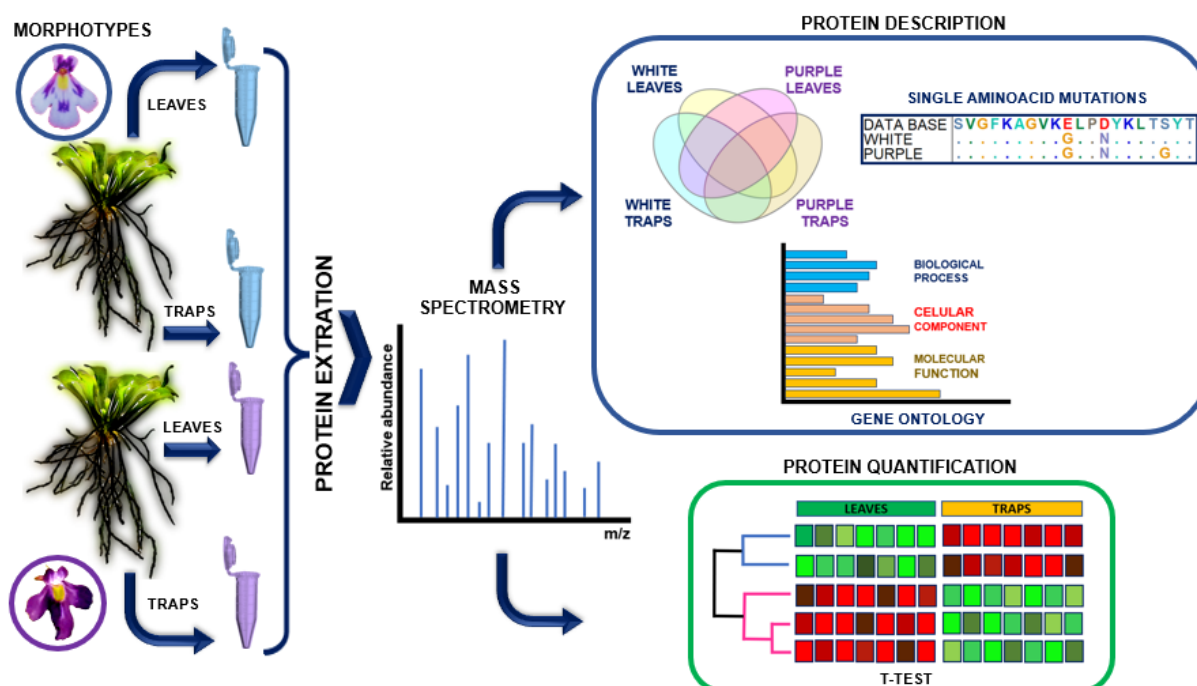
Abstract

The carnivorous plants of *Genlisea* genus devoid roots and display dimorphic leaf types: the epiterrestrial leaves, with photosynthetic function, and the utriculiferous subterrestrial leaves, which act to trap preys. To identify the proteins and to infer molecular processes in which they are involved, we performed a proteomic analysis of the two foliar types of two *Genlisea violacea* morphotypes, white- and purple-flowered. The proteins from photosynthetic leaves and leaf-modified traps were identified by in-gel tryptic digestion, *de novo* peptide sequencing, and homology searches against *Genlisea aurea* proteome. Also, a label-free quantification of shared proteins was conducted and protein biological and functional identification were assigned by Gene Ontology analysis. A total of 482 exclusive proteins were identified for photosynthetic leaves and 14 for traps, with 65 proteins shared by both organs. Functional analysis and quantification indicated that photosynthetic leaves proteins are mainly involved in photosynthesis and responses to stimuli, while trap proteins are involved in respiration, transport and digestion and the photosynthetic proteins leaves mainly in photosynthesis and responses to stimuli. The identification of these proteins can shed a light on the functional differences between photosynthetic-active leaves and traps at the proteome level.

Significance

Here we present the first proteomic analysis for photosynthetic leaves and traps of the rootless carnivorous plant *Genlisea violacea*. The proteomic analysis revealed the main processes occurring in each leaf type and provide relevant insights into the molecular processes related to carnivory in the genera. Also, the single amino acid substitutions in primary proteins sequences reveals intra and interspecific variation in the two morphotypes studied. Also, these proteins can provide targets for exploring the phylogenetic relations in *Genlisea*.

Graphical Abstract



Keywords: Carnivorous plants, *Genlisea*, *de novo* sequencing, proteome, LC-MS/MS

1. Introduction

To acquire nutrients the carnivorous plants present special adaptations to attract, capture and digest preys [1–3]. In the evolutionary history of angiosperms, carnivory syndrome has arisen in several times and carnivory is currently recognized in more than 10 families distributed in five orders [4,5]. The Lentibulariaceae (Lamiales) [6] is the largest among carnivorous plants families, grouping about 350 species distributed in three genera: *Pinguicula*, *Genlisea* and *Utricularia* [7,8]. The genus *Genlisea* consists of 31 species [7,9] including *Genlisea violacea*, which is a endemic species to Brazil and found in São Paulo and Minas Gerais states [10–13]. *G. violacea* is the type species of the subgenus *Tayloria* and exhibit a high variation in floral habit and morphology [7].

The species of *Genlisea* are rootless rosetted herbs that produce two leaf types, the photosynthesizing epiterrestrial leaves and the underground utriculiferous leaves. The latter are corkscrew-shaped traps formed by a basal petiole attached to a vesicle followed by a dichotomously bifurcated tubular neck at the apex in two helical fistulated arms [1,14–16]. Field and laboratory observations suggest that *Genlisea* has a variety of prey including bacteria, protozoa, algae and microfauna, such as nematodes, rotifers, annelids and small arthropods [15,17–20]. Inside the traps, trichomes allow the prey capture and produce prey digesting enzymes [16]. For example, in *Genlisea* phosphatase activity has been detected in the terminal cells of trichomes found inside the traps [19]. Nevertheless, knowledge about the production of hydrolytic enzymes and digestion mechanisms in the within Lentibulariaceae genera is scarce.

The comparative of the functional representation of Gene Ontology terms (GO) in carnivorous and non-carnivorous plants showed that in *Genlisea aurea* has few signals of genomic overrepresentation, including phospholipase activity [5]. However, the authors highlighted that the study was limited by the lack of available genomic sequence data for carnivorous plants, as well as the lack of thorough Gene Ontology annotation of plant taxa in general. So far few carnivorous plant species have their genomes available, including *Cephalotus follicularis* [21], *Drosera capensis* [22], *Genlisea hispidula*, *G. nigrocaulis* [23], *Utricularia gibba* [24], *Utricularia reniformis* [25] and *Genlisea aurea*, which shows one of the smallest genomes in angiosperms with ~60 megabases (Mb) [26]. Nevertheless, the availability of genomic data has contributed to the discovery of proteins and to understand mechanisms and evolution in different carnivorous plant families [27].

Experimental proteomic approaches have provided significant insights into carnivorous plant enzymes. In *Nepenthes* traps has been reported different proteases and defense related proteins [28–30]. In addition, studies based on transcriptomic data have served as a reference in proteomic analyses of carnivorous plants such as *Dionaea* [31]. Moreover, the transcriptome analysis

of *Genlisea nigrocaulis* and *G. hispidula* traps and leaves suggested that transcription factors are involved in transport and cellular metabolism of nitrogen and some hydrolases are highly up-regulated in traps when compared with photosynthetic leaves [32]. Also, in the sister genus *Utricularia*, the transcriptomic analysis showed the similarity between transcripts from vegetative shoots and traps, but traps presented gene overexpression of hydrolytic enzymes, and genes involved in respiration and phosphate uptake [33].

Among proteomics studies, the most common approaches used to identify proteins with tandem mass spectrometry data (MS/MS) depends on available database to compare with experimental data [34]. However, in *de novo* peptide sequencing, the identity of the peptides is inferred directly from the acquired mass spectra, allowing the identification of proteins without the existence of a reference genome [35]. Using this approach, Hatano and Hamada confirmed the presence of xylosidase, glucanase and chitinase in the digestive liquid of *Nepenthes* traps [29].

However, the protein and peptide components of different tissues are rarely discussed in Lentibulariaceae family. Aiming to mitigate this lacuna of knowledge, here we present, based on a large-scale proteomics approach, the proteomes of photosynthetic leaves and traps of two morphotypes of *Genlisea violacea* using mass spectrometry and *de novo* peptide sequencing coupled to label-free quantification methods, using as reference the available proteome of the closed related *Genlisea aurea* [26]. This study represents the first overview of leaf and trap proteomes describing the molecular function, biological process or localization in cellular components of the exclusive-organ and shared proteins by GO classification. The results revealed exclusive leaf proteins and exclusive trap proteins and proteins shared by the two foliar types and proteins up-regulated in both leaf types. These findings will help to enhance our understanding of the molecular basis of protein functions in carnivorous plants.

2. Material and Methods

2.1 Plant material and protein extraction

Blooming *Genlisea violacea* plants were collected in the Municipality of Capitólio, Minas Gerais State, Brazil. Adult plants of the two morphotypes, white- and purple-flowered, with uniform shape and size, were collected and identified. Vouchers were deposited in Herbarium Jaboti (Universidade Estadual Paulista, campus Jaboticabal). The photosynthetic leaves and utriculiferous leaves (hereinafter traps) from different plants, from the same growing spot were harvested and mixed until get 1 g of each leaf type for each morphotype. All the samples were frozen at -80 °C until protein extraction. Each treatment consisted of three biological replicates for each morphotype and specific leaf type, totalizing six biological replicates per morphotype and identified as PL (purple-flowered morphotype leaves), PT (purple-flowered morphotype traps), WL (white-flowered morphotype leaves), and WT (white-flowered morphotype traps).

For protein extraction, 1 g of each sample tissue was ground with liquid nitrogen and suspended sequentially with 10 mL extraction buffer (125 mM Tris-HCl (pH 6.8), Glycerol 20%, 1% SDS, 0.1% DTT) with slight stirring for 15 min at 4°C and then centrifuged for 5 min at 3200 g and 4 °C. The supernatant was transferred to 50 ml conical sterile tube and five volumes of cold acetone (99.5%) were added. The samples were stored at -30°C for 16 h to precipitate the proteins. After centrifugation for 5 min at 3200 g and 4 °C, the pellet was washed with cold acetone and resuspended in 40 µL of extraction buffer. Total protein concentration was determined via Bradford assay [36].

2.2 Peptide in-gel digestion and MS/MS acquisition

Equal amounts of total protein (50 µg) were separated with 12% SDS-PAGE gels [37]. The in-gel digestion protocol followed Shevchenko et al. (2007) [38]. The excised gel slices containing the proteins were cut into cubes,

transferred to microtubes and washed with 100 mM ammonium bicarbonate (AmBic): acetonitrile (ACN) solution (1:1, v/v) and dehydrated with ACN (100%), followed by reduction of disulfide bonds with 10 mM dithiothreitol (DTT) solution in 100 mM AmBic and incubated at 56°C for 30 min. Protein cysteine residues were carbamidomethylated by incubation in a 50 mM iodoacetamide (IAA) solution in 100 mM AmBic for 30 minutes at room temperature in darkness.

The proteins were digested with sequencing grade modified trypsin (Promega, Madison, WI, USA) at a ratio of 1:10 (trypsin:protein) at 37°C overnight. The tryptic peptides were recovered from the gel matrix using 5% formic acid: acetonitrile (1:2, v/v) with agitation for 60 min, followed by one cycle of pure acetonitrile for 30 min. The extracted peptides were dried in a vacuum and resuspended in 200 µL of 0.1% formic acid and peptides purified with Costar® Spin-X® Centrifuge Tube Filters (CORNING) and dried in a vacuum centrifuge.

2.3 UPLC-MS/MS analysis

For quantification analyses, three technical replicates of each biological sample were performed, totalizing nine runs for each leaf type of each morphotype. In order to increase the coverage and the total number of identified proteins by *de novo* sequencing analyses, the biological replicates of each leaf type were mixed and submitted to HPLC-MS five times. The digested peptides were resuspended in 0.1% formic acid in H₂O and subjected to liquid chromatography (LC)-MS/MS analysis on a chromatographic system EASY-nLC1000 (Thermo Fisher Scientific) using a Acclaim™ PepMap™ 100 C18 HPLC Columns (75 µm x 15 cm) (Thermo Fisher Scientific) on a constant flow rate of 400 nL/min for 65min. The solution A consisted of 0.1% formic acid in H₂O, and solvent B was 0.1% formic acid in acetonitrile. The separation gradient was adjusted starting with 5% to 70%, of solution B. Ionization and injection of the peptides into the mass spectrometer (Q-Exactive) was carried out through nano-electrospray (nESI) using 3.5 kV applied directly into the injection needle. Mass

spectrometry was used with the data-dependent acquisition method (DDA) for the twenty most abundant peptide ions. Full scans (MS1) and data-dependent scans (MS2) were acquired with a resolution equal to 70,000 for MS1 and 17,500 FWHM (full width at half maximum) for MS2. Fragment spectra were acquired using high-energy collision dissociation (HCD). An isolation mass window of 4.0 m/z was used for the precursor ion selection, and normalized collision energy of 30% was used for fragmentation with dynamic exclusion length of five seconds.

2.4 *De novo* sequencing, protein identification and GO analyses

For *de novo* sequencing the raw MS/MS files, of the five technical replicates of the mixed biological replicates and the files generated for the quantitative analyses, were analyzed with PEAKS Studio (version X+; Bioinformatics Solutions Inc., Waterloo) [34], which provides the peptide sequence without comparing to a protein sequence database. The deduced amino acid sequences with local alignment confidence (ALC) > 80% were used for sequence homology search. For the identification and removal of common MS contaminants were used the 41,502 entries of The common Repository of Adventitious Proteins (cRAP-03/04/2019) - <http://www.thegpm.org/crap/index.html>- and protein identification was performed through stringent database searches against the 17,735 entries of Uniprot *Genlisea aurea* proteome (UP000015453), with PEAKS Database algorithm (PEAKS DB) [39] and setting the parameters as follows: Enzyme, trypsin; Instrument type, Orbitrap; Parent Mass ion Tolerance, 10.0 ppm; Fragment Mass Ion Tolerance, 0.5 Da; Fixed modifications, Carbamidomethyl (C); Variable modifications: Oxidation(M); Max Missed Cleavages, 2. All the proteins with an FDR (Peptide-Spectrum Matches, Peptide Sequences, Protein) less than 1%, were retained for further downstream analysis, including single peptide substitutions detected by the SPIDER algorithm [40] embedded in the PEAKS software. The Single amino acid substitutions with 10% ion intensity and with more than two spectrum count in proteins identified in leaves of both morphotypes were selected for analysis, including validation, using as reference the chloroplast genome of *Genlisea violacea* [41]. In order to increase the number of identified

proteins, *de novo* peptides that were not used to identify proteins within the *Genlisea aurea* database, were used to perform a new search against the Viridiplantae database UniREF100 [42]. This database combines identical sequences from different organism into a single UniRef, totalizing 7,823,185 entries. The search was done with the same parameters of the first round. Gene Ontology analyses were obtained from the predicted gene annotations, available at UNIPROT website tool Retrieve/ID mapping (<https://www.uniprot.org/uploadlists/>).

2.5 Protein quantification and statistical analyses

The protein quantification was performed by sets of leaf types, totalizing 5 sets: (1) leaves and traps of purple-florewed morphotype, (2) leaves and traps of white-florewed morphotype, (3) leaves of purple- and white florewed morphotypes, (4) traps of purple- and white florewed morphotypes, and finally, (5) leaves of the two morphotypes and traps of the two morphotypes. For the label-free quantification (LFQ), the raw files were processed using the MaxQuant version 1.6.5.0 [43] and the MS/MS spectra were searched using the Andromeda search engine [44] against the Uniprot *Genlisea aurea* proteome (UP000015453). The maximal allowed mass tolerance was set to 20 ppm for precursor and 0.5 Da for fragment ions. Enzyme specificity was set to trypsin with a maximum of two missed cleavages. Carbamidomethylation of cysteine was set as a fixed modification, and oxidation of methionine was selected as variable modification. The minimum peptide length was set to 7 amino acids. The false discovery rates (FDRs) of peptide and protein were set to 0.01. Label-free quantification was performed using the normalized spectral protein intensity (LFQ intensity) to calculate protein intensity profiles across samples [45]. The protein ratios were calculated from the median of all normalized peptide ratios using unique peptides and peptides assigned to the protein group with the highest number of peptides (razor peptides), with two ratio count for each pairwise comparison step.

Data preparation and statistical analyses were performed using Perseus v.1.6.5.0 [46]. Reverse and contaminant entries were excluded for further analysis. Data obtained from independent experiments from each leaf type were annotated into groups. For the analysis of differentially accumulated proteins, the data were converted into Log2, and groups of proteins with valid values in at least two repetitions in each group were selected. After data imputation of missing values, a two-sample t-test analysis was applied with p-value 0.05 to identify protein for which abundance was significantly changed between pair set of leaves with at least two-fold change.

3. Results

3.1 *De novo* peptide sequencing, protein identification and Single amino acid substitutions

Through *de novo* peptide assembly approach, we collected between 60,213 and 117,114 MS scans and 191,471 and 315,623 MS/MS scans, representing in average 15,932 peptides (Table S1). Once no genome or proteome data are available for *Genlisea violacea*, the suggested peptide sequences were used for sequence homology searches using PEAKS DB and SPIDER algorithms against *Genlisea aurea* proteome and Viridiplantae UniREF100 database with Peptide-Spectrum Matches, Peptide Sequences, Protein Group FDR < 1% (Table S2). After filtration of redundant proteins in groups, 472 proteins were identified in PL, 52 in PT, 382 in WL and 66 in WT (Tables S3-S8), of which 39 were present in the four groups, 246 were shared by the leaves. Among traps, PT and WT show 6 and 8 exclusive proteins respectively, while among leaves, PL and WL show 162 and 74 exclusive proteins (Fig 1) (Supplementary Fig S1).

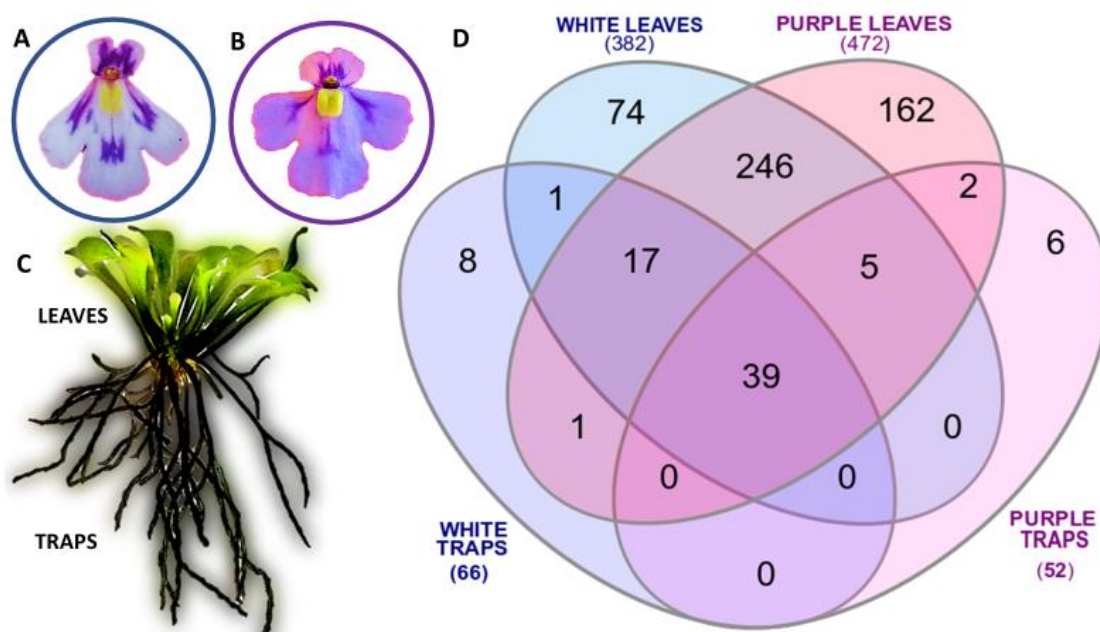


Fig. 1. *Genlisea violacea* white-flowered morphotype (A) and purple-flowered morphotype(B). C- *Genlisea violacea* showing photosynthetic leaves and traps. D- Venn diagram illustrating shared and exclusive proteins in leaves and traps of purple- and white-flowered morphotypes.

The Spider algorithm, embedded in the PEAKS software allowed the identification of 49 PL and 72 WL proteins of *Genlisea violacea* with at least one amino acid substitution when compared with *Genlisea aurea* sequences (Supplementary Table S8 and S9); 37 mutated proteins were shared by the two morphotypes and of these 33 proteins showed at least one identical single amino acid substitutions (Table 1) (Supplementary Fig S2). Of these 33 shared proteins, six have single amino acid substitutions confirmed by the amino acid sequences of *Genlisea violacea* chloroplastic proteins (Supplementary Table S10 and Supplementary Fig S3). Also, two proteins expressed in leaves from purple-flowered morphotype and three of white-flowered morphotype have single amino acid substitutions confirmed. These verified substitutions were identified by the SPIDER algorithm within a range of 2 and 42 spectrum count (Supplementary table S10 and supplementary Fig S4-S5).

Table 1. Shared proteins with single amino acid substitutions in proteins leaves of the two *Genlisea violacea* morphotypes.

Uniprot ID	Protein Description	Mutation			Protein identification				
		Leaf type	From	To	A.A Position	# Spect in mutated peptide	Sample Coverage (%)	# Peptides	# Unique peptides
S8D4F2	AAA domain-containing protein	PL	N	D	120	3	61	56	0
			T	L	387	21			
			T	L	573	2			
		WL	K	L	576	2			
			G	N	122	3	60	51	37
			T	L	387	37			
			E	G	551	3			
S8DYF2	Aminomethyltransferase	PL	A	Q	104	5	20	7	7
		WL	N	D	45	3	22	6	6
S8ENB1	Apocytochrome f	PL	S	T	301	2	25	13	13
		WL	Q	L	240	5	30	14	14
			I	V	252	8			
			D	E	333	3			
S8C8K3	ATPase_AAA_core domain-containing protein	PL	V	T	162	5	49	28	28
			N	D	165	36			
S8D424	ATP synthase subunit alpha, chloroplastic	WL	N	D	165	18	51	21	21
		PL	N	T	211	6	36	28	22
S8E474	Carbonic anhydrase	WL	N	T	211	9	38	26	20
		PL	P	A	70	3	53	16	16
S8E8M6	Chlorophyll a-b binding protein, chloroplastic	WL	P	A	70	27	54	15	15
			N	D	165	2			
		PL	N	D	356	3	16	15	15
			P	A	381	16		15	15
S8DZE1	Chlorophyll a-b binding protein, chloroplastic	WL	N	D	356	3	17	13	13
			P	A	381	28			
		PL	V	L	122	12	29	9	9
		WL	V	L	122	74	37	18	18
A0A2I6QD64	Cytochrome b559 subunit alpha		A	V	222	12			
		PL	A	D	77	4	37	4	2
		WL	A	D	77	13	48	5	2
S8CXJ8	Epimerase domain-containing protein	PL	F	V	132	2	21	7	7
		WL	F	V	132	7	21	8	8
S8CAG8	Fructose-bisphosphate aldolase	PL	D	E	41	12	47	22	8
		WL	D	E	41	30	41	19	8
			Q	E	236	24			
S8D1U0	Glutamine amidotransferase type-2 domain-	PL	I	V	125	2	12	16	16
		WL	I	V	125	4	11	12	12
S8BX77	Glyceraldehyde-3-phosphate dehydrogenase	PL	K	N	393	7	48	27	19
		WL	V	L	98	36	44	24	17
			K	N	393	21			
S8DEF3	Glyceraldehyde-3-phosphate dehydrogenase	PL	S	A	226	2	46	20	13
		WL	S	N	293	2	42	14	9
			S	T	325	3			
S8C4P9	GST N-terminal domain-containing protein	PL	A	G	168	8	11	3	3
		WL	A	G	168	15	11	3	3
S8CYV8	Histone H4	PL	A	Q	70	5	59	14	14
		WL	A	Q	70	4	63	11	11
S8CQW3	Malate dehydrogenase	PL	V	A	118	2	26	7	7
			A	E	200	5			
		WL	V	A	118	6	15	6	6
			A	E	200	5			
S8EAS0	Mitochondrial benzaldehyde dehydrogenase	PL	R	T	377	4	15	5	5
		WL	R	T	377	3	12	4	4
S8DNI1	NmrA domain-containing protein	PL	A	V	58	2	14	4	4
		WL	A	V	58	17	23	7	7
S8CBV6	Oxygen-evolving enhancer protein 1	PL	A	V	216	17	46	25	25
			S	G	225	21			
		WL	S	A	182	31	51	33	33
			A	V	216	51			
			K	E	273	4			

Uniprot ID	Protein Description	Mutation			Protein identification				
		Leaf type	From	To	A.A Position	# Spect in mutated peptide	Sample Coverage (%)	# Peptides	# Unique peptides
S8CYA5	PAP_fibrillin domain-containing protein	PL	G	A	124	3	4	2	2
		WL	G	A	124	5	4	1	1
S8CA75	Peroxidase_4 domain-containing protein	PL	A	S	51	7	41	8	8
			F	L	56	7			
		WL	A	S	51	16	39	8	8
			F	L	56	16			
S8CVD5	Peroxidase_4 domain-containing protein	PL	P	A	178	5	38	9	9
			S	T	189	5			
			V	A	236	6			
		WL	P	A	178	22	38	8	8
			S	T	189	22			
			V	A	236	15			
S8E173	Phosphoglycerate kinase	PL	E	D	193	9	54	26	21
			T	S	270	2			
			S	T	334	8			
		WL	D	E	113	38	50	24	19
			E	D	193	35			
			T	S	270	2			
			S	T	334	9			
			L	V	347	5			
S8CHM2	Phosphoglycerate kinase	PL	D	N	112	2	36	13	8
		WL	D	N	112	2	24	9	4
S8DAG9	Photosystem II CP47 reaction center protein	PL	Q	E	277	2	28	20	18
		WL	A	V	301	2	30	22	22
			N	D	407	2			
S8E188	PsbP domain-containing protein	PL	I	V	186	3	40	12	12
			A	T	215	4			
		WL	D	E	82	4	47	12	12
			G	T	103	2			
			I	V	105	2			
			A	S	182	18			
			I	V	186	20			
			A	T	215	2			
S8D398	Ribulose biphosphate carboxylase large chain	PL	Q	E	30	2	60	76	22
			G	N	150	11			
			V	L	341	5			
		WL	Q	E	30	7	45	63	9
			Q	E	149	3			
			G	N	150	10			
			V	L	341	8			
S8C9X5	Ribulose biphosphate carboxylase small chain	PL	R	Q	77	35	30	17	17
			R	E	77	4			
		WL	R	Q	77	282	35	25	25
			R	E	77	4			
S8C5P5	Thioredoxin domain-containing protein	PL	T	A	72	15	61	9	9
			N	A	73	15			
		WL	T	A	72	6	64	11	11
			N	A	73	6			
			D	E	92	7			
S8E0E9	Triosephosphate isomerase	PL	E	D	142	11	41	8	8
		WL	E	D	142	8	48	9	9
S8E065	Uncharacterized protein	PL	D	G	195	4	30	8	8
		WL	D	G	195	8	35	11	11
			H	Y	206	3			
S8D065	Uncharacterized protein	PL	E	D	85	7	30	6	6
		WL	E	D	85	2	14	3	3
S8CRY5	Uncharacterized protein	PL	A	T	434	10	26	16	16
		WL	A	T	434	4	21	11	11
S8CS62	Uncharacterized protein	PL	G	A	90	10	25	8	8
		WL	G	A	90	3	25	4	4
S8CIQ9	Uncharacterized protein	PL	V	A	182	2	13	3	3
		WL	V	A	182	4	9	2	2
S8D762	Uncharacterized protein	PL	D	E	80	2	17	2	2
		WL	D	E	80	2	6	1	1

PL: Purple flowered morphotype leaves

WL: White flowered morphotype leaves.

3.2 GO annotation of exclusive and shared leaves and traps proteins

To determine the functional and biological properties of the exclusive and shared proteins an overview was conducting using GO annotation with the Retrieve/ ID mapping tool in UNIPROT. For the analysis were selected one protein of each group representing proteins identified together. After filtration, 547 leaf and 79 trap proteins were selected, of which 65 proteins were shared by both leaf type and present at least in one of the *Genlisea violacea* morphotype (Fig 2A). The proteins were classified in three main domains according to their biological process, cellular component and molecular function (Fig 2). Annotation of all the identified proteins in the GO databases is provided in Supplementary Tables S11-S13.

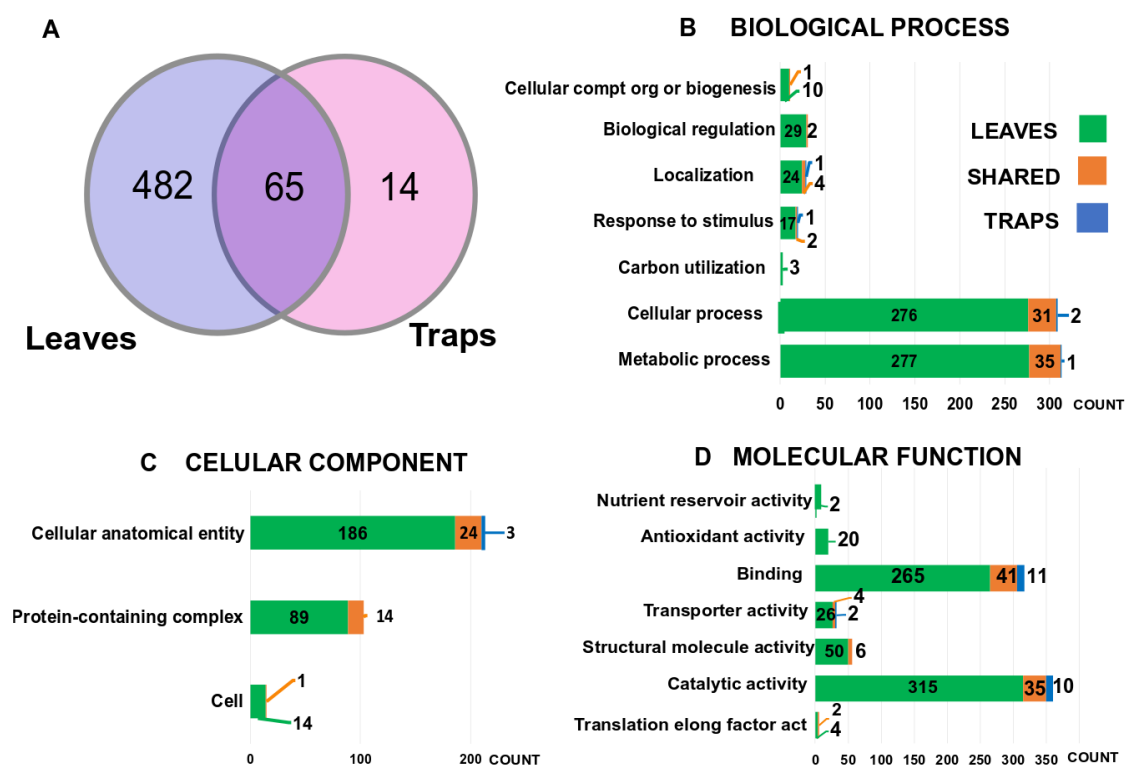


Fig. 2. Gene Ontology (GO) analysis. A- Proteins of leaves and traps used in GO classification. Distribution of leaf, trap and shared proteins into the Gene Ontology (GO) domains for Biological process (B), Cellular component (C) and Molecular function (D) in *Genlisea violacea*.

3.2.1 Biological process domain

In the Biological process domain, the majority of the leaf, trap and shared proteins were associated with cellular process and metabolic process categories (Fig 2B). In the cellular process exclusive leaf proteins were related to protein folding, cellular homeostasis, especially in cell redox homeostasis and cellular glucose homeostasis. Moreover, proteins acting in photosynthesis processes like light harvesting, electron transport, extrinsic component of membrane and oxygen evolving activity were also found. The leaves and traps shared proteins were related to protein folding, glycolytic process and acting in translation process. Also, proteins related to light harvesting in photosynthesis were found in traps and leaves of both morphotypes. In traps, in the cellular process category, were found the proteins Peroxidase (S8CL73) and Plasma membrane ATPase (S8DZJ2) acting in cellular metabolic process.

In the metabolic process category, proteins exclusively found in leaves in this category were related to cellular nitrogen compound metabolic process, ATP synthesis, glycolytic process, chlorophyll and jasmonic acid biosynthetic process, this one represented by the Allene oxide cyclase (S8CLT2). In turn, the shared proteins were related to nitrogen compound metabolic processes like translation, photosynthesis, ATP synthesis and glycolytic process. Also, the shared proteins were found in biosynthetic process category, with proteins of structural constituent of ribosome, elongation factor and in oxidation-reduction process proteins with electron transport in photosystem II activity, antioxidant activity, reductive processes in photorespiration, dehydrogenase in glucose metabolic process, electron transporter in photosynthesis and pentose phosphate pathway. In traps were found the Uncharacterized protein (S8CFM5) with iron ion binding with oxidoreductase activity.

Also, among proteins related with metabolic process where found proteins related to localization and response to stimulus. In leaves, exclusive proteins related to localization of macromolecule with GTP binding activity, protein import into nucleus and proteins with endoplasmic reticulum to Golgi vesicle-mediated

transport like the Wd_repeats_region domain-containing protein (S8CHE8). The shared proteins were related to nucleocytoplasmic transport, protein transport and proteins acting in the proton-transporting ATP synthase complex and transmembrane transporter activity and in traps were found the Plasma membrane ATPase (S8DZJ2).

In the category response to stimulus exclusive leaves proteins were found acting in defense response, represented by the Bet-v-1 domain-containing protein (S8DHI0) and in response to oxidative stress the proteins Peroxidase (S8EFM1, A0A067JCX4), Ascorbate peroxidase (A0A3S8TL14), L-ascorbate peroxidase (B9SGR9, A0A2I4EHK1, A0A067XJ96), AhpC-TSA domain-containing protein (K7MM65), NDK domain-containing protein (M5X8P7), and in response to high light intensity the Uncharacterized protein (S8D856) acting in photosynthetic electron transport in photosystem I. In traps responding to oxidative stress the protein Peroxidase (S8CL73). Also, the shared proteins responding to oxidative stress the proteins Catalase (S8E1K9) and response to stress, acting in photosynthetic electron transport the Photosystem II protein (A0A2I6QD25).

The exclusive leaf proteins in biological regulation category were associated to regulation of biological process with peroxidase activity, translation elongation factor activity, homeostasis cell redox, protein folding and calcium-mediated signaling, this one with the protein Calmodulin (S8CZ12), and in regulation of biological quality, the jasmonic acid biosynthetic process. In this category the shared protein Dihydrolipoyl dehydrogenase (S8CGC3) was related to regulation cell redox homeostasis.

In the Cellular component organization or biogenesis category, leaf proteins were related to actin depolymerization, photosystem II assembly, mitochondrial respiratory chain complex I assembly, ribosome biogenesis and in pollen development the Uncharacterized protein (S8BWE0). In this category the shared proteins were related to ribosome biogenesis.

Within the biological process domain leaves show the exclusive category carbon utilization with the protein carbonic anhydrase (S8E474, A0A4D9BLA3) found in both morphotypes.

3.2.2 Cellular component domain

Within cellular component domain the main category grouping leaf, trap and shared proteins were cellular anatomical entity (Fig 2C). Leaf proteins were found in the extracellular region, in the category apoplast, the protein Germin-like protein (S8E4K0) with nutrient reservoir activity. Also, were found proteins related to mitochondrial and chloroplast membranes. Moreover, different tubulin alpha chain proteins were found that are part of microtubules. In this category, the shared proteins were found in the cytoplasm with proteins of the chloroplast, thylakoid membrane, cytoskeleton and mitochondrial inner membrane. In traps were in the extracellular region the protein Peroxidase (S8CL73).

In this domain, were found leaf and shared proteins in the Protein-containing complex category. The leaf proteins acting in the photosystems and chloroplastic membrane protein complex with the PsbP domain-containing protein (S8E188, S8D7Q6) and in glycolytic process the Enolase (S8C2L7). Otherwise, the shared proteins were found acting in the glycolytic process, proton-transporting ATP synthase complex activity and proteins of the nucleosome and in leaves and traps of both morphotype proteins of membrane protein complex of the photosystems involved in photosynthetic electron transport in photosystem II, chlorophyll binding, light harvesting and chloroplast thylakoid membrane.

Also, in the category cell, were found leaf proteins with peroxidase activity like Peroxiredoxin (S8DVK0, S8CBR9), acting in cellular iron ion homeostasis the Ferritin (S8CG22), with ATP binding activity the Phosphotransferase (S8CZZ6) and involved in cell redox homeostasis the Protein disulfide-isomerase

(S8CV45). In the shared proteins, in traps and leaves of both morphotypes, involved in regulation cell redox homeostasis were found the Thioredoxin domain-containing protein (S8C8H1, S8D6C0, S8C5P5).

3.2.3 Molecular function domain

The main categories grouping leaves, traps and shared proteins were binding and catalytic activity (Fig 2D). In binding category leaves showed proteins acting in protein binding like 14-3-3 protein (S8BYG4), Actin-depolymerizing factor (S8D170), HATPase_c domain-containing protein (S8CRG0), Heat shock protein 90 (S8E095) and Calreticulin (S8C1N1) which acts in protein folding in the endoplasmic reticulum and calcium ion binding. In the category drug binding, proteins with a ATP binding activity and proteins involved in cellular amino acid metabolic process like Aspartate aminotransferase (S8DJJ3, S8DRZ1) and Serine hydroxymethyltransferase (S8CFW3). In small molecule binding category proteins involved in nucleotide binding, nucleoside binding and glucose binding. In ion binding the Calmodulin (S8CZ12), Cytochrome c oxidase subunit 2 (S8D4E0), Photosystem II CP47 reaction center (S8EC22) and Ferritin (S8CG22).

In binding category the shared proteins were found acting in protein binding, represented by Histones, 14-3-3 family proteins and the HATPase_c domain-containing protein (S8DFN4). In Nucleotide, nucleoside and ribosome binding the Eukaryotic translation initiation factor 5A (S8E4S5). With nucleoside binding activity the GTP-binding nuclear protein (S8EBF2), Elongation factor 1-alpha (S8CI40) and the Tr-type G domain-containing protein (S8CIP5). Binding to magnesium ion binding the Ribulose biphosphate carboxylase large chain (A0A2I6QD52) and the Iso dh domain-containing protein (S8BWD8) and iron binding the Photosystem II protein D1 (A0A2I6QD25).

Within binding category were found the traps proteins with ATP binding the protein Plasma membrane ATPase (S8DZJ2), protein binding the 14-3-3 h-1 protein (S8D779), thiamine pyrophosphate binding with the Pyruvate decarboxylase (S8D6K0), metal ion binding the Cu/Zn superoxide dismutase (H2DK20) and ion binding the proteins 10-hydroxygeraniol oxidoreductase (S8D5C1), Peroxidase (S8CL73), Uncharacterized proteins (S8CFM5, S8CYK9, S8DDM8, S8D1V3).

In the catalytic activity category the leaves showed proteins with cytochrome-c oxidase activity, ferroxidase activity, superoxide dismutase activity and oxidoreductase activity, within this category were found proteins like the Aldo_ket_red domain-containing (S8E6U3), Iso_dh domain-containing protein (S8E6J2), DHO_dh domain-containing protein (S8CZU4), NADPH-protochlorophyllide oxidoreductase (S8D6L3), Malate dehydrogenase (S8DYB4), Rieske domain-containing protein (S8CL66), and Superoxide dismutase (S8CV15), and with hydrolase activity the Inorganic pyrophosphatase (S8CLS8) and catalytic activity, acting on a protein the Peptidyl-prolyl cis-trans isomerase (S8CE21), Cytosol_ap domain-containing protein (S8CE03), PPIase cyclophilin-type domain-containing protein (S8CG73), ftsh-like protein (S8D0Y2), PPIase cyclophilin-type domain-containing protein (S8DMR4), Peptidyl-prolyl cis-trans isomerase (S8CBH1, S8CP19), Protein disulfide-isomerase (S8CV45), AAA domain-containing protein (S8DIK9) and within this category, proteins with threonine-type endopeptidase activity like the Proteasome subunit alpha type (S8CP75), and with serine-type endopeptidase activity the ATP-dependent Clp protease proteolytic subunit (S8EMJ4, S8CIS0), Subtilase family protein (S8EE25) and the PDZ domain-containing protein (S8EKZ6), with aspartic-type endopeptidase activity the Peptidase A1 domain-containing protein (S8EAQ4) and cysteine-type peptidase activity the Cysteine proteinase (S8CM96).

The shared proteins with catalytic activity show oxidoreductase activity with electron transporter and carbon fixation in photosynthesis, antioxidants acting in respiration process and cell redox homeostasis. Also, proteins acting in

transferring phosphorus-containing groups with hydrolase activity and acting in amino acid biosynthesis and the mitochondrial processing in leaves and traps of both morphotypes, the Mitochondrial processing peptidase (S8E5Q8). In traps, we found proteins with catalytic activity, like the Cysteine proteinase (S8E4V4) with cysteine-type peptidase activity, with oxidoreductase activity, the 10-hydroxygeraniol oxidoreductase (S8D5C1), and with hydrolase activity the Peroxidase (S8CL73), also, were found the Uncharacterized proteins (S8CYK9, S8DDM8).

The transmembrane transporter activity category in leaves was represented by the proteins Inorganic pyrophosphatase (S8CLS8), and the Uncharacterized protein (S8D3C4) of the mitochondrial inner membrane, in intracellular protein transport the AIG1-type G domain-containing protein (S8CYB6), in ATPase-coupled transmembrane transporter activity the ATP synthase subunit alpha (S8EC20, S8D0S6) and the V-type proton ATPase subunit G (S8EEI7) proteins, and nuclear import signal receptor activity with the IBB domain-containing protein (S8C6W0). The shared proteins show transmembrane transporter activity with proton-transporting ATP synthase activity the proteins ATP synthase subunit alpha (S8EF74), ATP synthase subunit beta (S8C857), AAA domain-containing protein (S8D4F2), and with the transmembrane transporter activity the Uncharacterized protein (S8CX03) mitochondrial inner membrane. Moreover, in traps were found the Plasma membrane ATPase (S8DZJ2) with proton-exporting ATPase activity.

The structural molecule activity category grouped leaves and shared proteins. In this, the leaf proteins were associated to the structural constituent of ribosome and cytoskeleton. Also, the shared proteins were grouped in the category structural constituent of ribosome and translation elongation factor activity. Besides, the leaves showed exclusive proteins with antioxidant activity like the Peroxidase (S8EFM,) Thylakoid-bound ascorbate peroxidase (S8CL08) and Peroxidase_4 domain-containing protein (S8CVD5, S8DGS9, S8CA75), with superoxide dismutase activity like Superoxide dismutase (S8E121, S8E1B9, S8CV15) and with peroxiredoxin activity the Peroxiredoxin (S8DVK0, S8CBR9),

Thioredoxin domain-containing protein (S8C8H1) and Cytosolic ascorbate peroxidase (A0A067XJ96).

3.3 Protein quantification

A label-free quantification and statistical analysis based on T-test approaches were employed to analyze the proteins expression changes between pair set of leaves of the two morphotypes studied (Table 2). The results showed that the largest number of proteins identified were found in the pair set of photosynthetic leaves against the traps of the two morphotypes combined; and the comparisons between the photosynthetic leaves of the two morphotypes presented the highest number of proteins with valid values, present in at least two repetitions of each group, and the largest number of differentially regulated proteins (Table 2).

Table 2. Label-free quantification and T-Test result in pair set of leaf types of *Genlisea violacea* white and purple morphotypes.

PAIR-SET	LFQ*		T-TEST**	
	Proteins groups	Proteins	Proteins after filtration	Differently regulated Proteins
WL-PL	402	381	64	16
WT-PT	145	130	17	3
WL-WT	229	211	12	2
PL-PT	389	373	17	11
LEAVES-TRAPS	476	456	19	8

*LFQ: Label Free Quantification (MAXQUANT)

**T-TEST: (PERSEUS)

The results of the significantly expressed proteins in the pair set are showed in Table 3 and heatmaps illustrate the differentially expressed proteins (Fig 3-4). When comparing the photosynthetic leaves between the two morphotypes we observed that chloroplast proteins related to photosynthesis and energy production and nucleosome proteins were exclusively up-regulated in the leaves of the purple morphotype, while in the leaves of the white morphotype, the

proteins up-regulated were mainly involved to chloroplast thylakoid membrane, photosystem II and one ribosomal protein (Table 3; Fig 3B). When comparing the traps between the two morphotypes, the histone H2B (S8CFM8) were up-regulated in the purple morphotype, while the Actin (S8DD77, S8CRU7) was up-regulated in the white morphotype (Fig 3D).

Considering the white-flowered morphotype, the chloroplast proteins related to photosynthesis were up-regulated in leaves comparing with traps (Table 3; Fig 3A), while when comparing leaves and traps in the purple-flowered morphotype (Fig 3C) the proteins related to the production of energy, photosynthesis, but also the proteins related to translation and histones were mainly up-regulated in the photosynthetic leaves (Fig 3C).

When the photosynthetic leaves and traps of the two morphotypes were grouped and compared (Fig 4), it was observed that eight proteins were differentially expressed; in the photosynthetic leaves were up-regulated proteins related to energy production like ATP synthase subunit alpha (S8EF74), chloroplast proteins such as Chlorophyll ab binding protein (S8CBA2) and Ribulose biphosphate carboxylase large chain (A0A2I6QD52), and also histones (S8CYV8) and Malate dehydrogenase (S8D4W0), and in the traps were up-accumulated Actin (S8DD77) and the uncharacterized protein (S8CX03) that is part of mitochondrial inner membrane (Fig 4).

Table 3. Differentially regulated proteins in pairs set of leaf types of *Genlisea violacea* white- and purple-flowered morphotypes.

Uniprot ID	Description	Up -Regulated Leave type	Peptides	Unique peptides	Sequence coverage [%]	MS/MS count	(-Log Student's T- test p-value)	Student's T- test Difference	Student's T- test Test statistic
PL-WL									
A0A2I6QD36	ATP synthase subunit b, chloroplastic	PL	3	3	14.1	56	1.3992	-0.9973	-2.2368
S8C6K2	Heat shock protein 70	PL	16	2	29.2	229	3.4804	-1.7794	-4.5456
S8CD85	Histone H2A	PL	4	4	31.3	103	2.0751	-1.3191	-3.0039
S8CFM8	Histone H2B	PL	5	5	37.7	84	1.7844	-1.6840	-2.6800
S8DRF8	Histone H3	PL	4	1	30.7	81	7.5974	-4.0085	-10.0601
S8CYV8	Histone H4	PL	11	11	67	305	6.3618	-1.6114	-8.1510
A0A2I6QD51	Photosystem I P700 chlorophyll a apoprotein	PL	7	7	12.4	172	1.6055	-1.0596	-2.4768
A0A2I6QD52	Ribulose biphosphate carboxylase large chain	PL	28	13	52.4	3158	4.1860	-1.0447	-5.3492
S8ELF0	Ribulose biphosphate carboxylase large chain	PL	14	3	24	86	2.2044	-2.4611	-3.1461
S8CBA2	Chlorophyll a-b binding protein, chloroplastic	WL	9	9	52.8	640	1.4753	0.8956	2.3262
A0A2I6QD64	Cytochrome b559 subunit alpha	WL	2	2	22.9	76	2.0237	1.0221	2.9470
S8CKD0	Nucleoside diphosphate kinase	WL	4	4	32.4	37	2.4437	0.9562	3.4078
S8CBV6	Oxygen-evolving enhancer protein 1,	WL	8	8	29.1	245	1.5074	1.1830	2.3636
S8DAG9	Photosystem II CP47 reaction center protein	WL	9	9	18.2	373	3.7779	1.3975	4.8802
S8CAG4	Phosphoribulokinase	WL	9	9	32.6	114	1.4177	1.3418	2.2587
S8E9X0	Uncharacterized protein	WL	1	1	10.6	45	2.8252	1.5073	3.8239
WT-PT									
S8CFM8	Histone H2B	PT	4	4	26.8	116	1.7914	-2.1335	-2.7333
S8CRU7	Actin	WT	5	4	10.1	153	1.6180	1.1269	2.5286
S8DD77	Actin	WT	5	4	15.3	112	4.7963	1.4988	6.4207
WL-WT									
S8CBA2	Chlorophyll a-b binding protein, chloroplastic	WL	9	9	52.8	420	6.8365	-2.7387	-8.8519
A0A2I6QD52	Ribulose biphosphate carboxylase large chain	WL	24	11	47.8	1132	6.2617	-5.5493	-8.0080
PL-PT									
S8EF74	ATP synthase subunit alpha	PL	12	10	26.7	83	2.0343	-2.2581	-3.0167
S8CBA2	Chlorophyll a-b binding protein, chloroplastic	PL	6	6	44.9	354	5.0183	-4.2928	-6.7325
S8CI40	Elongation factor 1-alpha	PL	8	8	15	113	1.6805	-1.9255	-2.6027
A0A2I6QD52	Ribulose biphosphate carboxylase large chain	PL	26	12	51.6	2118	6.5265	-7.0024	-9.0974
S8C6K2	Heat shock protein 70	PL	17	2	30.3	272	1.8572	-1.9787	-2.8104
S8CD85	Histone H2A	PL	4	4	31.3	106	1.9177	-1.8761	-2.8811
S8CFM8	Histone H2B	PL	5	5	37.7	119	5.5145	-1.8112	-7.4602
S8DRF8	Histone H3	PL	5	1	5.5	143	1.6000	-2.1068	-2.5071
S8CYV8	Histone H4	PL	11	11	67	356	2.2168	-2.1636	-3.2282
S8D4W0	Malate dehydrogenase	PL	4	4	11.5	83	3.8034	-2.0481	-5.1152
S8E4Y7	Uncharacterized protein	PL	11	3	40.6	179	4.4740	-2.4326	-5.9819
LEAVES (PL+WL) -TRAPS (PT+WT)									
S8EF74	ATP synthase subunit alpha	LEAVES	12	9	24.5	128	1.5594	1.1004	2.3086
S8CBA2	Chlorophyll a-b binding protein, chloroplastic	LEAVES	9	9	52.8	689	6.9898	3.2622	6.8236
S8CYV8	Histone H4	LEAVES	11	11	67	552	2.0832	1.4912	2.8161
S8D4W0	Malate dehydrogenase	LEAVES	4	4	11.5	130	3.6692	1.4916	4.1742
A0A2I6QD52	Ribulose biphosphate carboxylase large chain	LEAVES	28	13	52.4	3246	10.2421	6.1311	9.6251
S8E4Y7	Uncharacterized protein	LEAVES	11	3	40.6	295	2.5515	1.3091	3.2372
S8DD77	Actin	TRAPS	7	4	27.1	94	3.0458	-1.3949	-3.6603
S8CX03	Uncharacterized protein	TRAPS	10	4	22.2	117	3.9455	-2.5416	-4.3973

Fig.3. Heatmap of proteins identified as differentially regulated ($p < 0.05$) in *Genlisea violacea* pair set. A- White morphotype leaves and traps. B- Leaves of white and purple morphotypes. C- Purple morphotype leaves and traps. D- Traps and white and purple morphotypes. The color gradient range (-3 to 2) indicates the proportion of upregulated (Red) and down regulated (Green) proteins among treatments (Log2 transformed and normalized values).

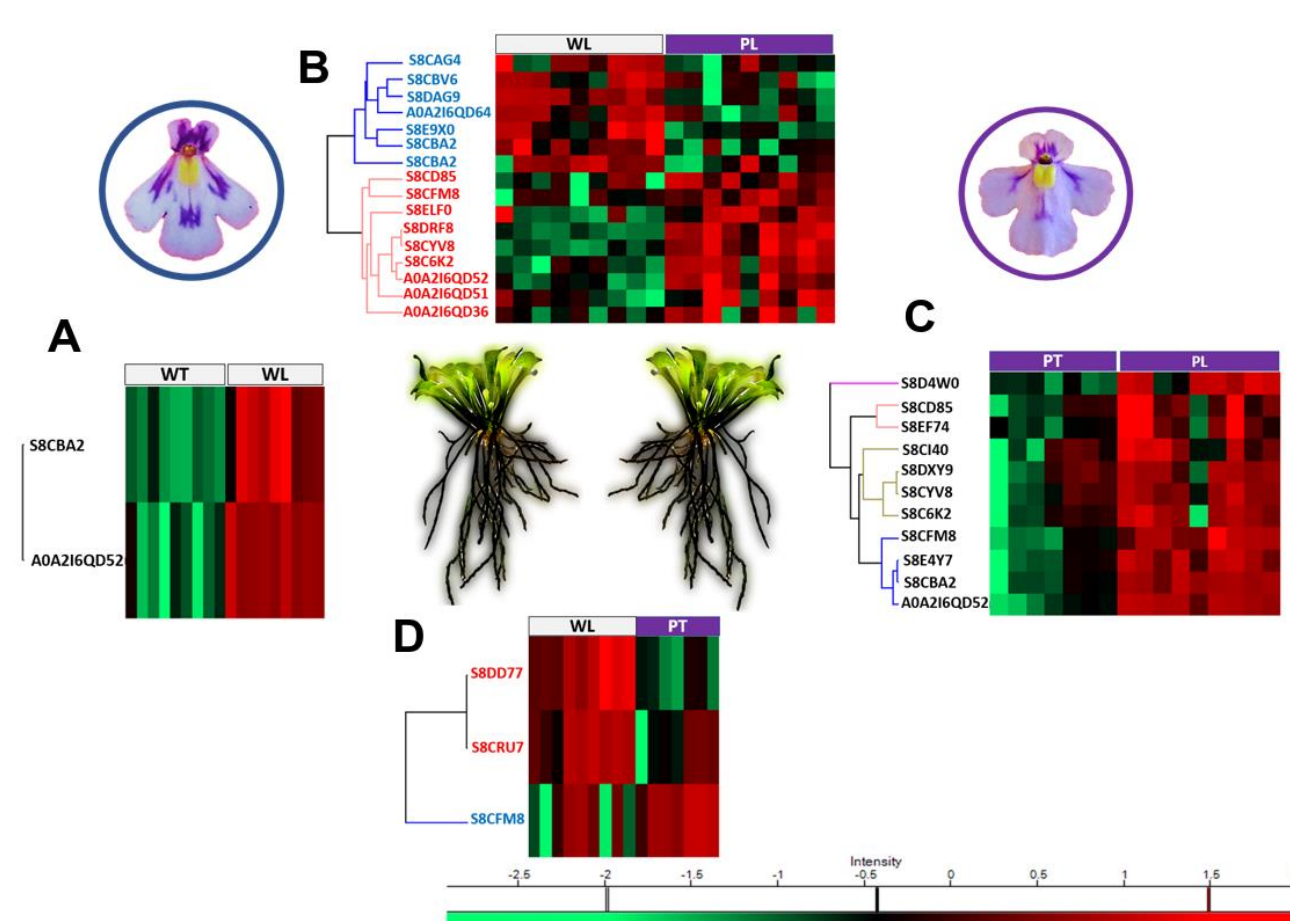
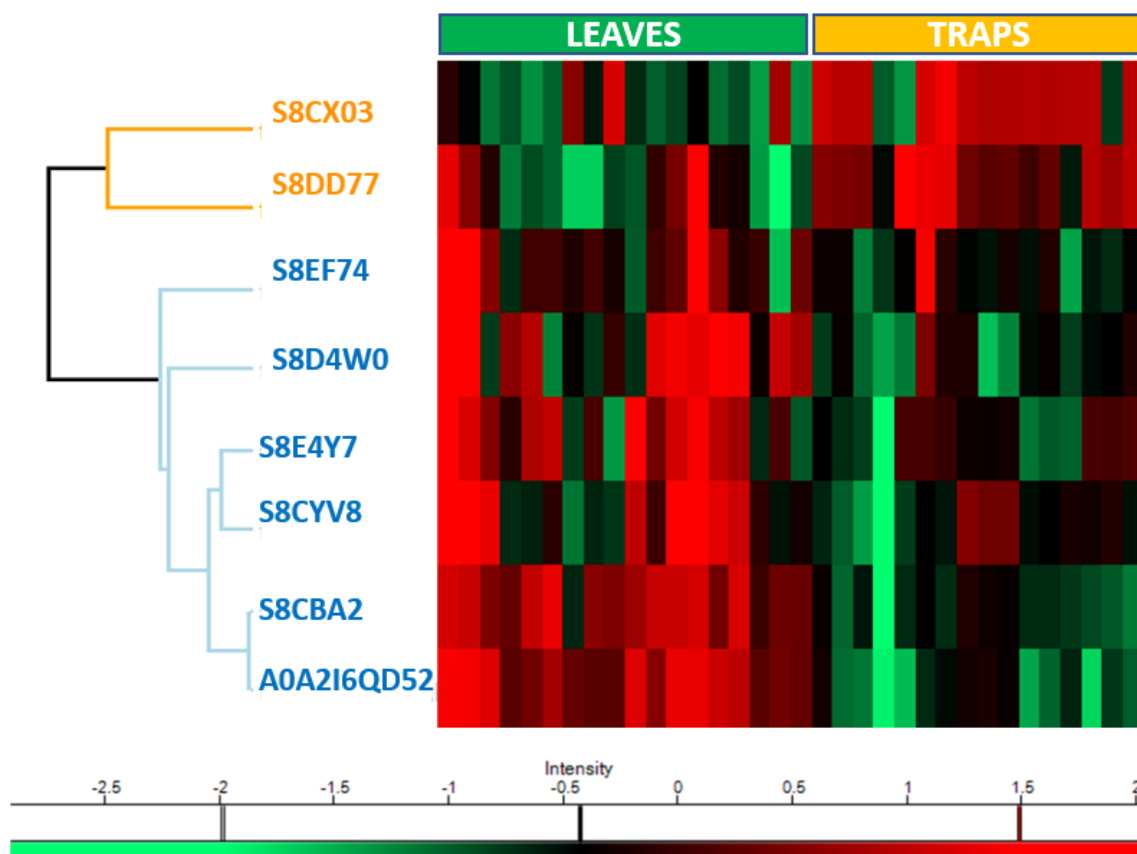


Fig.4. Leaves and traps differentially regulated proteins ($p < 0.05$) in *Genlisea violacea*. The color gradient range (-3 to 2) indicates the proportion of upregulated (Red) and down regulated (Green) proteins among treatments (Log2 transformed and normalized values).



4. Discussion

The Lentibulariaceae family includes structures with unusual vegetative morphologies [47,48]. In this family plants from the genera *Utricularia* and *Genlisea* lack roots and absorb nutrients through specialized leaves (traps) [1,49]. Since traps have foliar origin, it is expected that these organs share basic molecular functions and proteins. In our study with *Genlisea violacea*, the gene ontology classification shows that the two foliar types shared proteins involved in basic biological process, molecular functions and cellular components important for cellular homeostasis and development. Among the basic biological process shared by leaves and traps, were found proteins associated to nitrogen compounds metabolism, protein folding, glycolytic process, ATP synthesis,

transmembrane transporter activity, protein transport, photorespiration, light harvesting in photosynthesis and cellular components including, cytoplasm, integral component of chloroplast and mitochondrial membranes, structural constituent of chloroplast, ribosomes and cytoskeleton (Tables S11-S13). Among these basic processes, were identified in leaves and traps of both morphotypes, the proteins Ribulose biphosphate carboxylase small chain (S8C9X5) and Ribulose biphosphate carboxylase large chain (S8ELF0, A0A2I6QD52) both involved in in photorespiration and photosynthesis. Ribulose-1,5-bisphosphate (RuBP) carboxylase/oxygenase (Rubisco), is believed to be the most the most abundant protein in the world [50] and catalyzes the first step in photosynthetic CO₂ assimilation and photorespiratory carbon oxidation [51]. Similar results were found in the transcriptomic study of vegetative shoots and traps in the closed related *Utricularia gibba*, showing high similarities between the gene expression profiles and functional classification in these leaf-originated organs [33].

Among the common proteins present in leaves and traps of *Genlisea violacea*, we found proteins related to cellular homeostasis. In biological process domain *Genlisea* leaves and traps of both morphotypes share the proteins Catalase (S8E1K9) and Dihydrolipoyl dehydrogenase (S8CGC3) responding to oxidative stress. Others proteins with antioxidants effect were identified exclusive in leaves and in traps, among them, in traps were identified the Peroxidase (S8CL73). These proteins act against reactive oxygen species (ROS). During the course of metabolic process, the organism produces different ROS than can cause damage to a wide range of macromolecules, including DNA and different enzymes evolved to protect the cells, among these, superoxide dismutase, catalase and peroxidases [52]. Interestingly, compared to others angiosperms, the genera *Genlisea* and *Utricularia* show high DNA rate mutations [53], possibly caused in part due ROS action [33,54,55]. Besides the shared and exclusive tissue proteins associated with response to oxidative stress, leaves and traps display several proteins with oxidoreductase activity, which can produce ROS. For example, in leaves is present the Complex1-domain-containing protein (S8EEM8) with NADH dehydrogenase (ubiquinone) activity, it is known that proteins with that activity produce highly reactive oxygen species [56]. However,

in carnivorous plants NADH oxidases generates ROS for prey digestion, including in *Genlisea* [57] and *Nepenthes* [58]. Also, in the extracellular region of traps were found the protein Peroxidase EC 1.11.1.7 (S8CL73) classified as peroxidases class III family. This kind of peroxidases also can generate ROS [59,60] and in *Nepenthes* a single class III peroxidase act in defense against pathogens, controls the bacterial growth in the pitcher fluid and by the action of ROS, oxidize proteins than later are digested by proteolytic enzymes like aspartic proteases [61].

Additionally, other protein found in leaves of both morphotypes related to the jasmonic acid biosynthetic process was the Allene oxide cyclase (S8CLT2). In plants Jasmonic acid (JA) and its derivatives regulates several processes, including resistance to necrotrophic pathogens infections and herbivore insects. The JA signaling pathway includes the production of defense related proteins and secondary metabolites [62]. Several aspects in the carnivory evolution are related to plant defense, including jasmonates [63]. In carnivorous plants JA can regulate the production of defense and digestive proteins and even the carnivorous plant with passive traps regulates their digestive enzyme activities [64]. Signalization by Jasmonate has been reported in three genera of carnivorous plants in the Caryophyllales order, including the passive traps of *Nepenthes*, inducing the expression pathogenesis related proteins, hydrolytic protein and secondary metabolites (review in [64]). Also, in this order JA derivatives are involved in the induction of trap closing the Venus flytrap (*Dionaea muscipula*) [65] and production of endopeptidases, like Cysteine endopeptidases [66]. In *Drosera capensis* the increased concentrations of Jasmonates acts signaling the prey capture and promoting trap movement and enzymes secretion [67]. Pavlovič and Mithöfer (2019) highlight the importance of investigate if JA signaling is co-opted in other carnivorous genera not related with Caryophyllales, including *Genlisea* [64].

Interestingly, in flowering plants phytohormones like JA can induce PR-10 genes, pathogenesis related activity (PR) [68]. In this study one of the protein

found in leaves were related to the defense response, Bet_v_1 domain-containing protein (S8DHI0), this protein belongs to the pathogenesis related proteins class PR10, classified as intracellular proteins present in the cytoplasm, slightly acidic and resistant to proteases [69]. PR10 proteins have been identified in different carnivorous plants, including *Cephalotus follicularis* (A0A1Q3C0L0) [70]. In *Nepenthes* pitcher fluid proteins with PR activity are believed to inhibit the proliferation of putrefaction and symbiotic bacteria to ensure nutrients acquisition for plant growth [29]. In *Utricularia* and *Genlisea* traps the very low concentrations of oxygen may help to kill the prey and regulate the trap inhabitants adapted to facultative anoxia [71]. *Utricularia* supply organic carbon from photosynthesis to microbial community in traps and benefit from its products [72,73]. In *Genlisea filiformis* the mainly bacterial groups found in the traps were Firmicutes and Proteobacteria [20]. Also, in *Genlisea* algae occurring inside the traps were found that comes from the surrounding environment and can compete for organic phosphate [74]. The presence of microbes including Proteobacteria, green algae, fungi, metazoans, among others in *Genlisea* traps shed light on the complex food chains within the traps [32]. In *Nepenthes* the pitcher fluid contain proteases and PR proteins which have digestion and antibacterial functions, suggesting that the digestion of prey system evolved from the defense system in this genera, the main PR protein found in this genera were, class III peroxidase, β -1,3-glucanase, and class III chitinase [30,61]. PR proteins and transduction signal pathways are another similarity between plant defense and carnivory [64]. Besides, in *Nepenthes alata* the calcium mediated signaling may acts in downstream jasmonate signaling pathway that regulates the protease production [75]. Related to this signaling pathway in this study were found in leaves of *G. violacea* the protein Calmodulin acting in calcium-mediated signaling and the Calreticulin which acts in protein folding in the endoplasmic reticulum and calcium ion binding, stress response [76] and plant immunity [77].

Moreover, in this study proteins associated to the carnivory were found in leaves and traps of *G. violacea* like the Cysteine proteinase (S8CM96, S8E4V4) with peptidase activity, acting on L-amino acid peptides. According to the MEROPS peptidase database (<http://merops.sanger.ac.uk/>) the cysteine

proteinase of *G. violacea*, identified in the peptide database as MER0703873, belongs to peptidase family C1 (Papain family clan). Cysteine peptidases, serine-type carboxypeptidase and aspartic type endopeptidase were reported in *Utricularia gibba* like metabolic adaptations to carnivory [78] and also in *Dionaea* the prey degradation is mainly performed by cysteine endopeptidases supported by serine carboxypeptidase [31,79]. Besides, in this study proteins with serine-type endopeptidase and with metalloendopeptidase activity were found in leaves, and in leaves and traps the Mitochondrial processing peptidase (S8E5Q8). Also, the Peptidase A1 domain-containing protein (S8EAQ4) with aspartic-type endopeptidase activity were found in leaves of both morphotypes. In *Nepenthes*, aspartic proteinases are important for nitrogen acquisition from insect protein in the pitcher fluid. Thus, it is suggested that in *Nepenthes* these enzymes can be produced in other organs like leaves and stem and later secreted in the pitcher [80,81].

Otherwise, in our results *Genlisea violacea* photosynthetic leaves show distinct activities related to metabolic process and cellular component involved in photosynthesis and photorespiration and basic cellular cycles. Moreover, in *G. violacea* were found that the light-exposed leaves show exclusive proteins related to light reaction and photosynthesis. Among these proteins associated with the term response to high light intensity activity part of the response to stimulus category the Uncharacterized protein (S8D856) acting in photosynthetic electron transport in photosystem I. Another exclusive term found in the leaf proteins was carbon utilization with the protein carbonic anhydrase (S8E474) in leaves of both morphotypes, and this protein acts in the reversible hydration of carbon dioxide, carbonic anhydrase plays a key role in photosynthetic carbon dioxide fixation and one of its primary functions is convert carbonic acid for fixation by Rubisco [82].

Furthermore, in the cellular component domain, the leaves present the exclusive term apoplast represented by the germin-like protein (S8E4K0, A0A4P1REH7). The germin-like protein (GLP) was found in the extracellular region associated with nutrient reservoir activity. In *Arabidopsis thaliana* different GLPs proteins have been reported acting like a receptor in the extracellular matrix

involved in developmental processes and response to stress [83]. Probably GLPs proteins must have additional enzyme activities that have not been identified in specific tissues including in the extracellular environment [84]. Germin like proteins have been reported inhibits serine protease activity in the wheat leaf apoplast [85].

Comparisons between leaves and traps of each morphotype showed proteins up-regulated related to photosynthesis, energy production, translation and histones in leaves. Concordant results were observed when leaves and traps of both morphotypes were grouped and compared; also, it was observed that in the photosynthetic leaves proteins related to energy production were up-regulated. The Malate dehydrogenase is found in the chloroplasts and act in photosynthesis and in the Calvin cycle [86]. Supporting the idea, that in *Genlisea* subterrestrial traps, the rate of photosynthesis per unit leaf mass or area must be low or reduced when compared to the photosynthetic leaves [63]. Similar results were reported by the transcriptome analysis of *Genlisea nigrocaulis* photosynthetic leaves [32], *Utricularia gibba* vegetative shoots [33] and non-carnivorous leaves of *Cephalotus follicularis* [21] with differential expression of proteins related to photosynthesis and chloroplast. *Nepenthes*, pitcher shows a decreased amount of total soluble proteins related to Rubisco when compared to the photosynthetic tissues, but almost the same in the chlorophyll-binding proteins [63]. In transcriptomic analysis of *Utricularia gibba* the differential expressed genes in traps were related with hydrolytic enzymes, respiration, phosphate uptake and nitrogen compound transporters, suggesting that in traps respiration is the major metabolic activity [33]. Similarly, in *Genlisea nigrocaulis*, the differentially expressed genes in the traps were related to respiratory and mitochondrial activities including NADH oxidases [32]. Whereas in *Cephalotus follicularis* the main significantly enriched GO terms expressed in pitcher leaves were relative to nutrient transporters, involving amino acid transport, general substrate, AAA+ ATPase domain, sugar/inositol transporter, ATPase-associated domain transporter, among others [21].

However, the energetic or respiration cost of traps in comparison with the photosynthetic leaves depends if the traps are active or passive. The respiration rate in passive traps compared to leaves is lower probably due reduced photosynthesis and different leaf mass area [63]. In this study the quantification and statistical analysis showed the proteins Actin (S8DD77) and the uncharacterized protein (S8CX03), part of mitochondrial inner membrane, were up-regulated in traps. In the other hand, by *de novo* sequencing were identified in traps, the exclusive protein Plasma membrane ATPase (S8DZJ2). In *Nepenthes* Plasma membrane ATPase is responsible for the pitcher fluid acidification and molecular transport function [87,88] and it is known that the Actin protein forms part of the plants cytoskeletal network (microfilaments), which acts as one of the most important regulators of immune signaling cascade, controlling movements of organelles, proteins and chemical signals in defense signaling processes [89]. Also, actin cytoskeleton integrates immune signaling to coordinate large defense responses [90]. Cytoskeleton is also associated with mitochondrial structure, function and dynamics in cells [91] and in *Drosera* trichomes the actin-endoplasmic reticulum is associated with plasmalemma, mitochondria, chloroplast and other organelles [92]. Furthermore, in *Genlisea* traps, secretory hair displays mitochondria with a well-developed cristae. Such hairs are formed by three compartments, basal, middle and terminal cell; in subgenus *Tayloria*, the subgenus in which *G. violacea* is nested, the terminal cells are transfer cells with wall labyrinth and ER well developed, with a large vacuole and with numerous mitochondria near the wall ingrowths [93]. Due its wall labyrinth, transfers cell shows an increased surface area of the plasma membrane than support an increased capacity for nutrients and proteins transport [94,95]. The Actin network act in the formation of this wall labyrinths in transfer cells [96]. In *Genlisea* is believed that digestive enzymes are transported directly from ER to the cell wall via connecting ER membranes with the plasmalemma [93] and the pores in the cuticle act in both secretion of enzymes and absorption of the product of digestion [18,93].

In addition to the cysteine proteinase found in leaves and traps of *G. violacea*, traps display proteins related to respiration and metabolic process,

like glycolytic process and proteins with oxidoreductase activity, hydrolase activity and superoxide dismutase) and also the 14-3-3 h-1 protein (S8D779). 14-3-3 proteins regulate the activity of several important plant enzymes, including Plasma membrane ATPase [97].

Besides, proteins, different secondary metabolites are related to prey attraction, digestion, antimicrobial effect and protecting plant tissue during the prey digestion in carnivorous plants. However, there is no information about its presence and functions in the Lentibulariaceae family [98]. On the other hand, in this study the proteomic approach allows the identification of single amino acid substitutions in the primary sequences of both morphotypes of *G. violacea*. Purple and white-flowered morphotypes share mutations when compared to the *G. aurea* proteome and also show intraspecific mutations (Table 1 and supplementary Table S8 and S9). Amino acid substitutions can be neutral, or deleterious, and at conserved positions can cause negative effects on proteins function [99], like loss of proteins function [100]. In plants, single amino acid substitutions are proved to improve salt stress tolerance [101], enhanced carotenoid accumulation [102], alter response to pathogens [103,104], confer herbicide resistance [105–107], restore activity in non-functional enzymes [108], influence product and substrate specificity of enzymes [109], and even can cause phenotypic changes [110] and affect organs development [111]. Also intra and interspecific variations in single amino acid were reported in the chloroplastic genomes of three morphotypes of the closely related *Utricularia amethystina* and the authors highlight that this kind of variations can represent potential molecular markers to use in evolutionary studies [112]. In our results, single amino acid substitutions identified like Leucine (L) were confirmed as Isoleucine (I), in *Genlisea violacea* chloroplastic sequences. In peptide sequencing experiments, these amino acids residues are indistinguishable in MS2 spectrum since both are identified by the same molecular mass.

5. Conclusions

This is the first study in the *Genlisea* genus based in mass-spectrometry approach, using *de novo* peptide sequencing, together with a database search and proteins label free quantification of two morphotypes of *G. violacea* allowed the identification of exclusive leaves and traps proteins and differentially expression of shared proteins. The GO classification of shared proteins indicates that traps have foliar origin and performs common basic process, like response to oxidative stress and basic component organization and composition. The identification and quantification of this subset of proteins shed a light of photosynthetic-active leaves and leaf-modified traps specialized functions at the proteome level in *Genlisea*, like photosynthetic and response to stimuli in leaves, and respiration, digestion and nutrient transport in traps. Moreover, these approaches enable the identification of proteins related to signaling, plant defense, and production of enzymes and ROS related to carnivory in *Genlisea*. The functional mechanism of these proteins in the *Genlisea* interaction requires further investigation. Also, *de novo* sequencing allowed to identify differences between primary sequences in proteins of both morphotypes and when compared with protein sequences of *Genlisea aurea*. These, intra and inter single amino acid substitution may serve as informative sites for phylogenetic inferences. However, this kind of studies depends in the availability of proteins sequences and precise annotations from genomics and proteomics projects in this carnivory genera. Therefore, future studies focusing proteins related to carnivory and also secondary metabolites may contribute to understand the molecular mechanisms and signaling pathways in digestion and nutrient transport in this carnivorous plant genus and also phylogenetics and genomics studies can clarify the relationship within *Genlisea* species.

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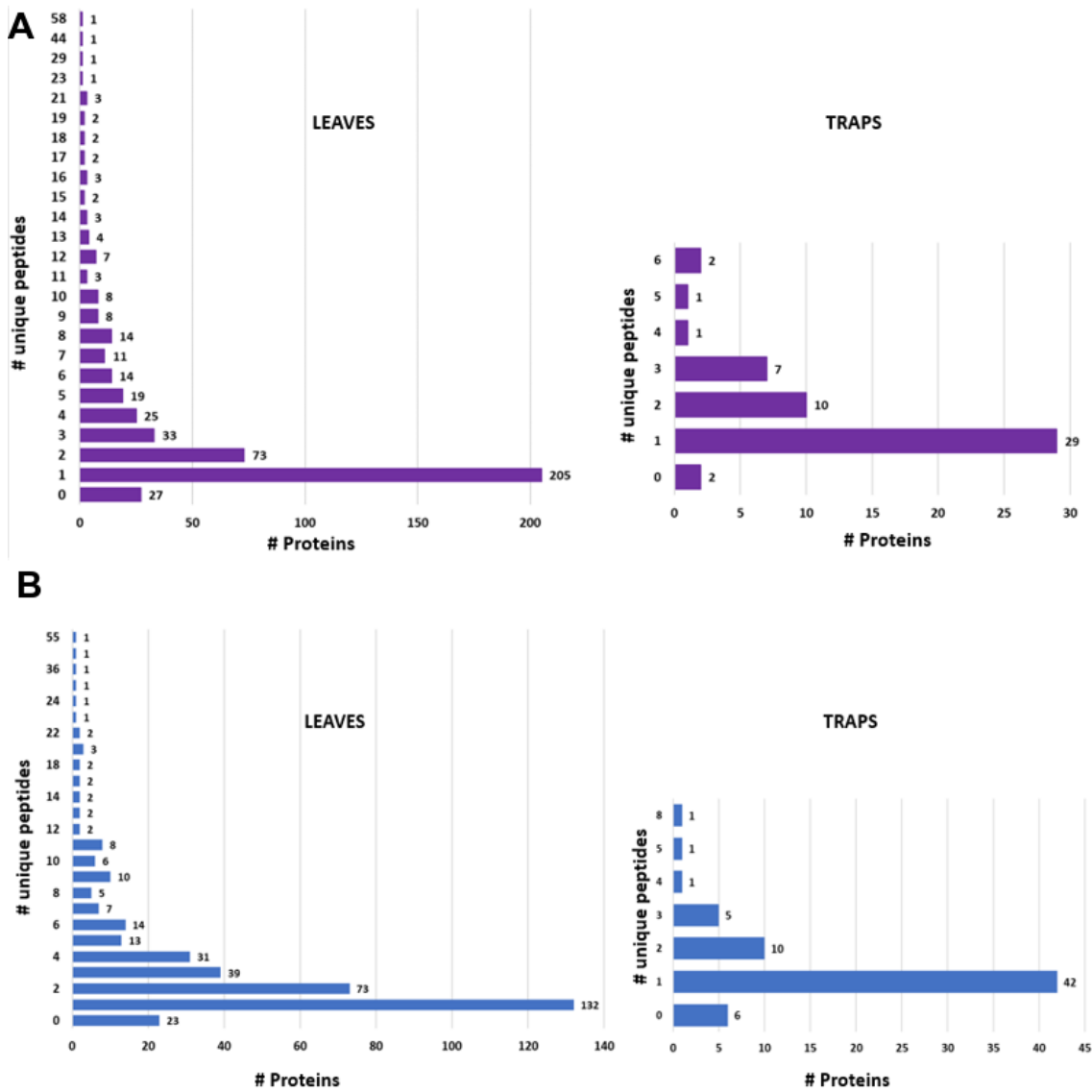
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SUPPLEMENTARY FIGURES

Figure S1. Identified proteins in leaves and traps by number of unique peptides with PEAKS. A- Purple-flowered morphotype, B- White-flowered morphotype.



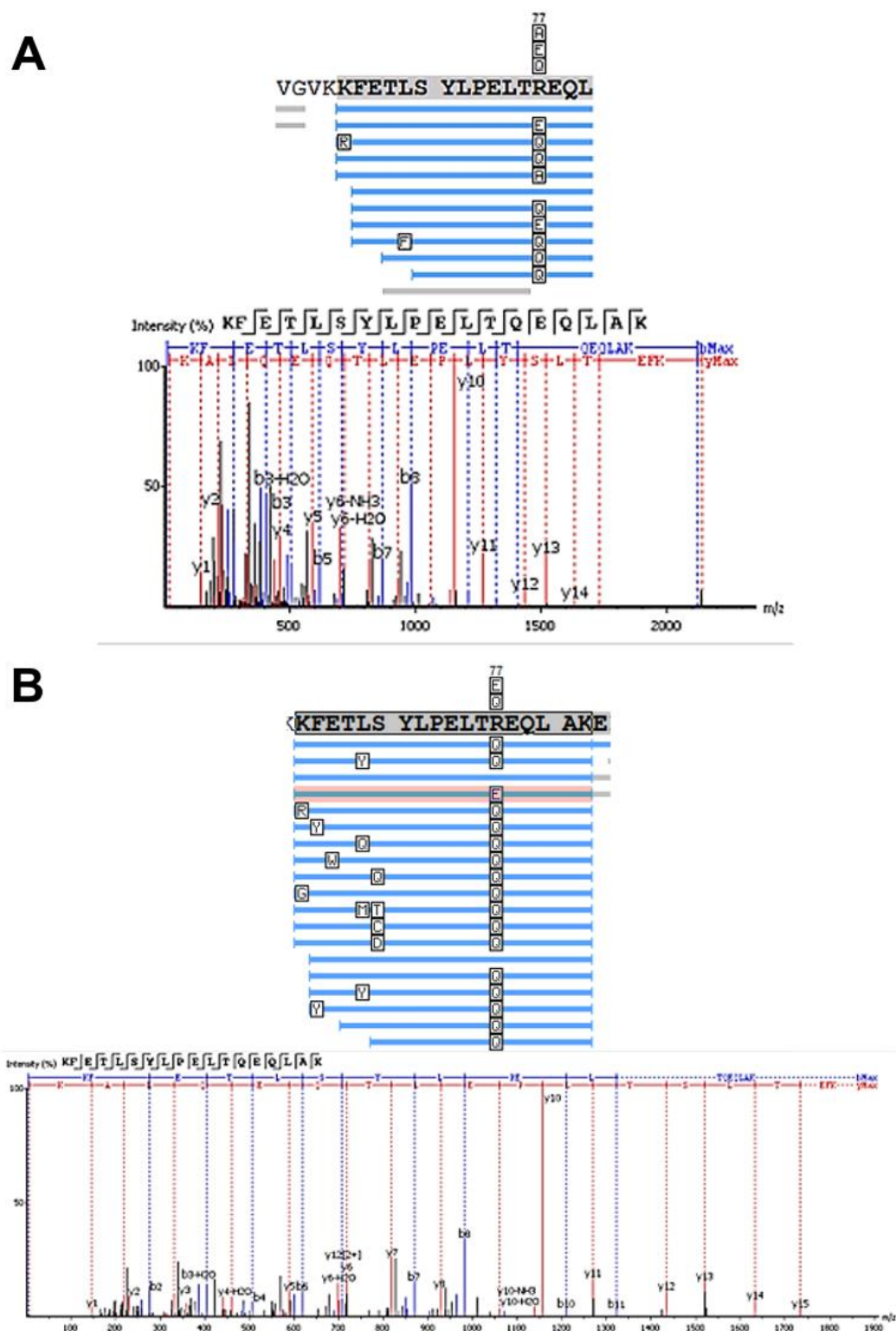


Figure S3. Partial alignment and comparison of shared protein sequences with single amino acid substitutions in purple- (PL) and white-flowered (WL) morphotypes of *Genlisea violacea*, identified by SPIDER algorithm in *Genlisea aurea* proteome and confirmed by chloroplastic proteins in *Genlisea violacea* and compared with sequence proteins of species of Lentibulariaceae family. The conserved amino acid residues are indicated by dots. A- AAA domain-containing protein, B- Apocytochrome f, C- ATP synthase subunit alpha, D- Cytochrome b559 subunit alpha, E- Photosystem II CP47 reaction center protein, F- Ribulose biphosphate carboxylase large chain.

A AAA domain-containing protein

Position: 387 T>L

	370	380	390	400
<i>G. aurea</i> (S8D4F2)	DSTSTMLQPRIVGEEHYETAQRVKQTLQRYKELQDIITAI			
<i>G. violacea</i> (YP_009466633)				
<i>G. violacea</i> -PL				
<i>G. violacea</i> -WL				
<i>G. aurea</i> (YP_009466255)				
<i>G. filiformis</i> (YP_009466331)				
<i>G. margaretae</i> (YP_009108445)				
<i>G. tuberosa</i> (YP_009466557)				
<i>U. amethystina</i> (QGT34450)				
<i>U. foliosa</i> (AQS79791)				
<i>U. reniformis</i> (YP_009272479)				
<i>U. macrorrhiza</i> (YP_009108505)				
<i>P. ehlersiae</i> (YP_009002262)				

B Apocytochrome f

WL Position: 240 Q>L

WL Position: 252 I>V

PL Position: 301 S>T

WL Position: 333 D>E

	230	240	250	260
<i>G. aurea</i> (S8ENB1)	ISPEIKKIGNLSFQSYRPNQKNIIVIGFVPGQKYTEI			
<i>G. violacea</i> (YP_009466639)				
<i>G. violacea</i> -PL				
<i>G. violacea</i> -WL				
<i>G. aurea</i> (YP_009466261)				
<i>G. filiformis</i> (YP_009466337)				
<i>G. margaretae</i> (YP_009108449)				
<i>G. pygmaea</i> (YP_009466412)				
<i>G. tuberosa</i> (YP_009466563)				
<i>U. amethystina</i> (QGT34543)				
<i>U. foliosa</i> (AQS79797.1)				
<i>U. gibba</i> (YP_008082594)				
<i>U. macrorrhiza</i> (YP_009108511)				
<i>U. reniformis</i> (YP_009272473)				
<i>P. ehlersiae</i> (YP_009002268)				

	300	310	320	330	341
<i>G. aurea</i> (S8ENB1)	RGQIYPDGSKSNNTVYNATGAGIVSKILRKEGGYEISITDPSDGR				
<i>G. violacea</i> (YP_009466639)					
<i>G. violacea</i> -PL					
<i>G. violacea</i> -WL					
<i>G. aurea</i> (YP_009466261)					
<i>G. filiformis</i> (YP_009466337)					
<i>G. margaretae</i> (YP_009108449)					
<i>G. pygmaea</i> (YP_009466412)					
<i>G. tuberosa</i> (YP_009466563)					
<i>U. amethystina</i> (QGT34543)					
<i>U. foliosa</i> (AQS79797.1)					
<i>U. gibba</i> (YP_008082594)					
<i>U. macrorrhiza</i> (YP_009108511)					
<i>U. reniformis</i> (YP_009272473)					
<i>P. Ehlersiae</i> (YP_009002268)					

C ATP synthase subunit alpha

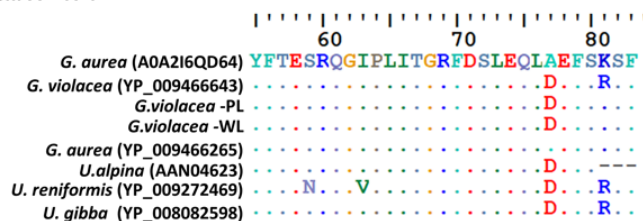
Position: 211 N>T

	200	210	220
<i>G. aurea</i> (S8D424)	ICVYVAIGQKASSVAQVNTLQERGAMEYITIVVAE'		
<i>G. violacea</i> (YP_009466614)			
<i>G. violacea</i> -PL			
<i>G. violacea</i> -WL			
<i>G. aurea</i> (YP_009466236)			
<i>G. filiformis</i> (YP_009466312)			
<i>G. margaretae</i> (YP_0091084270)			
<i>G. pygmaea</i> (YP_009466387)			
<i>U. amethystina</i> (QGT34428)			
<i>U. foliosa</i> (AQS79769.1)			
<i>U. gibba</i> (YP_008082566)			
<i>U. macrorrhiza</i> (YP_009108484)			
<i>U. reniformis</i> (YP_009272498)			
<i>P. ehlersiae</i> (YP_009002243)			

Figure S3.Continuation

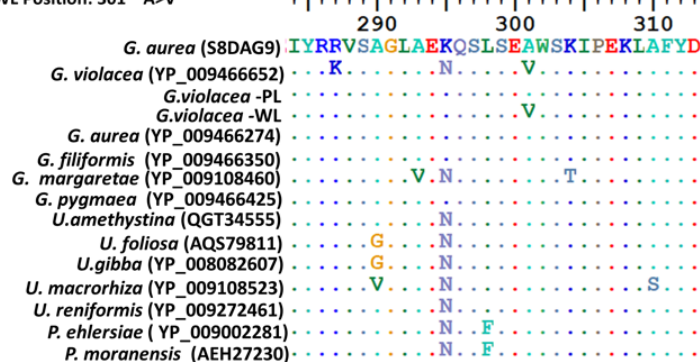
D Cytochrome b559 subunit alpha

Position: 77 A>T



E Photosystem II CP47 reaction center protein

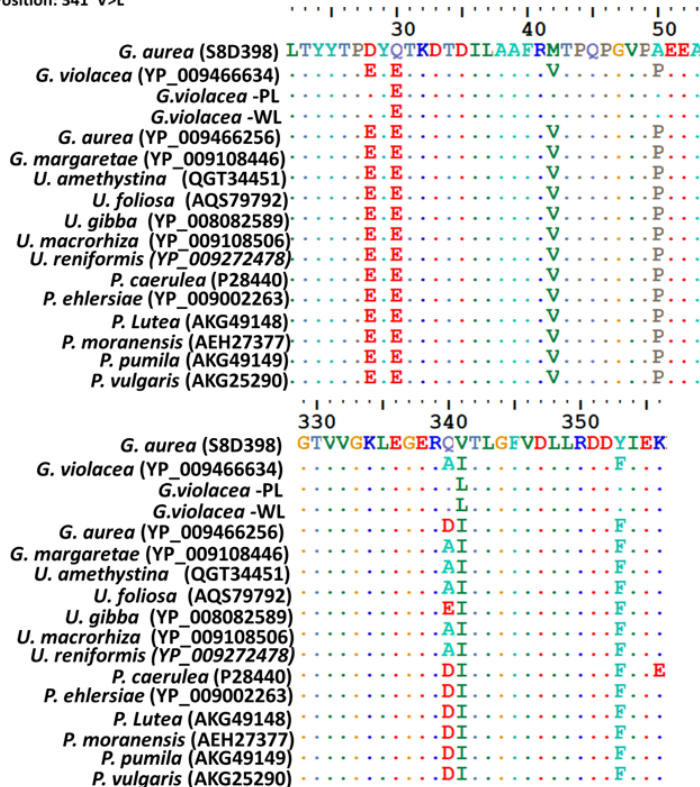
WL Position: 301 A>V



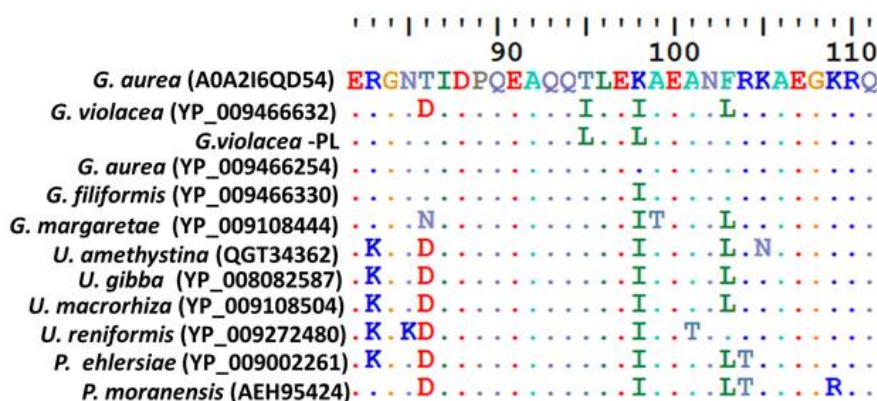
F Ribulose biphosphate carboxylase large chain

Position: 30 Q>E

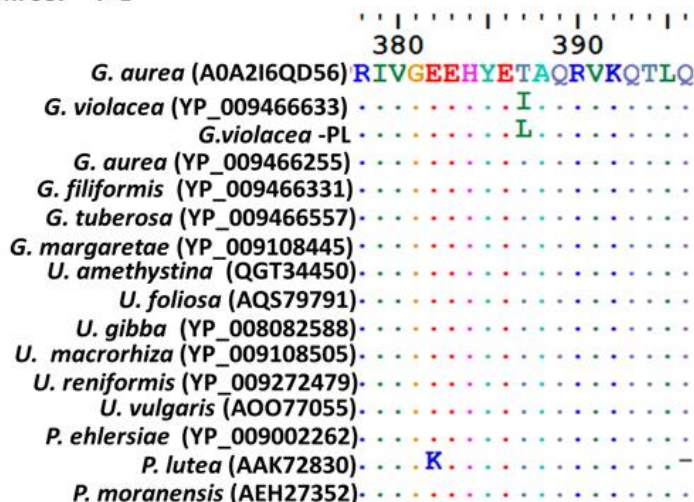
Position: 341 V>L



Position: 95 T>L
Position: 98 K>L



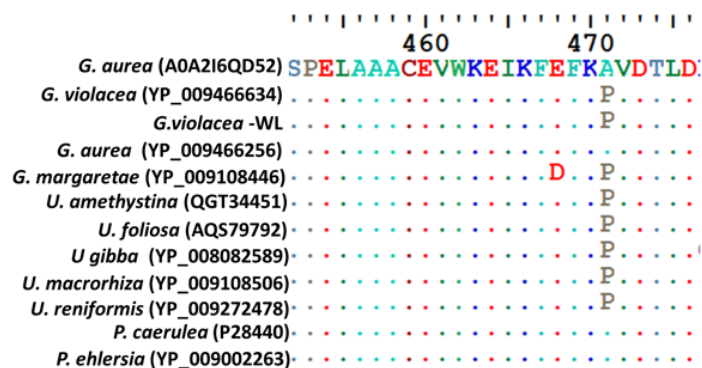
Position: 387 T>L



Position: 16 T>A

Position: 101 V>L

Position: 471 A>P



SUPPLEMENTARY TABLES

Table S1. *De novo* statistics of data of *Genlisea violacea* morphotypes with PEAKS.

	leave type			
	Purple Leaves	Purple Traps	White Leaves	White Traps
# of MS scans	62365	117114	60213	94133
# of MS/MS scans	315623	191471	309202	241025
#Features	336523	239671	305145	236818
De novo peptides after score filter Round 1	26240	4987	46631	18972
De novo peptides after score filter Round 2	10202	1991	12986	5447

Table S2. Statistics of PEAKS filtered results.

PURPLE LEAVES				
	PKS-DB GA	SPIDER GA	PKSDA VIR	SPIDER VIR
FDR (Peptide-Spectrum Matches)	0.10%	0.20%	0.20%	0.20%
FDR (Peptide Sequences)	0.80%	0.80%	0.80%	0.80%
FDR (Protein Group)	0.70%	0.80%	0.80%	0.80%
De Novo Only Spectra	22546	20941	9860	9833
PURPLE TRAPS				
	PKS-DB GA	SPIDER GA	PKSDA VIR	SPIDER VIR
FDR (Peptide-Spectrum Matches)	0.10%	0.10%	0.10%	0.10%
FDR (Peptide Sequences)	0.90%	0.90%	0.80%	0.80%
FDR (Protein Group)	0.00%	0.00%	0.00%	0.00%
De Novo Only Spectra	4467	4462	1987	1987
WITHE LEAVES				
	PKS-DB GA	SPIDER GA	PKSDA VIR	SPIDER VIR
FDR (Peptide-Spectrum Matches)	0.30%	0.30%	0.20%	0.30%
FDR (Peptide Sequences)	0.90%	0.80%	0.60%	0.80%
FDR (Protein Group)	0.70%	0.90%	0.80%	0.80%
De Novo Only Spectra	36924	18920	6502	12309
WITHE TRAPS				
	PKS-DB GA	SPIDER GA	PKSDA VIRI	SPIDER VIR
FDR (Peptide-Spectrum Matches)	0.00%	0.00%	0.00%	0.00%
FDR (Peptide Sequences)	0.00%	0.00%	0.00%	0.00%
FDR (Protein Group)	0.00%	0.00%	0.00%	0.00%
De Novo Only Spectra	16893	16861	5378	5377

* GA: *Genlisea aurea**VIR: *Viridiplantae*

Table S3. Total identified proteins with PEAKS algorithms.

PURPLE LEAVES							
	Identified			#Peptides	#Sequences	#Proteins	
	#PSMs	#Scans	#Features			Groups	Proteins
PEAKS DB: <i>Genlisea aurea</i>	8404	21819	19145	1137	1110	303	340
SPIDER: <i>Genlisea aurea</i>	11817	28105	19949	2195	2155	366	400
PEAKS DB: Viridiplantae	12271	29147	13541	2378	2298	471	505
SPIDER: Viridiplantae	12315	29269	13550	2390	2304	473	508
PURPLE TRAPS							
	Identified			#Peptides	#Sequences	#Proteins	
	#PSMs	#Scans	#Features			Groups	Proteins
PEAKS DB: <i>Genlisea aurea</i>	2291	5493	3550	223	223	49	63
SPIDER: <i>Genlisea aurea</i>	2305	5509	3552	234	234	50	66
PEAKS DB: Viridiplantae	2310	5523	2127	238	238	52	68
SPIDER: Viridiplantae	2310	5523	2127	238	238	52	68
WITHE LEAVES							
	Identified			#Peptides	#Sequences	#Proteins	
	#PSMs	#Scans	#Features			Groups	Proteins
PEAKS DB: <i>Genlisea aurea</i>	15571	15408	24302	1072	1047	279	318
SPIDER: <i>Genlisea aurea</i>	19772	19549	17638	1852	1818	324	356
PEAKS DB: Viridiplantae	19288	19085	10732	1889	1823	368	411
SPIDER: Viridiplantae	20517	20286	14248	2020	1945	384	417
WITHE TRAPS							
	Identified			#Peptides	#Sequences	#Proteins	
	#PSMs	#Scans	#Features			Groups	Proteins
PEAKS DB: <i>Genlisea aurea</i>	2632	6451	10728	210	210	60	78
SPIDER: <i>Genlisea aurea</i>	2687	6553	10743	227	227	60	78
PEAKS DB: Viridiplantae	2690	6557	4121	229	229	66	85
SPIDER: Viridiplantae	2691	6558	4121	229	229	66	85

Table S4. Identified proteins with PEAKS in leaves of the *Genlisea violacea* purple-flowered morphotype.

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
A0A2I6QD52	Ribulose biphosphate carboxylase large chain	532.64	77	118	58	1625	52828
S8D398	Ribulose biphosphate carboxylase large chain	398.51	56	73	21	672	48012
S8D4F2	AAA domain-containing protein	421.79	61	56	0	451	65998
S8CBA2	Chlorophyll a-b binding protein chloroplastic	391.93	56	44	44	295	28144
S8ELF0	Ribulose biphosphate carboxylase large chain	360.78	43	44	7	300	54568
S8D424	ATP synthase subunit alpha chloroplastic	329.53	36	28	19	232	55180
S8BX77	Glyceraldehyde-3-phosphate dehydrogenase	362.93	48	27	19	218	42461
S8C8K3	ATPase_AAA_core domain-containing protein	366.32	49	29	29	203	35153
S8C9X5	Ribulose biphosphate carboxylase small chain	274.33	30	18	17	167	19266
S8DCS9	AAA domain-containing protein	316.35	48	27	8	188	64784
S8E173	Phosphoglycerate kinase	336.64	54	27	21	174	50566
S8D525	Fructose-bisphosphate aldolase	317.71	55	26	9	185	38134
S8CAG8	Fructose-bisphosphate aldolase	326.99	47	22	8	152	37786
A0A2I6QD77	Photosystem II CP47 reaction center protein	312.55	30	20	18	158	55975
S8CYV8	Histone H4	240.91	59	14	14	127	11409
S8C857	ATP synthase subunit beta Oxygen-evolving enhancer protein 1 chloroplastic	327.99	47	23	1	128	57058
S8CBV6		317.71	46	25	23	129	34653
S8E474	Carbonic anhydrase	303.62	53	16	16	132	22765
S8DLI4	Uncharacterized protein	291.58	34	18	18	120	22118
S8C6K2	Heat shock protein 70	305.41	28	18	2	102	71263
S8E4Y7	Uncharacterized protein	259.87	38	12	4	105	41708
S8CXZ6	Chlorophyll a-b binding protein chloroplastic	326.70	27	21	21	106	51327
S8CTY8	Glycolate oxidase	274.98	49	19	16	96	39322
S8E8M6	Chlorophyll a-b binding protein chloroplastic	260.04	16	15	15	103	57243
S8DZE1	Chlorophyll a-b binding protein chloroplastic	238.60	29	9	9	97	30811
S8CVD3	Glyceraldehyde-3-phosphate dehydrogenase	301.72	25	15	7	88	46701
S8DAF4	Photosystem II CP43 reaction center protein	304.27	26	17	17	100	51932
S8CSZ4	Actin-97	271.24	32	14	5	88	41746
S8DI77	Uncharacterized protein	263.76	37	14	14	93	25784
S8DPH5	Uncharacterized protein	299.85	28	17	1	87	69648
S8CPA4	Uncharacterized protein FAD-binding FR-type domain-containing protein	296.48	23	16	0	82	71144
S8D6P3		262.78	32	12	12	89	31236
S8EF74	ATP synthase subunit alpha	242.25	28	13	12	74	54983
S8CAG4	Phosphoribulokinase	296.63	37	12	12	76	42000
S8CRU7	Actin	220.29	27	8	1	73	41788
S8DYF2	Aminomethyltransferase	191.71	20	7	7	69	43926
S8CDZ1	Uncharacterized protein	233.20	38	10	10	58	21516
S8DEF3	Glyceraldehyde-3-phosphate dehydrogenase	294.01	46	20	13	66	36532
S8E1K9	Catalase	253.66	23	10	10	69	57099

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
S8CHM2	Phosphoglycerate kinase	268.73	36	13	8	68	42185
S8CFW3	Serine hydroxymethyltransferase	228.74	22	12	12	62	51711
S8ENB1	Apocytochrome f	242.77	29	13	13	64	47237
S8CI40	Elongation factor 1-alpha	200.03	22	11	11	62	48652
S8EC20	ATP synthase subunit alpha	194.75	10	6	1	61	54698
S8D216	Chlorophyll a-b binding protein chloroplastic	242.32	35	10	10	60	27260
A0A2I6QD25	Photosystem II protein D1	229.30	19	9	4	64	38945
A0A2I6QD51	Photosystem I P700 chlorophyll a apoprotein A2	249.78	12	10	10	62	82658
S8DFY8	Elongation factor Tu	281.62	30	15	15	65	51970
S8D1U0	Glutamine amidotransferase type-2 domain-containing protein	244.97	12	16	16	50	155310
S8DFN4	HATPase_c domain-containing protein	242.84	17	10	10	57	80152
S8EAM3	Heat shock protein hsp70	259.88	15	12	1	54	68703
S8CRY5	Uncharacterized protein	274.00	26	16	14	56	61536
S8CWK8	Ubiquitin-like domain-containing protein	152.26	36	5	2	50	14799
S8D4W0	Malate dehydrogenase	211.63	14	6	6	52	37424
S8D2K5	Fructose-bisphosphate aldolase	273.82	32	14	10	52	38302
S8C474	Uncharacterized protein	220.72	27	9	9	47	40703
S8CA75	PEROXIDASE_4 domain-containing protein	219.96	41	8	8	44	23973
S8BZF0	Monodehydroascorbate reductase	216.39	29	12	12	44	47113
S8D4J3	Glutamine synthetase	300.98	37	13	11	41	31188
S8BXC1	Serine-glyoxylate aminotransferase	256.32	38	13	13	44	44089
S8CVW0	Histone H2B	175.27	34	8	8	43	17104
S8E0E9	Triosephosphate isomerase	212.53	41	8	8	49	27341
S8D0S6	ATP synthase subunit alpha	176.18	7	5	1	39	48951
S8EDT4	Photosystem I iron-sulfur center	192.04	44	4	2	44	9022
S8C5P5	Thioredoxin domain-containing protein	204.15	61	9	9	44	16319
S8DIK9	AAA domain-containing protein	205.48	21	11	11	42	73251
A0A2I6QD58	Photosystem I P700 chlorophyll a apoprotein A1	246.68	13	12	12	41	83068
A0A2I6QD76	Cytochrome b6	160.22	21	3	3	44	24181
S8CWV4	Glycine cleavage system P protein	165.01	9	5	5	37	60737
S8BXF4	TRANSKETOLASE_1 domain-containing protein	164.60	10	6	5	42	46944
S8CVD5	PEROXIDASE_4 domain-containing protein	203.73	38	9	8	40	27543
S8E188	PsbP domain-containing protein	222.57	40	12	12	29	26970
S8DLT5	14-3-3 h-1 protein	230.79	31	9	4	38	28683
S8C3A0	Chloroplast sedoheptulose-1 7-bisphosphatase	179.37	50	6	6	35	13663
A0A2I6QD42	Photosystem II D2 protein	179.48	13	6	6	38	39549
S8D8M8	Transket_pyr domain-containing protein	170.74	29	6	5	37	33978
S8DTS5	Uncharacterized protein	192.01	32	6	5	38	20590
S8CIP5	Tr-type G domain-containing protein	182.00	12	9	9	32	93742
S8E065	Uncharacterized protein	199.48	30	8	8	31	25030
S8E7B3	Uncharacterized protein	156.74	28	4	4	27	20658
S8C8H1	Thioredoxin domain-containing protein	216.17	30	10	10	34	29355
S8EE95	Uncharacterized protein	193.50	37	5	5	31	14796

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
S8E2N0	Histone H3	126.70	20	4	1	31	15268
S8CRS6	Fructose-bisphosphate aldolase	174.25	20	7	4	34	38096
S8E325	Malate dehydrogenase	174.69	17	7	7	28	37101
S8D490	AAA domain-containing protein	186.13	18	6	6	35	37668
S8DD77	Actin	209.86	27	7	3	33	32298
S8CX03	Uncharacterized protein	187.15	16	7	2	29	41206
S8CZK7	Uncharacterized protein	222.96	31	13	13	30	61389
S8CBN4	Histone H3	121.55	20	4	1	28	15406
S8C5B9	PAP_fibrillin domain-containing protein	134.85	27	6	6	28	22309
S8ELF4	Photosystem II protein D1	206.36	13	6	1	33	38317
S8D9H7	Uncharacterized protein	172.68	16	3	3	30	21894
S8CE03	CYTOSOL_AP domain-containing protein	197.52	15	6	6	29	58141
S8C3Q5	Chloroplast heat shock protein 70-2	203.57	23	8	8	27	31402
S8CQW3	Malate dehydrogenase	215.82	26	7	6	25	47366
S8DR98	Uncharacterized protein	118.75	16	2	2	30	16068
S8D3C4	Uncharacterized protein	173.59	19	7	2	21	34316
S8CUE3	Aminotran_1_2 domain-containing protein	187.34	16	7	7	25	53500
S8DMR4	PPLase cyclophilin-type domain-containing protein	196.54	15	4	4	28	26576
S8CXJ8	Epimerase domain-containing protein	171.52	21	7	7	27	42213
S8E9K5	Chlorophyll a-b binding protein chloroplastic	223.79	32	10	10	28	23147
S8CV15	Superoxide dismutase	125.69	20	4	3	25	24518
S8DPI8	Chloroplast sedoheptulose-1 7-bisphosphatase	158.71	42	7	7	21	21945
S8D270	Vacuolar proton pump subunit B	223.32	23	9	9	22	54294
S8CGU2	Uncharacterized protein	162.77	26	4	4	24	16456
S8CMY8	Histone H2A	132.12	25	3	3	22	16340
S8DUY5	Fructose-bisphosphate aldolase	155.18	19	4	0	25	23145
S8D903	Uncharacterized protein	190.40	28	7	7	24	44176
S8CH69	Gp_dh_N domain-containing protein	243.22	34	10	5	23	21054
S8C8L5	Tubulin beta chain	139.37	9	3	1	21	49498
S8CGR9	Cytochrome b6-f complex iron-sulfur subunit	161.50	18	4	4	23	23864
S8E1F6	Luminal-binding protein 5	205.28	12	8	4	23	72872
S8BWD8	Iso_dh domain-containing protein	142.75	10	4	1	19	46579
S8CS62	Uncharacterized protein	201.31	25	8	8	23	15058
S8C9G3	Aspartate aminotransferase	129.15	29	4	4	22	21786
A0A2I6QD64	Cytochrome b559 subunit alpha	122.37	37	4	2	19	9315
S8D4L6	Uncharacterized protein	167.84	19	6	6	18	28175
S8DIH8	PSII_BNR domain-containing protein	193.25	31	7	7	21	38467
S8CSI1	Precursor of carboxylase p-protein 1 glycine decarboxylase complex	187.95	18	9	9	21	44701
S8D0Y2	Precursor of protein cell division protease ftsh-like protein	149.92	12	7	7	21	74450
S8E8N2	Uncharacterized protein	113.90	16	3	3	21	14363
A0A2I6QD80	Cytochrome b6-f complex subunit 4	69.84	6	1	1	18	17401
S8CU40	Aldedh domain-containing protein	189.73	15	7	7	21	52882
S8CK62	Uncharacterized protein	173.50	21	8	8	17	46703

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
S8E6J2	Iso_dh domain-containing protein	151.31	10	4	1	17	46097
S8CXR1	Uncharacterized protein	163.72	16	6	6	20	34336
S8CGH1	Tubulin beta chain	138.11	10	3	1	17	49649
S8CDY1	Tubulin alpha chain	151.00	13	4	2	17	44821
S8E5C8	Malate dehydrogenase	148.87	20	6	6	15	35533
S8D400	Uncharacterized protein	173.12	21	5	3	21	31252
S8D065	Uncharacterized protein	197.90	30	6	6	18	25508
S8D1L1	Cytochrome b559 subunit alpha	107.23	33	3	1	17	10673
Q6USJ7	Ribulose biphosphate carboxylase large chain	60.24	5	1	1	18	48542
S8CXH8	Quinone oxidoreductase-like protein	191.37	19	8	8	16	34621
S8CCA7	Uncharacterized protein	146.73	10	5	5	15	41348
S8CBH1	Peptidyl-prolyl cis-trans isomerase	156.83	11	2	2	16	18111
S8E581	Tubulin alpha chain	134.90	16	3	1	17	29585
S8E6J7	Expansin-like EG45 domain-containing protein	75.60	10	1	1	16	13172
Q0ZPA3	Plastid lipid associated protein CHRC	102.34	9	2	0	19	35650
S8C765	Uncharacterized protein	158.55	8	4	4	15	68942
S8CGC3	Dihydrolipoyl dehydrogenase	169.65	17	6	6	14	50261
S8CRI9	Stachyose synthase	174.78	5	4	4	17	94627
S8E5Q8	Mitochondrial processing peptidase	146.40	12	4	4	14	58684
S8EK09	14-3-3 a-1 protein	200.70	18	6	1	15	28616
S8DSK8	Uncharacterized protein	167.14	11	5	5	16	31992
S8EBF2	GTP-binding nuclear protein	169.49	24	6	6	17	25082
S8D4Q8	Uncharacterized protein	163.85	23	5	5	17	22481
S8CKD0	Nucleoside diphosphate kinase	157.82	32	5	5	18	16488
S8CTT6	Uncharacterized protein	106.15	25	3	3	15	20623
S8C1I3	Chlorophyll a-b binding protein chloroplastic	171.13	16	5	4	15	19844
A0A5B7A6S3	Uncharacterized protein	93.66	7	2	1	15	43152
S8CNJ1	40S ribosomal protein S8	167.89	13	4	4	15	46307
S8EAS0	Mitochondrial benzaldehyde dehydrogenase	162.36	15	5	5	13	56190
S8CNM7	Fructokinase-like protein	187.70	23	5	5	16	33889
A0A2I6QE85	Ribulose biphosphate carboxylase large chain	135.09	5	4	0	7	52765
S8CC21	Uncharacterized protein	86.61	18	1	1	15	7483
S8D2Z7	Phosphoenolpyruvate carboxykinase	194.49	11	6	6	13	71071
S8EC22	Photosystem II CP47 reaction center protein	134.07	7	3	1	15	43023
S8BXZ7	Ribosomal_S7 domain-containing protein	138.75	30	3	3	14	10607
S8DLB7	S5 DRBM domain-containing protein	125.25	9	2	2	15	27967
S8C7U2	Uncharacterized protein	159.76	23	4	4	15	21947
S8C037	Uncharacterized protein	83.68	4	1	1	15	29587
S8D6C0	Thioredoxin domain-containing protein	140.95	24	4	4	13	19658
A0A0A0Y4Q2	Fibrillin 1 protein	97.06	9	2	0	15	35230
S8CEN8	Uncharacterized protein	143.55	16	8	8	10	85842
S8CMR4	Methionine synthase	147.48	8	5	2	14	84912
S8CV70	Glycolate oxidase	107.20	15	3	1	12	39095
S8DIS1	Triosephosphate isomerase	201.35	30	8	8	14	33401

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
S8DYB4	Malate dehydrogenase	63.88	4	1	1	13	33107
S8CDH5	Ribos_L4_asso_C domain-containing protein	130.00	19	5	5	12	38779
S8D949	Chloroplast chaperonin 21	153.90	13	4	4	15	30888
S8CHY4	Uncharacterized protein	120.30	5	3	3	12	83432
S8CF09	Clp_N domain-containing protein	122.01	20	2	2	15	21161
A0A2G9FWJ5	Uncharacterized protein	68.53	9	1	1	13	15978
S8C4P9	GST N-terminal domain-containing protein	107.80	11	3	3	13	29141
A0A5B6YNS3	Putative chaperonin 60 subunit beta 2	106.24	7	3	2	10	64320
S8DYR8	CoA_binding domain-containing protein	94.39	10	2	2	13	34346
S8CCI5	Uncharacterized protein	160.41	23	4	1	13	26552
S8C9K9	Malic enzyme	144.85	17	5	5	11	48720
S8E2K9	Uncharacterized protein	47.42	0	1	1	7	389080
S8EEI2	Methionine synthase	136.40	7	4	0	13	91588
S8E3C6	HATPase_c domain-containing protein	139.50	11	4	1	12	51710
S8C8U7	Ribosomal_L7Ae domain-containing protein	85.09	10	2	2	10	29671
S8CRG9	AA_TRNA_LIGASE_II domain-containing protein	165.45	9	5	5	12	69114
S8E1E6	Uncharacterized protein	115.33	5	4	1	6	110222
S8E9X0	Uncharacterized protein	75.55	11	1	1	12	14339
S8CHW1	FBPase domain-containing protein	150.97	13	3	3	7	36790
S8EDZ6	Formate dehydrogenase mitochondrial	132.08	10	2	2	10	42740
S8DZG3	Peptide methionine sulfoxide reductase	78.32	7	2	2	5	27876
S8EJ11	Adenosylhomocysteinase	93.44	4	2	2	11	62251
Q67HJ0	Cytochrome b559 subunit alpha	56.11	16	1	1	10	8598
S8DH12	SOR_SNZ domain-containing protein	119.43	5	2	2	7	33231
S8CCZ2	KH type-2 domain-containing protein	139.15	17	3	3	9	26011
S8CTL4	6-phosphogluconate dehydrogenase decarboxylating	94.66	6	3	3	6	55583
S8E780	Uncharacterized protein	128.84	11	4	3	7	51920
S8C490	ADK_lid domain-containing protein	107.92	10	2	2	9	26381
S8C1N1	Calreticulin	112.51	23	2	2	10	8837
S8E1B9	Superoxide dismutase	78.17	3	1	0	8	31020
S8D528	CAAD domain-containing protein	108.18	7	3	3	6	16701
S8CIQ9	Uncharacterized protein	89.61	13	3	3	8	33988
S8CDW0	NAD(P)-bd_dom domain-containing protein	67.20	5	1	1	11	28007
S8CSD6	Uncharacterized protein	96.55	16	2	2	7	23443
S8CIS6	PAP_fibrillin domain-containing protein	85.31	9	2	2	10	24661
A0A2I6QE76	ATP synthase epsilon chain chloroplastic	138.91	28	3	2	10	14633
A0A1S2Y8F1	isoflavone reductase-like protein	67.32	4	1	1	10	34235
S8D170	Actin-depolymerizing factor	81.50	8	1	1	11	16524
A0A4P1REH7	Germin-like protein	67.55	5	2	2	5	22364
S8C6W0	IBB domain-containing protein	129.47	4	3	3	7	58930
S8EKZ6	PDZ domain-containing protein	164.88	13	5	5	10	43791
S8CVY3	Extracellular calcium sensing receptor	207.41	22	9	9	10	39377
S8CX13	60S ribosomal protein L13	77.72	5	1	1	8	23705

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
S8EAM5	14-3-3 protein	97.69	14	3	2	8	27562
S8C5Q3	Uncharacterized protein	136.58	15	3	3	8	25647
A0A024HR93	Ribulose biphosphate carboxylase large chain	75.41	2	1	0	2	45424
I1ULG6	Ribulose biphosphate carboxylase large chain	85.53	15	2	1	3	20367
S8EDN5	NAD(P)-bd_dom domain-containing protein	174.10	13	3	3	8	39811
S8CL66	Rieske domain-containing protein	146.99	12	2	2	7	28316
W1IK53	ATP synthase subunit alpha chloroplastic	101.56	6	2	0	7	55240
A0A1R3I2S6	PAP_fibrillin domain-containing protein	106.93	9	2	0	8	35485
A0A426Y333	Nucleoside diphosphate kinase	56.03	9	1	1	8	20361
S8D0H0	Elongation factor Tu	136.35	4	2	2	9	48862
S8BTK9	Uncharacterized protein	86.93	11	1	1	8	19863
S8C3Z8	Phosphoenolpyruvate carboxylase	120.23	7	4	1	6	75837
S8DNI1	NmrA domain-containing protein	121.87	14	4	3	5	35984
S8D2R1	Alcohol dehydrogenase	135.23	10	4	4	8	32947
S8CMA5	Uncharacterized protein	130.08	26	4	4	7	17870
A0A2I6QD54	ATP synthase epsilon chain chloroplastic	101.07	36	4	1	7	14687
S8D988	Uncharacterized protein	106.27	5	2	2	9	53316
S8E383	RRM domain-containing protein	52.86	6	1	1	8	17159
S8DSS9	Glucose-1-phosphate adenylyltransferase	140.20	14	5	5	7	54796
S8BUN5	Nucleoside diphosphate kinase	66.65	5	1	1	8	25740
A0A2G9IBF3	Molecular chaperones mortalin/PBP74/GRP75 HSP70 superfamily	105.15	5	3	3	9	74975
S8BSE7	Uncharacterized protein	74.33	14	1	1	8	10928
S8CE21	Peptidyl-prolyl cis-trans isomerase	128.03	31	4	4	7	18065
O81372	Nucleoside diphosphate kinase 1	76.87	9	1	1	8	16351
A0A2G9GMS2	PAP_fibrillin domain-containing protein	101.25	8	2	0	8	34493
Q8WKQ8	Ribulose biphosphate carboxylase large chain	91.67	7	2	1	8	49232
S8CP12	Aldo_ket_red domain-containing protein	127.31	8	3	3	7	36756
S8D3B8	PHB domain-containing protein	144.28	15	4	4	7	30974
S8CWY3	Uncharacterized protein	100.59	14	3	3	5	30361
S8CFQ6	Fructose-bisphosphate aldolase	83.89	7	1	1	7	21624
S8E3P5	PHB domain-containing protein	97.16	10	2	2	8	31338
S8C3Y2	Uncharacterized protein	97.84	11	3	3	6	33647
S8BSC9	40S ribosomal protein S24	91.45	11	1	1	8	15741
S8DPM6	Glucose-1-phosphate adenylyltransferase	112.57	8	3	3	7	51441
S8C9Q9	Hydroxypyruvate reductase	111.57	8	3	3	5	42463
S8C2S9	Uncharacterized protein	83.55	9	1	1	6	17833
S8DM13	Uncharacterized protein	87.26	6	2	2	6	31931
S8CWB2	p0 ribosomal protein-like protein	88.38	7	2	2	7	35081
S8BST7	S5 DRBM domain-containing protein	58.88	6	1	1	7	23294
S8D413	Geraniol dehydrogenase 1	74.10	4	1	1	6	38352
S8CLT2	Allene oxide cyclase	118.12	15	2	2	8	19253
S8CUF0	Uncharacterized protein	89.75	11	2	2	5	25386
S8DSD6	Cysteine synthase	91.15	7	2	2	6	34557

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
S8E4S5	Eukaryotic translation initiation factor 5A	51.17	6	1	1	5	17356
S8DS50	Uncharacterized protein	116.16	19	3	3	6	19985
S8D544	Uncharacterized protein	46.93	7	1	1	7	16810
S8C3B0	2-methyl-6-phytylbenzoquinone methyltransferase	99.78	14	3	3	7	31996
S8E788	PAP_fibrillin domain-containing protein	81.80	7	2	2	7	21847
S8BT37	Glutathione reductase	88.86	8	2	2	8	44877
S8CBR9	Peroxiredoxin	74.68	11	1	1	7	17000
W8SQU3	Chlorophyll a-b binding protein chloroplastic	57.89	6	1	1	6	20241
A0A453L9A1	Pyruvate dehydrogenase E1 component subunit beta	74.24	4	1	1	3	31214
K7MM65	AhpC-TSA domain-containing protein	75.70	11	1	1	8	14291
S8CL08	Thylakoid-bound ascorbate peroxidase	179.18	17	6	5	6	39191
S8CM36	Ribosomal_L6e_N domain-containing protein	92.04	12	2	2	6	26032
S8CET3	AAA domain-containing protein	85.61	7	2	2	5	40555
S8EEM8	Complex1_30kDa domain-containing protein	88.30	6	1	1	7	22534
S8CFK3	NAD(P)-bd_dom domain-containing protein	108.90	15	3	3	7	27811
S8C489	Remorin_C domain-containing protein	70.70	15	2	2	5	14841
S8ELH0	4Fe-4S ferredoxin-type domain-containing protein	122.22	18	2	0	6	8815
S8D431	Uncharacterized protein	115.21	15	3	1	7	31355
S8E121	Superoxide dismutase	74.88	12	2	2	4	25035
V4W5U2	Uncharacterized protein	76.32	5	2	2	4	63295
S8CXP8	TCTP domain-containing protein	64.87	5	1	1	5	18898
W9QUC7	Photosystem I reaction center subunit N	70.78	15	2	2	3	18288
S8CXH7	PsbP domain-containing protein	83.85	10	2	2	5	26904
A0A444FTJ0	Uncharacterized protein	84.52	10	3	1	5	45480
A0A4U5PYS7	Fructose-bisphosphate aldolase	72.23	6	2	1	6	42751
S8DTZ0	Cysteine synthase	66.93	16	1	1	7	7848
A0A2G2ZE93	photosystem I reaction center subunit XI chloroplastic-like	123.50	15	3	3	7	23120
M5X8P7	NDK domain-containing protein	84.19	17	1	1	6	10557
A0A444XLN7	TPM_phosphatase domain-containing protein	62.13	6	1	1	6	23776
Q32434	Ribulose bisphosphate carboxylase large chain	56.17	4	1	1	5	52630
S8CRG0	HATPase_c domain-containing protein	89.02	4	3	3	6	93194
S8EJW3	ANK_REP_REGION domain-containing protein	81.34	5	1	1	6	33258
S8CXK0	PHB domain-containing protein	91.30	6	1	1	5	30498
S8CSL6	Aldo_ket_red domain-containing protein	77.16	4	1	1	4	40145
S8EBQ7	Nucleoside diphosphate kinase	138.44	24	4	4	6	18110
S8DNC6	Uncharacterized protein	84.81	2	1	1	5	74183
A0A2I6QD88	50S ribosomal protein L2 chloroplastic	69.21	12	2	2	2	29876
S8CSI2	S-adenosylmethionine synthase	83.80	4	2	2	2	42727
M0ZSM1	Uncharacterized protein	95.60	7	3	1	5	34962
S8DEB4	Uncharacterized protein	72.12	6	1	1	4	22749
B9SGR9	L-ascorbate peroxidase cytosolic putative	59.48	4	1	0	1	28776
S8CV45	Protein disulfide-isomerase	56.91	2	1	1	6	48477
S8DT71	Uncharacterized protein	82.37	12	2	2	5	23224

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
S8C309	Alpha-galactosidase	98.72	8	2	2	4	41792
A0A2I6QD87	50S ribosomal protein L16 chloroplastic	62.66	10	1	1	4	15500
S8BXS5	Uncharacterized protein	52.48	6	1	1	3	21147
S8E3U3	Uncharacterized protein	48.36	2	1	1	4	47846
S8D3V6	Uncharacterized protein	67.15	20	2	2	3	12131
A0A4D9BLA3	Carbonic anhydrase	60.53	5	1	1	6	36205
A0A4Y7J1J5	Uncharacterized protein	74.93	4	1	1	6	44481
S8BYG4	14-3-3 protein	83.43	8	2	0	2	28271
S8C2L7	Enolase	108.53	20	4	4	4	31628
S8CA49	Ribosomal_L16 domain-containing protein	97.50	14	4	4	5	24216
S8CJE3	Ribosomal_L2_C domain-containing protein	92.08	12	2	2	3	28113
S8EDK9	Uncharacterized protein	62.54	9	2	2	2	23641
S8CA82	Ribosomal_L18_c domain-containing protein	61.72	6	1	1	3	27431
S8BYT7	Uncharacterized protein	51.63	8	1	1	3	15545
O47073	Ribulose biphosphate carboxylase large chain	65.08	6	2	0	2	44332
Q43848	Transketolase chloroplastic	72.94	2	1	1	1	79992
S8CYA5	PAP_fibrillin domain-containing protein	85.22	4	2	2	5	35076
A0A5A7R1Y0	Cold shock protein 1	61.87	8	1	1	5	19746
S8CBV7	PDZ domain-containing protein	91.51	17	2	2	5	9737
M8BRS6	Putative 2-Cys peroxiredoxin BAS1 chloroplastic	55.24	7	1	1	4	22811
A0A2C9U8K7	PAP_fibrillin domain-containing protein	95.97	8	2	0	4	35273
A0A4U5NMA0	PAP_fibrillin domain-containing protein	53.40	5	1	1	4	27774
S8DNX3	Uncharacterized protein	107.07	7	1	0	2	41501
S8DN02	Uncharacterized protein	79.76	5	2	2	4	53747
S8CXQ3	Uncharacterized protein	67.55	3	2	1	4	117486
S8CAH8	NAD(P)-bd_dom domain-containing protein	94.32	5	1	1	4	28768
S8CQK5	Ribosomal protein	79.29	11	2	2	4	33075
S8DW35	Uncharacterized protein	130.13	14	3	3	4	36011
S8C5N3	Uncharacterized protein	79.66	10	2	0	2	24086
S8CYW0	Uncharacterized protein	73.76	7	2	2	3	36670
S8CDH4	Uncharacterized protein	67.92	5	1	1	3	23550
S8CAI9	Uncharacterized protein	46.88	3	1	1	3	43085
S8CPQ1	Cupin_2 domain-containing protein	82.32	3	1	1	2	33309
S8DRL0	Uncharacterized protein	103.75	7	2	2	4	24320
S8EFY6	Aldo_ket_red domain-containing protein	83.41	8	2	2	4	37890
S8BWT7	Enolase	83.01	14	1	1	4	11666
S8EE25	Subtilase family protein	103.65	3	2	2	4	78807
S8CMJ8	Succinate-CoA ligase subunit beta	91.13	6	2	2	2	44740
S8D4E0	Cytochrome c oxidase subunit 2	69.77	13	1	1	3	17075
S8D555	Uncharacterized protein	80.43	5	1	1	3	17608
S8D0M9	NmrA domain-containing protein	96.66	5	1	1	2	36842
S8CXD9	Uncharacterized protein	82.94	18	1	1	4	10122
S8C019	Guanine nucleotide regulatory protein	79.33	17	2	0	2	15063

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
S8CG22	Ferritin	56.53	4	1	1	2	25026
A0A2I4EHK1	L-ascorbate peroxidase cytosolic	66.37	9	2	0	2	27398
A0A3S8TL14	Ascorbate peroxidase	61.98	8	2	1	2	27103
S8CM96	Cysteine proteinase	88.57	9	2	2	4	36744
S8C7X0	TauD domain-containing protein	67.12	4	1	1	3	35814
A0A2G9GAZ9	Iridoid synthase	48.30	4	1	1	4	44754
S8DP00	Uncharacterized protein	46.70	8	1	1	2	24373
S8D3H5	Chlorophyll a-b binding protein chloroplastic	103.38	17	2	2	3	28049
S8C3R9	Malic enzyme	72.16	6	1	1	4	16686
A0A4D9BCT0	NmrA domain-containing protein	69.98	4	1	1	2	34215
A0A2G3C7W3	ATP synthase subunit b' chloroplastic	79.75	12	2	2	4	14682
Q9AWA8	Glutamine synthetase	85.19	7	2	1	4	47431
A0A4D6NK45	F-type H ⁺ -transporting ATPase subunit beta	77.40	4	1	1	4	63911
S8D3D9	Glyceraldehyde-3-phosphate dehydrogenase	86.52	4	1	0	1	42406
S8C1V8	APH domain-containing protein	87.51	6	2	2	3	47897
S8D4U2	14_3_3 domain-containing protein	73.71	9	2	2	3	24906
S8BZX0	SHSP domain-containing protein	48.70	6	1	1	1	22021
S8D2V7	Uncharacterized protein	74.20	2	1	1	2	101130
S8CML0	Elongation factor 1 gamma-like protein	92.66	5	1	1	2	48208
S8EFM1	Peroxidase	50.79	3	1	1	2	32597
S8CZZ6	Phosphotransferase	74.69	3	1	1	3	53502
S8CX39	Alpha-galactosidase	73.49	4	2	2	3	47057
S8EAY5	FAD_binding_2 domain-containing protein	78.79	4	1	1	3	35117
S8EAQ4	Peptidase A1 domain-containing protein	73.77	2	1	1	2	44749
S8CHV8	Betaine aldehyde dehydrogenase	59.54	4	1	1	2	36196
S8BWK0	Tr-type G domain-containing protein	66.05	3	1	1	2	67552
S8BZB0	Chloroplast lipocalin	67.71	3	1	1	2	30767
S8EMJ4	ATP-dependent Clp protease proteolytic subunit	48.73	5	1	1	2	31466
S8DWP6	Xylose isomerase	58.10	3	1	1	2	52649
S8D762	Uncharacterized protein	80.96	17	2	2	3	22861
S8CSZ2	Glutamate decarboxylase	51.32	3	1	1	2	57215
S8E095	Heat shock protein 90	69.36	6	1	1	3	24466
S8DA95	Uncharacterized protein	55.08	8	1	1	2	16751
S8DDT9	Ribosomal_L5 domain-containing protein	59.66	19	1	1	3	8377
B7FJ53	Uncharacterized protein	86.22	10	2	1	2	28070
S8DJJ3	Aspartate aminotransferase	46.69	3	1	1	1	47772
S8C0M0	Uncharacterized protein	51.86	17	1	1	2	8483
Q33585	Ribulose biphosphate carboxylase large chain	66.42	5	2	0	2	52728
A0A1S3UFS1	Fructose-bisphosphate aldolase	77.33	7	2	0	3	38405
W9R689	Uncharacterized protein	72.28	4	1	1	3	45131
S8C612	Uncharacterized protein	55.99	11	1	1	3	14776
A0A4S8IYE1	Uncharacterized protein	75.46	3	1	1	2	60732
A0A2G9H7L1	Cysteine proteinase Cathepsin L	94.73	7	2	2	3	51892

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
A0A4D8Y9C2	Chaperonin GroEL	93.74	3	2	1	3	104477
A0A1U8F7J0	Adenosylhomocysteinase	86.96	4	1	1	3	53187
S8CP19	Peptidyl-prolyl cis-trans isomerase	65.61	4	1	1	1	19817
S8CIS0	ATP-dependent Clp protease proteolytic subunit	48.40	4	1	1	2	43045
S8D409	Uncharacterized protein	52.78	3	1	1	2	39404
S8DRZ1	Aspartate aminotransferase	70.87	6	1	1	2	25822
S8CLS8	Inorganic pyrophosphatase	56.60	2	1	1	1	80063
A0A5A7RAZ6	Ferredoxin--NADP reductase	59.07	3	1	1	1	40694
S8DMW3	Uncharacterized protein	77.14	3	1	1	1	41431
S8CUH2	Lipocln_cytosolic_FA-bd_dom domain-containing protein	62.51	11	2	2	2	20907
S8E759	Isopentenyl pyrophosphate isomerase	56.27	5	1	1	2	27580
S8EEI7	V-type proton ATPase subunit G	61.69	10	1	1	1	11953
S8CP75	Proteasome subunit alpha type	46.33	5	1	1	1	25867
S8CZU4	DHO_dh domain-containing protein	49.22	2	1	1	2	42816
S8CZ12	Calmodulin	62.58	11	2	2	2	16848
S8CIS4	Cysteine synthase	61.12	14	2	2	2	27387
S8EDR7	10-formyltetrahydrofolate synthetase	50.79	2	1	1	1	67864
S8DJF6	S10_plectin domain-containing protein	47.72	7	1	1	1	19649
S8CG73	PPIase cyclophilin-type domain-containing protein	46.25	4	1	1	1	31467
A0A388K5H9	Chlorophyll a-b binding protein chloroplastic	84.63	4	2	1	2	27179
G7JPH8	Photosystem II stability/assembly factor HCF136	60.85	4	1	1	1	43691
X2D1B6	Ribulose biphosphate carboxylase large chain	69.75	7	2	0	2	44583
S8D856	Uncharacterized protein	61.97	15	1	1	2	8228
M1D096	ATP synthase subunit beta	48.97	4	1	1	2	59569
S8CHE8	WD_REPEATS_REGION domain-containing protein	55.00	3	1	1	2	46979
A0A484K5I4	Uncharacterized protein	77.16	4	2	0	2	64290
V9PE85	ATP synthase subunit beta chloroplastic	103.44	4	1	1	2	53578
A0A4Y7KRT9	Uncharacterized protein	66.71	4	1	1	1	29648
A0A0B2R4F5	Transketolase chloroplastic	51.47	2	1	1	1	80079
S8DVQ7	Uncharacterized protein	51.45	8	1	1	2	24117
A9NVA3	Phosphoglycerate kinase	76.09	6	2	1	2	52938
S8DV76	Ribosomal_L18e/L15P domain-containing protein	77.38	12	2	2	2	20993
A0A1J7HAM6	Thioredoxin	47.71	9	1	1	2	13078
S8CMZ7	Uncharacterized protein	46.43	13	1	1	2	15044
A0A2I6QE99	Photosystem II CP47 reaction center protein	70.76	3	1	1	1	55960
A0A022QWP2	Dihydrolipoyl dehydrogenase	60.77	2	1	1	2	53563
A0A2R6R3T3	Glyceraldehyde-3-phosphate dehydrogenase	66.78	4	1	1	2	48117
A0A2G3BID8	Monodehydroascorbate reductase	61.00	4	1	1	2	45698
A0A4P1REY1	Uncharacterized protein	55.45	3	1	1	2	51454
A0A5A7QTK3	Oxygen-evolving enhancer protein 2	46.02	5	1	1	2	29442
A0A4D9BSX4	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	76.18	4	2	1	2	84638
A0A087SHJ4	Peptidyl-prolyl cis-trans isomerase	85.87	15	2	2	2	23892

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
A0A2I4F2B2	Fructose-bisphosphate aldolase	80.72	6	1	1	2	38399
A0A4D8YMP6	Ribulose-phosphate 3-epimerase	73.48	9	1	1	2	16911
A0A022RPY1	Chitin-binding type-1 domain-containing protein	73.91	6	1	1	2	29053
M0TDY7	Uncharacterized protein	47.71	32	1	1	2	4622
S8BT19	Uncharacterized protein	46.44	6	1	1	1	22981
S8CLG1	Geraniol dehydrogenase 1	66.44	6	1	1	1	39126
S8CXM5	Uncharacterized protein	50.92	2	1	1	1	87020
S8CYB6	AIG1-type G domain-containing protein	48.71	3	1	1	1	33462
S8C9L2	S4 RNA-binding domain-containing protein	54.50	5	1	1	1	29634
S8E3C7	Uncharacterized protein	54.91	5	1	1	1	25239
S8CLA5	SRP54 domain-containing protein	49.92	3	1	1	1	52483
S8BYC7	Geranylgeranyl reductase	74.34	11	1	1	1	18860
S8DEF5	Geranylgeranyl reductase	74.34	11	1	1	1	18950
S8CCK1	Uncharacterized protein	59.75	4	1	1	1	34158
S8CQT5	Uncharacterized protein	47.69	7	1	1	1	13139
S8D6L3	NADPH-protochlorophyllide oxidoreductase	50.33	5	1	1	1	37950
S8CF55	Uncharacterized protein	55.01	10	1	1	1	22668
S8CJD3	Glucose-6-phosphate 1-dehydrogenase	51.72	2	1	1	1	59952
S8D453	30S ribosomal protein S7 chloroplastic	46.84	12	1	1	1	17347
S8CEY0	Beta-hydroxyacyl-acyl carrier protein dehydratase	49.02	4	1	1	1	23686
S8ECI2	30S ribosomal protein S14 chloroplastic	50.10	10	1	1	1	11832
S8CGN1	Epimerase domain-containing protein	53.16	4	1	1	1	42515
S8C347	2-C-methyl-D-erythritol 2 4-cyclodiphosphate synthase	65.92	8	1	1	1	24401
A0A5A7QH3	Fructose-1 6-bisphosphatase class 1	59.06	5	1	1	1	40586
S8DS25	Iso_dh domain-containing protein	56.14	3	1	1	1	37206
S8C3H3	Uncharacterized protein	54.26	2	1	1	1	70721
S8EC55	PfkB domain-containing protein	47.85	6	1	1	1	32166
A0A5E4EDM5	PREDICTED: L-ascorbate peroxidase	46.53	5	1	0	1	40099
S8ED92	Usp domain-containing protein	46.12	4	1	1	1	25076
Q9LKZ0	Chlorophyll a-b binding protein chloroplastic	53.17	11	1	1	1	16677
A0A068U890	Aminomethyltransferase	46.53	3	1	1	1	48037
A0A4D9B866	Chlorophyll a-b binding protein chloroplastic	46.70	5	1	1	1	28029
A0A2U1PVG5	Band 7 protein	49.35	5	1	1	1	33970
S8D037	Uncharacterized protein	67.27	10	1	1	1	13142
B9RVK2	Ribosomal protein	48.88	4	1	1	1	38746
A0A5B7AL20	Putative Ribosomal protein S10p/S20e family protein isoform 1	47.11	11	1	1	1	11943
S8E4K0	Germin-like protein	67.85	11	1	1	1	21469
V4U6P5	Carbonic anhydrase	62.68	6	1	1	1	31586
K3XGJ1	Serine hydroxymethyltransferase	61.96	3	1	1	1	57274
A0A067JCX4	Peroxidase	59.20	5	1	1	1	35045
Q9LKY5	Tubulin alpha chain	56.07	9	1	1	1	17771
Q677D0	Chlorophyll a-b binding protein chloroplastic	53.70	6	1	1	1	22495
A0A5A7RBM6	Photosystem II CP43 chlorophyll apoprotein	48.11	3	1	1	1	65358

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
A0A2P5WF81	Uncharacterized protein	47.04	3	1	1	1	55501
A0A1J6ID15	Dihydrolipoyl dehydrogenase	46.50	4	1	1	1	53470
S8CBU5	Uncharacterized protein	48.60	15	1	1	1	11127

Table S5. Identified proteins with PEAKS in traps of the *Genlisea violacea* purple-flowered morphotype.

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
S8CWK8	Ubiquitin-like domain-containing protein	155.54	24	4	1	89	14799
S8CYV8	Histone H4	170.74	36	6	6	81	11409
A0A2I6QD52	Ribulose biphosphate carboxylase large chain	197.10	23	10	6	58	52828
S8E2N0	Histone H3	121.87	20	4	1	27	15268
S8CBN4	Histone H3	122.60	20	4	1	28	15406
S8DPH5	Uncharacterized protein	143.08	8	4	1	45	69648
S8C6K2	Heat shock protein 70	143.39	8	4	1	44	71263
S8CRU7	Actin	147.63	8	4	1	41	41788
S8CBA2	Chlorophyll a-b binding protein chloroplastic	147.66	17	3	3	41	28144
S8ENH4	Histone H2B	113.43	18	3	3	22	16419
S8CSZ4	Actin-97	129.43	6	3	0	35	41746
S8CMY8	Histone H2A	81.00	6	1	1	31	16340
S8EF74	ATP synthase subunit alpha	161.09	12	5	5	19	54983
S8CX03	Uncharacterized protein	119.37	7	3	3	19	41206
S8ELF0	Ribulose biphosphate carboxylase large chain	139.17	9	5	1	18	54568
S8E6J7	Expansin-like EG45 domain-containing protein	80.63	10	1	1	21	13172
S8BWD8	Iso_dh domain-containing protein	100.47	6	2	2	18	46579
S8CI40	Elongation factor 1-alpha	130.90	7	3	3	9	48652
S8DD77	Actin	129.58	10	3	3	14	32298
S8CL73	Peroxidase	77.15	6	2	2	9	33296
S8D4W0	Malate dehydrogenase	81.87	4	2	2	7	37424
S8DR98	Uncharacterized protein	99.27	16	2	2	13	16068
S8BZF0	Monodehydroascorbate reductase	95.78	8	3	3	7	47113
S8E1F6	Luminal-binding protein 5	95.38	3	2	1	8	72872
S8DLT5	14-3-3 h-1 protein	64.69	4	1	1	6	28683
S8E4S5	Eukaryotic translation initiation factor 5A	51.24	6	1	1	8	17356
S8CIP5	Tr-type G domain-containing protein	127.17	6	4	4	9	93742
S8D4L6	Uncharacterized protein	109.97	11	2	2	8	28175
S8EAM5	14-3-3 protein	69.71	5	1	1	6	27562
S8D2K5	Fructose-bisphosphate aldolase	94.10	2	1	1	4	38302
S8EJ11	Adenosylhomocysteinase	84.13	2	2	2	5	62251
S8C9X5	Ribulose biphosphate carboxylase small chain	68.51	5	1	1	2	19266
A0A2I6QD25	Photosystem II protein D1	69.34	4	1	1	9	38945
S8CSD6	Uncharacterized protein	72.24	4	1	1	5	23443
S8EBF2	GTP-binding nuclear protein	95.02	9	2	2	8	25082
S8DFN4	HATPase_c domain-containing protein	80.19	4	2	2	3	80152

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
S8DLP5	Aconitate hydratase	62.10	1	1	1	4	93970
S8DAF4	Photosystem II CP43 reaction center protein	70.04	3	1	1	7	51932
S8CTL4	6-phosphogluconate dehydrogenase decarboxylating	91.05	6	3	3	3	55583
S8CWY3	Uncharacterized protein	77.56	4	1	1	2	30361
S8CAG8	Fructose-bisphosphate aldolase	59.28	3	1	1	4	37786
S8C857	ATP synthase subunit beta	101.05	4	2	2	3	57058
S8CUF0	Uncharacterized protein	59.32	4	1	1	1	25386
S8E5Q8	Mitochondrial processing peptidase	64.25	4	2	2	2	58684
S8DEF3	Glyceraldehyde-3-phosphate dehydrogenase	69.51	4	1	1	2	36532
S8DDM8	Uncharacterized protein	78.64	5	1	0	1	23938
S8CGC3	Dihydrolipoyl dehydrogenase	58.01	2	1	1	2	50261
S8CYK9	Uncharacterized protein	67.45	8	2	1	2	26555
S8DNI1	NmrA domain-containing protein	62.29	3	1	1	1	35984
S8D4F2	AAA domain-containing protein	55.76	2	1	1	3	65998
H2DK20	Cu/Zn superoxide dismutase	65.50	10	1	1	1	12508
A0A2P5F6N2	Hopanoid-associated sugar epimerase	53.35	4	1	1	1	34094

Table S6. Identified proteins with PEAKS in leaves of *Genlisea violacea* white-flowered morphotype.

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
A0A2I6QD52	Ribulose biphosphate carboxylase large chain	548.07	72	110	55	3373	52828
S8D398	Ribulose biphosphate carboxylase large chain	402.74	41	59	9	1314	48012
S8D4F2	AAA domain-containing protein	403.51	60	51	36	864	65998
S8C9X5	Ribulose biphosphate carboxylase small chain	286.20	35	25	24	790	19266
S8CBA2	Chlorophyll a-b binding protein chloroplastic	425.01	58	39	39	758	28144
S8ELF0	Ribulose biphosphate carboxylase large chain	366.26	41	38	4	491	54568
S8BX77	Glyceraldehyde-3-phosphate dehydrogenase	391.07	44	24	17	499	42461
S8D424	ATP synthase subunit alpha chloroplastic	314.67	38	26	19	533	55180
S8DCS9	AAA domain-containing protein	317.05	33	18	4	434	64784
S8CBV6	Oxygen-evolving enhancer protein 1 chloroplastic	361.72	51	33	31	389	34653
S8DZE1	Chlorophyll a-b binding protein chloroplastic	296.41	37	18	18	377	30811
S8E173	Phosphoglycerate kinase	336.56	50	24	19	367	50566
A0A2I6QD77	Photosystem II CP47 reaction center protein	338.90	32	22	22	357	55975
S8D525	Fructose-bisphosphate aldolase	316.10	57	19	6	296	38134
S8C8K3	ATPase_AAA_core domain-containing protein	372.65	51	22	22	296	35153
S8CXZ6	Chlorophyll a-b binding protein chloroplastic	326.83	32	23	23	269	51327
S8CAG8	Fructose-bisphosphate aldolase	323.87	41	19	7	234	37786
S8DLI4	Uncharacterized protein	279.05	32	11	11	241	22118
S8CTY8	Glycolate oxidase	259.00	53	19	17	213	39322
S8C857	ATP synthase subunit beta	323.09	45	19	18	201	57058
S8E474	Carbonic anhydrase	321.03	54	15	14	228	22765
S8E8M6	Chlorophyll a-b binding protein chloroplastic	232.80	17	13	13	201	57243
S8CVD3	Glyceraldehyde-3-phosphate dehydrogenase	330.90	30	16	9	184	46701
S8EC20	ATP synthase subunit alpha	203.10	16	7	2	204	54698
S8DI77	Uncharacterized protein	234.37	32	9	9	179	25784
S8EF74	ATP synthase subunit alpha	230.48	25	12	9	154	54983
S8CYV8	Histone H4	225.06	63	11	11	159	11409
S8ENB1	Apocytochrome f	277.67	30	14	9	151	47237
S8E4Y7	Uncharacterized protein	280.58	32	10	2	149	41708
A0A2I6QD25	Photosystem II protein D1	258.65	22	13	5	153	38945
S8DEF3	Glyceraldehyde-3-phosphate dehydrogenase	272.24	42	14	9	137	36532
S8D216	Chlorophyll a-b binding protein chloroplastic	250.53	35	11	11	126	27260
S8CDZ1	Uncharacterized protein	246.39	39	10	10	102	21516
S8DAF4	Photosystem II CP43 reaction center protein	337.86	37	19	19	135	51932
S8D0S6	ATP synthase subunit alpha	160.21	7	4	0	125	48951
S8D6P3	FAD-binding FR-type domain-containing protein	256.16	34	10	10	129	31236
A0A2I6QD42	Photosystem II D2 protein	214.31	19	9	9	120	39549
S8CSZ4	Actin-97	269.28	32	11	2	116	41746
S8CHM2	Phosphoglycerate kinase	261.40	24	9	4	117	42185

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
S8CRU7	Actin	240.50	27	8	1	110	41788
A0A2I6QD76	Cytochrome b6	167.97	21	4	4	109	24181
S8EE95	Uncharacterized protein	187.20	27	3	3	97	14796
S8CI40	Elongation factor 1-alpha	188.12	20	9	9	84	48652
A0A2I6QD64	Cytochrome b559 subunit alpha	158.48	48	5	2	85	9315
S8CFW3	Serine hydroxymethyltransferase	241.21	24	11	11	81	51711
S8CWK8	Ubiquitin-like domain-containing protein	159.43	24	4	4	82	14799
S8C474	Uncharacterized protein	198.23	26	10	10	87	40703
S8E1K9	Catalase	235.57	15	7	6	95	57099
S8E7B3	Uncharacterized protein	161.23	28	4	4	76	20658
S8CAG4	Phosphoribulokinase	299.05	40	13	13	72	42000
S8CA75	PEROXIDASE_4 domain-containing protein	189.48	39	8	8	83	23973
S8C8H1	Thioredoxin domain-containing protein	238.31	32	10	10	71	29355
A0A2I6QD51	Photosystem I P700 chlorophyll a apoprotein A2	226.84	13	9	6	81	82658
S8E065	Uncharacterized protein	188.77	35	11	11	57	25030
S8C6K2	Heat shock protein 70	273.42	23	15	1	78	71263
S8D8M8	Transket_pyr domain-containing protein	148.10	12	3	3	68	33978
S8EFG8	Histone H2B	166.10	40	6	6	55	16063
S8CVD5	PEROXIDASE_4 domain-containing protein	228.00	38	8	5	73	27543
S8D1L1	Cytochrome b559 subunit alpha	142.84	42	4	1	75	10673
S8CPA4	Uncharacterized protein	271.49	21	14	0	70	71144
S8E0E9	Triosephosphate isomerase	195.66	48	9	9	71	27341
S8D4J3	Glutamine synthetase	316.03	57	14	14	68	31188
S8DPH5	Uncharacterized protein	273.26	22	14	1	67	69648
S8DYF2	Aminomethyltransferase	176.45	22	6	6	64	43926
S8DFY8	Elongation factor Tu	228.59	23	9	9	63	51970
A0A2I6QD58	Photosystem I P700 chlorophyll a apoprotein A1	208.40	11	7	7	58	83068
S8DUY5	Fructose-bisphosphate aldolase	146.22	25	4	1	59	23145
S8ELF4	Photosystem II protein D1	233.76	15	9	1	60	38317
S8D4W0	Malate dehydrogenase	181.03	20	5	5	54	37424
S8D3C4	Uncharacterized protein	168.79	22	7	2	58	34316
S8DIK9	AAA domain-containing protein	225.70	22	10	10	62	73251
S8CV15	Superoxide dismutase	132.25	20	4	3	58	24518
S8D9H7	Uncharacterized protein	188.96	21	6	6	63	21894
S8CX03	Uncharacterized protein	175.79	18	7	2	57	41206
S8CS62	Uncharacterized protein	147.35	25	4	4	42	15058
S8E188	PsbP domain-containing protein	215.36	47	12	12	52	26970
S8C5P5	Thioredoxin domain-containing protein	215.32	64	11	11	49	16319
S8EDT4	Photosystem I iron-sulfur center	170.82	63	4	4	58	9022
S8E9K5	Chlorophyll a-b binding protein chloroplastic	192.00	36	6	6	56	23147
S8DFN4	HATPase_c domain-containing protein	190.34	9	5	5	52	80152
S8CMY8	Histone H2A	118.41	25	3	3	44	16340
S8D1U0	Glutamine amidotransferase type-2 domain-containing protein	221.38	11	12	12	46	2E+05

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
S8EAM3	Heat shock protein hsp70	230.36	12	10	0	42	68703
S8DNI1	NmrA domain-containing protein	148.13	23	7	5	41	35984
S8CRY5	Uncharacterized protein	220.08	21	11	11	37	61536
S8BXC1	Serine-glyoxylate aminotransferase	263.32	42	10	10	40	44089
S8BXF4	TRANSKETOLASE_1 domain-containing protein	182.09	25	8	8	35	46944
S8CU40	Aldedh domain-containing protein	183.47	15	7	7	47	52882
S8C3Q5	Chloroplast heat shock protein 70-2	193.60	21	7	7	33	31402
S8CQW3	Malate dehydrogenase	178.45	15	6	6	42	47366
S8CGU2	Uncharacterized protein	144.66	26	3	3	37	16456
S8D2K5	Fructose-bisphosphate aldolase	259.26	36	11	8	33	38302
S8E5C8	Malate dehydrogenase	137.81	16	5	5	27	35533
S8CWV4	Glycine cleavage system P protein	191.03	12	7	7	36	60737
S8D270	Vacuolar proton pump subunit B	204.56	26	8	8	41	54294
S8DD77	Actin	190.86	20	5	2	40	32298
A0A5B7A6S3	Uncharacterized protein	107.91	7	2	1	37	43152
S8E6J7	Expansin-like EG45 domain-containing protein	100.87	10	1	1	38	13172
S8CXJ8	Epimerase domain-containing protein	197.41	21	8	8	30	42213
S8D7P3	Uncharacterized protein	137.74	3	3	0	36	82350
S8C3A0	Chloroplast sedoheptulose-1,7-bisphosphatase	172.34	54	7	7	33	13663
S8E2N0	Histone H3	118.48	20	4	1	24	15268
S8E9X0	Uncharacterized protein	77.18	11	1	1	33	14339
S8CBH1	Peptidyl-prolyl cis-trans isomerase	137.67	16	2	2	37	18111
S8DPI8	Chloroplast sedoheptulose-1,7-bisphosphatase	144.39	29	6	6	35	21945
S8CBN4	Histone H3	119.03	20	4	1	22	15406
S8E8N2	Uncharacterized protein	117.87	16	3	3	24	14363
S8C1I3	Chlorophyll a-b binding protein chloroplastic	180.94	16	5	4	33	19844
A0A2I6QE76	ATP synthase epsilon chain chloroplastic	146.18	27	2	1	36	14633
S8CTT6	Uncharacterized protein	131.54	31	4	4	18	20623
A0A4D9A0J4	Photosystem II oxygen-evolving enhancer protein 2	59.90	4	1	1	32	28110
S8DTS5	Uncharacterized protein	175.97	36	5	5	28	20590
S8CXH8	Quinone oxidoreductase-like protein	164.71	17	6	6	25	34621
S8CV70	Glycolate oxidase	86.28	6	2	1	26	39095
S8CIP5	Tr-type G domain-containing protein	156.84	6	3	3	20	93742
S8CZK7	Uncharacterized protein	219.95	29	11	11	25	61389
S8CRS6	Fructose-bisphosphate aldolase	179.49	28	9	6	21	38096
S8C8L5	Tubulin beta chain	160.75	9	4	1	29	49498
S8DMR4	PP1ase cyclophilin-type domain-containing protein	206.93	15	4	4	31	26576
S8CC21	Uncharacterized protein	89.45	18	1	1	31	7483
S8CH69	Gp_dh_N domain-containing protein	207.67	29	7	5	23	21054
S8CUE3	Aminotran_1_2 domain-containing protein	213.31	14	6	6	27	53500
S8DR98	Uncharacterized protein	118.24	16	2	2	24	16068
S8D3H5	Chlorophyll a-b binding protein chloroplastic	157.62	17	4	4	29	28049
S8C4P9	GST N-terminal domain-containing protein	120.36	11	3	3	21	29141

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
A0A0A0Y4Q2	Fibrillin 1 protein	94.68	9	2	0	26	35230
S8CGH1	Tubulin beta chain	146.76	6	3	0	26	49649
S8DYB4	Malate dehydrogenase	60.31	4	1	1	24	33107
S8D0Y2	Precursor of protein cell division protease ftsh-like protein	141.91	9	4	4	21	74450
S8BZF0	Monodehydroascorbate reductase	193.08	18	5	5	19	47113
S8C2S9	Uncharacterized protein	109.56	22	3	3	21	17833
S8CGR9	Cytochrome b6-f complex iron-sulfur subunit	171.78	26	5	5	24	23864
S8CE03	CYTOSOL_AP domain-containing protein	169.51	10	4	4	19	58141
S8E325	Malate dehydrogenase	119.61	8	3	3	22	37101
S8C9K9	Malic enzyme	148.74	12	4	2	22	48720
S8E1F6	Luminal-binding protein 5	205.04	11	8	3	24	72872
S8E383	RRM domain-containing protein	62.17	6	1	1	22	17159
A0A5A7Q8A9	60 kDa chaperonin	63.11	2	1	1	25	67727
S8D528	CAAD domain-containing protein	129.71	7	3	3	18	16701
S8BVR5	Malic enzyme	127.71	8	3	1	20	65182
S8EDZ6	Formate dehydrogenase mitochondrial	141.02	15	4	4	24	42740
S8CKD0	Nucleoside diphosphate kinase	128.64	22	4	4	22	16488
A1IW05	Subunit IV of photosystem I (PSI-E)	57.47	25	1	1	19	5884
S8C9Q9	Hydroxypyruvate reductase	161.70	12	4	4	15	42463
A0A4P1REH7	Germin-like protein	66.53	5	2	1	15	22364
S8D4L6	Uncharacterized protein	197.78	26	6	6	16	28175
S8BWD8	Iso_dh domain-containing protein	124.85	10	3	1	17	46579
S8CSI1	Precursor of carboxylase p-protein 1 glycine decarboxylase complex	185.76	18	5	5	23	44701
S8D413	Geraniol dehydrogenase 1	134.39	12	4	4	20	38352
S8D490	AAA domain-containing protein	109.74	9	3	3	18	37668
S8CM36	Ribosomal_L6e_N domain-containing protein	80.76	6	1	1	20	26032
S8BXZ7	Ribosomal_S7 domain-containing protein	150.11	39	4	4	14	10607
S8CXR1	Uncharacterized protein	140.15	12	4	4	15	34336
S8BUN5	Nucleoside diphosphate kinase	94.55	9	2	2	15	25740
S8C5Q3	Uncharacterized protein	147.31	10	2	2	19	25647
S8CHY4	Uncharacterized protein	100.78	4	2	2	16	83432
S8E5Q8	Mitochondrial processing peptidase	134.58	10	5	5	14	58684
S8CRI9	Stachyose synthase	152.13	5	4	4	16	94627
S8E6J2	Iso_dh domain-containing protein	121.50	10	3	1	16	46097
S8E581	Tubulin alpha chain	98.83	11	2	1	15	29585
S8BYT7	Uncharacterized protein	61.48	8	1	1	17	15545
Q6XGX6	Putative photosystem I reaction center subunit N	84.86	27	2	2	15	9797
S8D544	Uncharacterized protein	84.74	16	3	3	9	16810
S8CMA5	Uncharacterized protein	160.53	16	3	3	13	17870
S8D400	Uncharacterized protein	172.36	19	3	2	14	31252
S8BXW0	Polyphenoloxidase	137.07	11	4	4	13	63588
S8D6C0	Thioredoxin domain-containing protein	121.04	23	3	3	15	19658
S8E1B9	Superoxide dismutase	80.92	3	1	0	13	31020

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
S8EEI7	V-type proton ATPase subunit G	62.56	10	1	1	16	11953
S8C7U2	Uncharacterized protein	137.80	23	3	3	16	21947
A0A2G9IBF3	Molecular chaperones mortalin/PBP74/GRP75 HSP70 superfamily	93.15	2	1	1	15	74975
A0A067XJ96	Cytosolic ascorbate peroxidase	67.27	8	2	0	6	27592
S8DLT5	14-3-3 h-1 protein	142.08	19	5	3	11	28683
S8CVY3	Extracellular calcium sensing receptor	186.43	16	6	6	16	39377
S8EAS0	Mitochondrial benzaldehyde dehydrogenase	165.58	12	4	4	13	56190
S8CF09	Clp_N domain-containing protein	103.39	20	2	2	15	21161
S8CL08	Thylakoid-bound ascorbate peroxidase	152.83	18	4	4	9	39191
S8DSK8	Uncharacterized protein	115.71	11	3	3	9	31992
S8D949	Chloroplast chaperonin 21	177.23	22	7	7	10	30888
S8C3Y2	Uncharacterized protein	103.58	7	2	2	6	33647
S8CCA7	Uncharacterized protein	111.58	10	3	3	12	41348
S8CNM7	Fructokinase-like protein	136.90	17	4	4	10	33889
S8D903	Uncharacterized protein	108.91	14	4	4	8	44176
A0A2I6QD80	Cytochrome b6-f complex subunit 4	88.05	11	2	2	11	17401
S8CLT2	Allene oxide cyclase	113.35	15	2	2	14	19253
A0A2I6QE92	Cytochrome f	125.16	17	4	2	11	35269
S8CLG1	Geraniol dehydrogenase 1	104.00	6	1	1	10	39126
A0A3S8TL14	Ascorbate peroxidase	64.21	4	1	0	5	27103
H9MBH0	Chlorophyll a-b binding protein chloroplastic	84.60	20	1	1	13	9033
S8CP12	Aldo_ket_red domain-containing protein	138.29	8	2	2	5	36756
S8C5B9	PAP_fibrillin domain-containing protein	95.41	22	3	3	7	22309
S8D065	Uncharacterized protein	149.24	14	3	3	10	25508
S8EDN5	UDP-glucose 4-epimerase	158.37	14	4	4	12	39811
S8CXP8	TCTP domain-containing protein	87.92	5	1	1	12	18898
S8D170	Actin-depolymerizing factor	74.14	8	1	1	12	16524
S8DSD6	Cysteine synthase	131.15	8	4	4	11	34557
S8D4Q8	Uncharacterized protein	113.57	6	1	1	9	22481
S8E9I9	Uncharacterized protein	63.95	6	1	1	9	20502
S8E3U3	Uncharacterized protein	67.45	2	1	1	9	47846
S8DIS1	Triosephosphate isomerase	143.16	18	4	4	11	33401
S8C490	ADK_lid domain-containing protein	112.53	10	2	2	11	26381
S8CDY1	Tubulin alpha chain	88.72	7	2	1	6	44821
S8CUF0	Uncharacterized protein	118.86	15	3	3	5	25386
A0A2G3C7W3	ATP synthase subunit b' chloroplastic	104.69	12	2	2	10	14682
S8CIS6	PAP_fibrillin domain-containing protein	94.62	12	3	2	5	24661
S8CDH4	Uncharacterized protein	107.59	11	2	2	8	23550
O81372	Nucleoside diphosphate kinase 1	66.58	9	1	1	9	16351
S8BST7	S5 DRBM domain-containing protein	91.56	10	2	2	8	23294
S8CGC3	Dihydrolipoyl dehydrogenase	124.60	9	4	4	5	50261
S8EEI2	Methionine synthase	125.36	4	3	1	8	91588
S8EK09	14-3-3 a-1 protein	104.40	12	3	1	4	28616

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
S8DAM5	Uncharacterized protein	104.55	14	2	2	6	15933
S8CEN8	Uncharacterized protein	104.84	5	3	3	4	85842
S8CWY3	Uncharacterized protein	85.97	7	2	2	6	30361
S8EBF2	GTP-binding nuclear protein	110.42	16	3	3	8	25082
S8C765	Uncharacterized protein	136.29	5	2	2	5	68942
S8D3D9	Glyceraldehyde-3-phosphate dehydrogenase	115.08	7	3	0	6	42406
S8EAM5	14-3-3 protein	101.74	15	3	2	6	27562
S8E3C6	HATPase_c domain-containing protein	119.83	6	2	1	6	51710
S8EFY6	Aldo_ket_red domain-containing protein	107.16	9	3	3	5	37890
S8CSD6	Uncharacterized protein	98.95	16	2	2	8	23443
S8EBQ7	Nucleoside diphosphate kinase	120.07	24	3	3	9	18110
S8EKZ6	PDZ domain-containing protein	131.15	16	4	4	8	43791
S8BSC9	40S ribosomal protein S24	86.07	11	1	1	9	15741
S8DYR8	CoA_binding domain-containing protein	73.38	4	1	1	6	34346
S8CT12	Uncharacterized protein	61.60	5	1	1	6	20387
S8CIQ9	Uncharacterized protein	81.52	9	2	2	5	33988
S8CK62	Uncharacterized protein	110.48	9	3	3	7	46703
S8C9L2	S4 RNA-binding domain-containing protein	76.89	7	3	3	5	29634
S8CL66	Rieske domain-containing protein	94.24	6	1	1	8	28316
S8E788	PAP_fibrillin domain-containing protein	72.61	7	2	2	8	21847
A0A4S8IYE1	Uncharacterized protein	65.36	3	1	1	9	60732
A0A4V3WK35	Uncharacterized protein	64.89	9	1	1	9	24720
S8CNJ1	40S ribosomal protein S8	148.14	7	2	2	8	46307
S8CMR4	Methionine synthase	108.99	3	2	0	6	84912
S8CCI5	Uncharacterized protein	116.76	13	2	1	7	26552
S8CJE3	Ribosomal_L2_C domain-containing protein	111.55	16	3	3	5	28113
A0A565CXF0	Ferredoxin--NADP reductase chloroplastic	63.04	5	2	2	5	40940
S8CUD3	40S ribosomal protein S7	104.20	12	1	1	6	21584
S8CBR9	Peroxisredoxin	96.49	23	3	3	8	17000
A0A2G2ZE93	photosystem I reaction center subunit XI chloroplastic-like	105.02	14	2	2	8	23120
S8CRG9	AA_TRNA_LIGASE_II domain-containing protein	102.01	5	2	2	6	69114
S8D0H0	Elongation factor Tu	104.79	4	1	1	3	48862
S8E2K9	Uncharacterized protein	58.71	0	1	1	1	4E+05
S8CDH5	Ribos_L4_asso_C domain-containing protein	111.86	12	3	3	7	38779
S8CUH2	Lipocln_cytosolic_FA-bd_dom domain-containing protein	79.08	11	3	3	5	20907
S8BUV6	Uncharacterized protein	80.39	5	1	1	5	30846
S8C019	Guanine nucleotide regulatory protein	84.00	17	2	1	6	15063
S8D431	Uncharacterized protein	118.52	12	2	1	4	31355
S8EEF3	Uncharacterized protein	59.36	7	1	1	5	19713
S8DIH8	PSII_BNR domain-containing protein	125.92	20	5	5	7	38467
S8CDW0	NAD(P)-bd_dom domain-containing protein	68.05	5	1	1	7	28007
S8BWT7	Enolase	76.47	14	1	0	7	11666
S8DP00	Uncharacterized protein	93.58	17	2	2	5	24373

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
S8DDT9	Ribosomal_L5 domain-containing protein	72.56	19	1	1	7	8377
S8DXW1	Uncharacterized protein	57.30	14	1	1	4	9559
S8CLD8	Uncharacterized protein	67.42	3	1	1	3	46578
A0A5A7PDG4	Oxygen-evolving enhancer protein 1	94.21	7	2	1	6	35154
Q8H534	Os07g0484800 protein	65.36	8	1	1	6	20219
A0A5A7R1Y0	Cold shock protein 1	66.62	8	1	1	6	19746
S8CM96	Cysteine proteinase	86.11	5	2	2	6	36744
S8C6W0	IBB domain-containing protein	110.91	3	1	1	3	58930
S8CL64	Uncharacterized protein	104.02	8	1	1	5	20008
S8BTK9	Uncharacterized protein	75.09	11	1	1	6	19863
S8D3B8	Prohibitin	144.50	15	3	3	6	30974
S8E9H9	Malic enzyme	70.48	4	2	1	3	60554
S8E759	Isopentenyl pyrophosphate isomerase	85.04	9	2	2	5	27580
S8D524	50S ribosomal protein L14 chloroplastic	81.99	19	2	2	3	13678
S8DNC6	Uncharacterized protein	79.88	2	1	1	4	74183
S8EJW3	ANK_REP_REGION domain-containing protein	79.56	5	1	1	4	33258
S8C802	Lactoylglutathione lyase	108.22	8	2	2	6	25789
S8D406	40S ribosomal protein S25	75.79	12	2	2	5	11369
S8D3J4	Uncharacterized protein	79.88	6	1	0	4	21996
S8C1N1	Calreticulin	81.41	23	1	1	6	8837
S8CF55	Uncharacterized protein	100.95	14	2	2	2	22668
S8CMJ8	Succinate-CoA ligase subunit beta	102.94	4	1	1	2	44740
A0A1R3HY13	NmrA-like protein	87.50	8	2	2	5	34125
S8D8K7	S4 RNA-binding domain-containing protein	96.87	19	3	3	3	23038
W9RGV2	Phosphoglucomutase	88.41	5	2	2	4	63512
M0ZSM1	Uncharacterized protein	95.82	7	2	0	3	34962
S8CYA5	PAP_fibrillin domain-containing protein	84.81	4	1	1	5	35076
S8DVK0	Peroxiredoxin	86.49	10	1	1	6	17495
A0A2C9U8K7	PAP_fibrillin domain-containing protein	76.95	8	2	0	5	35273
A0A2I4F2B2	Fructose-bisphosphate aldolase	88.48	6	1	1	6	38399
S8C2L7	Enolase	106.64	15	3	3	5	31628
S8DA78	Uncharacterized protein	94.41	13	2	2	3	14921
S8D2R1	Alcohol dehydrogenase	92.57	16	3	3	3	32947
S8CAH8	NAD(P)-bd_dom domain-containing protein	108.82	5	1	1	4	28768
S8DM13	Uncharacterized protein	99.56	6	2	2	5	31931
S8D2E2	Uncharacterized protein	92.18	16	2	2	4	21479
S8DHI0	Bet_v_1 domain-containing protein	80.85	10	3	3	3	16780
S8DGS9	PEROXIDASE_4 domain-containing protein	71.08	10	2	2	4	27354
V4S7U5	Uncharacterized protein	77.31	4	1	1	2	47818
S8DRL0	Uncharacterized protein	71.33	7	1	1	5	24320
S8BWE0	Uncharacterized protein	56.52	4	1	1	5	23381
S8EE25	Subtilase family protein	57.88	2	1	1	5	78807
S8BWK0	Tr-type G domain-containing protein	90.39	5	2	2	4	67552

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
S8D0M9	NmrA domain-containing protein	82.90	5	1	1	3	36842
A0A1D1ZKQ0	Oxygen-evolving enhancer protein 1 chloroplastic	79.31	8	2	0	2	39368
S8EEM8	Complex1_30kDa domain-containing protein	82.27	6	1	1	4	22534
A0A2G9GAZ9	Iridoid synthase	77.95	4	1	1	3	44754
S8DA36	Uncharacterized protein	72.12	10	1	1	5	24553
A0A5A7NWH1	mRNA-binding family protein	87.53	7	2	1	4	43703
A0A1J3EV72	Oxygen-evolving enhancer protein 1 chloroplastic	91.30	15	2	0	3	23781
A0A2I6QD88	50S ribosomal protein L2 chloroplastic	108.56	12	2	2	3	29876
S8CZ12	Calmodulin	80.81	11	1	1	3	16848
S8C1V8	APH domain-containing protein	60.08	4	1	1	4	47897
S8CTL4	6-phosphogluconate dehydrogenase decarboxylating	82.38	4	2	2	2	55583
S8CX13	60S ribosomal protein L13	59.58	5	1	1	2	23705
S8EC55	PfkB domain-containing protein	125.72	12	3	3	4	32166
S8CPQ1	Cupin_2 domain-containing protein	67.49	3	1	1	1	33309
S8CXH7	PsbP domain-containing protein	107.84	11	2	2	3	26904
S8EMJ4	ATP-dependent Clp protease proteolytic subunit	86.32	9	2	2	3	31466
S8EEC7	WD_REPEATS_REGION domain-containing protein	72.51	10	2	2	3	36136
S8E3P5	PHB domain-containing protein	70.70	8	2	2	3	31338
S8E780	Uncharacterized protein	87.23	5	1	1	3	51920
Q43848	Transketolase chloroplastic	80.42	4	2	2	3	79992
I1N2I4	NAD(P)-bd_dom domain-containing protein	78.22	6	1	1	4	27631
S8C037	Uncharacterized protein	68.43	4	1	1	2	29587
S8CHW1	FBPase domain-containing protein	61.26	4	1	1	4	36790
S8CX39	Alpha-galactosidase	70.13	4	2	2	3	47057
A0A0D9VHX1	Gp_dh_N domain-containing protein	58.18	8	2	0	2	34127
Q7FAH2	Glyceraldehyde-3-phosphate dehydrogenase 2 cytosolic	56.71	3	1	0	1	36773
S8CWB2	p0 ribosomal protein-like protein	73.26	7	2	2	3	35081
A0A4D9BH81	Nucleoside-diphosphate kinase	61.63	2	1	1	4	74024
A0A1R3I2S6	PAP_fibrillin domain-containing protein	73.75	9	2	0	3	35485
A0A164Z1J4	Epimerase domain-containing protein	66.41	3	1	0	1	43581
S8CE21	Peptidyl-prolyl cis-trans isomerase	79.11	7	1	1	1	18065
S8CBV7	PDZ domain-containing protein	101.87	17	1	1	4	9737
S8CJI5	RRM domain-containing protein	69.38	10	1	1	2	15394
S8D2Z7	Phosphoenolpyruvate carboxykinase	87.47	4	2	2	3	71071
S8D762	Uncharacterized protein	75.71	6	1	1	2	22861
S8C8U7	Ribosomal_L7Ae domain-containing protein	62.84	10	2	2	3	29671
S8BWA3	Uncharacterized protein	75.66	9	2	2	2	26334
S8CCZ2	KH type-2 domain-containing protein	57.10	6	1	1	3	26011
S8EAX8	Uncharacterized protein	71.66	4	1	1	1	53165
S8CSL6	Aldo_ket_red domain-containing protein	75.07	4	1	1	2	40145
S8CBU5	Uncharacterized protein	81.59	15	1	1	3	11127
S8DWY3	M16C_associated domain-containing protein	68.93	3	2	2	3	1E+05

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
B8LLV3	Serine hydroxymethyltransferase	66.45	4	1	1	1	47221
A0A5D3E5W9	Stromal 70 kDa heat shock-related protein	85.32	3	2	2	2	56959
S8D7Q6	PsbP domain-containing protein	64.04	5	1	1	2	25949
A0A1L5JKB2	Glyceraldehyde-3-phosphate dehydrogenase	67.90	3	1	0	1	36529
A0A2I6QD87	50S ribosomal protein L16 chloroplastic	56.53	10	1	1	3	15500
D5LY28	Soluble acid invertase 1	76.07	2	1	1	3	73128
A0A4D8YMP6	Ribulose-phosphate 3-epimerase	66.91	9	1	1	3	16911
W5S7M9	Cu-Zn superoxide dismutase	57.66	17	1	1	3	7753
S8DH12	SOR_SNZ domain-containing protein	76.66	5	1	1	1	33231
S8EDR7	10-formyltetrahydrofolate synthetase	58.35	2	1	1	2	67864
S8E6U3	Aldo_ket_red domain-containing protein	93.97	8	2	2	2	41141
S8E584	Nascent polypeptide-associated complex subunit beta	83.26	12	1	1	2	17776
S8DN02	Uncharacterized protein	77.03	6	2	2	2	53747
S8CP75	Proteasome subunit alpha type	71.23	11	2	2	2	25867
S8E878	PKS_ER domain-containing protein	56.20	4	1	1	1	34605
S8CFK3	NAD(P)-bd_dom domain-containing protein	75.35	6	2	2	2	27811
S8DLJ5	RRM domain-containing protein	61.05	9	1	1	2	15421
S8C0M0	Uncharacterized protein	62.82	17	1	1	2	8483
S8C3B0	2-methyl-6-phytylbenzoquinone methyltransferase	88.76	5	1	1	1	31996
S8DJL3	Uncharacterized protein	59.86	5	1	1	1	28915
S8D3H1	30S ribosomal protein S4 chloroplastic	68.71	8	2	2	2	23440
S8EAQ4	Peptidase A1 domain-containing protein	61.62	2	1	1	2	44749
S8DSS9	Glucose-1-phosphate adenylyltransferase	58.38	2	1	1	1	54796
S8CMZ7	Uncharacterized protein	66.84	13	2	2	2	15044
D7T9G8	PSII_BNR domain-containing protein	81.73	7	2	2	2	44272
S8D0N8	Uncharacterized protein	58.45	4	1	1	1	25844
V7D036	Glyceraldehyde-3-phosphate dehydrogenase	57.21	4	1	0	1	36900
S8CUG6	Uncharacterized protein	102.30	32	2	2	2	14406
A0A540MUY0	Aspartate aminotransferase	73.59	4	1	1	1	38915
A0A444EGL7	PKS_ER domain-containing protein	66.00	4	1	1	2	31980
S8CZZ6	Phosphotransferase	71.29	3	1	1	1	53502
S8BXS5	Uncharacterized protein	58.53	6	1	1	1	21147
S8C612	Uncharacterized protein	64.21	11	1	1	1	14776
S8DJJ3	Aspartate aminotransferase	63.91	3	1	1	1	47772
S8EIS5	Uncharacterized protein	60.02	8	1	1	1	19503
A0A1U8F7J0	Adenosylhomocysteinase	93.29	4	1	1	1	53187
A0A4D8Y9C2	Chaperonin GroEL	86.90	2	1	1	1	1E+05
A0A2I6QE99	Photosystem II CP47 reaction center protein	85.15	4	1	1	1	55960
A0A5D2NFF5	Uncharacterized protein	85.21	7	1	1	1	29753
A0A022RPY1	Chitin-binding type-1 domain-containing protein	65.76	6	1	1	1	29053
A0A445B273	CN hydrolase domain-containing protein	61.48	4	1	1	1	42012
J3MR75	Uncharacterized protein	60.92	3	1	1	1	59114
A0A1J3JPV7	Proteasome subunit alpha type	56.99	13	1	1	1	12089

Table S7. Identified proteins with PEAKS in traps of the *Genlisea violacea* white-flowered morphotype.

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
S8CWK8	Ubiquitin-like domain-containing protein	155.01	17	3	0	99	14799
S8CSZ4	Actin-97	152.67	9	4	1	68	41746
A0A2I6QD52	Ribulose biphosphate carboxylase large chain	196.47	18	8	8	53	52828
S8CRU7	Actin	147.53	8	4	1	69	41788
S8CYV8	Histone H4	146.24	31	3	3	66	11409
S8E4Y7	Uncharacterized protein	146.46	9	4	1	64	41708
S8DD77	Actin	141.38	10	3	3	48	32298
S8CBA2	Chlorophyll a-b binding protein chloroplastic	201.13	17	5	5	47	28144
S8C6K2	Heat shock protein 70	157.07	8	4	1	37	71263
S8CBN4	Histone H3	113.39	13	2	0	13	15406
S8E2N0	Histone H3	114.50	13	2	0	13	15268
S8DPH5	Uncharacterized protein	142.85	6	3	0	28	69648
S8CX03	Uncharacterized protein	103.07	7	3	3	21	41206
S8CVW0; S8EFG8; S8ENH4; S8CFM8	Histone H2B	117.10	12	2	2	8	17104
S8CMY8	Histone H2A	84.03	6	1	1	22	16340
S8EF74	ATP synthase subunit alpha	187.68	10	4	4	19	54983
S8E6J7	Expansin-like EG45 domain-containing protein	79.89	10	1	1	25	13172
S8CIP5	Tr-type G domain-containing protein	150.29	3	3	3	16	93742
S8CI40	Elongation factor 1-alpha	151.24	7	3	3	7	48652
S8BWD8	Iso_dh domain-containing protein	102.61	6	2	2	16	46579
S8D4W0	Malate dehydrogenase	94.39	4	2	2	16	37424
S8DFN4	HATPase_c domain-containing protein	91.25	4	2	2	8	80152
S8DR98	Uncharacterized protein	78.89	7	1	1	21	16068
S8E0E9	Triosephosphate isomerase	104.48	10	2	2	17	27341
S8DLT5	14-3-3 h-1 protein	111.02	9	2	1	8	28683
S8D4L6	Uncharacterized protein	113.35	6	1	1	9	28175
S8C9X5	Ribulose biphosphate carboxylase small chain	78.71	5	1	1	6	19266
S8D6K0	Pyruvate decarboxylase	64.46	2	1	1	9	63268
A0A2I6QD25	Photosystem II protein D1	75.81	4	1	1	11	38945
S8BWT7	Enolase	103.37	20	1	1	14	11666
S8C857	ATP synthase subunit beta	118.79	4	1	1	6	57058
S8DEF3	Glyceraldehyde-3-phosphate dehydrogenase	112.35	7	2	2	3	36532
S8EAM5	14-3-3 protein	65.31	5	1	1	9	27562
S8CPQ1	Cupin_2 domain-containing protein	54.54	3	1	1	3	33309
S8CUF0	Uncharacterized protein	97.87	9	2	2	2	25386

Uniprot ID	Description	-10lgP	Coverage (%)	# Peptides	# Unique	# Spec	Avg. Mass
S8D525	Fructose-bisphosphate aldolase	49.24	3	1	1	2	38134
S8EK09	14-3-3 a-1 protein	94.85	5	1	0	3	28616
S8CAG8	Fructose-bisphosphate aldolase	78.26	3	1	1	1	37786
S8BZF0	Monodehydroascorbate reductase	102.37	5	2	2	4	47113
S8E5C8	Malate dehydrogenase	45.86	2	1	1	2	35533
S8DYR8	CoA_binding domain-containing protein	59.74	4	1	1	6	34346
S8D779	14-3-3 h-1 protein	94.28	5	1	0	3	28738
S8EBF2	GTP-binding nuclear protein	94.35	9	2	2	4	25082
S8E4V4	Cysteine proteinase	56.05	3	1	1	2	38986
S8CGC3	Dihydrolipoyl dehydrogenase	93.19	2	1	1	1	50261
S8E1F6	Luminal-binding protein 5	94.49	3	2	1	3	72872
S8DZJ2	Plasma membrane ATPase	81.56	2	1	1	2	1E+05
S8CX13	60S ribosomal protein L13	67.20	5	1	1	3	23705
S8BXW0	Polyphenoloxidase	88.81	4	1	1	3	63588
S8CA49	Ribosomal_L16 domain-containing protein	64.79	6	1	1	2	24216
S8E3U3	Uncharacterized protein	60.26	2	1	1	3	47846
S8CSD6	Uncharacterized protein	75.60	4	1	1	2	23443
S8C9K9	Malic enzyme	82.20	3	1	1	1	48720
S8E173	Phosphoglycerate kinase	66.76	2	1	1	1	50566
S8E1K9	Catalase	81.93	2	1	1	1	57099
S8D4F2	AAA domain-containing protein	52.02	2	1	1	3	65998
S8DAF4	Photosystem II CP43 reaction center protein	55.80	3	1	1	3	51932
A0A411HB20	Plasma membrane intrinsic protein 2	44.71	4	1	1	1	30047
S8CHM2	Phosphoglycerate kinase	91.22	7	2	2	2	42185
S8C8U7	Ribosomal_L7Ae domain-containing protein	52.21	4	1	1	2	29671
S8D2K5	Fructose-bisphosphate aldolase	45.05	2	1	1	1	38302
S8D5C1	10-hydroxygeraniol oxidoreductase	45.47	3	1	1	1	38103
S8CFM5	Uncharacterized protein	44.97	2	1	1	1	54476
S8D216	Chlorophyll a-b binding protein chloroplastic	57.86	7	1	1	1	27260
S8D1V3	Uncharacterized protein	48.21	1	1	1	1	74572
S8EDN5	UDP-glucose 4-epimerase	48.30	5	1	1	1	39811

Table S8. Proteins with single aminoacid substitutions identified in leaves of purple-flowered morphotype of *Genlisea violacea*. Shared proteins by the two morphotypes are in bold.

Uniprot ID	Protein Description	Mutation				Protein identification		
		From	To	A.A Position	# Spect in mutated peptide	Sample Coverage	# Peptides	# Unique peptides
S8D398	Ribulose biphosphate carboxylase large chain	Q	E	30	2	60	76	22
		G	N	150	11			
		V	L	341	5			
A0A2I6QD56	ATP synthase subunit beta, chloroplastic	N	D	120	3	67	54	1
		T	L	387	21			
S8D4F2	AAA domain-containing protein	N	D	120	3	61	56	0
		T	L	387	21			
		T	L	573	2			
		K	L	576	2			
S8C8K3	ATPase_AAA_core domain-containing protein	V	T	162	5	49	28	28
		N	D	165	36			
S8BX77	Glyceraldehyde-3-phosphate dehydrogenase	K	N	393	7	48	27	19
S8E173	Phosphoglycerate kinase	E	D	193	9	54	26	21
		T	S	270	2			
		S	T	334	8			
S8D424	ATP synthase subunit alpha, chloroplastic	N	T	211	6	36	28	22
S8CAG8	Fructose-bisphosphate aldolase	D	E	41	12	47	22	8
S8CBV6	Oxygen-evolving enhancer protein 1, chloroplastic	A	V	216	17	46	25	25
		S	G	225	21			
S8DAG9	Photosystem II CP47 reaction center protein	Q	E	277	2	28	20	18
S8E474	Carbonic anhydrase	P	A	70	3	53	16	16
S8DEF3	Glyceraldehyde-3-phosphate dehydrogenase	S	A	226	2	46	20	13
S8CRY5	Uncharacterized protein	A	T	434	10	26	16	16
S8C9X5	Ribulose biphosphate carboxylase small chain	R	E	77	4	30	17	17
		R	Q	77	35	30	17	17
S8CSZ4	Actin-97	V	L	249	5	32	14	5
S8CHM2	Phosphoglycerate kinase	D	N	112	2	36	13	8
S8E8M6	Chlorophyll a-b binding protein, chloroplastic	N	D	356	3	16	15	15
		P	A	381	16	16	15	15
S8D1U0	Glutamine amidotransferase type-2 domain-containing protein (Fragment)	I	V	125	2	12	16	16
S8ENB1	Apocytochrome f	S	T	301	2	25	13	13

Uniprot ID	Protein Description	Mutation				Protein identification		
		From	To	A.A Position	# Spect in mutated peptide	Sample Coverage	# Peptides	# Unique peptides
S8CYV8	Histone H4	A	Q	70	5	59	14	14
S8DZE1	Chlorophyll a-b binding protein, chloroplastic	V	L	122	12	29	9	9
S8E188	PsbP domain-containing protein	I	V	186	3	40	12	12
		A	T	215	4	40	12	12
S8CA75	PEROXIDASE_4 domain-containing protein	A	S	51	7	41	8	8
		F	L	56	7	41	8	8
S8CQW3	Malate dehydrogenase	V	A	118	2	26	7	7
		A	E	200	5			
S8E0E9	Triosephosphate isomerase	E	D	142	11	41	8	8
S8CVD5	PEROXIDASE_4 domain-containing protein	P	A	178	5	38	9	9
		S	T	189	5			
		V	A	236	6			
S8C5P5	Thioredoxin domain-containing protein	T	A	72	15	61	9	9
		N	A	73	15			
S8CS62	Uncharacterized protein	G	A	90	10	25	8	8
S8E065	Uncharacterized protein	D	G	195	4	30	8	8
S8D065	Uncharacterized protein	E	D	85	7	30	6	6
S8DMR4	PPase cyclophilin-type domain-containing protein	N	D	54	7	15	4	4
S8DTS5	Uncharacterized protein (Fragment)	A	S	173	5	32	6	6
S8DYF2	Aminomethyltransferase	A	Q	104	5	20	7	7
S8CXH8	Quinone oxidoreductase-like protein	L	V	148	2	19	8	8
S8CXJ8	Epimerase domain-containing protein	Q	E	153	2			
		F	Y	132	2	21	7	7
S8EDN5	NAD(P)-bd_dom domain-containing protein	K	T	59	2	13	3	3
S8EAS0	Mitochondrial benzaldehyde dehydrogenase	R	T	377	4	15	5	5
A0A2I6QD76X	Cytochrome b6	T	A	116	2	21	3	3
S8C5B9	PAP_fibrillin domain-containing protein (Fragment)	T	S	48	5	27	6	6
A0A2I6QD64	Cytochrome b559 subunit alpha	A	D	77	4	37	4	2
S8DNI1	NmrA domain-containing protein	A	V	58	2	14	4	4
S8CFK3	NAD(P)-bd_dom domain-containing protein	V	L	123	4	15	3	3
S8C4P9	GST N-terminal domain-containing protein	A	G	168	8	11	3	3
A0A2I6QD54	ATP synthase epsilon chain, chloroplastic	T	L	95	2	36	4	1
		K	L	98	2			
S8CIQ9	Uncharacterized protein	V	A	182	2	13	3	3

Uniprot ID	Protein Description	Mutation				Protein identification		
		From	To	A.A Position	# Spect in mutated peptide	Sample Coverage	# Peptides	# Unique peptides
S8CYA5	PAP_fibrillin domain- containing protein	G	A	124	3	4	2	2
S8BYG4	14-3-3 protein	G	S	74	2	8	2	0
S8D762	Uncharacterized protein	D	E	80	2	17	2	2
S8D4U2	14_3_3 domain-containing protein	S	D	51	2	9	2	2

Table S9. Proteins with single aminoacid substitutions identified in leaves of white-flowered morphotype of *Genlisea violacea*. Shared proteins by the two morphotypes are in bold.

Uniprot ID	Protein Description	Mutation				Protein identification		
		From	To	A.A Position	# Spect in mutated peptide	Sample Coverage	# Peptides	# Unique peptides
A0A2I6QD52	Ribulose biphosphate carboxylase large chain	E	W	30	6	72	112	49
		Q	E	149	3			
		G	N	150	10			
		G	N	261	4			
		A	P	471	42			
S8CBA2	Chlorophyll a-b binding protein, chloroplastic	A	V	44	4	58	39	39
		T	A	90	15			
		I	V	113	7			
		Y	F	257	2			
		V	A	262	2			
S8D398	Ribulose biphosphate carboxylase large chain	Q	E	30	7	45	63	9
		Q	E	149	3			
		G	N	150	10			
		V	L	341	8			
S8D4F2	AAA domain-containing protein	G	N	122	3	60	51	37
		T	L	387	37			
		E	G	551	3			
		V	L	554	3			
S8BX77	Glyceraldehyde-3-phosphate dehydrogenase	V	L	98	36	44	24	17
		K	N	393	21			
S8C8K3	ATPase_AAA_core domain-containing protein	N	D	165	18	51	21	21
S8CBV6	Oxygen-evolving enhancer protein 1, chloroplastic	S	A	182	31	51	33	33
		A	V	216	51			
		K	E	273	4			
S8DAG9	Photosystem II CP47 reaction center protein	A	V	301	2	30	22	22
		N	D	407	2			
S8E173	Phosphoglycerate kinase	D	E	113	38	50	24	19
		E	D	193	35			
		T	S	270	2			
		S	T	334	9			
		L	V	347	5			
S8CVD3	Glyceraldehyde-3-phosphate dehydrogenase (Fragment)	N	Y	408	2	30	16	9
S8CAG8	Fructose-bisphosphate aldolase	D	E	41	30	41	19	8
		Q	E	236	24			

Uniprot ID	Protein Description	Mutation				Protein identification		
		From	To	A.A Position	# Spect in mutated peptide	Sample Coverage	# Peptides	# Unique peptides
S8E474	Carbonic anhydrase	P	A	70	27	54	15	15
		N	D	165	2			
S8D525	Fructose-bisphosphate aldolase	D	E	43	28	57	19	6
		Q	E	238	20			
S8D424	S8D424_9LAMI ATP synthase subunit alpha, chloroplastic	N	T	211	9	38	26	20
S8DZE1	S8DZE1_9LAMI Chlorophyll a-b binding protein, chloroplastic	V	L	122	74	37	18	18
		A	V	222	12			
S8C9X5	Ribulose bisphosphate carboxylase small chain	R	Q	77	282	35	25	25
		R	E	77	4			
S8E4Y7	Uncharacterized protein	I	V	249	7	32	10	2
S8DLI4	Uncharacterized protein	V	L	60	7	32	11	11
		F	Y	136	5			
S8ENB1	Apocytochrome f	Q	L	240	5	30	14	14
		I	V	252	8			
		D	E	333	3			
S8DEF3	Glyceraldehyde-3-phosphate dehydrogenase	S	N	293	2	42	14	9
		S	T	325	3			
S8BXC1	Serine-glyoxylate aminotransferase	V	L	266	2	42	10	10
		A	S	276	2			
S8CHM2	Phosphoglycerate kinase	D	N	112	2	24	9	4
S8D2K5	Fructose-bisphosphate aldolase	N	D	164	2	36	11	8
A0A2I6QD25	Photosystem II protein D1	N	D	266	2	22	13	5
S8D216	S8D216_9LAMI Chlorophyll a-b binding protein, chloroplastic	I	V	170	19	35	11	11
S8C8H1	Thioredoxin domain-containing protein	I	V	157	4	32	10	10
S8E1K9	Catalase	V	L	48	2	15	7	7
S8E8M6	Chlorophyll a-b binding protein, chloroplastic	N	D	356	3	17	13	13
		P	A	381	28			
S8ELF4	Photosystem II protein D1	N	D	266	2	15	9	1
S8CVD5	PEROXIDASE_4 domain-containing protein	P	A	178	22	38	8	8
		S	T	189	22			
		V	A	236	15			
A0A2I6QD51	Photosystem I P700 chlorophyll a apoprotein A2	V	L	101	2	13	9	6
S8CYV8	Histone H4	A	Q	70	4	63	11	11
S8D1U0	Glutamine amidotransferase type-2 domain-containing protein	I	V	125	4	11	12	12
S8CRY5	Uncharacterized protein	A	T	434	4	21	11	11
S8E188	PsbP domain-containing protein	D	E	82	4	47	12	12
		G	T	103	2			

Uniprot ID	Protein Description	Mutation			Protein identification			
		From	To	A.A Position	# Spect in mutated peptide	Sample Coverage	# Peptides	# Unique peptides
		I	V	105	2			
		A	S	182	18			
		I	V	186	20			
		A	T	215	2			
S8C5P5	Thioredoxin domain-containing protein	T	A	72	6	64	11	11
		N	A	73	6			
		D	E	92	7			
S8CXJ8	Epimerase domain-containing protein	F	V	132	7	21	8	8
S8E0E9	Triosephosphate isomerase	E	D	142	8	48	9	9
S8CWW4	Glycine cleavage system P protein	K	E	464	3	12	7	7
S8CA75	PEROXIDASE_4 domain-containing protein	A	S	51	16	39	8	8
		F	L	56	16			
S8E065	Uncharacterized protein	D	G	195	8	35	11	11
		H	Y	206	3			
S8CI40	Elongation factor 1-alpha	T	V	257	3	20	9	9
S8CVY3	Extracellular calcium sensing receptor	V	L	313	2	16	6	6
S8BXF4	TRANSKETOLASE_1 domain-containing protein	Y	F	337	6	25	8	8
S8C1I3	Chlorophyll a-b binding protein, chloroplastic	C	G	27	5	16	5	5
S8CQW3	Malate dehydrogenase	V	A	118	6	15	6	6
		A	E	200	5			
S8D949	Chloroplast chaperonin 21	V	A	283	2	22	7	7
S8DYF2	Aminomethyltransferase	N	D	45	3	22	6	6
A0A2I6QD76	Cytochrome b6	T	A	16	13	21	4	4
S8EAS0	Mitochondrial benzaldehyde dehydrogenase	R	T	377	3	12	4	4
8CXH8	Quinone oxidoreductase-like protein	L	V	148	7	17	6	6
		Q	R	153	13			
		Q	E	153	7			
S8E7B3	Uncharacterized protein	S	A	102	5	28	4	4
		G	Q	121	20			
		G	E	121	3			
A0A2I6QD64	Cytochrome b559 subunit alpha	A	D	77	13	48	5	2
S8D065	Uncharacterized protein	E	D	85	2	14	3	3
S8DNI1	NmrA domain-containing protein	A	V	58	17	23	7	7
S8D8M8	Transket_pyr domain-containing protein	V	L	312	3	12	3	3
S8CS62	Uncharacterized protein	G	A	90	3	25	4	4
S8DPI8	Chloroplast sedoheptulose-1,7-bisphosphatase	A	S	183	4	29	6	6
S8BXW0	Polyphenoloxidase	M	L	329	6	11	4	4
		K	A	424	4			

Uniprot ID	Protein Description	Mutation				Protein identification		
		From	To	A.A Position	# Spect in mutated peptide	Sample Coverage	# Peptides	# Unique peptides
S8EC55	PfkB domain-containing protein	V	L	215	4	12	3	3
S8D6C0	Thioredoxin domain-containing protein	A	S	143	6	23	3	3
S8C4P9	GST N-terminal domain-containing protein	A	G	168	15	11	3	3
S8D3D9	Glyceraldehyde-3-phosphate dehydrogenase	N	T	384	5	7	3	0
S8CJE3	Ribosomal_L2_C domain-containing protein	V	L	137	2	16	3	3
8CMJ8	Succinate-CoA ligase subunit beta	A	T	188	2	4	1	1
S8BWK0	Tr-type G domain-containing protein	Q	E	220	2	5	2	2
S8CYA5	PAP_fibrillin domain-containing protein	G	A	124	5	4	1	1
S8D544	Uncharacterized protein	D	E	67	7	16	3	3
S8CIQ9	Uncharacterized protein	V	A	182	4	9	2	2
S8D762	Uncharacterized protein	D	E	80	2	6	1	1
S8DA36	Uncharacterized protein	N	G	65	5	10	1	1
S8D7Q6	PsbP domain-containing protein	D	E	142	2	5	1	1

Table S10. Shared and exclusive single amino acid substitutions found in the two morphotypes of *Genlisea violacea* identified by SPIDER algorithm in *Genlisea aurea* proteome and confirmed by amino acid sequences of *Genlisea violacea* chloroplast sequences.

			MUTATION				
UNIPROT Accession	Protein Description	Leaf type	From	To	A.A Position	# Spect in mutate d peptide	Mutation present in <i>G.violacea</i> (NCBI I.D)
SHARED							
S8D4F2	AAA domain- containing protein (Fragment)	PL	N	D	120	3	
			T	L	387	21	YP_009466633
			T	L	573	2	
			K	L	576	2	
		WL	G	N	122	3	
			T	L	387	37	YP_009466633
			E	G	551	3	
			V	L	554	3	
S8ENB1	Apocytochrome f	PL	S	T	301	2	YP_009466639
		WL	Q	L	240	5	YP_009466639
			I	V	252	8	YP_009466639
			D	E	333	3	YP_009466639
S8D424	ATP synthase subunit alpha,	PL	N	T	211	6	YP_009466614
		WL	N	T	211	9	YP_009466614
A0A2I6QD64	Cytochrome b559 subunit	PL	A	D	77	4	YP_009466643
		WL	A	D	77	13	YP_009466643
S8DAG9	Photosystem II CP47 reaction center protein	PL	Q	E	277	2	
		WL	A	V	301	2	YP_009466652
			N	D	407	2	
S8D398	Ribulose bisphosphate carboxylase large chain (Fragment)	PL	Q	E	30	2	YP_009466634
			G	N	150	11	
			V	L	341	5	YP_009466634
		WL	Q	E	30	7	YP_009466634
			Q	E	149	3	
			G	N	150	10	
			V	L	341	8	YP_009466634
LEAF PURPLE MORPHOTYPE							
A0A2I6QD56	ATP synthase subunit beta,	PL	N	D	120	3	
		PL	T	L	387	21	YP_009466633
A0A2I6QD54	ATP synthase epsilon chain,	PL	T	L	95	2	YP_009466632
		PL	K	L	98	2	YP_009466632
LEAF WHITE MORPHOTYPE							
A0A2I6QD76	Cytochrome b6	WL	T	A	16	13	YP_009466656
A0A2I6QD51	Photosystem I P700 chlorophyll a apoprotein A2	WL	V	L	101	2	YP_009466628
A0A2I6QD52	Ribulose bisphosphate carboxylase large chain	WL	E	W	30	6	
		WL	Q	E	149	3	
		WL	G	N	150	10	
		WL	G	N	261	4	
		WL	A	P	471	42	YP_009466634

Table S11. GO annotation of photosynthetic leaves exclusive proteins of white and purple-flowered morphotypes of *Genlisea violacea* identified with PEAKS.

Uniprot ID	Leave type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component)
S8D398	WL-PL	Ribulose biphosphate carboxylase	<i>Genlisea aurea</i>	magnesium ion binding; ribulose-biphosphate carboxylase activity	carbon fixation	
S8BX77	WL-PL	Glyceraldehyde-3-phosphate dehydrog	<i>Genlisea aurea</i>	NAD binding; NADP binding; oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	glucose metabolic process	
S8D424	WL-PL	ATP synthase subunit alpha, chlorop	<i>Genlisea aurea</i>	ATP binding; proton-transporting ATP synthase activity, rotational mechanism	ATP synthesis coupled proton transport	chloroplast thylakoid membrane; proton-transporting ATP synthase complex, catalytic core F(1)
S8DCS9	WL-PL	AAA domain-containing protein	<i>Genlisea aurea</i>	ATP binding; proton-transporting ATP synthase activity, rotational mechanism	ATP synthesis coupled proton transport	proton-transporting ATP synthase complex, catalytic core F(1)
S8CBV6	WL-PL	Oxygen-evolving enhancer protein 1	<i>Genlisea aurea</i>	oxygen evolving activity	photosystem II assembly; photosystem II stabilization	photosystem II oxygen evolving complex chloroplast thylakoid membrane; integral component of membrane; photosystem I; photosystem II
S8DZE1	WL-PL	Chlorophyll a-b binding protein	<i>Genlisea aurea</i>	chlorophyll binding	photosynthesis, light harvesting; protein-chromophore linkage	chloroplast thylakoid membrane; integral component of membrane; photosystem I; photosystem II
A0A2I6QD77	WL-PL	Photosystem II CP47 reaction center	<i>Genlisea aurea</i>	chlorophyll binding; electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity	photosynthetic electron transport in photosystem II; protein-chromophore linkage	chloroplast thylakoid membrane; integral component of membrane; photosystem II
S8C8K3	WL-PL	ATPase_AAA_core domain-containing p	<i>Genlisea aurea</i>	ATP binding		
S8CXZ6	WL-PL	Chlorophyll a-b binding protein	<i>Genlisea aurea</i>	chlorophyll binding	photosynthesis, light harvesting; protein-chromophore linkage	chloroplast thylakoid membrane; integral component of membrane; photosystem I; photosystem II
S8DLI4	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>			chloroplast; integral component of membrane
S8CTY8	WL-PL	Glycolate oxidase	<i>Genlisea aurea</i>	FMN binding; oxidoreductase activity		
S8E474	WL-PL	Carbonic anhydrase	<i>Genlisea aurea</i>	carbonate dehydratase activity; zinc ion binding	carbon utilization	

Uniprot ID	Leave type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component)
S8E8M6	WL-PL	Chlorophyll a-b binding protein	<i>Genlisea aurea</i>	chlorophyll binding	photosynthesis, light harvesting; protein-chromophore linkage	chloroplast thylakoid membrane; integral component of membrane; photosystem I; photosystem II
S8CVD3	WL-PL	Glyceraldehyde-3-phosphate dehydrog	<i>Genlisea aurea</i>	NAD binding; NADP binding; oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	glucose metabolic process	
S8EC20	WL-PL	ATP synthase subunit alpha	<i>Genlisea aurea</i>	ATP binding; proton-transporting ATP synthase activity, rotational mechanism	ATP synthesis coupled proton transport	proton-transporting ATP synthase complex, catalytic core F(1)
S8DI77	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>		photosynthesis	photosystem I reaction center integral component of thylakoid membrane; photosystem I
S8ENB1	WL-PL	Apocytochrome f	<i>Genlisea aurea</i>	electron transfer activity; heme binding; iron ion binding	photosynthesis	photosystem I reaction center proton-transporting ATP synthase complex, catalytic core F(1)
S8CDZ1	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>		photosynthesis	photosystem I reaction center proton-transporting ATP synthase complex, catalytic core F(1)
S8D0S6	WL-PL	ATP synthase subunit alpha	<i>Genlisea aurea</i>	ATP binding; proton-transporting ATP synthase activity, rotational mechanism	ATP synthesis coupled proton transport	
S8D6P3	WL-PL	FAD-binding FR-type domain-containi	<i>Genlisea aurea</i>	oxidoreductase activity		
A0A2I6QD42	WL-PL	Photosystem II D2 protein	<i>Genlisea aurea</i>	chlorophyll binding; electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity; iron ion binding	photosynthetic electron transport in photosystem II; protein-chromophore linkage	chloroplast thylakoid membrane; integral component of membrane; photosystem II
A0A2I6QD76	WL-PL	Cytochrome b6	<i>Genlisea aurea</i>	electron transporter, transferring electrons within cytochrome b6/f complex of photosystem II activity; metal ion binding	photosynthesis; respiratory electron transport chain	chloroplast thylakoid membrane; integral component of membrane photosystem I reaction center chloroplast thylakoid membrane; integral component of membrane; photosystem II reaction center
S8EE95	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>		photosynthesis	
A0A2I6QD64	WL-PL	Cytochrome b559 subunit alpha	<i>Genlisea aurea</i>	electron transfer activity; heme binding; iron ion binding	photosynthetic electron transport chain	
S8CFW3	WL-PL	Serine hydroxymethyltransferase	<i>Genlisea aurea</i>	glycine hydroxymethyltransferase activity; methyltransferase activity; pyridoxal phosphate binding	glycine biosynthetic process from serine; methylation; tetrahydrofolate interconversion	
S8C474	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	proton-transporting ATP synthase activity, rotational mechanism	ATP synthesis coupled proton transport	proton-transporting ATP synthase complex,

Uniprot ID	Leave type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component) catalytic core F(1)
S8E7B3	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	proton-transporting ATP synthase activity, rotational mechanism	ATP synthesis coupled proton transport	membrane
S8CAG4	WL-PL	Phosphoribulokinase	<i>Genlisea aurea</i>	ATP binding; phosphoribulokinase activity	carbohydrate metabolic process	
S8CA75	WL-PL	PEROXIDASE_4 domain-containing prot	<i>Genlisea aurea</i>	heme binding; peroxidase activity	response to oxidative stress	
S8C8H1	WL-PL	Thioredoxin domain-containing prote	<i>Genlisea aurea</i>	peroxiredoxin activity	cell redox homeostasis	cell
A0A2I6QD51	WL-PL	Photosystem I P700 chlorophyll a ap	<i>Genlisea aurea</i>	4 iron, 4 sulfur cluster binding; chlorophyll binding; electron transfer activity; magnesium ion binding	photosynthesis; protein-chromophore linkage	chloroplast thylakoid membrane; integral component of membrane; photosystem I extrinsic component of membrane; photosystem II oxygen evolving complex
S8E065	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	calcium ion binding	photosynthesis	
S8D8M8	WL-PL	Transket_pyr domain-containing prot	<i>Genlisea aurea</i>	catalytic activity		
S8CVD5	WL-PL	PEROXIDASE_4 domain-containing prot	<i>Genlisea aurea</i>	heme binding; peroxidase activity	response to oxidative stress	chloroplast thylakoid membrane; integral component of membrane; photosystem II reaction center
S8D1L1	WL-PL	Cytochrome b559 subunit alpha	<i>Genlisea aurea</i>	heme binding; metal ion binding	photosynthetic electron transport chain	
S8CPA4	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	ATP binding		
S8D4J3	WL-PL	Glutamine synthetase	<i>Genlisea aurea</i>	glutamate-ammonia ligase activity	glutamine biosynthetic process	
S8DYF2	WL-PL	Aminomethyltransferase	<i>Genlisea aurea</i>	aminomethyltransferase activity; transaminase activity	glycine catabolic process; methylation	mitochondrion
S8DFY8	WL-PL	Elongation factor Tu	<i>Genlisea aurea</i>	GTPase activity; GTP binding; translation elongation factor activity		
A0A2I6QD58	WL-PL	Photosystem I P700 chlorophyll a ap	<i>Genlisea aurea</i>	4 iron, 4 sulfur cluster binding; chlorophyll binding; electron transfer activity; magnesium ion binding	photosynthesis; protein-chromophore linkage	chloroplast thylakoid membrane; integral component of membrane; photosystem I
S8DUY5	WL-PL	Fructose-bisphosphate aldolase	<i>Genlisea aurea</i>	fructose-bisphosphate aldolase activity	glycolytic process	
S8ELF4	WL-PL	Photosystem II protein D1	<i>Genlisea aurea</i>	electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity; metal ion binding	photosynthetic electron transport in photosystem II	integral component of membrane; photosystem II
S8D3C4	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	transmembrane transporter activity		integral component of membrane; mitochondrial inner membrane
S8DIK9	WL-PL	AAA domain-containing protein	<i>Genlisea aurea</i>	ATP binding; metalloendopeptidase activity		integral component of membrane

Uniprot ID	Leave type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component)
S8CV15	WL-PL	Superoxide dismutase	<i>Genlisea aurea</i>	metal ion binding; superoxide dismutase activity		integral component of membrane;
S8D9H7	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	proton transmembrane transporter activity	ATP synthesis coupled proton transport	proton-transporting ATP synthase complex, coupling factor F(o) integral component of membrane;
S8CS62	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>		photosynthesis	photosystem I extrinsic component of membrane;
S8E188	WL-PL	PsbP domain-containing protein	<i>Genlisea aurea</i>	calcium ion binding	photosynthesis	photosystem II oxygen evolving complex
S8C5P5	WL-PL	Thioredoxin domain-containing prote	<i>Genlisea aurea</i>	antioxidant activity; oxidoreductase activity	cell redox homeostasis	cell
S8EDT4	WL-PL	Photosystem I iron-sulfur center	<i>Genlisea aurea</i>	4 iron, 4 sulfur cluster binding; electron transfer activity; metal ion binding	photosynthetic electron transport in photosystem I	chloroplast thylakoid membrane; photosystem I chloroplast thylakoid membrane;
S8E9K5	WL-PL	Chlorophyll a-b binding protein, ch	<i>Genlisea aurea</i>	chlorophyll binding	photosynthesis, light harvesting; protein-chromophore linkage	integral component of membrane; photosystem I; photosystem II
S8D1U0	WL-PL	Glutamine amidotransferase type-2 d	<i>Genlisea aurea</i>	glutamate synthase activity	glutamate biosynthetic process	
S8EAM3	WL-PL	Heat shock protein hsp70	<i>Genlisea aurea</i>	ATP binding		
S8CRY5	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	ATP binding	protein refolding	
S8BXC1	WL-PL	Serine-glyoxylate aminotransferase	<i>Genlisea aurea</i>	transaminase activity		
S8BXF4	WL-PL	TRANSKETOLASE_1 domain-containing p	<i>Genlisea aurea</i>			
S8CU40	WL-PL	Aldedh domain-containing protein	<i>Genlisea aurea</i>	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor		
S8C3Q5	WL-PL	Chloroplast heat shock protein 70-2	<i>Genlisea aurea</i>			
S8CQW3	WL-PL	Malate dehydrogenase	<i>Genlisea aurea</i>	malate dehydrogenase (NADP+) activity	carbohydrate metabolic process; malate metabolic process	
S8CGU2	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome
S8CWV4	WL-PL	Glycine cleavage system P protein	<i>Genlisea aurea</i>	glycine dehydrogenase (decarboxylating) activity	glycine catabolic process	mitochondrion
S8D270	WL-PL	Vacuolar proton pump subunit B	<i>Genlisea aurea</i>	ATP binding	ATP metabolic process; proton transmembrane transport	proton-transporting V-type ATPase, V1 domain
S8CXJ8	WL-PL	Epimerase domain-containing protein	<i>Genlisea aurea</i>	catalytic activity; coenzyme binding		

Uniprot ID	Leave type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component)
S8C3A0	WL-PL	Chloroplast sedoheptulose-1,7-bisph	<i>Genlisea aurea</i>	phosphatase activity	carbohydrate metabolic process	
S8E9X0	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome
S8CBH1	WL-PL	Peptidyl-prolyl cis-trans isomerase	<i>Genlisea aurea</i>	peptidyl-prolyl cis-trans isomerase activity	protein folding	
S8DP18	WL-PL	Chloroplast sedoheptulose-1,7-bisph	<i>Genlisea aurea</i>	phosphatase activity	carbohydrate metabolic process	
S8E8N2	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>		photosynthesis	photosystem I reaction center chloroplast thylakoid membrane; integral component of membrane; photosystem I; photosystem II
S8C1I3	WL-PL	Chlorophyll a-b binding protein, ch	<i>Genlisea aurea</i>	chlorophyll binding	photosynthesis, light harvesting; protein-chromophore linkage	
S8CTT6	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	GTP binding		
S8DTS5	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	ATP binding		
S8CXH8	WL-PL	Quinone oxidoreductase-like protein	<i>Genlisea aurea</i>	oxidoreductase activity; zinc ion binding		
S8CV70	WL-PL	Glycolate oxidase	<i>Genlisea aurea</i>	FMN binding; oxidoreductase activity		
S8CZK7	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	ATP binding; proton-transporting ATPase activity, rotational mechanism	ATP metabolic process	proton-transporting V-type ATPase, V1 domain
S8CRS6	WL-PL	Fructose-bisphosphate aldolase	<i>Genlisea aurea</i>	fructose-bisphosphate aldolase activity	glycolytic process	
S8C8L5	WL-PL	Tubulin beta chain	<i>Genlisea aurea</i>	GTPase activity; GTP binding; structural constituent of cytoskeleton	microtubule-based process	cytoplasm; microtubule
S8DMR4	WL-PL	PP1ase cyclophilin-type domain-cont	<i>Genlisea aurea</i>	peptidyl-prolyl cis-trans isomerase activity		
S8CC21	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome
S8CH69	WL-PL	Gp_dh_N domain-containing protein	<i>Genlisea aurea</i>	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor		
S8CUE3	WL-PL	Aminotran_1_2 domain-containing pro	<i>Genlisea aurea</i>	catalytic activity; pyridoxal phosphate binding	biosynthetic process	
S8D3H5	WL-PL	Chlorophyll a-b binding protein, ch	<i>Genlisea aurea</i>	chlorophyll binding	photosynthesis, light harvesting; protein-chromophore linkage	chloroplast thylakoid membrane; integral component of membrane; photosystem I; photosystem II
S8C4P9	WL-PL	GST N-terminal domain-containing pr	<i>Genlisea aurea</i>			
S8CGH1	WL-PL	Tubulin beta chain	<i>Genlisea aurea</i>	GTPase activity; GTP binding; structural constituent of cytoskeleton	microtubule-based process	cytoplasm; microtubule
S8DYB4	WL-PL	Malate dehydrogenase	<i>Genlisea aurea</i>	L-malate dehydrogenase activity	carbohydrate metabolic process; malate metabolic process; tricarboxylic acid cycle	

Uniprot ID	Leave type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component)
S8D0Y2	WL-PL	Precursor of protein cell division	<i>Genlisea aurea</i>	ATP binding; metalloendopeptidase activity	cell division	integral component of membrane
S8C2S9	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome
S8CGR9	WL-PL	Cytochrome b6-f complex iron-sulfur	<i>Genlisea aurea</i>	2 iron, 2 sulfur cluster binding; electron transporter, transferring electrons within cytochrome b6/f complex of photosystem II activity; metal ion binding; plastoquinol--plastocyanin reductase activity; ubiquinol-cytochrome-c reductase activity		chloroplast thylakoid membrane; integral component of membrane
S8CE03	WL-PL	CYTOSOL_AP domain-containing protei	<i>Genlisea aurea</i>	aminopeptidase activity; manganese ion binding; metalloexopeptidase activity		cytoplasm
S8E325	WL-PL	Malate dehydrogenase	<i>Genlisea aurea</i>	L-malate dehydrogenase activity	carbohydrate metabolic process; malate metabolic process; tricarboxylic acid cycle	
S8E383	WL-PL	RRM domain-containing protein	<i>Genlisea aurea</i>	RNA binding		
S8D528	WL-PL	CAAD domain-containing protein	<i>Genlisea aurea</i>			integral component of membrane; thylakoid
S8EDZ6	WL-PL	Formate dehydrogenase, mitochondria	<i>Genlisea aurea</i>	formate dehydrogenase (NAD+) activity; NAD binding; oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	formate catabolic process	formate dehydrogenase complex; mitochondrion
S8CKD0	WL-PL	Nucleoside diphosphate kinase	<i>Genlisea aurea</i>	ATP binding; nucleoside diphosphate kinase activity	CTP biosynthetic process; GTP biosynthetic process; UTP biosynthetic process	
S8C9Q9	WL-PL	Hydroxypyruvate reductase	<i>Genlisea aurea</i>	NAD binding; oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor		
S8CS11	WL-PL	Precursor of carboxylase p-protein	<i>Genlisea aurea</i>	glycine dehydrogenase (decarboxylating) activity	glycine catabolic process	
S8D413	WL-PL	Geraniol dehydrogenase 1	<i>Genlisea aurea</i>	oxidoreductase activity; zinc ion binding		
S8D490	WL-PL	AAA domain-containing protein	<i>Genlisea aurea</i>	ATP binding	protein metabolic process	
S8CM36	WL-PL	Ribosomal_L6e_N domain-containing p	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome
S8BXZ7	WL-PL	Ribosomal_S7 domain-containing prot	<i>Genlisea aurea</i>		translation	
S8CXR1	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	phosphatase activity		
S8BUN5	WL-PL	Nucleoside diphosphate kinase	<i>Genlisea aurea</i>	ATP binding; nucleoside diphosphate kinase activity	CTP biosynthetic process; GTP biosynthetic process; UTP biosynthetic process	
S8C5Q3	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>		photosystem II assembly	

Uniprot ID	Leave type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component)
S8CHY4	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>			
S8CRI9	WL-PL	Stachyose synthase	<i>Genlisea aurea</i>			
S8E6J2	WL-PL	Iso_dh domain-containing protein	<i>Genlisea aurea</i>	isocitrate dehydrogenase (NADP+) activity; magnesium ion binding; NAD binding	isocitrate metabolic process	
S8E581	WL-PL	Tubulin alpha chain	<i>Genlisea aurea</i>	GTPase activity; GTP binding; structural constituent of cytoskeleton	microtubule-based process	microtubule
S8BYT7	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	small ribosomal subunit
S8D544	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>			integral component of membrane
S8CMA5	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome
S8D400	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	cytoplasm; small ribosomal subunit
S8D6C0	WL-PL	Thioredoxin domain-containing prote	<i>Genlisea aurea</i>	protein disulfide oxidoreductase activity	cell redox homeostasis; glycerol ether metabolic process	cell
S8E1B9	WL-PL	Superoxide dismutase	<i>Genlisea aurea</i>	metal ion binding; superoxide dismutase activity		
S8EEI7	WL-PL	V-type proton ATPase subunit G	<i>Genlisea aurea</i>	ATPase-coupled transmembrane transporter activity	proton transmembrane transport	vacuolar proton-transporting V-type ATPase complex
S8C7U2	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	GTP binding	intracellular protein transport; vesicle-mediated transport	endoplasmic reticulum; Golgi apparatus
S8CVY3	WL-PL	Extracellular calcium sensing recep	<i>Genlisea aurea</i>			integral component of membrane
S8EAS0	WL-PL	Mitochondrial benzaldehyde dehydrog	<i>Genlisea aurea</i>	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor		
S8CF09	WL-PL	Clp_N domain-containing protein	<i>Genlisea aurea</i>		protein metabolic process	
S8CL08	WL-PL	Thylakoid-bound ascorbate peroxidase	<i>Genlisea aurea</i>	heme binding; peroxidase activity	response to oxidative stress	integral component of membrane
S8DSK8	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>			integral component of membrane
S8D949	WL-PL	Chloroplast chaperonin 21	<i>Genlisea aurea</i>	ATP binding; transition metal ion binding	positive regulation of superoxide dismutase activity; protein folding	
S8C3Y2	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	ATP binding	protein refolding	
S8CCA7	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>			
S8CNM7	WL-PL	Fructokinase-like protein	<i>Genlisea aurea</i>	kinase activity; phosphotransferase activity, alcohol group as acceptor		
S8D903	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	ATP binding		

Uniprot ID	Leave type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component)
A0A2I6QD80	WL-PL	Cytochrome b6-f complex subunit 4	<i>Genlisea aurea</i>	electron transporter, transferring electrons within cytochrome b6/f complex of photosystem II activity; electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity	photosynthetic electron transport chain	chloroplast thylakoid membrane; integral component of membrane
S8CLT2	WL-PL	Allene oxide cyclase	<i>Genlisea aurea</i>	allene-oxide cyclase activity	jasmonic acid biosynthetic process	
S8CLG1	WL-PL	Geraniol dehydrogenase 1	<i>Genlisea aurea</i>	oxidoreductase activity; zinc ion binding		
S8CP12	WL-PL	Aldo_ket_red domain-containing prot	<i>Genlisea aurea</i>	oxidoreductase activity		
S8C5B9	WL-PL	PAP_fibrillin domain-containing pro	<i>Genlisea aurea</i>			
S8D065	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	ribose-5-phosphate isomerase activity	pentose-phosphate shunt, non-oxidative branch	
S8CXP8	WL-PL	TCTP domain-containing protein	<i>Genlisea aurea</i>			
S8D170	WL-PL	Actin-depolymerizing factor	<i>Genlisea aurea</i>	actin binding	actin filament depolymerization	actin cytoskeleton
S8DSD6	WL-PL	Cysteine synthase	<i>Genlisea aurea</i>	cysteine synthase activity	cysteine biosynthetic process from serine	
S8D4Q8	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>			integral component of membrane
S8DIS1	WL-PL	Triosephosphate isomerase	<i>Genlisea aurea</i>	triose-phosphate isomerase activity	glycolytic process	
S8C490	WL-PL	ADK_lid domain-containing protein	<i>Genlisea aurea</i>	adenylate kinase activity; ATP binding		
S8CDY1	WL-PL	Tubulin alpha chain	<i>Genlisea aurea</i>	GTPase activity; GTP binding; structural constituent of cytoskeleton	microtubule-based process	microtubule
S8CIS6	WL-PL	PAP_fibrillin domain-containing pro	<i>Genlisea aurea</i>			
S8CDH4	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>			
S8BST7	WL-PL	S5 DRBM domain-containing protein	<i>Genlisea aurea</i>	RNA binding; structural constituent of ribosome	translation	small ribosomal subunit
S8EEI2	WL-PL	Methionine synthase	<i>Genlisea aurea</i>	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity; zinc ion binding	methionine biosynthetic process	
S8CEN8	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	ATP binding; hydrolase activity		
S8C765	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	ATP binding; unfolded protein binding	protein folding	
S8D3D9	WL-PL	Glyceraldehyde-3-phosphate dehydrog	<i>Genlisea aurea</i>	NAD binding; NADP binding; oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	glucose metabolic process	
S8E3C6	WL-PL	HATPase_c domain-containing protein	<i>Genlisea aurea</i>	ATP binding; unfolded protein binding	protein folding	
S8EFY6	WL-PL	Aldo_ket_red domain-containing prot	<i>Genlisea aurea</i>	oxidoreductase activity		
S8EBQ7	WL-PL	Nucleoside diphosphate kinase	<i>Genlisea aurea</i>	ATP binding; nucleoside diphosphate kinase activity	CTP biosynthetic process; GTP biosynthetic process; UTP biosynthetic process	

Uniprot ID	Leave type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component)
S8EKZ6	WL-PL	PDZ domain-containing protein	<i>Genlisea aurea</i>	serine-type endopeptidase activity		
S8BSC9	WL-PL	40S ribosomal protein S24	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome
S8CIQ9	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>			
S8CK62	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	ATP binding; helicase activity; nucleic acid binding		
S8C9L2	WL-PL	S4 RNA-binding domain-containing pr	<i>Genlisea aurea</i>	rRNA binding; structural constituent of ribosome	translation	ribosome
S8CL66	WL-PL	Rieske domain-containing protein	<i>Genlisea aurea</i>	2 iron, 2 sulfur cluster binding; nitrite reductase [NAD(P)H] activity		
S8E788	WL-PL	PAP_fibrillin domain-containing pro	<i>Genlisea aurea</i>			
S8CNJ1	WL-PL	40S ribosomal protein S8	<i>Genlisea aurea</i>	GTPase activity; GTP binding; structural constituent of ribosome	translation	ribosome
S8CMR4	WL-PL	Methionine synthase	<i>Genlisea aurea</i>	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity; zinc ion binding	methionine biosynthetic process	
S8CCI5	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	ATP binding; unfolded protein binding	protein folding	
S8CJE3	WL-PL	Ribosomal_L2_C domain-containing pr	<i>Genlisea aurea</i>	RNA binding; structural constituent of ribosome	translation	large ribosomal subunit
S8CBR9	WL-PL	Peroxioredoxin	<i>Genlisea aurea</i>	peroxidase activity; peroxiredoxin activity	cell redox homeostasis	cell
S8CRG9	WL-PL	AA_TRNA_LIGASE_II domain-containing	<i>Genlisea aurea</i>	ATP binding; glycine-tRNA ligase activity	glycyl-tRNA aminoacylation	cytoplasm
S8D0H0	WL-PL	Elongation factor Tu	<i>Genlisea aurea</i>	GTPase activity; GTP binding; translation elongation factor activity		
S8E2K9	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>			
S8CDH5	WL-PL	Ribos_L4_asso_C domain-containing p	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome
S8CUH2	WL-PL	Lipocln_cytosolic_FA-bd_dom domain-	<i>Genlisea aurea</i>			
S8C019	WL-PL	Guanine nucleotide regulatory prote	<i>Genlisea aurea</i>	GTPase activity; GTP binding		
S8D431	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	cytoplasm; small ribosomal subunit
S8DIH8	WL-PL	PSII_BNR domain-containing protein	<i>Genlisea aurea</i>			
S8CDW0	WL-PL	NAD(P)-bd_dom domain-containing pro	<i>Genlisea aurea</i>			
S8DP00	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	proton-transporting ATP synthase activity, rotational mechanism	ATP synthesis coupled proton transport	proton-transporting ATP synthase complex, catalytic core F(1)
S8DDT9	WL-PL	Ribosomal_L5 domain-containing prot	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome
S8CM96	WL-PL	Cysteine proteinase	<i>Genlisea aurea</i>	cysteine-type peptidase activity		
S8C6W0	WL-PL	IBB domain-containing protein	<i>Genlisea aurea</i>	nuclear import signal receptor activity	protein import into nucleus	cytoplasm; nucleus
S8BTK9	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	ATP binding	protein refolding	

Uniprot ID	Leave type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component)
S8D3B8	WL-PL	Prohibitin	<i>Genlisea aurea</i>			mitochondrial inner membrane
S8E759	WL-PL	Isopentenyl pyrophosphate isomerase	<i>Genlisea aurea</i>	hydrolase activity; isopentenyl-diphosphate delta-isomerase activity	isoprenoid biosynthetic process	
S8DNC6	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	ATP binding; kinase activity; pyruvate, phosphate dikinase activity	pyruvate metabolic process	
S8EJW3	WL-PL	ANK_REP_REGION domain-containing pr	<i>Genlisea aurea</i>			
S8C1N1	WL-PL	Calreticulin	<i>Genlisea aurea</i>	calcium ion binding; unfolded protein binding	protein folding	endoplasmic reticulum
S8CF55	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>			
S8CMJ8	WL-PL	Succinate-CoA ligase subunit beta	<i>Genlisea aurea</i>	ATP binding; ligase activity; metal ion binding	tricarboxylic acid cycle	
S8CYA5	WL-PL	PAP_fibrillin domain-containing pro	<i>Genlisea aurea</i>			
S8C2L7	WL-PL	Enolase	<i>Genlisea aurea</i>	magnesium ion binding; phosphopyruvate hydratase activity	glycolytic process	phosphopyruvate hydratase complex
S8D2R1	WL-PL	Alcohol dehydrogenase	<i>Genlisea aurea</i>	oxidoreductase activity; zinc ion binding		
S8CAH8	WL-PL	NAD(P)-bd_dom domain-containing pro	<i>Genlisea aurea</i>			
S8DM13	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	RNA binding		ribonucleoprotein complex
S8DRL0	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	metal ion binding; ribulose-phosphate 3-epimerase activity	carbohydrate metabolic process; pentose-phosphate shunt	
S8EE25	WL-PL	Subtilase family protein	<i>Genlisea aurea</i>	serine-type endopeptidase activity		
S8BWK0	WL-PL	Tr-type G domain-containing protein	<i>Genlisea aurea</i>	GTPase activity; GTP binding; translation elongation factor activity		
S8D0M9	WL-PL	NmrA domain-containing protein	<i>Genlisea aurea</i>			
S8EEM8	WL-PL	Complex1_30kDa domain-containing pr	<i>Genlisea aurea</i>	NADH dehydrogenase (ubiquinone) activity		thylakoid
A0A2I6QD88	WL-PL	50S ribosomal protein L2, chloropla	<i>Genlisea aurea</i>	rRNA binding; structural constituent of ribosome; transferase activity	translation	chloroplast; large ribosomal subunit
S8CZ12	WL-PL	Calmodulin	<i>Genlisea aurea</i>	calcium ion binding	calcium-mediated signaling	
S8C1V8	WL-PL	APH domain-containing protein	<i>Genlisea aurea</i>	S-methyl-5-thioribose kinase activity	methionine biosynthetic process	
S8EC55	WL-PL	PfkB domain-containing protein	<i>Genlisea aurea</i>	adenosine kinase activity	purine ribonucleoside salvage	
S8CXH7	WL-PL	PsbP domain-containing protein	<i>Genlisea aurea</i>	calcium ion binding	photosynthesis	extrinsic component of membrane; photosystem II oxygen evolving complex
S8EMJ4	WL-PL	ATP-dependent Clp protease proteoly	<i>Genlisea aurea</i>	serine-type endopeptidase activity		
S8E3P5	WL-PL	PHB domain-containing protein	<i>Genlisea aurea</i>			
S8E780	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	UTP:glucose-1-phosphate uridylyltransferase activity	UDP-glucose metabolic process	

Uniprot ID	Leave type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component)
S8C037	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	voltage-gated anion channel activity		mitochondrial outer membrane
S8CHW1	WL-PL	FBPase domain-containing protein	<i>Genlisea aurea</i>	fructose 1,6-bisphosphate 1-phosphatase activity	carbohydrate metabolic process	
S8CX39	WL-PL	Alpha-galactosidase	<i>Genlisea aurea</i>	raffinose alpha-galactosidase activity	carbohydrate metabolic process	
S8CWB2	WL-PL	p0 ribosomal protein-like protein	<i>Genlisea aurea</i>		ribosome biogenesis	ribosome
S8CE21	WL-PL	Peptidyl-prolyl cis-trans isomerase	<i>Genlisea aurea</i>	peptidyl-prolyl cis-trans isomerase activity	protein folding	
S8CBV7	WL-PL	PDZ domain-containing protein	<i>Genlisea aurea</i>			
S8D2Z7	WL-PL	Phosphoenolpyruvate carboxykinase	<i>Genlisea aurea</i>	ATP binding; kinase activity; phosphoenolpyruvate carboxykinase (ATP) activity	gluconeogenesis	
S8D762	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>			
S8CCZ2	WL-PL	KH type-2 domain-containing protein	<i>Genlisea aurea</i>	RNA binding; structural constituent of ribosome	translation	small ribosomal subunit
S8CSL6	WL-PL	Aldo_ket_red domain-containing prot	<i>Genlisea aurea</i>	oxidoreductase activity		
S8CBU5	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	proton-transporting ATP synthase activity, rotational mechanism	ATP synthesis coupled proton transport	proton-transporting ATP synthase complex, catalytic core F(1)
A0A2I6QD87	WL-PL	50S ribosomal protein L16, chloropl	<i>Genlisea aurea</i>	rRNA binding; structural constituent of ribosome	translation	chloroplast; ribosome
S8DH12	WL-PL	SOR_SNZ domain-containing protein	<i>Genlisea aurea</i>	catalytic activity	pyridoxal phosphate biosynthetic process	
S8EDR7	WL-PL	10-formyltetrahydrofolate synthetas	<i>Genlisea aurea</i>	ATP binding; formate-tetrahydrofolate ligase activity		
S8DN02	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>		mitochondrial respiratory chain complex I assembly	
S8CP75	WL-PL	Proteasome subunit alpha type	<i>Genlisea aurea</i>	threonine-type endopeptidase activity	proteasome-mediated ubiquitin-dependent protein catabolic process	cytoplasm; nucleus; proteasome core complex, alpha-subunit complex
S8CFK3	WL-PL	NAD(P)-bd_dom domain-containing pro	<i>Genlisea aurea</i>			
S8C0M0	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	ubiquinol-cytochrome-c reductase activity		mitochondrial inner membrane; respirasome
S8C3B0	WL-PL	2-methyl-6-phytylbenzoquinone methy	<i>Genlisea aurea</i>	methyltransferase activity	methylation	integral component of membrane
S8EAQ4	WL-PL	Peptidase A1 domain-containing prot	<i>Genlisea aurea</i>	aspartic-type endopeptidase activity		
S8DSS9	WL-PL	Glucose-1-phosphate adenylyltransfe	<i>Genlisea aurea</i>	ATP binding; glucose-1-phosphate adenylyltransferase activity	glycogen biosynthetic process; starch biosynthetic process	chloroplast
S8CMZ7	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome

Uniprot ID	Leave type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component)
S8CZZ6	WL-PL	Phosphotransferase	<i>Genlisea aurea</i>	ATP binding; glucose binding; hexokinase activity	cellular glucose homeostasis; glycolytic process	cell
S8BXS5	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>			
S8C612	WL-PL	Uncharacterized protein	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome
S8DJJ3	WL-PL	Aspartate aminotransferase	<i>Genlisea aurea</i>	L-aspartate:2-oxoglutarate aminotransferase activity; pyridoxal phosphate binding	biosynthetic process; cellular amino acid metabolic process	
S8C9G3	PL	Aspartate aminotransferase	<i>Genlisea aurea</i>	pyridoxal phosphate binding; transaminase activity	biosynthetic process; cellular amino acid metabolic process	
S8EC22	PL	Photosystem II CP47 reaction center	<i>Genlisea aurea</i>	chlorophyll binding; electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity	photosynthetic electron transport in photosystem II; protein-chromophore linkage	integral component of membrane; photosystem II
S8DLB7	PL	S5 DRBM domain-containing protein	<i>Genlisea aurea</i>	RNA binding; structural constituent of ribosome	translation	small ribosomal subunit
S8E1E6	PL	Uncharacterized protein	<i>Genlisea aurea</i>	phosphoenolpyruvate carboxylase activity	carbon fixation; tricarboxylic acid cycle	
S8DZG3	PL	Peptide methionine sulfoxide reduct	<i>Genlisea aurea</i>	peptide-methionine (S)-S-oxide reductase activity		
S8C3Z8	PL	Phosphoenolpyruvate carboxylase	<i>Genlisea aurea</i>	phosphoenolpyruvate carboxylase activity	carbon fixation; tricarboxylic acid cycle	
A0A2I6QD54	PL	ATP synthase epsilon chain, chlorop	<i>Genlisea aurea</i>	ATP binding; proton-transporting ATP synthase activity, rotational mechanism	ATP synthesis coupled proton transport	chloroplast thylakoid membrane; proton-transporting ATP synthase complex, catalytic core F(1)
S8D988	PL	Uncharacterized protein	<i>Genlisea aurea</i>	selenium binding		
S8BSE7	PL	Uncharacterized protein	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome
S8CFQ6	PL	Fructose-bisphosphate aldolase	<i>Genlisea aurea</i>	fructose-bisphosphate aldolase activity	glycolytic process	
S8DPM6	PL	Glucose-1-phosphate adenylyltransfe	<i>Genlisea aurea</i>	ATP binding; glucose-1-phosphate adenylyltransferase activity	glycogen biosynthetic process; starch biosynthetic process	chloroplast
S8DS50	PL	Uncharacterized protein	<i>Genlisea aurea</i>	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase activity	terpenoid biosynthetic process	
S8BT37	PL	Glutathione reductase	<i>Genlisea aurea</i>	oxidoreductase activity, acting on a sulfur group of donors, NAD(P) as acceptor		
S8CET3	PL	AAA domain-containing protein	<i>Genlisea aurea</i>	ATP binding; hydrolase activity	protein catabolic process	cytoplasm
S8C489	PL	Remorin_C domain-containing protein	<i>Genlisea aurea</i>			
S8ELH0	PL	4Fe-4S ferredoxin-type domain-conta	<i>Genlisea aurea</i>	4 iron, 4 sulfur cluster binding; electron transfer activity	photosynthetic electron transport in photosystem I	photosystem I; thylakoid membrane
S8E121	PL	Superoxide dismutase	<i>Genlisea aurea</i>	metal ion binding; superoxide dismutase activity		

Uniprot ID	Leave type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component)
S8DTZ0	PL	Cysteine synthase	<i>Genlisea aurea</i>			
S8CRG0	PL	HATPase_c domain-containing protein	<i>Genlisea aurea</i>	ATP binding; unfolded protein binding	protein folding	
S8CXK0	PL	Prohibitin	<i>Genlisea aurea</i>			mitochondrial inner membrane
S8CSI2	PL	S-adenosylmethionine synthase	<i>Genlisea aurea</i>	ATP binding; metal ion binding; methionine adenosyltransferase activity	one-carbon metabolic process; S-adenosylmethionine biosynthetic process	
S8DEB4	PL	Uncharacterized protein	<i>Genlisea aurea</i>	rRNA binding; structural constituent of ribosome	translation	ribosome
S8CV45	PL	Protein disulfide-isomerase	<i>Genlisea aurea</i>	protein disulfide isomerase activity	cell redox homeostasis	cell
S8DT71	PL	Uncharacterized protein	<i>Genlisea aurea</i>	GTPase activity; GTP binding		
S8C309	PL	Alpha-galactosidase	<i>Genlisea aurea</i>	raffinose alpha-galactosidase activity	carbohydrate metabolic process	
S8D3V6	PL	Uncharacterized protein	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome
S8BYG4	PL	14-3-3 protein	<i>Genlisea aurea</i>	protein domain specific binding		
S8EDK9	PL	Uncharacterized protein	<i>Genlisea aurea</i>			
S8CA82	PL	Ribosomal_L18_c domain-containing p	<i>Genlisea aurea</i>	5S rRNA binding; structural constituent of ribosome	translation	ribosome
S8DNX3	PL	Uncharacterized protein	<i>Genlisea aurea</i>			
S8CXQ3	PL	Uncharacterized protein	<i>Genlisea aurea</i>	phosphoenolpyruvate carboxylase activity	carbon fixation; tricarboxylic acid cycle	
S8CQK5	PL	Ribosomal protein	<i>Genlisea aurea</i>	RNA binding; structural constituent of ribosome	translation	large ribosomal subunit
S8DW35	PL	Uncharacterized protein	<i>Genlisea aurea</i>	UTP:glucose-1-phosphate uridylyltransferase activity	UDP-glucose metabolic process	
S8C5N3	PL	Uncharacterized protein	<i>Genlisea aurea</i>	GTPase activity; GTP binding		
S8CYW0	PL	Uncharacterized protein	<i>Genlisea aurea</i>	1-deoxy-D-xylulose-5-phosphate reductoisomerase activity; metal ion binding; NADPH binding	isoprenoid biosynthetic process	
S8CAI9	PL	Uncharacterized protein	<i>Genlisea aurea</i>	L-malate dehydrogenase activity	carbohydrate metabolic process; malate metabolic process; tricarboxylic acid cycle	
S8D4E0	PL	Cytochrome c oxidase subunit 2	<i>Genlisea aurea</i>	copper ion binding; cytochrome-c oxidase activity		membrane
S8D555	PL	Uncharacterized protein	<i>Genlisea aurea</i>	RNA binding; structural constituent of ribosome	translation	ribosome
S8CXD9	PL	Uncharacterized protein	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome
S8CG22	PL	Ferritin	<i>Genlisea aurea</i>	ferric iron binding; ferroxidase activity	cellular iron ion homeostasis; iron ion transport	cell
S8C7X0	PL	TauD domain-containing protein	<i>Genlisea aurea</i>	oxidoreductase activity		
S8C3R9	PL	Malic enzyme	<i>Genlisea aurea</i>	NAD binding		

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S8D4U2	PL	14_3_3 domain-containing protein	<i>Genlisea aurea</i>	protein domain specific binding		
S8BZX0	PL	SHSP domain-containing protein	<i>Genlisea aurea</i>			
S8D2V7	PL	Uncharacterized protein	<i>Genlisea aurea</i>	ATP binding	protein metabolic process	
S8CML0	PL	Elongation factor 1 gamma-like prot	<i>Genlisea aurea</i>	translation elongation factor activity		
S8EFM1	PL	Peroxidase	<i>Genlisea aurea</i>	heme binding; metal ion binding; peroxidase activity	hydrogen peroxide catabolic process; response to oxidative stress	extracellular region
S8EAY5	PL	FAD_binding_2 domain-containing pro	<i>Genlisea aurea</i>	oxidoreductase activity		
S8CHV8	PL	Betaine aldehyde dehydrogenase	<i>Genlisea aurea</i>	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor		
S8BZB0	PL	Chloroplast lipocalin	<i>Genlisea aurea</i>	small molecule binding		
S8DWP6	PL	Xylose isomerase	<i>Genlisea aurea</i>	metal ion binding; xylose isomerase activity	D-xylose metabolic process	
S8CSZ2	PL	Glutamate decarboxylase	<i>Genlisea aurea</i>	glutamate decarboxylase activity; pyridoxal phosphate binding	glutamate metabolic process	
S8E095	PL	Heat shock protein 90	<i>Genlisea aurea</i>	ATP binding; unfolded protein binding	protein folding	
S8DA95	PL	Uncharacterized protein	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome
S8CP19	PL	Peptidyl-prolyl cis-trans isomerase	<i>Genlisea aurea</i>	peptidyl-prolyl cis-trans isomerase activity	protein folding	
S8CIS0	PL	ATP-dependent Clp protease proteoly	<i>Genlisea aurea</i>	serine-type endopeptidase activity		
S8D409	PL	Uncharacterized protein	<i>Genlisea aurea</i>			
S8DRZ1	PL	Aspartate aminotransferase	<i>Genlisea aurea</i>	pyridoxal phosphate binding; transaminase activity	biosynthetic process; cellular amino acid metabolic process	
S8CLS8	PL	Inorganic pyrophosphatase	<i>Genlisea aurea</i>	inorganic diphosphatase activity; pyrophosphate hydrolysis-driven proton transmembrane transporter activity		integral component of membrane
S8DMW3	PL	Uncharacterized protein	<i>Genlisea aurea</i>	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides		
S8CZU4	PL	DHO_dh domain-containing protein	<i>Genlisea aurea</i>	oxidoreductase activity, acting on the CH-CH group of donors		cytoplasm
S8CIS4	PL	Cysteine synthase	<i>Genlisea aurea</i>	cysteine synthase activity	cysteine biosynthetic process from serine	
S8DJF6	PL	S10_pectin domain-containing prote	<i>Genlisea aurea</i>			
S8CG73	PL	PPase cyclophilin-type domain-cont	<i>Genlisea aurea</i>	peptidyl-prolyl cis-trans isomerase activity		
S8D856	PL	Uncharacterized protein	<i>Genlisea aurea</i>		photosynthetic electron transport in photosystem I; response to high light intensity	
S8CHE8	PL	WD_REPEATS_REGION domain-containing	<i>Genlisea aurea</i>		endoplasmic reticulum to Golgi vesicle-	cytoplasm

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					mediated transport	
S8DVQ7	PL	Uncharacterized protein	<i>Genlisea aurea</i>	inorganic diphosphatase activity; magnesium ion binding	phosphate-containing compound metabolic process	cytoplasm
S8DV76	PL	Ribosomal_L18e/L15P domain-containi	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome
S8BT19	PL	Uncharacterized protein	<i>Genlisea aurea</i>	ATP binding; nucleic acid binding		
S8CXM5	PL	Uncharacterized protein	<i>Genlisea aurea</i>	catalytic activity		
S8CYB6	PL	AIG1-type G domain-containing prote	<i>Genlisea aurea</i>	GTP binding; metal ion binding; P-P-bond-hydrolysis-driven protein transmembrane transporter activity	intracellular protein transport	chloroplast outer membrane
S8E3C7	PL	Uncharacterized protein	<i>Genlisea aurea</i>			
S8CLA5	PL	SRP54 domain-containing protein	<i>Genlisea aurea</i>	7S RNA binding; GTPase activity; GTP binding	SRP-dependent cotranslational protein targeting to membrane	signal recognition particle
S8BYC7	PL	Geranylgeranyl reductase	<i>Genlisea aurea</i>	FAD binding		
S8DEF5	PL	Geranylgeranyl reductase	<i>Genlisea aurea</i>	FAD binding		
S8CCK1	PL	Uncharacterized protein	<i>Genlisea aurea</i>	ATP binding; unfolded protein binding	protein folding	
S8CQT5	PL	Uncharacterized protein	<i>Genlisea aurea</i>		photosynthesis	photosystem I
S8D6L3	PL	NADPH-protochlorophyllide oxidoredu	<i>Genlisea aurea</i>	protochlorophyllide reductase activity	chlorophyll biosynthetic process; photosynthesis glucose metabolic process; pentose-phosphate shunt	chloroplast
S8CJD3	PL	Glucose-6-phosphate 1-dehydrogenase	<i>Genlisea aurea</i>	glucose-6-phosphate dehydrogenase activity; NADP binding		
S8D453	PL	30S ribosomal protein S7, chloropla	<i>Genlisea aurea</i>	rRNA binding; structural constituent of ribosome	translation	chloroplast; small ribosomal subunit
S8CEY0	PL	Beta-hydroxyacyl-acyl carrier prote	<i>Genlisea aurea</i>	hydro-lyase activity	fatty acid biosynthetic process	
S8ECI2	PL	30S ribosomal protein S14, chloropl	<i>Genlisea aurea</i>	rRNA binding; structural constituent of ribosome	translation	chloroplast; ribosome
S8CGN1	PL	Epimerase domain-containing protein	<i>Genlisea aurea</i>	GDP-mannose 3,5-epimerase activity; NAD binding		
S8C347	PL	2-C-methyl-D-erythritol 2,4-cyclodi	<i>Genlisea aurea</i>	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase activity	terpenoid biosynthetic process	
S8DS25	PL	Iso_dh domain-containing protein	<i>Genlisea aurea</i>	isocitrate dehydrogenase (NAD+) activity	tricarboxylic acid cycle	
S8C3H3	PL	Uncharacterized protein	<i>Genlisea aurea</i>			
S8ED92	PL	Usp domain-containing protein	<i>Genlisea aurea</i>			
S8D037	PL	Uncharacterized protein	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome
S8E4K0	PL	Germin-like protein	<i>Genlisea aurea</i>	manganese ion binding; nutrient reservoir activity		apoplast; cell wall
S8D7P3	WL	Uncharacterized protein	<i>Genlisea aurea</i>		photosynthesis	integral component of

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S8BVR5	WL	Malic enzyme	<i>Genlisea aurea</i>	malate dehydrogenase (decarboxylating) (NAD+) activity; metal ion binding; NAD binding		membrane; photosystem I
S8E9I9	WL	Uncharacterized protein	<i>Genlisea aurea</i>			
S8DAM5	WL	Uncharacterized protein	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome
S8CT12	WL	Uncharacterized protein	<i>Genlisea aurea</i>			
S8CUD3	WL	40S ribosomal protein S7	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome
S8BUV6	WL	Uncharacterized protein	<i>Genlisea aurea</i>			
S8EEF3	WL	Uncharacterized protein	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome
S8DXW1	WL	Uncharacterized protein	<i>Genlisea aurea</i>			
S8CLD8	WL	Uncharacterized protein	<i>Genlisea aurea</i>	glutamate-1-semialdehyde 2,1-aminomutase activity; pyridoxal phosphate binding; transaminase activity	tetrapyrrole biosynthetic process	
S8CL64	WL	Uncharacterized protein	<i>Genlisea aurea</i>			
S8E9H9	WL	Malic enzyme	<i>Genlisea aurea</i>	malate dehydrogenase (decarboxylating) (NAD+) activity; metal ion binding; NAD binding		
S8D524	WL	50S ribosomal protein L14, chloropl	<i>Genlisea aurea</i>	rRNA binding; structural constituent of ribosome	translation	chloroplast; large ribosomal subunit
S8C802	WL	Lactoylglutathione lyase	<i>Genlisea aurea</i>	lactoylglutathione lyase activity; metal ion binding		
S8D406	WL	40S ribosomal protein S25	<i>Genlisea aurea</i>			ribosome
S8D3J4	WL	Uncharacterized protein	<i>Genlisea aurea</i>	GTPase activity; GTP binding		
S8D8K7	WL	S4 RNA-binding domain-containing pr	<i>Genlisea aurea</i>	rRNA binding; structural constituent of ribosome	translation	small ribosomal subunit
S8DVK0	WL	Peroxiredoxin	<i>Genlisea aurea</i>	peroxidase activity; peroxiredoxin activity	cell redox homeostasis	cell
S8DA78	WL	Uncharacterized protein	<i>Genlisea aurea</i>			
S8D2E2	WL	Uncharacterized protein	<i>Genlisea aurea</i>			integral component of membrane
S8DHI0	WL	Bet_v_1 domain-containing protein	<i>Genlisea aurea</i>		defense response	
S8DGS9	WL	PEROXIDASE_4 domain-containing prot	<i>Genlisea aurea</i>	heme binding; peroxidase activity	response to oxidative stress	integral component of membrane
S8BWE0	WL	Uncharacterized protein	<i>Genlisea aurea</i>		pollen development	
S8DA36	WL	Uncharacterized protein	<i>Genlisea aurea</i>			
S8EEC7	WL	WD_REPEATS_REGION domain-containing	<i>Genlisea aurea</i>			
S8CJI5	WL	RRM domain-containing protein	<i>Genlisea aurea</i>	RNA binding		
S8BWA3	WL	Uncharacterized protein	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome
S8EAX8	WL	Uncharacterized protein	<i>Genlisea aurea</i>	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase activity; iron ion binding	terpenoid biosynthetic process	
S8DWY3	WL	M16C-associated domain-containing p	<i>Genlisea aurea</i>	catalytic activity; metal ion binding	proteolysis	

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S8D7Q6	WL	PsbP domain-containing protein	<i>Genlisea aurea</i>	calcium ion binding	photosynthesis	extrinsic component of membrane; photosystem II oxygen evolving complex
S8E6U3	WL	Aldo_ket_red domain-containing prot	<i>Genlisea aurea</i>	oxidoreductase activity		
S8E584	WL	Nascent polypeptide-associated comp	<i>Genlisea aurea</i>			
S8E878	WL	PKS_ER domain-containing protein	<i>Genlisea aurea</i>	oxidoreductase activity		
S8DLJ5	WL	RRM domain-containing protein	<i>Genlisea aurea</i>	RNA binding		
S8DJL3	WL	Uncharacterized protein	<i>Genlisea aurea</i>	ATPase-coupled transmembrane transporter activity		
S8D3H1	WL	30S ribosomal protein S4, chloropla	<i>Genlisea aurea</i>	rRNA binding; structural constituent of ribosome	translation	chloroplast; small ribosomal subunit
S8D0N8	WL	Uncharacterized protein	<i>Genlisea aurea</i>	proton-transporting ATPase activity, rotational mechanism		proton-transporting two-sector ATPase complex, catalytic domain
S8CUG6	WL	Uncharacterized protein	<i>Genlisea aurea</i>			
A0A5B7A6S3	WL-PL	Uncharacterized protein	<i>Davidia involucrata</i>			
A0A2I6QE76	WL-PL	ATP synthase epsilon chain, chlorop	<i>Genlisea violacea</i>	ATP binding; proton-transporting ATP synthase activity, rotational mechanism	ATP synthesis coupled proton transport	chloroplast thylakoid membrane; proton-transporting ATP synthase complex, catalytic core F(1)
A0A0A0Y4Q2	WL-PL	Fibrillin 1 protein	<i>Capsicum annuum</i>			
A0A4P1REH7	WL-PL	Germin-like protein	<i>Lupinus angustifolius</i>	manganese ion binding; nutrient reservoir activity		apoplast; cell wall
A0A2G9IBF3	WL-PL	Molecular chaperones mortalin/PBP74	<i>Handroanthus impetiginosus</i>	ATP binding; unfolded protein binding	protein folding	
A0A3S8TL14	WL-PL	Ascorbate peroxidase	<i>Datisca glomerata</i>	heme binding; peroxidase activity	response to oxidative stress	
A0A2G3C7W3	WL-PL	ATP synthase subunit b', chloroplas	<i>Capsicum chinense</i>	proton transmembrane transporter activity	ATP synthesis coupled proton transport	integral component of membrane; proton-transporting ATP synthase complex, coupling factor F(o)
O81372	WL-PL	Nucleoside diphosphate kinase 1	<i>Mesembryanthemum crystallinum</i>	ATP binding; metal ion binding; nucleoside diphosphate kinase activity	CTP biosynthetic process; GTP biosynthetic process; UTP biosynthetic process	
A0A4S8IYE1	WL-PL	Uncharacterized protein	<i>Musa balbisiana</i>	cysteine-type peptidase activity		integral component of membrane
A0A5A7R1Y0	WL-PL	Cold shock protein 1	<i>Striga asiatica</i>			
M0ZSM1	WL-PL	Chloroplast manganese stabilizing p	<i>Solanum tuberosum</i>	oxygen evolving activity	photosystem II assembly; photosystem II stabilization	photosystem II oxygen evolving complex

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A0A2C9U8K7	WL-PL	PAP_fibrillin domain-containing pro	<i>Manihot esculenta</i>			
A0A2I4F2B2	WL-PL	Fructose-bisphosphate aldolase	<i>Juglans regia</i>	fructose-bisphosphate aldolase activity	glycolytic process	
A0A2G9GAZ9	WL-PL	Iridoid synthase	<i>Handroanthus impetiginosus</i>	oxidoreductase activity		
Q43848	WL-PL	Transketolase, chloroplastic	<i>Solanum tuberosum</i>	metal ion binding; transketolase activity	reductive pentose-phosphate cycle	chloroplast thylakoid membrane
A0A1R3I2S6	WL-PL	PAP_fibrillin domain-containing pro	<i>Corchorus capsularis</i>			
A0A4D8YMP6	WL-PL	Ribulose-phosphate 3-epimerase	<i>Salvia splendens</i>	racemase and epimerase activity, acting on carbohydrates and derivatives	carbohydrate metabolic process	
A0A1U8F7J0	WL-PL	Adenosylhomocysteinase	<i>Capsicum annuum</i>	adenosylhomocysteinase activity	one-carbon metabolic process	
A0A4D8Y9C2	WL-PL	Chaperonin GroEL	<i>Salvia splendens</i>	ATP binding	protein refolding	
A0A2I6QE99	WL-PL	Photosystem II CP47 reaction center	<i>Genlisea violacea</i>	chlorophyll binding; electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity	photosynthetic electron transport in photosystem II; protein-chromophore linkage	chloroplast thylakoid membrane; integral component of membrane; photosystem II
A0A022RPY1	WL-PL	Chitin-binding type-1 domain-contai	<i>Erythranthe guttata</i>	chitinase activity; chitin binding	carbohydrate metabolic process; cell wall macromolecule catabolic process; chitin catabolic process	
Q6USJ7	PL	Ribulose bisphosphate carboxylase l	<i>Pyrrosia rupestris</i>	magnesium ion binding; monooxygenase activity; ribulose-bisphosphate carboxylase activity	photorespiration; reductive pentose-phosphate cycle	chloroplast
Q0ZPA3	PL	Plastid lipid associated protein CH	<i>Solanum lycopersicum</i>			
A0A2I6QE85	PL	Ribulose bisphosphate carboxylase l	<i>Pinguicula primuliflora</i>	magnesium ion binding; monooxygenase activity; ribulose-bisphosphate carboxylase activity	photorespiration; reductive pentose-phosphate cycle	chloroplast
A0A2G9FWJ5	PL	Uncharacterized protein	<i>Handroanthus impetiginosus</i>		photosynthesis	photosystem I reaction center
A0A5B6YNS3	PL	Putative chaperonin 60 subunit beta	<i>Davidia involucrata</i>			
Q67HJ0	PL	Cytochrome b559 subunit alpha	<i>Alania cunninghamii</i>	heme binding; metal ion binding	photosynthetic electron transport chain	chloroplast thylakoid membrane; integral component of membrane; photosystem II reaction center
A0A1S2Y8F1	PL	isoflavone reductase-like protein	<i>Cicer arietinum</i>			
A0A024HR93	PL	Ribulose bisphosphate carboxylase l	<i>Vincetoxicum mollissimum</i>	magnesium ion binding; monooxygenase activity; ribulose-bisphosphate carboxylase activity	photorespiration; reductive pentose-phosphate cycle	chloroplast
I1ULG6	PL	Ribulose bisphosphate carboxylase l	<i>Stizophyllum riparium</i>	magnesium ion binding; monooxygenase activity; ribulose-bisphosphate carboxylase activity	photorespiration; reductive pentose-phosphate cycle	chloroplast

Uniprot ID	Leave type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component)
W1IK53	PL	ATP synthase subunit alpha, chlorop	<i>Pinguicula ehlersiae</i>	ATP binding; proton-transporting ATP synthase activity, rotational mechanism	ATP synthesis coupled proton transport	chloroplast thylakoid membrane; proton-transporting ATP synthase complex, catalytic core F(1)
A0A426Y333	PL	Nucleoside diphosphate kinase	<i>Ensete ventricosum</i>	ATP binding; nucleoside diphosphate kinase activity	CTP biosynthetic process; GTP biosynthetic process; UTP biosynthetic process	
A0A2G9GMS2	PL	PAP_fibrillin domain-containing pro	<i>Handroanthus impetiginosus</i>			
Q8WKQ8	PL	Ribulose biphosphate carboxylase l	<i>Tigridia pavonia</i>	magnesium ion binding; monooxygenase activity; ribulose-bisphosphate carboxylase activity	photorespiration; reductive pentose-phosphate cycle	chloroplast
W8SQU3	PL	Chlorophyll a-b binding protein, ch	<i>Pyrus x bretschneideri</i>	chlorophyll binding	photosynthesis, light harvesting; protein-chromophore linkage	chloroplast thylakoid membrane; integral component of membrane; photosystem I; photosystem II
A0A453L9A1	PL	Pyruvate dehydrogenase E1 component	<i>Aegilops tauschii subsp. strangulata</i>	pyruvate dehydrogenase (acetyl-transferring) activity	acetyl-CoA biosynthetic process from pyruvate cell redox homeostasis; hydrogen peroxide catabolic process; response to oxidative stress	
K7MM65	PL	AhpC-TSA domain-containing protein	<i>Glycine max</i>	thioredoxin peroxidase activity		cell; integral component of membrane
V4W5U2	PL	Uncharacterized protein	<i>Citrus clementina</i>	intramolecular transferase activity, phosphotransferases; magnesium ion binding	carbohydrate metabolic process	
W9QUC7	PL	Photosystem I reaction center subun	<i>Morus notabilis</i>		photosynthesis	photosystem I
A0A444FTJ0	PL	Uncharacterized protein	<i>Ensete ventricosum</i>	ATP binding	protein refolding	
A0A4U5PYS7	PL	Fructose-bisphosphate aldolase	<i>Populus alba</i>	fructose-bisphosphate aldolase activity	glycolytic process	
M5X8P7	PL	NDK domain-containing protein	<i>Prunus persica</i>	nucleoside diphosphate kinase activity	cellular response to hydrogen peroxide	
A0A444XLN7	PL	TPM_phosphatase domain-containing p	<i>Arachis hypogaea</i>			
Q32434	PL	Ribulose biphosphate carboxylase l	<i>Peucedanum elegans</i>	magnesium ion binding; monooxygenase activity; ribulose-bisphosphate carboxylase activity	photorespiration; reductive pentose-phosphate cycle cellular response to oxidative stress;	chloroplast
B9SGR9	PL	L-ascorbate peroxidase, cytosolic,	<i>Ricinus communis</i>	heme binding; L-ascorbate peroxidase activity; peroxidase activity	hydrogen peroxide catabolic process; response to reactive oxygen species	chloroplast
A0A4D9BLA3	PL	Carbonic anhydrase	<i>Salvia splendens</i>	carbonate dehydratase activity; zinc ion binding	carbon utilization	

Uniprot ID	Leave type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component)
A0A4Y7J1J5	PL	Uncharacterized protein	<i>Papaver somniferum</i>	adenine phosphoribosyltransferase activity	adenine salvage; nucleoside metabolic process	cytoplasm
O47073	PL	Ribulose biphosphate carboxylase l	<i>Didymoglossum ekmanii</i>	magnesium ion binding; monooxygenase activity; ribulose-bisphosphate carboxylase activity	photorespiration; reductive pentose-phosphate cycle	chloroplast
M8BRS6	PL	Putative 2-Cys peroxiredoxin BAS1,	<i>Aegilops tauschii</i>	peroxiredoxin activity	cell redox homeostasis	cell
A0A4U5NMA0	PL	PAP_fibrillin domain-containing pro	<i>Populus alba</i>			
A0A2I4EHK1	PL	L-ascorbate peroxidase, cytosolic	<i>Juglans regia</i>	heme binding; peroxidase activity	response to oxidative stress	
A0A4D9BCT0	PL	NmrA domain-containing protein	<i>Salvia splendens</i>			
Q9AWA8	PL	Glutamine synthetase	<i>Beta vulgaris</i>	ATP binding; glutamate-ammonia ligase activity	glutamine biosynthetic process; response to cadmium ion	apoplast; chloroplast envelope; chloroplast stroma; chloroplast thylakoid membrane; cytosolic ribosome; mitochondrion
A0A4D6NK45	PL	F-type H ⁺ -transporting ATPase subun	<i>Vigna unguiculata</i>	ATP binding; proton-transporting ATP synthase activity, rotational mechanism	ATP synthesis coupled proton transport	proton-transporting ATP synthase complex, catalytic core F(1)
B7FJ53	PL	Uncharacterized protein	<i>Medicago truncatula</i>			chloroplast; integral component of membrane
Q33585	PL	Ribulose biphosphate carboxylase l	<i>Diphasiastrum complanatum</i>	magnesium ion binding; monooxygenase activity; ribulose-bisphosphate carboxylase activity	photorespiration; reductive pentose-phosphate cycle	chloroplast
A0A1S3UFS1	PL	Fructose-bisphosphate aldolase	<i>Vigna radiata</i>	fructose-bisphosphate aldolase activity	glycolytic process	
W9R689	PL	Uncharacterized protein	<i>Morus notabilis</i>	magnesium ion binding; phosphopyruvate hydratase activity	glycolytic process	phosphopyruvate hydratase complex
A0A2G9H7L1	PL	Cysteine proteinase Cathepsin L	<i>Handroanthus impetiginosus</i>	cysteine-type peptidase activity		
A0A5A7RAZ6	PL	Ferredoxin--NADP reductase, chlorop	<i>Striga asiatica</i>			
A0A388K5H9	PL	Chlorophyll a-b binding protein, ch	<i>Chara braunii</i>	chlorophyll binding	photosynthesis, light harvesting; protein-chromophore linkage	chloroplast thylakoid membrane; integral component of membrane; photosystem I; photosystem II
G7JPH8	PL	Photosystem II stability/assembly f	<i>Medicago truncatula</i>			
X2D1B6	PL	Ribulose biphosphate carboxylase l	<i>Tectaria impressa</i>	magnesium ion binding; monooxygenase activity; ribulose-bisphosphate carboxylase activity	photorespiration; reductive pentose-phosphate cycle	chloroplast
M1D096	PL	ATP synthase subunit beta	<i>Solanum tuberosum</i>	ATPase activity; ATP binding; proton-transporting ATP synthase activity, rotational mechanism	ATP synthesis coupled proton transport	mitochondrial proton-transporting ATP synthase complex, catalytic core F(1)

Uniprot ID	Leave type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component)
V9PE85	PL	ATP synthase subunit beta, chloropl	<i>Agrostemma githago</i>	ATP binding; proton-transporting ATP synthase activity; rotational mechanism	ATP synthesis coupled proton transport	chloroplast thylakoid membrane; proton-transporting ATP synthase complex, catalytic core F(1)
A0A4Y7KR T9	PL	Uncharacterized protein	<i>Papaver somniferum</i>			
A0A0B2R4 F5	PL	Transketolase, chloroplastic	<i>Glycine soja</i>	1-deoxy-D-xylulose-5-phosphate synthase activity; transketolase activity		
A0A0B2R4 F5	PL	TRANSKETOLASE_1 domain-containing p	<i>Glycine max</i>	transketolase activity	pentose-phosphate shunt glycolytic process cell redox homeostasis; glycerol ether metabolic process	cytosol
A9NVA3	PL	Phosphoglycerate kinase	<i>Picea sitchensis</i>	phosphoglycerate kinase activity		
A0A1J7HA M6	PL	Thioredoxin	<i>Lupinus angustifolius</i>	protein disulfide oxidoreductase activity		cell
A0A022QW P2	PL	Dihydrolipoyl dehydrogenase	<i>Erythranthe guttata</i>	dihydrolipoyl dehydrogenase activity; electron transfer activity; flavin adenine dinucleotide binding	cell redox homeostasis	cell
A0A2R6R3 T3	PL	Glyceraldehyde-3-phosphate dehydrog	<i>Actinidia chinensis var. chinensis</i>	NAD binding; NADP binding; oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	glucose metabolic process	
A0A2G3BI D8	PL	Monodehydroascorbate reductase	<i>Capsicum chinense</i>	flavin adenine dinucleotide binding; oxidoreductase activity		
A0A4P1RE Y1	PL	Uncharacterized protein	<i>Lupinus angustifolius</i>	cysteine-type peptidase activity		
A0A5A7QT K3	PL	Oxygen-evolving enhancer protein 2	<i>Striga asiatica</i>			
A0A4D9BS X4	PL	5-methyltetrahydropteroyltriglutama	<i>Salvia splendens</i>	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity; zinc ion binding	methionine biosynthetic process; methylation	
A0A087SHJ 4	PL	Peptidyl-prolyl cis-trans isomerase	<i>Auxenochlorella protothecoides</i>	peptidyl-prolyl cis-trans isomerase activity	protein folding	
M0TDY7	PL	60S ribosomal protein L23A-like	<i>Trifolium medium</i>	structural constituent of ribosome	translation	ribosome
A0A5A7QH G3	PL	Fructose-1,6-bisphosphatase class 1	<i>Striga asiatica</i>			
A0A5E4ED M5	PL	PREDICTED: L-ascorbate peroxidase	<i>Prunus dulcis</i>	peroxidase activity		
Q9LKZ0	PL	Chlorophyll a-b binding protein, ch	<i>Picea glauca</i>	chlorophyll binding	photosynthesis, light harvesting; protein-chromophore linkage	chloroplast thylakoid membrane; integral component of membrane; photosystem I; photosystem II
A0A068U89 0	PL	Aminomethyltransferase	<i>Coffea canephora</i>	aminomethyltransferase activity; transaminase activity	glycine catabolic process	mitochondrion
A0A4D9B8 66	PL	Chlorophyll a-b binding protein, ch	<i>Salvia splendens</i>	chlorophyll binding	photosynthesis, light harvesting; protein-chromophore linkage	chloroplast thylakoid membrane; integral component of membrane;

Uniprot ID	Leave type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component)
						photosystem I; photosystem II
A0A2U1PV G5	PL	Band 7 protein	<i>Artemisia annua</i>			
B9RVK2	PL	Ribosomal protein	<i>Ricinus communis</i>	RNA binding; structural constituent of ribosome	translation	large ribosomal subunit
A0A5B7AL 20	PL	Putative Ribosomal protein S10p/S20	<i>Davidia involucrata</i>			ribosome
V4U6P5	PL	Carbonic anhydrase	<i>Citrus clementina</i>	carbonate dehydratase activity; zinc ion binding	carbon utilization cellular response to tetrahydrofolate ; folic acid metabolic process; glycine biosynthetic process from serine; glycine metabolic process; L-serine catabolic process; one-carbon metabolic process; tetrahydrofolate interconversion ; tetrahydrofolate metabolic process hydrogen peroxide catabolic process; response to oxidative stress	
K3XGJ1	PL	Serine hydroxymethyltransferase	<i>Setaria italica</i>	amino acid binding; cobalt ion binding; glycine hydroxymethyltransferase activity; pyridoxal phosphate binding; serine binding; zinc ion binding		
A0A067JC X4	PL	Peroxidase	<i>Jatropha curcas</i>	heme binding; metal ion binding; peroxidase activity		extracellular region
Q9LKY5	PL	Tubulin alpha chain	<i>Zea mays</i>	GTPase activity; GTP binding; structural constituent of cytoskeleton	microtubule-based process	microtubule
Q677D0	PL	Chlorophyll a-b binding protein, ch	<i>Hyacinthus orientalis</i>	chlorophyll binding	photosynthesis, light harvesting; protein-chromophore linkage	chloroplast thylakoid membrane; integral component of membrane; photosystem I; photosystem II
A0A5A7RB M6	PL	Photosystem II CP43 reaction center	<i>Striga asiatica</i>			
A0A2P5WF 81	PL	Uncharacterized protein	<i>Gossypium barbadense</i>	metal ion binding; metalloendopeptidase activity		
A0A1J6IDI 5	PL	Dihydrolipoyl dehydrogenase	<i>Nicotiana attenuata</i>	dihydrolipoyl dehydrogenase activity; electron transfer activity; flavin adenine dinucleotide binding	cell redox homeostasis	cell
A0A4D9A0 J4	WL	Photosystem II oxygen-evolving enh	<i>Salvia splendens</i>	calcium ion binding	photosynthesis	extrinsic component of membrane; photosystem II oxygen evolving complex
A0A5A7Q8 A9	WL	60 kDa chaperonin	<i>Striga asiatica</i>			

Uniprot ID	Leave type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component)
A1IW05	WL	Subunit IV of photosystem I (PSI-E)	<i>Phillyrea latifolia</i>		photosynthesis	photosystem I reaction center
Q6XGX6	WL	Putative photosystem I reaction cen	<i>Vitis vinifera</i>		photosynthesis	photosystem I
A0A067XJ96	WL	Cytosolic ascorbate peroxidase	<i>Pyrus pyrifolia</i>	heme binding; L-ascorbate peroxidase activity	response to oxidative stress	
A0A2I6QE92	WL	Cytochrome f	<i>Genlisea violacea</i>	electron transfer activity; heme binding; iron ion binding	photosynthesis	chloroplast thylakoid membrane; integral component of thylakoid membrane chloroplast thylakoid membrane
H9MBH0	WL	Chlorophyll a-b binding protein, ch	<i>Pinus radiata</i>	chlorophyll binding	photosynthesis, light harvesting; protein-chromophore linkage	integral component of membrane; photosystem I; photosystem II extrinsic component of membrane; photosystem II oxygen evolving complex chloroplast
A0A4V3WK35	WL	Uncharacterized protein	<i>Camellia sinensis</i>	calcium ion binding	photosynthesis	
A0A565CXF0	WL	Ferredoxin--NADP reductase, chlorop	<i>Arabis nemorensis</i>	ferredoxin-NADP+ reductase activity		chloroplast
A0A5A7PDG4	WL	Oxygen-evolving enhancer protein 1	<i>Striga asiatica</i>			
Q8H534	WL	Os07g0484800 protein	<i>Oryza sativa</i>	adenine phosphoribosyltransferase activity	adenine salvage; nucleoside metabolic process	cytosol
A0A1R3HY13	WL	NmrA-like protein	<i>Corchorus olitorius</i>			
W9RGV2	WL	Phosphoglucomutase	<i>Morus notabilis</i>	intramolecular transferase activity, phosphotransferases; magnesium ion binding	carbohydrate metabolic process	
V4S7U5	WL	Uncharacterized protein	<i>Citrus clementina</i>	magnesium ion binding; phosphopyruvate hydratase activity	glycolytic process	phosphopyruvate hydratase complex
A0A1D1ZKQ0	WL	Oxygen-evolving enhancer protein 1,	<i>Anthurium amnicola</i>	oxygen evolving activity	photosystem II assembly; photosystem II stabilization	photosystem II oxygen evolving complex
A0A5A7NWH1	WL	mRNA-binding family protein	<i>Striga asiatica</i>			
A0A1J3EV72	WL	Oxygen-evolving enhancer protein 1,	<i>Nocca caerulea</i>	oxygen evolving activity	photosystem II assembly; photosystem II stabilization	photosystem II oxygen evolving complex
I1N2I4	WL	NAD(P)-bd_dom domain-containing pro	<i>Glycine max</i>			chloroplast
A0A0D9VHX1	WL	Gp_dh_N domain-containing protein	<i>Leersia perrieri</i>	nucleotide binding; oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor		
Q7FAH2	WL	Glyceraldehyde-3-phosphate dehydrog	<i>Oryza barthii</i>	NAD binding; NADP binding; oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	glucose metabolic process	
A0A4D9BH81	WL	Nucleoside-diphosphate kinase	<i>Salvia splendens</i>	hydrolase activity; nucleoside diphosphate kinase activity	CTP biosynthetic process; GTP biosynthetic process; UTP	

Uniprot ID	Leave type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component)
					biosynthetic process	
A0A164Z1J4	WL	Epimerase domain-containing protein	<i>Daucus carota</i>	catalytic activity; coenzyme binding		
B8LLV3	WL	Serine hydroxymethyltransferase	<i>Picea sitchensis</i>	glycine hydroxymethyltransferase activity; pyridoxal phosphate binding	glycine biosynthetic process from serine; tetrahydrofolate interconversion	
A0A5D3E5W9	WL	Stromal 70 kDa heat shock-related p	<i>Cucumis melo</i>			
A0A1L5JKB2	WL	Glyceraldehyde-3-phosphate dehydrog	<i>Sesuvium portulacastrum</i>	NAD binding; NADP binding; oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	glucose metabolic process	
D5LY28	WL	Soluble acid invertase 1	<i>Phelipanche ramosa</i>	sucrose alpha-glucosidase activity	carbohydrate metabolic process	integral component of membrane
W5S7M9	WL	Cu-Zn superoxide dismutase	<i>Aegiceras corniculatum</i>	metal ion binding	superoxide metabolic process	
D7T9G8	WL	PSII_BNR domain-containing protein	<i>Vitis vinifera</i>			
V7D036	WL	Glyceraldehyde-3-phosphate dehydrog	<i>Phaseolus vulgaris</i>	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor		
A0A540MU Y0	WL	Aspartate aminotransferase	<i>Malus baccata</i>	L-aspartate:2-oxoglutarate aminotransferase activity		
A0A444EGL7	WL	PKS_ER domain-containing protein	<i>Ensete ventricosum</i>	oxidoreductase activity		
A0A5D2NFF5	WL	Uncharacterized protein	<i>Gossypium tomentosum</i>			
A0A445B273	WL	CN hydrolase domain-containing prot	<i>Arachis hypogaea</i>		nitrogen compound metabolic process	
J3MR75	WL	Uncharacterized protein	<i>Oryza brachyantha</i>	pyridoxal phosphate binding; transaminase activity		
A0A1J3JPV7	WL	Proteasome subunit alpha type	<i>Noccaea caerulea</i>	threonine-type endopeptidase activity	ubiquitin-dependent protein catabolic process	cytoplasm; nucleus; proteasome core complex, alpha-subunit complex

Table S12. GO annotation of shared proteins in leaves and traps of white and purple-flowered morphotypes of *Genlisea violacea* identified with PEAKS.

Uniprot ID	Leave Type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component)
S8EJ11	PL-PT	Adenosylhomocysteinase	<i>Genlisea aurea</i>	adenosylhomocysteinase activity	one-carbon metabolic process; positive regulation of translational elongation; positive regulation of translational termination; translational frameshifting	
S8E4S5	PL-PT	Eukaryotic translation initiation f	<i>Genlisea aurea</i>	ribosome binding; translation elongation factor activity		
S8E4Y7	WL-WT-PL	Uncharacterized protein	<i>Genlisea aurea</i>	ATP binding		cytoplasm; cytoskeleton
S8E0E9	WL-WT-PL	Triosephosphate isomerase	<i>Genlisea aurea</i>	triose-phosphate isomerase activity	glycolytic process	
S8BWT7	WL-WT-PL	Enolase	<i>Genlisea aurea</i>	magnesium ion binding; phosphopyruvate hydratase activity	glycolytic process	phosphopyruvate hydratase complex
S8CPQ1	WL-WT-PL	Cupin_2 domain-containing protein	<i>Genlisea aurea</i>	isomerase activity	carbohydrate metabolic process	
S8D525	WL-WT-PL	Fructose-bisphosphate aldolase	<i>Genlisea aurea</i>	fructose-bisphosphate aldolase activity	glycolytic process	
S8EK09	WL-WT-PL	14-3-3 a-1 protein	<i>Genlisea aurea</i>	protein domain specific binding		
S8E5C8	WL-WT-PL	Malate dehydrogenase	<i>Genlisea aurea</i>	L-malate dehydrogenase activity	carbohydrate metabolic process; malate metabolic process; tricarboxylic acid cycle	
S8DYR8	WL-WT-PL	CoA_binding domain-containing prote	<i>Genlisea aurea</i>	cofactor binding; ligase activity		
S8CX13	WL-WT-PL	60S ribosomal protein L13	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome
S8E3U3	WL-WT-PL	Uncharacterized protein	<i>Genlisea aurea</i>	ATP binding; galactokinase activity; galactose binding	galactose metabolic process	cytoplasm
S8C9K9	WL-WT-PL	Malic enzyme	<i>Genlisea aurea</i>	malate dehydrogenase (decarboxylating) (NAD ⁺) activity; metal ion binding; NAD binding		
S8E173	WL-WT-PL	Phosphoglycerate kinase	<i>Genlisea aurea</i>	phosphoglycerate kinase activity	glycolytic process; hydrogen peroxide catabolic process; response to oxidative stress	
S8E1K9	WL-WT-PL	Catalase	<i>Genlisea aurea</i>	catalase activity; heme binding; metal ion binding		
S8CHM2	WL-WT-PL	Phosphoglycerate kinase	<i>Genlisea aurea</i>	ATP binding; phosphoglycerate kinase activity	glycolytic process	
S8C8U7	WL-WT-PL	Ribosomal_L7Ae domain-containing pr	<i>Genlisea aurea</i>		ribosome biogenesis	ribonucleoprotein complex

Uniprot ID	Leave Type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component)
S8D216	WL-WT-PL	Chlorophyll a-b binding protein, ch	<i>Genlisea aurea</i>	chlorophyll binding	photosynthesis , light harvesting; protein-chromophore linkage	chloroplast thylakoid membrane; integral component of membrane; photosystem I; photosystem II
S8EDN5	WL-WT-PL	UDP-glucose 4-epimerase	<i>Genlisea aurea</i>	UDP-glucose 4-epimerase activity	galactose metabolic process	
S8CWK8	WL-WT-PL-PT	Ubiquitin-like domain-containing pr	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome
S8CSZ4	WL-WT-PL-PT	Actin-97	<i>Genlisea aurea</i>	ATP binding		cytoplasm; cytoskeleton
A0A2I6QD52	WL-WT-PL-PT	Ribulose biphosphate carboxylase large chain, RuBisCO large subunit	<i>Genlisea aurea</i>	magnesium ion binding; monooxygenase activity; ribulose-biphosphate carboxylase activity	photorespiration; reductive pentose-phosphate cycle	chloroplast
S8CRU7	WL-WT-PL-PT	Actin	<i>Genlisea aurea</i>	ATP binding		cytoplasm; cytoskeleton
S8CYV8	WL-WT-PL-PT	Histone H4	<i>Genlisea aurea</i>	DNA binding; protein heterodimerization activity		nucleosome; nucleus
S8DD77	WL-WT-PL-PT	Actin	<i>Genlisea aurea</i>			
S8CBA2	WL-WT-PL-PT	Chlorophyll a-b binding protein, ch	<i>Genlisea aurea</i>	chlorophyll binding	photosynthesis , light harvesting; protein-chromophore linkage	chloroplast thylakoid membrane; integral component of membrane; photosystem I; photosystem II
S8C6K2	WL-WT-PL-PT	Heat shock protein 70	<i>Genlisea aurea</i>	ATP binding		
S8CBN4	WL-WT-PL-PT	Histone H3	<i>Genlisea aurea</i>	DNA binding; protein heterodimerization activity		nucleosome; nucleus
S8E2N0	WL-WT-PL-PT	Histone H3	<i>Genlisea aurea</i>	DNA binding; protein heterodimerization activity		nucleosome; nucleus
S8DPH5	WL-WT-PL-PT	Uncharacterized protein	<i>Genlisea aurea</i>	ATP binding		
S8CX03	WL-WT-PL-PT	Uncharacterized protein	<i>Genlisea aurea</i>	transmembrane transporter activity		integral component of membrane; mitochondrial inner membrane
S8ENH4	WL-WT-PL-PT	Histone H2B	<i>Genlisea aurea</i>	DNA binding; protein heterodimerization activity		nucleosome; nucleus
S8CMY8	WL-WT-PL-PT	Histone H2A	<i>Genlisea aurea</i>	DNA binding; protein heterodimerization activity		nucleosome; nucleus
S8EF74	WL-WT-PL-PT	ATP synthase subunit alpha	<i>Genlisea aurea</i>	ATP binding; proton-transporting ATP synthase activity, rotational mechanism	ATP synthesis coupled proton transport	proton-transporting ATP synthase complex, catalytic core F(1)
S8E6J7	WL-WT-PL-PT	Expansin-like EG45 domain-containin	<i>Genlisea aurea</i>			
S8CIP5	WL-WT-PL-PT	Tr-type G domain-containing protein	<i>Genlisea aurea</i>	GTPase activity; GTP binding		

Uniprot ID	Leave Type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component)
S8CI40	WL-WT- PL-PT	Elongation factor 1-alpha	<i>Genlisea aurea</i>	GTPase activity; GTP binding; translation elongation factor activity isocitrate dehydrogenase (NADP+) activity; magnesium ion binding; NAD binding	isocitrate metabolic process	
S8BWD8	WL-WT- PL-PT	Iso_dh domain-containing protein	<i>Genlisea aurea</i>		carbohydrate metabolic process; malate metabolic process; tricarboxylic acid cycle	
S8D4W0	WL-WT- PL-PT	Malate dehydrogenase	<i>Genlisea aurea</i>	L-malate dehydrogenase activity		
S8DFN4	WL-WT- PL-PT	HATPase_c domain-containing protein	<i>Genlisea aurea</i>	ATP binding; unfolded protein binding structural	protein folding	
S8DR98	WL-WT- PL-PT	Uncharacterized protein	<i>Genlisea aurea</i>	constituent of ribosome	translation	ribosome
S8DLT5	WL-WT- PL-PT	14-3-3 h-1 protein	<i>Genlisea aurea</i>	protein domain specific binding structural		
S8D4L6	WL-WT- PL-PT	Uncharacterized protein	<i>Genlisea aurea</i>	constituent of ribosome	translation	ribosome
S8C9X5	WL-WT- PL-PT	Ribulose biphosphate carboxylase small chain	<i>Genlisea aurea</i>	monooxygenase activity; ribulose- biphosphate carboxylase activity	carbon fixation; photorespiratio n; photosynthesis	chloroplast
A0A2I6Q D25	WL-WT- PL-PT	Photosystem II protein D1	<i>Genlisea aurea</i>	chlorophyll binding; electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity; iron ion binding; oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor	photosynthetic electron transport in photosystem II; protein- chromophore linkage; response to herbicide	chloroplast thylakoid membrane; integral component of membrane; photosystem II
S8C857	WL-WT- PL-PT	ATP synthase subunit beta	<i>Genlisea aurea</i>	ATP binding; proton-transporting ATP synthase activity, rotational mechanism	ATP synthesis coupled proton transport	proton- transporting ATP synthase complex, catalytic core F(1)
S8DEF3	WL-WT- PL-PT	Glyceraldehyde-3-phosphate dehydrog	<i>Genlisea aurea</i>	NAD binding; NADP binding; oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	glucose metabolic process	
S8EAM5	WL-WT- PL-PT	14-3-3 protein	<i>Genlisea aurea</i>	protein domain specific binding		
S8CUF0	WL-WT- PL-PT	Uncharacterized protein	<i>Genlisea aurea</i>			integral component of membrane
S8CAG8	WL-WT- PL-PT	Fructose-bisphosphate aldolase	<i>Genlisea aurea</i>	fructose- bisphosphate aldolase activity flavin adenine dinucleotide binding; oxidoreductase activity	glycolytic process	
S8BZF0	WL-WT- PL-PT	Monodehydroascorbate reductase	<i>Genlisea aurea</i>			

Uniprot ID	Leave Type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component)
S8EBF2	WL-WT- PL-PT	GTP-binding nuclear protein	<i>Genlisea aurea</i>	GTPase activity; GTP binding	nucleocytoplas mic transport; protein transport	nucleus
S8CGC3	WL-WT- PL-PT	Dihydrolipoyl dehydrogenase	<i>Genlisea aurea</i>	dihydrolipoyl dehydrogenase activity; electron transfer activity; flavin adenine dinucleotide binding	cell redox homeostasis	cell
S8E1F6	WL-WT- PL-PT	Luminal-binding protein 5	<i>Genlisea aurea</i>	ATP binding		
S8CSD6	WL-WT- PL-PT	Uncharacterized protein	<i>Genlisea aurea</i>			
S8D4F2	WL-WT- PL-PT	AAA domain-containing protein	<i>Genlisea aurea</i>	ATP binding; proton-transporting ATP synthase activity, rotational mechanism	ATP synthesis coupled proton transport	proton- transporting ATP synthase complex, catalytic core F(1)
S8DAF4	WL-WT- PL-PT	Photosystem II CP43 reaction center	<i>Genlisea aurea</i>	chlorophyll binding; electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity; metal ion binding	photosynthetic electron transport in photosystem II; protein- chromophore linkage	chloroplast thylakoid membrane; integral component of membrane; photosystem II
S8D2K5	WL-WT- PL-PT	Fructose-bisphosphate aldolase	<i>Genlisea aurea</i>	fructose- bisphosphate aldolase activity	glycolytic process	
S8BXW0	WT-WL	Polyphenoloxidase	<i>Genlisea aurea</i>	catechol oxidase activity; metal ion binding	pigment biosynthetic process	
S8ELF0	WL-PL-PT	Ribulose bisphosphate carboxylase large chain	<i>Genlisea aurea</i>	magnesium ion binding; ribulose- bisphosphate carboxylase activity	carbon fixation	
S8DNI1	WL-PL-PT	NmrA domain-containing protein	<i>Genlisea aurea</i>			
S8E5Q8	WL-PL-PT	Mitochondrial processing peptidase	<i>Genlisea aurea</i>	metal ion binding; metalloendopeptida se activity		
S8CWY3	WL-PL-PT	Uncharacterized protein	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	cytoplasm; ribosome
S8CTL4	WL-PL-PT	6-phosphogluconate dehydrogenase, d	<i>Genlisea aurea</i>	NADP binding; phosphogluconate dehydrogenase (decarboxylating) activity	D-gluconate metabolic process; pentose- phosphate shunt	
S8CA49	WT-PL	Ribosomal_L16 domain-containing pro	<i>Genlisea aurea</i>	structural constituent of ribosome	translation	ribosome

Table S13. GO annotation of traps exclusive proteins of white and purple-flowered morphotypes of *Genlisea violacea* identified with PEAKS.

Uniprot ID	Leave Type	Protein names	Organism	Gene ontology (molecular function)	Gene ontology (biological process)	Gene ontology (cellular component)
S8D6K0	WT	Pyruvate decarboxylase	<i>Genlisea aurea</i>	carboxy-lyase activity; magnesium ion binding; thiamine pyrophosphate binding		
S8D779	WT	14-3-3 h-1 protein	<i>Genlisea aurea</i>	protein domain specific binding		
S8E4V4	WT	Cysteine proteinase	<i>Genlisea aurea</i>	cysteine-type peptidase activity		
S8DZJ2	WT	Plasma membrane ATPase	<i>Genlisea aurea</i>	ATP binding; proton-exporting ATPase activity, phosphorylative mechanism	proton export across plasma membrane	integral component of membrane; plasma membrane
S8D5C1	WT	10-hydroxygeraniol oxidoreductase	<i>Genlisea aurea</i>	oxidoreductase activity; zinc ion binding; heme binding; iron ion binding; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen		
S8CFM5	WT	Uncharacterized protein	<i>Genlisea aurea</i>	metal ion binding		
S8D1V3	WT	Uncharacterized protein	<i>Genlisea aurea</i>	channel activity		integral component of membrane
A0A411HB20	WT	Plasma membrane intrinsic protein 2	<i>Narcissus tazetta (Cream narcissus)</i>	heme binding; metal ion binding; peroxidase activity	hydrogen peroxide catabolic process; response to oxidative stress	extracellular region
S8CL73	PT*	Peroxidase	<i>Genlisea aurea</i>	4 iron, 4 sulfur cluster binding; aconitate hydratase activity; citrate dehydratase activity		
S8DLP5	PT	Aconitate hydratase	<i>Genlisea aurea</i>	GTPase activity; GTP binding		
S8DDM8	PT	Uncharacterized protein	<i>Genlisea aurea</i>	GTPase activity; GTP binding		
S8CYK9	PT	Uncharacterized protein	<i>Genlisea aurea</i>	metal ion binding; superoxide dismutase activity		
H2DK20	PT	Cu/Zn superoxide dismutase	<i>Camellia oleifera</i>			
A0A2P5F6N2	PT	Hopanoid-associated sugar epimerase	<i>Trema orientale</i>			