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IDENTIFICAÇÃO, CARACTERIZAÇÃO, ATIVIDADE BIOLÓGICA E AVALIAÇÃO DO MECANISMO DE AÇÃO DE PEPTÍDEOS DO NÉCTAR FLORAL DE *Nicotiana sp.*

FORTALEZA

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Dissertação apresentada à Coordenação do Programa de Pós-Graduação em Bioquímica do Centro de Ciências, da Universidade Federal do Ceará, como requisito parcial para obtenção do título de Mestre em Bioquímica. Área de concentração: Bioquímica de Macromoléculas.

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Aos meus pais, Lucila e Jose.
Aos meus irmãos, Danilo e Angela.
À Akitoy e o Paco.
A mim.

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RESUMO

Embora o néctar floral seja uma rica fonte de nutrientes, raramente é infectado por microrganismos. Nesse sentido, moléculas de defesa como proteínas têm sido identificadas nesse fluido, mas o estudo de peptídeos é escasso. Portanto, o objetivo deste estudo foi realizar uma análise peptidômica do néctar floral de tabaco ornamental para identificar peptídeos envolvidos na defesa da planta. Após análises por LC-MS/MS, 794 peptídeos foram identificados e caracterizados. Após uma extensa análise bioinformática das características físico-químicas e biológicas como massa molecular, ponto isoelétrico, carga liquida neta, ração hidrofóbica, índice de Bowman e probabilidade de ter atividade antifúngica e antibacteriana, seis peptídeos foram selecionados para posterior síntese e avaliação de suas propriedades antimicrobianas contra fungos e bactérias fitopatogênicos. Os resultados dos testes de sensibilidade aos peptídeos feitos sobre os microrganismos fitopatogênicos mostraram que todos os peptídeos apresentaram alguma atividade antimicrobiana. No entanto, os resultados foram heterogêneos com base na concentração dos peptídeos e no microrganismo. No caso das bactérias os peptídeos ativos presentam atividade a valores maiores de 125 e 62 µM enquanto nos fungos se obteve atividade inibitória em até 15 µM. A análise do mecanismo de ação, usando microscopia de fluorescência, indicou danos na membrana celular induzidos pelos peptídeos. Os resultados mostram que o néctar floral é rico em peptídeos que são responsáveis pela defesa da planta contra diferentes microrganismos, aproximadamente 20% dos peptídeos identificados tiveram atividade antimicrobial predita superior a um 60%. Estes são resultados promissores que levam a um melhor entendimento da defesa do néctar floral e a possível obtenção de biomoléculas alternativas para o combate de doenças agrícolas infecciosas.

Palavras-chave: Peptídeos antimicrobianos (AMP); peróxido de hidrogênio; Nicotiana sp; Nectarinas; Peptidoma.

ABSTRACT

Although floral nectar is a rich source of nutrients, it is rarely infected by microorganisms. Defense molecules such as proteins have been identified in this fluid, but defense peptides have been largely overlooked. Thus, the aim of this study was to perform an extensive peptidomic analysis of the ornamental tobacco floral nectar to seek peptides involved in nectar defense. Using LC-MS/MS, 794 peptides were sequenced and characterized. After extensive bioinformatics analysis of physicochemical and biological characteristics as molecular mass, isoelectric point, net charge, hydrophobic ratio, Bowman index and probability of having antifungal and antibacterial activity, six peptides were selected for further synthesis and evaluation of their properties. antimicrobials against phytopathogenic fungi and bacteria. Results of peptide sensitivity tests performed on phytopathogenic microorganisms were that all peptides showed some antimicrobial activity. However, the results were heterogeneous based on the concentration of the peptides and the microorganism. In the case of bacteria, active peptides presented activity at minimal values of 125 and 62 µM, while in fungi, inhibitory activity was obtained at 15 µM. Analysis of the mechanism of action, using fluorescence microscopy, indicated cell membrane damage induced by peptides. The results show that floral nectar is rich in peptides that are responsible for plant defense against different microorganisms, approximately 20% of the identified peptides had predicted antimicrobial activity greater than 60%. These are promising results that lead to a better understanding of floral nectar defense and to possible obtain alternatives biomolecules to combat infectious agricultural diseases.

Keywords: Antimicrobial peptides (AMP); hydrogen peroxide; Nicotiana sp; Nectarins; Peptidome.

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1 INTRODUÇÃO

1.1 Compostos naturais e sua importância na agricultura

De acordo com o Panorama Agrícola de 2021-2030 da OCDE-FAO, a população mundial terá um aumento anual de 0,9% e, até o ano de 2030, será um total de 8,5 bilhões de pessoas. O aumento constante da população tem um impacto direto sobre a demanda de alimentos, incluindo cereais, oleaginosas, raízes, tubérculos, leguminosas, cana de açúcar, beterraba, óleo de palma e algodão, além de produtos pecuários (carne, laticínios, ovos e peixes) (FAO, 2021a). Diante do aumento constante da população e, portanto, suas demandas, o acesso aos alimentos para atender às necessidades das pessoas é um dos maiores desafios atualmente (FAO, 2021b). Além do problema da demanda, diversos fatores como luz, água, chuva, temperatura, umidade relativa do ar, vento e fatores bióticos e abióticos podem gerar a diminuição da produtividade das plantas (EILENBERG; HAJEK; LOMER, 2001).

Entre os fatores bióticos estão incluídos os microrganismos fitopatogênicos (fungos, bactérias e vírus), que afetam as culturas e suas produtividades. Os fungos *Fusarium* spp., *Pythium* spp., *Colletotrichum* spp., *Alternaria* spp., *Plasmodiophora* spp., *Taphrina* spp., *Puccinia* spp. são os mais comumente encontrados, atacando as principais plantas cultivadas, geralmente permeando seus tecidos para posteriormente matá-los e beneficiar-se dos nutrientes (LINDSEY; MURUGAN; RENITTA, 2020). Bactérias como *Pseudomonas* spp., *Xanthomonas* spp., *Erwinia* spp., *Ralstonia* spp., *Agrobacterium* spp., *Xylella* spp., *Pectobacterium* spp. and *Dickeya* spp são capazes de sobreviver no material vegetal e entram nele através do solo (MANSFIELD et al., 2012). Finalmente, os vírus geram doenças tais como folha do mosaico, topo encaracolado e amarelecimento da folha, que são infecções sistêmicas, o que causa nanismo e crescimento atrofiado da planta, levando a uma redução no rendimento do cultivo (LINDSEY; MURUGAN; RENITTA, 2020).

Atualmente, a forma mais utilizada de combate aos microrganismos fitopatogênicos é a aplicação de múltiplos agrotóxicos. Porém, tem sido amplamente comprovado os efeitos nocivos desses produtos comerciais sobre o meio ambiente e na saúde e qualidade de vida da população humana (AKTAR; SENGUPTA; CHOWDHURY, 2009). Conscientes dessas desvantagens, os setores agrícolas começaram a optar por opções ecologicamente corretas. Práticas como exclusão, evasão e erradicação (evitar o contato do patógeno com a planta hospedeira em crescimento por meio da desinfecção das sementes ou outras partes, usando produtos químicos ou calor) são algumas delas (PELCZAR et al., 2020). Adicionalmente, estão se aplicando estratégias biológicas, tais como: 1- aplicação de organismos endófitos, os quais são simbióticos com as plantas e as proveem com proteção antimicrobiana (TAN; ZOU, 2001); 2- aplicação de metabólitos secundários de plantas (CHENG; CHENG, 2015); 3- aplicação de peptídeos antimicrobianos (AMP), que constituem uma das primeiras linhas de defesa na maioria dos organismos contra grupos de microrganismos patogênicos (SALAS et al., 2015). Na agricultura moderna, isso significa que a aplicação destes tipos de práticas verdes podem levar a processos mais sustentáveis (SURESH WALIA,SUPRADIP SAHA, VANDANA TRIPATHI, 2017).

1.2 Mecanismos de defesa das plantas contra patógenos

As plantas estão constantemente expostas a microrganismos por diversos componentes ambientais, tais como solo, água, ar. Essas interações podem ser benéficas ou prejudiciais, o que significa que podem ser interações mutualísticas ou patogênicas (RODRIGUEZ et al., 2019; THRALL et al., 2007). Em caso de contato com microrganismos nocivos, as plantas possuem uma série de estratégias de resposta de defesa, por isso, a perda total de uma colheita não é algo comum (NISHAD et al., 2020). De forma geral, os mecanismos de defesa das plantas podem ser vistos de duas formas, constitutivos e induzidos.

Primeiramente, os mecanismos constitutivos envolvem uma primeira linha de frente, que consistem em barreiras físicas como cutículas cerosas, paredes celulares rígidas e a acumulação de proteínas e peptídeos em tecidos como frutas e sementes (NISHAD et al., 2020). No caso dos patógenos superarem essas primeiras defesas, o sistema de defensa induzível é ativado e pode ser de dois tipos: imunidade desencadeada por patógenos e herbívoros (PTI) e imunidade desencadeada por efetores (ETI) (ALI et al., 2018). Os padrões moleculares associados a patógenos (PAMPs) são estruturas microbianas ou patogênicas, como flagelinas, lipopolissacarídeos e componentes da parede celular fúngica (quitinas e glucanos), os quais são reconhecidos por receptores de plantas chamados receptores de reconhecimento de padrões (PRRs) que ativam ainda mais o PTI. Por outro lado, patógenos microbianos secretam proteínas efetoras que são reconhecidas por um grupo especial de proteínas de resistência (PR) que estimulam a ativação da resposta de defesa induzida, denominada ETI. Esses reconhecimentos geram respostas complexas que envolvem produção de espécies reativas de oxigênio (ROS), reticulação da parede celular, síntese de moléculas antimicrobianas, como fitoalexinas e, eventualmente, a produção de proteínas e peptídeos relacionados à patogênese (ALI et al., 2018).

As primeiras proteínas relacionadas à patogênese (PR-Proteínas) relatadas foram de plantas de Tabaco infectadas pelo vírus do mosaico do tabaco (TMV),(LOON; KAMMEN, 1970). Até o momento, existem 17 grupos em que essas proteínas podem ser classificadas de acordo com semelhanças de sequência, atividades enzimáticas e outras características biológicas (SELS et al., 2008). Dentre esses grupos estão quitinase, glucanase, taumatina, defensina e tionina, que têm a função de restringir a invasão do patógeno e sua replicação (ALI et al., 2018).

Além das PR-Proteínas, existem peptídeos antimicrobianos (AMPs), cujas funções parecem melhorar a defesa. Os AMPs têm sido identificados em folhas, tubérculos, flores, vagens e sementes, desempenhando um papel importante na proteção de sementes em germinação e plântulas em desenvolvimento. Tendo em conta que existem vários estudos descrevendo a atividade biológica de AMPs, esses metabólitos se mostram como bons candidatos para o controle do crescimento microbiano indesejado nos cultivos de grande importância econômica (LACERDA et al., 2014).

1.3 Peptídeos antimicrobianos

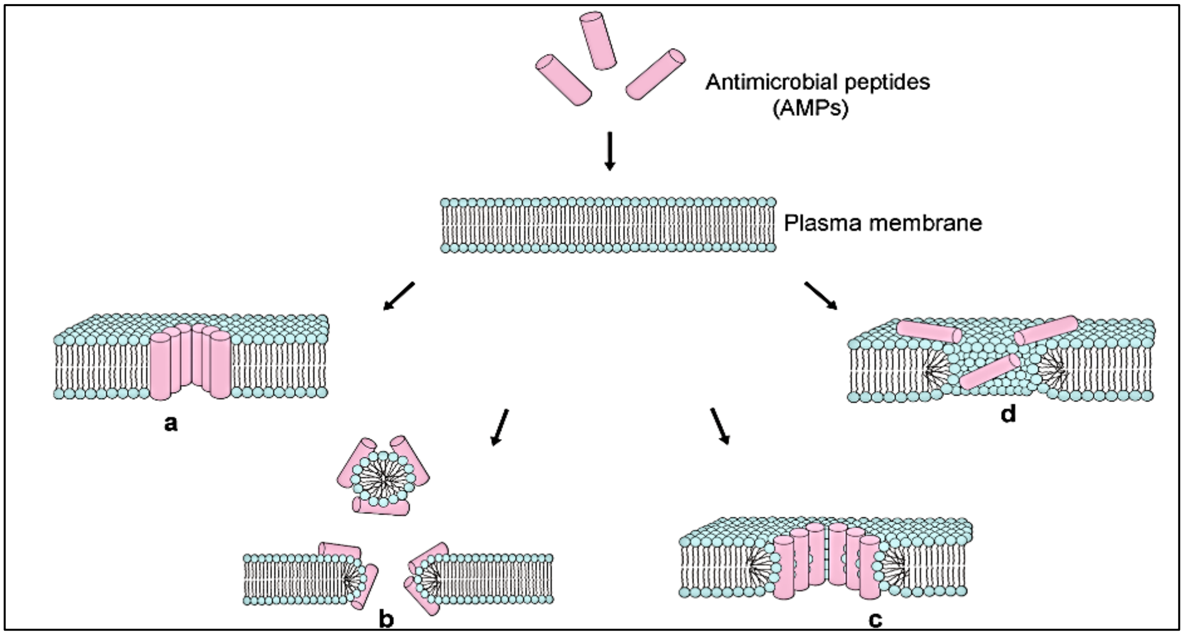
De acordo com o mencionado anteriormente, as plantas têm mecanismos de defesa para combater ataques de fungos, bactérias e vírus patogênicos. Como resposta à infecção por uma variedade de patógenos, as plantas apresentam regulação positiva de um conjunto de genes associados à resistência adquirida sistêmica. Dentre tais respostas, está a produção de peptídeos antimicrobianos (AMPs), que possuem expressão ubíqua e são encontrados como defesa contra patógenos e pragas (EGOROV et al., 2005). Suas formas moleculares são variadas, porém, a maioria são peptídeos lineares (TAM et al., 2015). Estes tipos de peptídeos estão sendo pesquisados como uma alternativa para combater uma ampla gama de infecções microbianas, uma vez que os tratamentos comerciais convencionais não estão mais sendo eficazes como antes. Ao contrário dos tratamentos convencionais, que geralmente funcionam através de um alvo molecular de alta afinidade definido, o que pode induzir resistência em microrganismos, os AMPs possuem múltiplas atividades antimicrobianas que podem fornecer uma estratégia para evitar que patógenos desenvolvam resistência (PESCHEL; SAHL, 2006). A atividade antimicrobiana de peptídeos é determinada por alguns parâmetros físico-químicos e estruturais, tais como, resíduos de aminoácidos, carga líquida positiva, hidrofobicidade, índice de Boman e helicidade. Além disso, fatores externos (pH, temperatura e íons metálicos) podem afetar a atividade dos AMPs vegetais. Vale ressaltar que todos esses fatores estão inter-relacionados e uma mudança em um desses fatores levaria a alterações nos outros (LI et al., 2021).

De uma forma geral, os AMPs vegetais podem ser classificados como peptídeos catiônicos ou aniônicos. No entanto, sua classificação pode ser mais complexa e geralmente baseada em sua similaridade de sequência, presença de motivos de cisteína e estruturas terciárias (HAMMAMI et al., 2009). Os grupos dentro dos quais os AMPs de plantas estão classificados são: tioninas (HUGHES et al., 2000), defensinas de plantas (GRAHAM; SILVERSTEIN; VANDENBOSCH, 2008), peptídeos do tipo heveína (PORTO et al., 2012), peptídeos do tipo knottin (LE NGUYEN et al., 1990), família α-hairpin (SLAVOKHOTOVA; ROGOZHIN, 2020) , proteínas de transferência de lipídios (YEATS; ROSE, 2008), snakins (SEGURA et al., 1999) e família de ciclotídeos (HARRIS et al., 2006).

Atualmente, é amplamente aceito que os peptídeos antimicrobianos exercem sua atividade principalmente por interações com as membranas dos microrganismos alvo (QUEMÉ-PEÑA et al., 2019). No caso das bactérias, as membranas apresentam em sua estrutura lipídios aniônicos (como o são a fosfatidilserina e cardiolipina), o que permite que os peptídeos de carga líquida positiva interajam com esses compostos aniônicos, e como resultado há um aumento da permeabilidade da membrana e uma morte celular rápida (BIOLOGY et al., 2017). Resultados prévios demostram que os AMPs podem se ligar a regiões não específicas da membrana das células-alvo (o que dependerá diretamente da conformação intrínseca ou dinâmica do peptídeo) (DORSCHNER et al., 2006). As interações entre os AMPs e a membrana celular são classificadas em quatro modelos, “barrel-stave”, “carpet”, “toroidal” e “disordered toroidal” (Fig.1) (LI et al., 2021).

No modelo “barrel-stave”, os AMPs se ligam inicialmente de forma paralela à superfície de uma membrana lipídica, formando assim um poro transmembranar permanente, enquanto os peptídeos se alinham com o núcleo hidrofóbico da bicamada lipídica (Fig. 1a). Há evidências de que após a formação dos poros, alguns AMPs entram na célula e interagem com componentes intracelulares específicos (TRAVKOVA; MOEHWALD; BREZESINSKI, 2017). No mecanismo “carpet”, se produz um efeito semelhante ao efeito dos detergentes. O peptídeo é adsorvido paralelamente à bicamada fosfolipídica, uma vez que haja uma cobertura peptídica suficiente se formam agregados cíclicos com lipídios da membrana, o que produz a ruptura da membrana (Fig.1b) (JÄRVÅ et al., 2018). Em relação ao modelo “toroidal” (Fig.1c), é apresentado como um ponto médio entre os modelos “carpet” e “barrel-stave”. Uma vez que a molécula de AMP é adsorvida na superfície da bicamada e transformada estruturalmente, a membrana se dobra e o peptídeo passa pela bicamada formando se um poro (WIMLEY, 2010). Finalmente, no mecanismo “disordered toroidal”, poros aleatórios são formados na membrana plasmática e, após isso, os lipídios se dobram para dentro e as cavidades dos poros são organizadas por grupos de cabeças de fosfolipídios. Os peptídeos incorporados estabilizam os poros circulares retos, enquanto os peptídeos restantes estão dispostos nas aberturas dos poros e estabilizam a curvatura da membrana (Fig. 1d) (CIRAC et al., 2011). Apesar das interações com as membranas serem o mecanismo de ação mais aceito de AMPs, há evidências recentes provando que os AMPs podem atuar em outros alvos, incluindo a inibição de componentes da parede celular, síntese de DNA ou proteínas (SAHL, 2012).

Figura 1. Principais mecanismos de ação dos AMPs vegetais.



Quatro principais mecanismos de ação dos AMPs vegetais. **(a)** Modelo Barril-stave: Os AMPs inserem se verticalmente na membrana plasmática para formar os poros na transmembrana. **(b)** Modelo Carpet: Os peptídeos são adsorvidos paralelamente à bicamada lipídica cobrindo assim a superfície celular, gerando a ruptura da membrana. **(c)** Modelo Toroidal: um tipo intermediário entre o mecanismo Carpet e o Barril-stave. Peptídeos e lipídios formam os poros. **(d)** Modelo Disordered toroidal: A formação de poros é mais aleatória e envolve menos peptídeos, mas são necessários peptídeos adicionais para estabilizar a abertura.

Fonte: LI, J. et al. Plant antimicrobial peptides: structures, functions, and applications. **Botanical Studies**, v. 62, n. 1, 2021

1.4 Néctar floral

A reprodução da planta ocorre em duas formas: sexuada e assexuada. Os dois métodos de reprodução têm suas próprias vantagens. Contudo, na reprodução sexuada, a planta recém-formada é uma combinação de genes, dando-lhe alguma vantagem adaptativa (HENRY et al., 2018). Na reprodução sexuada, a polinização é uma ferramenta indispensável, desde que ela é responsável pelo fluxo gênico e diversidade genética (SILVA et al., 2020). Para isso, as plantas com flores produzem o néctar, que é uma solução aquosa complexa, composta por açúcares (principalmente sacarose, frutose e glicose), aminoácidos, proteínas, vitaminas, lipídios, ácidos orgânicos e inorgânicos, entre outros compostos, e geralmente é secretado na base de uma flor (CARTER; THORNBURG, 2004c). A riqueza de metabólitos no néctar expõe esse fluido a infecções que podem também serem provenientes dos próprios polinizadores (desde que não são estéreis e podem transportar patógenos). Uma infecção pode afetar seriamente a qualidade e quantidade dos componentes do néctar e assim suas características, tais como: voláteis (RERING et al., 2018; SCHAEFFER et al., 2019), açúcares (CANTO; HERRERA, 2012; VANNETTE; FUKAMI, 2018), aminoácidos (GOOD et al., 2014; JUNKER et al., 2014; VANNETTE; FUKAMI, 2016), além do volume do néctar (VANNETTE; FUKAMI, 2018). Sendo assim, essas mudanças podem afetar diretamente a fecundidade das plantas (PARK; THORNBURG, 2009).

Para evitar e eventualmente combater infecções, as plantas com flores desenvolveram estratégias para lidar com esses potenciais invasores microbianos e proteger a integridade do néctar. Foi descoberto que algumas proteínas do néctar estão envolvidas na defesa da planta e que elas podem ser secretadas indutivamente por estresse biótico ou abiótico (SILVA et al., 2020). Uma dessas estratégias é a acumulação de proteínas com funções de defesa. As Nectarinas (Nec I-V), têm sido relatadas como proteínas relacionadas à defesa do néctar floral da *Nicotiana spp*. (PARK; THORNBURG, 2009), e sua identificação permitiu a determinação de uma via bioquímica que gera altos níveis de peróxido de hidrogênio, que auxiliam no processo de defesa contra microrganismos (CARTER; THORNBURG, 2004c). A nectarina I é a proteína mais abundante, e foi caracterizada como uma superóxido dismutase, o que significa que transforma espécies de superóxido em peróxido de hidrogênio, que por sua vez se acumula em valores tão elevados quanto 4 mM(CARTER; GRAHAM; THORNBURG, 1999). As nectarinas II e III estão diretamente relacionadas em estabilizar o pH do néctar. A atividade da superóxido dismutase consome prótons o que podem gerar um pH básico no néctar, portanto, acredita-se que as Nectarinas II e III tem a função de equilibrar o pH, mantendo condições fisiológicas para a função adequada do néctar (CARTER; THORNBURG, 2004a). Por fim, a Nectarina IV e V apresentam atividade de glicose oxidase, que ao oxidar a glicose contribui para a produção de peróxido de hidrogênio (CARTER; THORNBURG, 2004b). Esse ciclo não foi identificado em outros néctares. Vale ressaltar que o proteoma de cada néctar floral parece ser único. Por exemplo, uma β-1,3-glucanase foi identificada no néctar extrafloral da *Hemerocallis citrina* Baroni (HONG-XIA, ZHOU. et al., 2022), uma L-ascorbato oxidase em *Nitraria tangutorum* (CHEN et al., 2021) e uma quitinase ácida (Machi3-1) no néctar floral de plantas de maçã (KURILLA et al., 2020).

1.5 Nicotiana spp.

A planta *Nicotiana* é classificada no gênero de ervas anuais e perenes, arbustos e pequenas árvores da família das solanáceas (Solanaceae). Suas flores possuem cinco pétalas, cálice de cinco lóbulos e folhas alternadas, e geralmente um cimo terminal tipo panícula e um fruto em forma de cápsula com grande número de pequenas sementes. Este gênero inclui as espécies conhecidas como plantas de tabaco, que são cultivadas para produzir tabaco (CHEN et al., 2012). Muitas espécies de *Nicotiana* (como *Nicotiana alata* e *Nicotiana sanderae*) são cultivadas como plantas ornamentais (Fig. 2). Suas flores perfumadas abrem à noite para ser visitadas por mariposas e outros polinizadores. Esses tipos de plantas são autóctones da América do Norte e do Sul, Austrália, sudoeste da África e Pacífico Sul (LI, 2008). Alguns tipos de plantas de *Nicotiana* demonstraram possuir compostos com importante potencial biotecnológico para serem utilizados como inseticidas, anestésicos, diaforéticos e sedativos. Esses resultados sugerem que as plantas podem secretar metabólitos secundários, por exemplo, para prevenir as possíveis infestações por comunidades microbianas deletérias (CHEN et al., 2012).

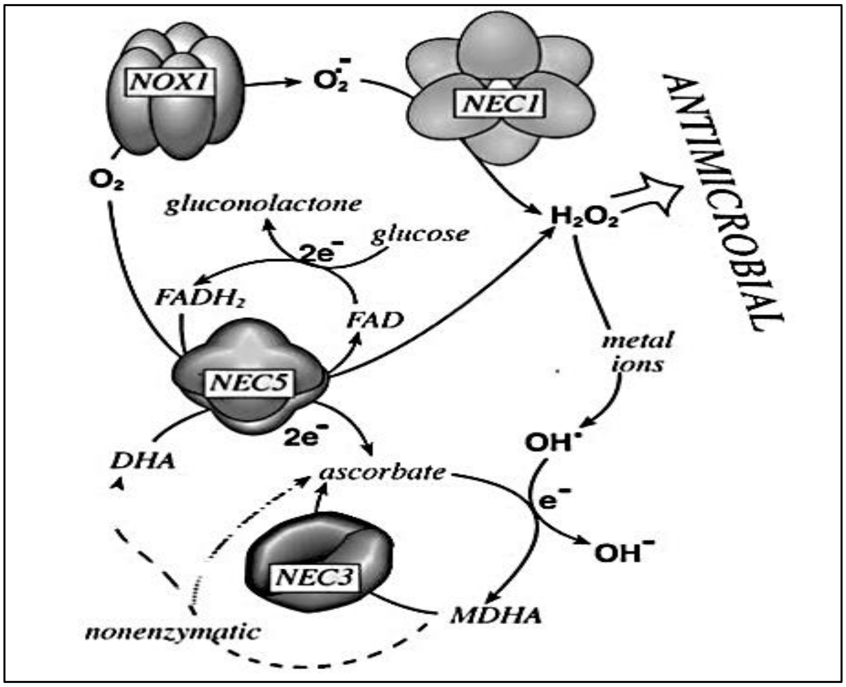
Figura 2. Flores das espécies *Nicotiana alata* (esquerda) e *Nicotiana sanderae* (direita).

Retirado em 12 de Janeiro de 2022:
https://www.newworldencyclopedia.org/p/index.php?title=Nicotiana&oldid=814719

A planta ornamental de Tabaco tem sido amplamente utilizada como modelo para estudar as proteínas do néctar floral e seu possível papel na defesa. Thornburg e colaboradores fizeram uma extensa pesquisa relacionada às nectarinas encontradas (CARTER; GRAHAM; THORNBURG, 1999; CARTER; THORNBURG, 2004b, 2004a, 2000, 2004c; THORNBURG et al., 2003). Como resultado dessas pesquisas, foi possível elucidar o ciclo redox do néctar "Carter–Thornburg redox cycle". Como já foi dito antes, apesar do néctar ser um meio enriquecido e o fato de os insetos que o visitam não serem estéreis, as infecções nas flores são relativamente raras. Isso sugere que as plantas desenvolveram sistemas de defesa para protegerem o néctar, e as nectarinas que se acumulam no néctar do Tabaco ornamental, estão envolvidas em um desses sistemas. Durante o ciclo redox do néctar (Fig. 3) são gerados altos níveis de peróxido de hidrogênio, além de fornecer os meios necessários para a planta lidar com altas concentrações de espécies reativas de oxigênio. Durante o ciclo, as proteínas NEC I e NEC 5 fornecem diretamente o peróxido de hidrogênio e o NEC 3 ajuda à planta a lidar com os produtos tóxicos, consequência desses altos níveis de peróxido de hidrogênio (PARK; THORNBURG, 2009). Os estudos permitem afirmar que esses altos níveis de peróxido de hidrogênio são antimicrobianos, levando a consideração que o néctar inibe o crescimento de bactérias, enquanto o néctar tratado com catalase, para destruir o peróxido de hidrogênio, é incapaz de inibir o crescimento bacteriano (THORNBURG et al., 2003; CARTER et al., 2007).

Recentemente, Silva e colaboradores (SILVA et al., 2020) realizaram um perfil proteômico comparativo do néctar floral de *Nicotiana spp*., *Petunia hybrida* e *Datura stramonium*. A análise LC-MS/MS permitiu identificar 22 proteínas de *P. hybrida*, 35 proteínas de *D. stramonium* e 144 proteínas de 23 espécies de *Nicotiana*. A maior parte do proteoma (105) do néctar de Nicotiana *spp*. identificou proteínas de transferência de lipídios (LTPs), proteínas do Ciclo Redox do Néctar, inibidores de proteases e PR-proteínas, que estão relacionadas com funções de defesa/estresse. *Petunia hybrida* apresentou 14 PR-proteínas nas quais se incluem quitinases ácidas, osmotinas e peroxidases. Apesar dos estudos com proteínas de néctar, trabalhos sobre peptídeos de néctar floral têm sido pouco explorados. Até o momento, há apenas um manuscrito na literatura que descreve a composição peptídica do néctar floral e não há nenhum estudo que descreva uma extensa análise peptidômica desse fluido (SANTOS et al., 2017). Embora a compreensão atual dos peptídeos do néctar e sua função biológica permaneçam pouco investigadas, foi levantada a hipótese que os peptídeos biologicamente ativos são secretados e se acumulam no néctar floral, protegendo este fluido contra a infecção microbiana.

Figura 3. Ciclo redox do néctar “Carter–Thornburg redox cycle”.



O ciclo redox do néctar é iniciado por uma NADPH oxidase ligada à membrana (NOX1) que converte o oxigênio molecular em superóxido. A nectarina I (NEC1) funciona como uma superóxido dismutase que desprotona o superóxido em peróxido de hidrogênio, resultando no acúmulo de peróxido de hidrogênio no néctar. Simultaneamente, a Nectarina V (NEC5) funciona como uma glicose oxidase que utiliza uma molecula FAD ligada covalentemente e glicose em uma redução de dois elétrons do oxigênio molecular para gerar peróxido de hidrogênio adicional. A partir dessas duas reações, o peróxido de hidrogênio resultante se acumula no néctar solúvel em níveis muito altos, até 4 mM. A nectarina III (NEC3) é uma monodesidroascorbato redutase capaz de converter diretamente MDHA em ascorbato. Adicionalmente, há uma reação não enzimática que também converterá MDHA em ascorbato. Se duas moléculas de MDHA interagem em solução, o elétron extra em uma molécula de MDHA pode ser passado para a segunda molécula de MDHA. Isso resulta na redução do primeiro MDHA a ascorbato e a oxidação do segundo MDHA ao desidroascorbato deficiente em dois elétrons (DHA). A enzima Nectarin V também pode utilizar o DHA como um aceptor de elétrons terminal e, ao fazê-lo, converte o DHA novamente em ascorbato.

Fonte: PARK, S.; THORNBURG, R. W. Biochemistry of nectar proteins. **Journal of Plant Biology**, v. 52, n. 1, p. 27–34, 2009.

2 OBJETIVOS

2.1 Objetivos Gerais

Determinar a peptidômica do néctar floral de *Nicotiana spp*., caracterizar seus peptídeos e avaliar a atividade antimicrobiana e os mecanismos de ação de alguns peptídeos sobre fitopatógenos.

2.2 Objetivos Específicos

- Determinar a peptidômica do néctar floral do tabaco ornamental (*Nicotiana alata x N. sanderae*).
- Caracterizar, por bioinformática, todos os peptídeos obtidos, principalmente quanto às características de peptídeos antimicrobianos;
- Escolher e sintetizar seis peptídeos com características de peptídeos antimicrobianos;
- Avaliar se os peptídeos têm atividade contra bactérias e fungos fitopatogênicos;
- Estabelecer os possíveis mecanismos de ação pelos quais os peptídeos atingem sua ação antimicrobiana.

3 ARTIGO CIENTÍFICO

Title:
Ornamental Tobacco Floral Nectar is a Rich Source of Antimicrobial Peptides

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Abstract

Although floral nectar is a rich source of nutrients, it is rarely infected by microorganisms. Defense molecules such as proteins have been identified in this fluid, but defense peptides have been largely overlooked. Thus, the aim of this study was to perform an extensive peptidomic analysis of the ornamental tobacco floral nectar to seek peptides involved in nectar defense. Using LC-MS/MS, 793 peptides were sequenced and characterized. After extensive bioinformatics analysis, six peptides were selected for further characterization, synthesis, and evaluation of their antimicrobial properties against phytopathogenic fungi and bacteria. All six peptides had antimicrobial activity to some extent. However, the activity varied by peptide concentration and microorganism tested. An analysis of the action mechanism revealed damage in the cell membrane induced by peptides. The results show that floral nectar is rich in peptides and that, together with proteins and hydrogen peroxide, they contribute to plant defense against microorganisms during pollination.

Keywords: Antimicrobial peptide (AMP); hydrogen peroxide; *Nicotiana* sp; Nectarins; Peptidome.

1. Introduction

Floral nectar has been defined as an energy-rich aqueous secretion composed of sugars (mainly sucrose, fructose, and glucose), amino acids, proteins, vitamins, lipids, and both organic and inorganic acids. It serves to attract and reward pollinators [1,2]. However, because a pollinator might be in a barnyard one day and in a plant's reproductive tract the next, mechanisms must exist that reduce or eliminate the introduction of phytopathogenic bacteria and fungi into ovaries. Thus, pollinators are also vectors of microorganisms [3,4] which can decrease plant reproduction and alter the frequency of pollinators' visits [5].

To fight against infection, flowering plants have protective mechanisms for reducing the effect of potential invaders while simultaneously protecting nectar integrity [6]. An important discovery was the identification and characterization of nectar-specific proteins (called nectarins), whose function is to generate high levels of the antimicrobial molecule hydrogen peroxide (up to 4 mM). First characterized from ornamental tobacco in the mid-1990s by the Thornburg laboratory, these proteins are involved in a novel biochemical cycle named the "Carter-Thornburg" Nectar Redox Cycle [2].

Subsequently, other studies on the nectar proteome have been performed, identifying new proteins. Currently, the view is that proteomes of floral nectars appear to be unique, i.e. species-specific. Therefore, it is difficult to make generalizations about the protein profile of floral nectars. However, most studies hypothesize a defensive function for these nectar proteins. Antimicrobial proteins have been described, including β-1,3- glucanase identified in *Hemerocallis citrina* [7], L-ascorbate oxidase in *Nitraria tangutorum* [8], and acidic chitinase III (Machi3-1) in floral nectar of common apple [9].

In contrast, only recently have studies begun of antimicrobial peptides in floral nectar [10]. As yet, there is no systematic peptidomic analysis of this fluid. We hypothesize that biologically active peptides are secreted into and accumulate in floral nectar, protecting it against microbial infection. We used ornamental tobacco as a model plant. Its floral nectar was harvested and the peptides within it were extracted, purified, and sequenced. Afterwards, all peptide sequences were characterized using bioinformatics tools, and six peptides were subsequently synthetized. Finally, these six peptides were tested *in vitro* for their antibacterial and antifungal activity.

2. Material and Methods

2.1. Nectar harvesting, sample preparation, and peptidomic analysis

Raw floral nectar samples were collected from ornamental tobacco plants (*Nicotiana alata* x *N. sanderae*) grown in a greenhouse at 25 ºC with 16/8 h (light/dark) photoperiod, as described previously [11]. One mL of nectar was mixed with 2 mL of 0.1 % trifluoroacetic acid (TFA), and the resulting solution was mixed with 3 mL of hexane-ethyl acetate (1:1 v/v) to remove less-polar low molecular weight compounds. After centrifugation at 10,000 x g for 10 min at 4 ºC, the aqueous phase was collected and loaded onto a methanol-preconditioned polymeric reversed-phase cartridge, followed by 0.1 % TFA washes to remove the sugars in the sample. The retained peptides and small proteins, together with other polar small-molecule compounds, were eluted using an acetonitrile:water solution (90:10) containing 0.1 % TFA. After lyophilization, the samples containing the peptides were reconstituted in 0.1 % TFA, and nanoscale LC-MS/MS analyses were performed using an ABI QStar mass spectrometer.

2.2. Characterization of nectar peptides

Molecular masses and isoelectric points were calculated using the pI/molecular mass tool of the ExPASy Server (https://web.expasy.org/compute_pi/) [12], while net charge, hydrophobic ratio, and Boman index (which indicates the binding potential to proteins) were predicted using the Antimicrobial Peptide Database (https://aps.unmc.edu/prediction) [13–15]. All peptide sequences were compared to protein sequences using Basic Local Alignment Search Tool (BLAST) (https://blast.ncbi.nlm.nih.gov/Blast.cgi). Antifungal and antibacterial activities were predicted using the iAMPpred tool (http://cabgrid.res.in:8080/amppred/) [16]. DNA- and RNA-binding activities were determined using the DRNApred online tool (http://biomine.cs.vcu.edu/servers/DRNApred/) [17].

2.3 Choice, synthesis, and purity of synthetic peptides

Five criteria were considered in selecting nectar peptides for further synthesis and antimicrobial-activity investigation [18]: 1) positive net charge, 2) low molecular weight (10-25 amino acids), 3) Boman index of $\leq$ 2.5, 4) hydrophobic ratio (30-55%), and 5) predicted antimicrobial potential greater than 80%. The top six peptides to meet these criteria were chemically synthesized by Chempeptide Limited (China) (www.chempeptide.com) using solid-phase peptide chemistry. The purity of these peptides was subsequently determined by reversed-phase high-pressure liquid chromatography (RP-HPLC) and mass spectrometry.

2.4 Molecular modeling

The three-dimensional (3D) models of the peptides were simulated using the online PEP-FOLD server (http://bioserv.rpbs.univ-paris-diderot.fr/services/PEP-FOLD/) [19]. The best models were chosen considering both Tm and sOPEP scores from the PEP-FOLD server. The Tm score is a metric for measuring the similarity among two structures; these range from 0 up to 1, where 1 indicates a perfect match between two structures. sOPEP is the coarse-grained energy of PEP-FOLD. The clustered representatives correspond to the models with the best scores, i.e. the lowest sOPEP energy represents the highest Tm value. The Ramachandran plot analysis were assessed by using the online server RAMPAGE (http://mordred.bioc.cam.ac.uk/~rapper/rampage.php). The PyMol Molecular Graphics System (http://www.pymol.org) was employed to analyze the 3D structures.

2.5 Antimicrobial activity

2.5.1 Antibacterial assay

The antibacterial action of peptides was tested against *Pseudomonas syringae pv. syringae*, *P. syringae pv. tomato*, *Erwinia amylovora*, and *Xanthomonas perforans*, according to previously published protocols [20], which were obtained from the Department of Plant Pathology and Microbiology, Iowa State University, USA. Stock cultures (10 µL) were incubated overnight at 37 °C in 100 mL of LB (Luria-Bertani) liquid broth and the bacterial growth was measured at 600 nm. Afterwards, 100 µL of cell suspension (Abs_{600nm}: 0.1) was added to 96-well plates followed by the addition of 100 µL of synthetic peptides, with concentrations ranging from 15 µM to 250 µM (in 0.9% NaCl containing 5% DMSO). The bacterial growth was monitored for 24 h, at 37 °C, by using a SpectraMax Multi-Mode Microplate Reader. H_2O_2 (2 and 4 µM) and 0.9% NaCl containing 5% DMSO were used as positive and negative controls, respectively. Similarly, the bacterium *Escherichia coli* MC 4100 (H_2O_2-sensitive, Oxy R-deficient) was also used as control. All experiments were performed three times, with three replicates per treatment.

2.5.2 Antifungal assay

The antifungal potential of the peptides was tested against *Aspergillus niger*, *Colletotrichum spp.*, and *Penicillium digitatum*, which had been obtained from the Department of Biochemistry and Molecular Biology, Federal University of Ceara, Brazil, using methods described by Lima et al. [21]. The fungi were inoculated in YPD (Yeast Extract-Peptone-Dextrose) agar and left to grow for 14 days at 30 °C. The cultures were harvested using 10 mL of sterile saline solution and filtered through cotton to harvest the spores. The spore concentrations were adjusted to 1×10^6 spore/mL, assuming an absorbance of 0.1 at 600 nm. Subsequently, 100 µL of spore suspension was mixed with 100 µL of peptides (15 to 250 µM, in 0.9% NaCl containing 5% DMSO) and added to 96-well plates. The mixtures were incubated at 37 °C and the growth was monitored for 48 h with an automated microplate reader (Model Elx800, Bio-Tek Instruments). H_2O_2 (2 and 4 µM) and 0.9% NaCl containing 5% DMSO were used as positive and negative growth controls, respectively. All experiments were performed three times, with three replicates per treatment.

2.6 Mechanism of action of peptides

The cell membrane integrity was evaluated with a propidium iodide uptake assay, as previously described [21]. The bacteria or spore suspensions were incubated at 37 ºC in presence of the peptides for 24 or 48 h, respectively. Treated cells were centrifuged at 5,000 x g for 5 min at 4 °C, after which the supernatant was discarded, and the resulting pellet resuspended in 50 µL of sterile saline solution to which 1 µM propidium iodide had been added. The mixtures were incubated at 37 ºC for 30 min in the dark, and were centrifuged again. The pellets were washed three times and resuspended in 50 µL of sterile saline. Finally, propidium iodide uptake was observed by fluorescence microscope equipped with a measurement system (Olympus microscope system; excitation wavelength 400–500 nm, emission wavelength 600–700 nm).

3. Results and discussion

3.1. Identification and characterization of nectar peptides

Supplementary Table 1 shows the 793 peptides identified from ornamental tobacco floral nectar and their main characteristics as obtained from bioinformatics tools. The peptides contained 5 to 47 amino acids, with molecular weights ranging from 467 to 6198 Da. The average pI was 5.48. The highest proportion, 67.8% of all identified peptides (539), had pIs below 6.0, 15.8% (126) had a pI between 6.0 and 7.0, and 16.4% (128) had a pI between 7.1 and 10.0. With regard to the net charge, 49% of peptides had negative net charge, ranging from -7 to -1, 19% had zero net charge, and 31% had positive net charge, from +1 to +9. The hydrophobic ratio of 35% of the peptides ranged of 0-30%, while 60% of the peptides had hydrophobic ratios between 31% and 59%. Only 4.4% of peptides had hydrophobic ratio between 60% and 70%. Ten antifungal peptides (1.2%) and 149 antibacterial peptides (18.7%) had predicted antimicrobial activities of greater than 60% (Supplementary Table 1).

Considering the main features described for antimicrobial peptides (AMPs) [22], the top six peptides were selected for further characterization, synthesis, and biological activity determination (Table 1). The selection was first based on the predicted antibacterial and antifungal activities, with all six peptides having a probability of >84% to be antifungal or antibacterial. The six peptides also had relatively short sequences (13-25 AA), which is common for AMPs [23]. For example, Chen et. al. [24] reported a pore forming AMP of 14 amino acid residues, which was used as template for new AMPs. All six of these selected peptides had a positive net charge (+1 to +6).

Five of the six chosen peptides had basic isoelectric points, which ranged from 8.5 to 9.4 (Table 1). These values are in agreement with other previously reported AMPs, such as *RcAlb*-PepI (pI 8.8), *RcAlb*-PepII (pI 7.8), *Mo*-CBP$_3$-PepI (pI 7.97), *Mo*-CBP$_3$-PepII (pI 7.97), and *Mo*-CBP$_3$-PepIII (pI 8.11), which were bioinspired from plant proteins [20,25]. The positive net charge is an important feature since this permits the negatively-charged peptides to establish electrostatic interactions with the microbial cell membranes [18]. The hydrophobic ratios of all six peptides were > 40%. This feature is also important since, after the electrostatic interaction, the peptides can bind to phospholipids to further disturb the cell membrane [26]. The Boman index of all peptides was ≤ 2.0. The Boman index indicates the binding potential to proteins, such as membrane receptors. A value ≤ 2.5 indicates a low potential of interaction with receptors, suggesting that the binding of peptides to microbial cell membranes involves lipids rather than proteins [27]. The six peptides also showed a capacity to bind to DNA. This function has been described for some AMPs, such as the peptide MBP-1 isolated from maize, which showed affinity to DNA and its possible intervention of transcription or translation processes [28]. Finally, no peptide showed RNA-binding activity based on our bioinformatics analysis (Table 1).

We also evaluated the three-dimensional structure of the top six peptides (Fig. 1). Peptides 1 and 3 did not show any organized secondary structure, while Peptides 2, 4, 5, and 6 exhibited α-helical structures. Amphipathic α-helical peptides usually present a higher antimicrobial activity than those with less-defined secondary structures, because they can induce pore formation in the cell membrane of microorganisms [20,29–31]. Lipid transfer proteins (LTPs) are among the many classes of proteins with antimicrobial activity that have been isolated from plants, and one of their main features is the presence of an α-helical structure. Similarly, Cc-LTP2 and Cc-GRP, two antifungal peptides obtained from *Coffea canephora* seeds, showed activity against phytopathogenic fungi, by promoting permeability of the cell membrane and reactive oxygen species (ROS) overproduction [32]. EcAMP1, which was isolated from *Echinochloa crusgalli* seeds, is another example of a cationic α-helical antimicrobial peptide [33]. Even though there are several reports describing α-helical antimicrobial peptides, this is only one of the features that can influence peptide function, since peptides with non-helical structures have also been reported as potent antimicrobial molecules [34,35].

3.2. Antibacterial activity

The antibacterial activity of the six nectar peptides was tested against four phytopathogenic bacteria (Fig. 2). Peptide 6 was the most active, inhibiting 100% the growth of *P. syringae* pv. *syringae*, *P. syringae* pv. *tomato*, and *X. perforans*, and approximately 35% of the growth of *E. amylovora*. Interestingly, the action of peptide 6 on *P. syringae* pv. *syringae* indicated membrane damage and leakage of cell content, as indicated by negative absorbance after addition of the peptide. Similarly, the peptide epsilon-poly-l-lysine exhibited activity against different phytopathogenic bacteria in the form of cell lysis [36].

Other peptides, such as peptide 4 inhibited the growth of *P. syringae* pv. *tomato* by ca. 50% and *X. perforans* by 90%, and was partially active against *P. syringae* pv. *syringae* and inactive against *E. amylovora.* In contrast, peptide 2 and peptide 3 were active only against *P. syringae* pv. *syringae.* Interestingly, peptide 1 and peptide 5 did not show any antibacterial activity *in vitro* (Fig. 2), although both had predicted antibacterial activity > 95% (Table 1). Because peptide 4 and peptide 6 presented the best antibacterial activities, new assays were performed using each peptide at a variety of concentrations ranging between 15 and 250 µM.

Supplementary Fig. 1 shows that 125 µM was the lowest concentration at which peptide 4 was active against *P. syringae* pv. *syringae, P. syringae* pv. *tomato,* and *X. perforans.* By comparison, peptide 6 showed antibacterial activity even at 62 µM, inhibiting the growth of *P. syringae* pv. *tomato* and *P. syringae* pv. *syringae* by 100% and 50%, respectively. Even at 15 µM, peptide 6 exhibited a slight activity on all bacteria tested (Supplementary Fig. 2). In comparison, the peptide MBP-1 reached full antimicrobial activity at a concentration of 25 µM [28] and the peptide C6 was active against Gram-positive and Gram-negative bacteria at 2-16 µM [37]. There are also reports of peptides which presented antibacterial activity at higher concentrations. For instance, Mendes and collaborators [38] reported five AMPs active against *Erwinia amylovora* at concentrations of 50-100 µM, and the peptides Leg1 and Leg2 showed activity against different Gram-positive and Gram-negative bacteria at 125, 250, and 500 µM [39].

3.3 Antifungal activity

The antifungal activities of the six nectar peptides are shown in Fig. 3. *A. niger* and *P. digitatum* were more susceptible to all peptides. In general, the peptides inhibited the spore germination by ca. 70-80%. In contrast, *Colletotrichum spp*. showed the lowest sensitivity to these peptides, but even they showed antifungal activities of ca. 40-75%. Further assays were performed using all peptides at different concentration (15-250 µM) (Supplementary Fig. 3, 4, and 5).

In general, all of the selected tobacco nectar peptides showed antifungal activities even at 15 µM, although to different degrees. For comparison, the peptides Ac-AMP2 and MiAMP1 presented inhibitory activity on spore germination of *P. expansum* at 100 µM [40] and the peptides ETD151 [41] and Thanatin exhibited antifungal activities against *Botrytis cinerea* and *Penicillium digitatum* at 6.25 and 2 µM, respectively [42]. This variability in active concentrations has been attributed to differences in the composition of the fungal cell membranes and the peptides' biochemical features, resulting in different degrees of interaction between peptide and microbial cell membranes [43].

3.4 Function of hydrogen peroxide (H_2O_2)

H_2O_2 is constitutively produced in the floral nectar of ornamental tobacco plants. Its concentration can range up to 4 mM [44] . According to Park et al. [45], H_2O_2 has an important role in the nectar's defense, since it is produced in high concentrations during the nectar redox cycle, which is coordinated by two major proteins called Nectarins I and V. We tested the antibacterial and antifungal activity of the H_2O_2 (2 and 4 µM) to evaluate if it alone would be sufficient to protect the plant, and if the peptides could have a key or complementary role in this process. Additionally, an *E. coli* strain (*E. coli* MC 4100), that is known to be unable to degrade H_2O_2 [46], was included in the assays as control.

In general, H_2O_2 inhibited the growth of all bacteria (Supplementary Fig.1 and 2) and fungi (Supplementary Fig. 3, 4, and 5), thus corroborating the hypothesis of that it plays a role in defense. However, even at 4 mM H_2O_2, bacterial and fungal growth was still observed. Only *E. coli* MC 4100 and *P. digitatum* had their growth completely inhibited by 2 mM H_2O_2. It is worthwhile noting that, even at concentrations as low as 31 µM, the nectar peptides 4 and peptide 6 exhibited antibacterial activity against *E. coli* MC 4100 (Supplementary Fig. 1 and 2).

These results show that H_2O_2 alone is not enough to protect the floral nectar and reinforce the crucial role of peptides or proteins as a complementary mechanism of defense. This interpretation is supported by the work of Silva and collaborators [1] who used LC-MS/MS to identify 144 proteins from 23 species of *Nicotiana* and found that defense proteins were the single largest group of proteins in the nectar (34%). They also identified lipid transfer proteins, proteinase inhibitors, and chitinases. All these proteins are classified as Pathogenesis-Related (PR) Proteins and are well known as plant defense molecules against microorganisms [47–49].

3.4 Mechanism of action of peptides

The ability to damage membranes − by pore formation and/or destruction of the plasma membrane − are among the best-known mechanisms of action of antimicrobial peptides [50]. Thus, we used the fungus *A. niger* and the bacterium *E. coli* as models to investigate the action mechanism of nectar peptides. The action of these peptides on the cell membrane was evaluated using the propidium iodide (PI) fluorophore, which is a DNA-binding and membrane-impermeable chemical. Thus, it only enters into cells if the membrane is damaged.

Fig. 4 shows that both *A. niger* and *E. coli* cells displayed strong red fluorescence, indicating alterations in the permeability of the cell membrane, which can result in the disruption of the lipid layer, pore formation, and/or unbalance of intracellular electrochemical gradients, thereby leading to loss of membrane functions and cell death [51–53]. Similarly, the plant protein-derived synthetic peptides *RcAlb*-PepI, *RcAlb*-PepII, *RcAlb*-PepII, PepGAT, PepKAA, *Mo*-CBP$_3$-PepI, *Mo*-CBP$_3$-PepII, and *Mo*-CBP$_3$-PepIII targeted fungal membranes, leading to pore formation, loss of internal content, and death [20,25]. Once inside the cell, predicted DNA-binding activities of the peptides suggested that these tobacco nectar peptides would interact with cellular DNA (Table 1). This function has been described for some AMPs, such as the peptide MBP-1 isolated from maize that showed affinity to DNA and possible disruption of transcription or translation processes [28]. However, further assays will be needed to prove whether the six peptides studied here affect these processes.

3.5 Other functions for nectar peptides

Pollinators are attracted by smell as well as carbohydrate content. It is of note that several peptides contain at least one tryptophan residue, which may be used by symbiotic bacteria or yeasts to produce aromatic compounds that may have an important effect on nectar's smell [54,55]. Moreover, some pollinators prefer a floral nectar with a large number of yeasts. There is evidence that the health and longevity of pollinators that consume nectar containing yeast is better than that of pollinators that consume yeast-free nectar [56].

In our survey of total peptidome of ornamental tobacco nectar, we found that a high number of peptides (around 80%) had low predicted antifungal and antibacterial activity (Supplementary Table 1). In addition, several peptides were either unmatched, or were matched to uncharacterized, putative, or hypothetical plant proteins. This led us to hypothesize that most of these peptides were not hydrolytic products of the nectar proteins but instead might be from cellular proteins that were secreted by the nectary gland or even trafficked from other plant organs to the nectary gland via the phloem. Thus, the many potential antimicrobial peptides that we find in nectar might have evolved from the entire genome of flowering plants. In addition, we hypothesize that − since phloem is likely to be the ultimate origin of nectar [57] − it is possible that phloem could also be provisioning the nectar with a rich source of antimicrobial peptides.

Conclusion

Tobacco floral nectar is a rich source of peptides, with varied sequences and biochemical properties. At least 159 peptides, representing 20% of the sequenced peptides, were identified as being antimicrobial according to bioinformatic analysis. Although only six peptides were tested, all showed antifungal or antibacterial activity to varying degrees, and the mechanism of action of the peptides seems to involve damage to the cell membrane. These results suggest that not only the peptides, but also the proteins and hydrogen peroxide, together, are responsible for floral nectar defense. In addition, the results show that floral nectar is rich in other peptides which can be used by symbiote bacteria or yeasts to produce aromatic compounds that are important to the nectar's smell, which can then attract pollinators.

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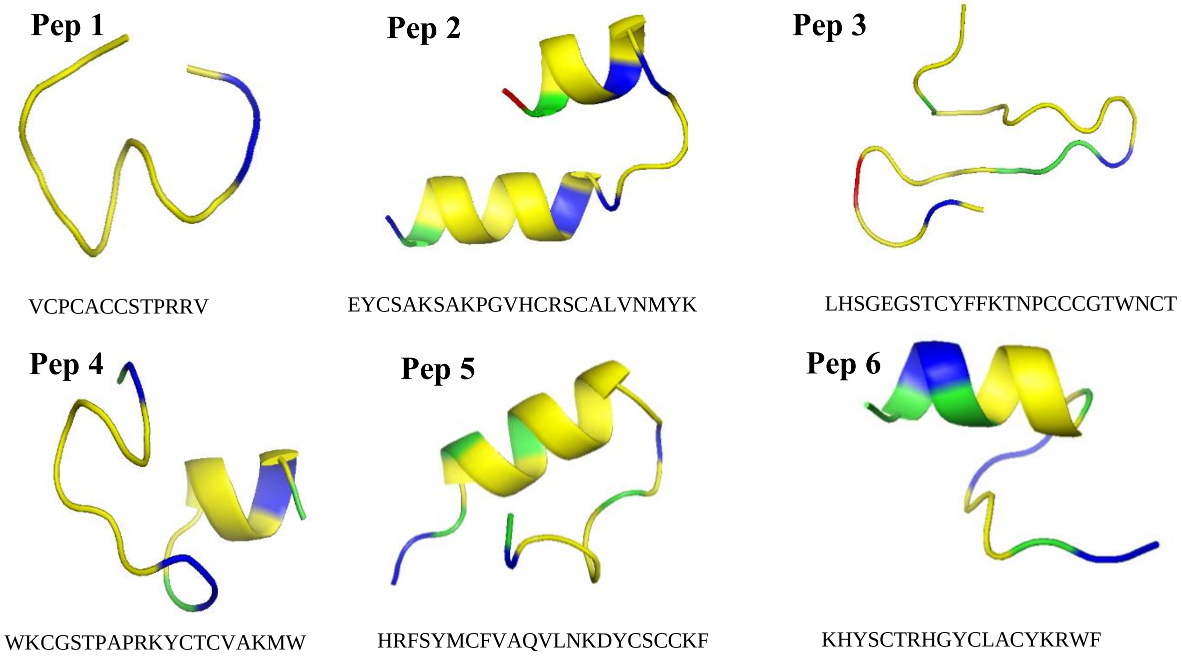


Fig 1. Three-dimensional models of six peptides identified from ornamental tobacco nectar. Models were built using the online tool PEPfold server 3.0 (http://bioserv.rpbs.univ-paris-diderot.fr/services/PEP-FOLD/) and visualized by Pymol program. Blue, red, yellow, and green represent positively, negatively, non-polar, and hydrophobic amino acid residues, respectively.

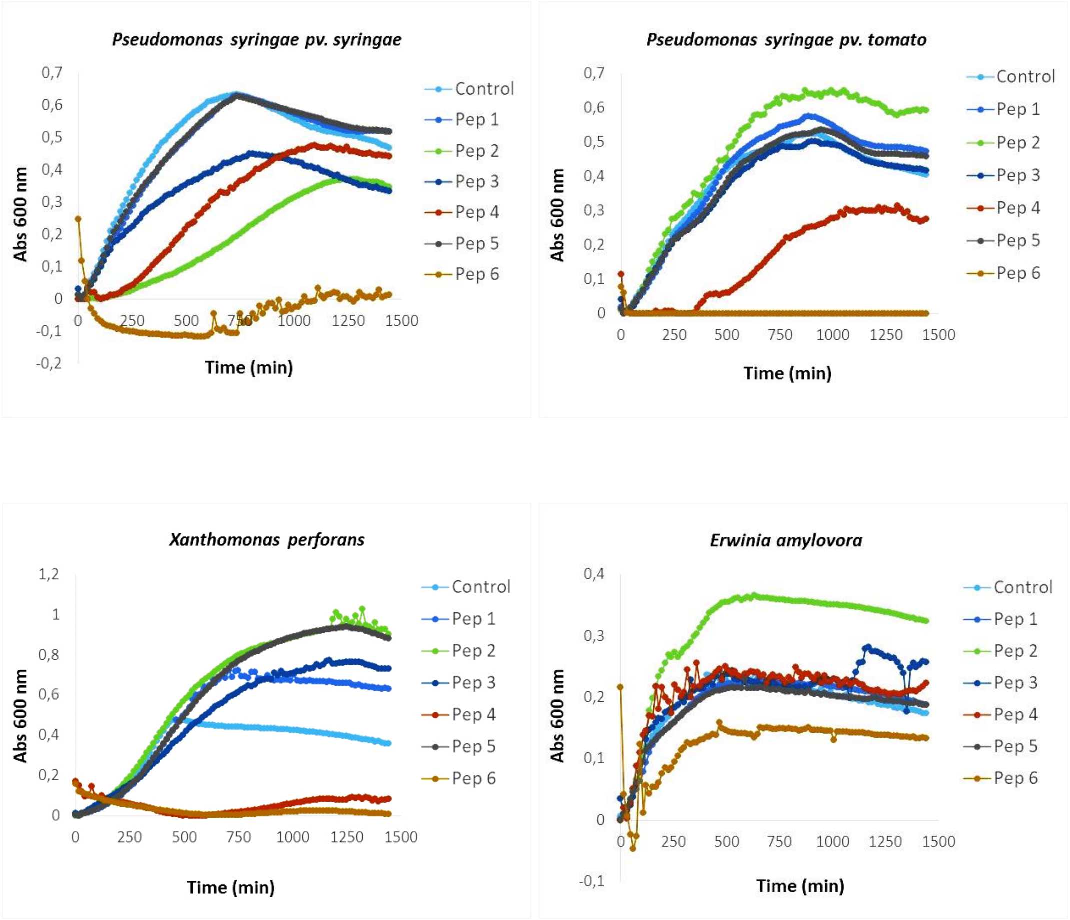


Fig. 2. Antibacterial activity of six peptides identified from ornamental tobacco floral nectar. All peptides were tested at 250 µM and dissolved in 0.9% NaCl, containing 5% DMSO, which was used as control. The bacterial growth was monitored by absorbance at 600 nm, for 24 h, 37 °C, using a SpectraMax Multi-Mode Microplate Reader.

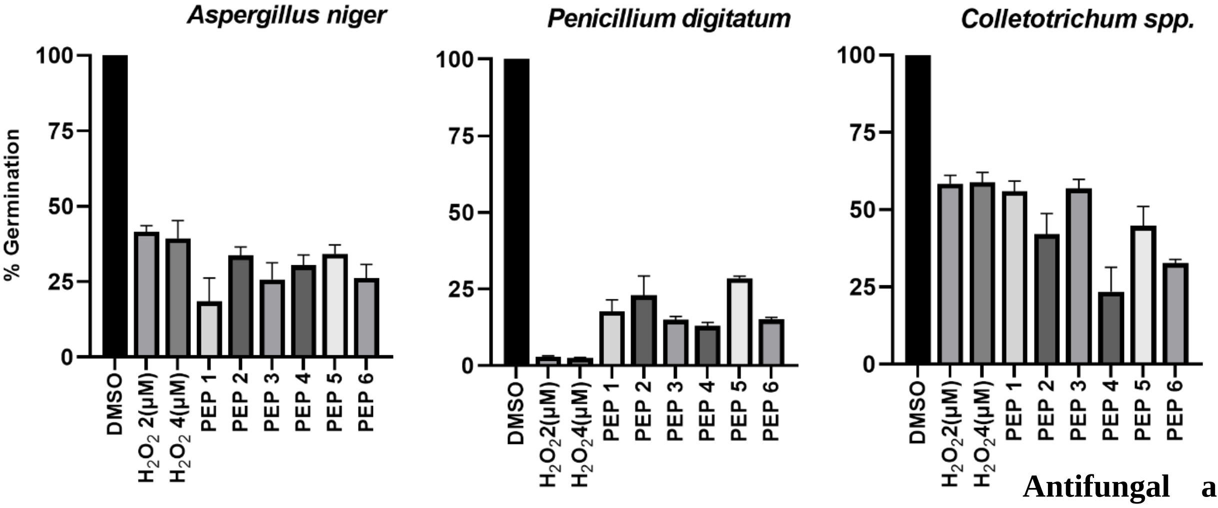


Fig. 3. Antifungal activity of six peptides identified from ornamental tobacco floral nectar. All peptides were tested at 250 µM and dissolved in 0.9% NaCl, containing 5% DMSO, which was used as control. The spore germination was monitored for 48 h, at 600 nm, by using an automated microplate reader (Model Elx800, Bio-Tek Instruments)**.**

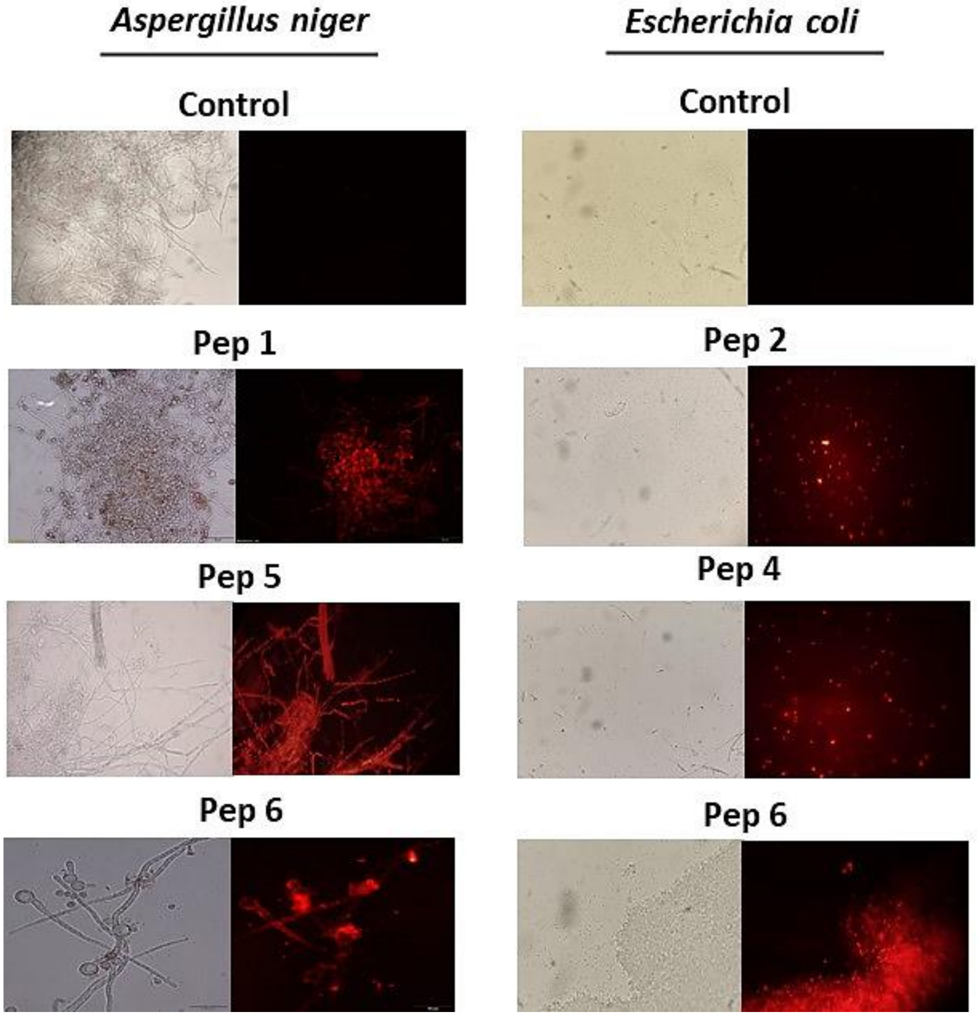
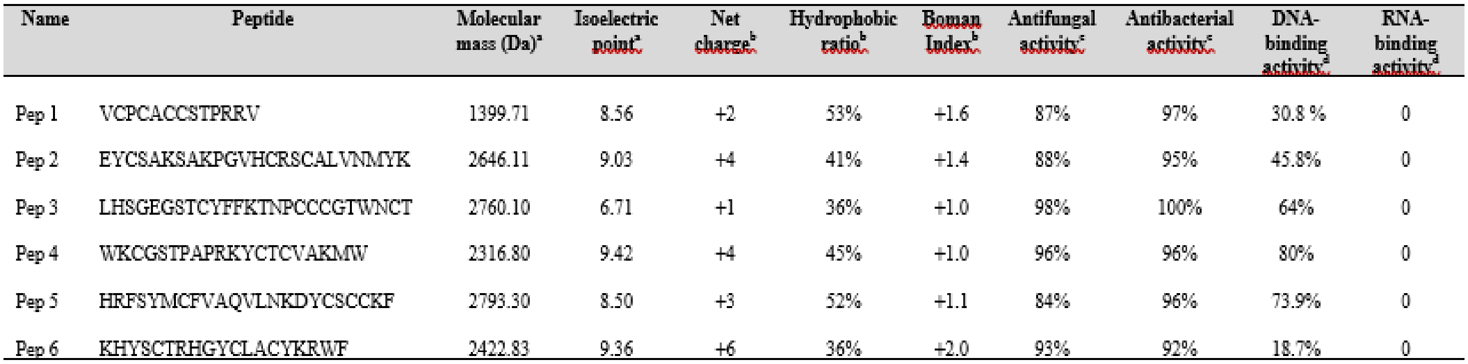


Fig. 4. Action mechanism of peptides identified from ornamental tobacco floral nectar on *A. niger* and *E. coli* cells. Spores and cells were incubated with peptides and propidium iodide (PI) to determine the pore formation at the cell membrane. Control: Spores were treated with 0.9% NaCl, containing 5% DMSO. All peptides were tested at 125 µM. Imagens were taken with a fluorescence measurement system (Olympus microscope system; excitation wavelength 400–500 nm, emission wavelength 600–700 nm).

Table 1. List of nectar peptides used in the antimicrobial assays and some of their biochemical characteristics.



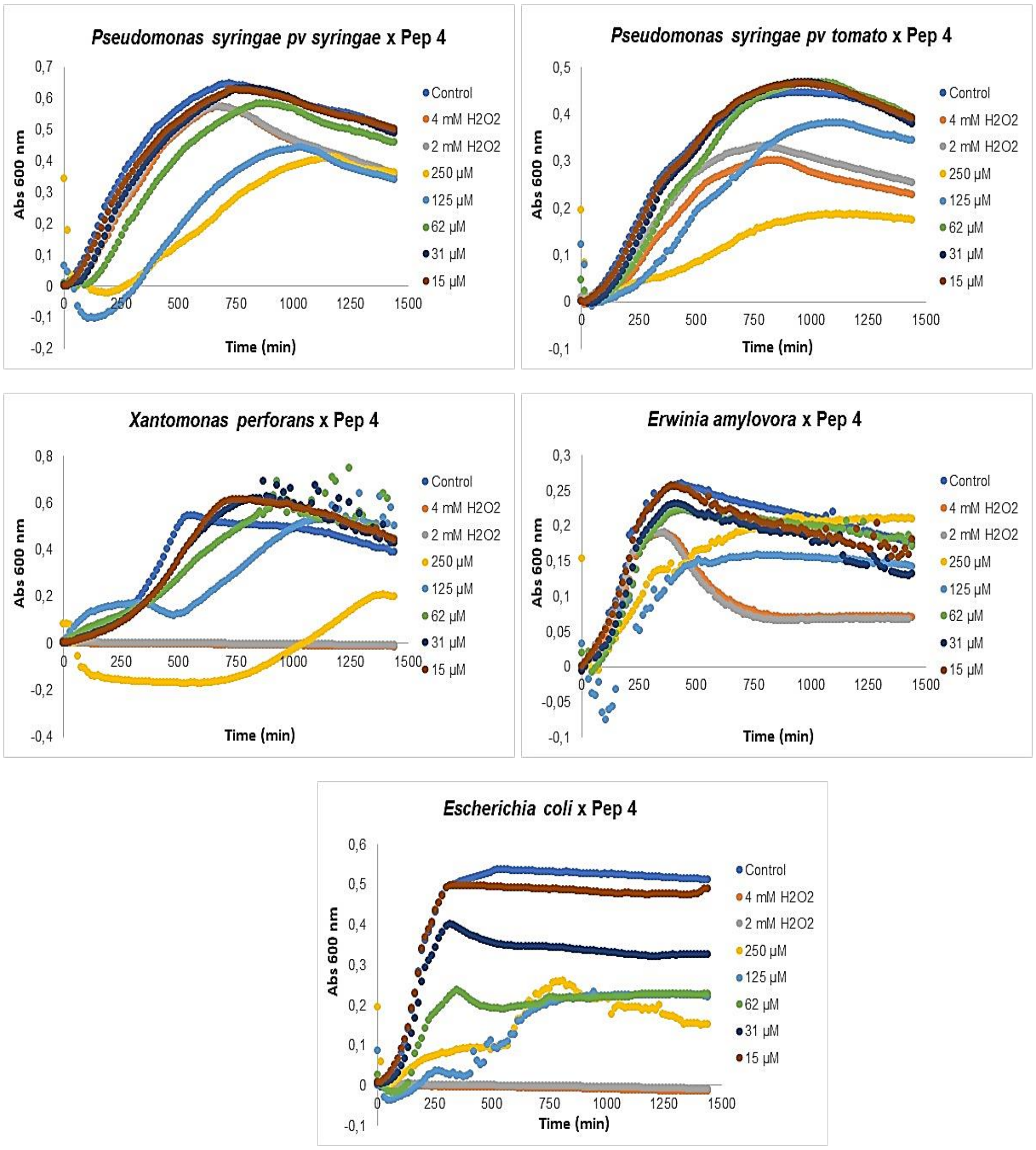
Name	Peptide	Molecular mass (Da)[a]	Isoelectric point[a]	Net charge[b]	Hydrophobic ratio[b]	Boman Index[b]	Antifungal activity[c]	Antibacterial activity[c]	DNA-binding activity[d]	RNA-binding activity[d]
Pep 1	VCPCACCSTPRRV	1399.71	8.56	+2	53%	+1.6	87%	97%	30.8 %	0
Pep 2	EYCSAKSAKPGVHCRSCALVNMYK	2646.11	9.03	+4	41%	+1.4	88%	95%	45.8%	0
Pep 3	LHSGEGSTCYFFKTNPCCCGTWNCT	2760.10	6.71	+1	36%	+1.0	98%	100%	64%	0
Pep 4	WKCGSTPAPRKYCTCVAKMW	2316.80	9.42	+4	45%	+1.0	96%	96%	80%	0
Pep 5	HRFSYMCFVAQVLNKDYCSCCKF	2793.30	8.50	+3	52%	+1.1	84%	96%	73.9%	0
Pep 6	KHYSCTRHGYCLACYKRWF	2422.83	9.36	+6	36%	+2.0	93%	92%	18.7%	0

[a] Molecular mass and isoelectric point were calculated using https://web.expasy.org/compute_pi/

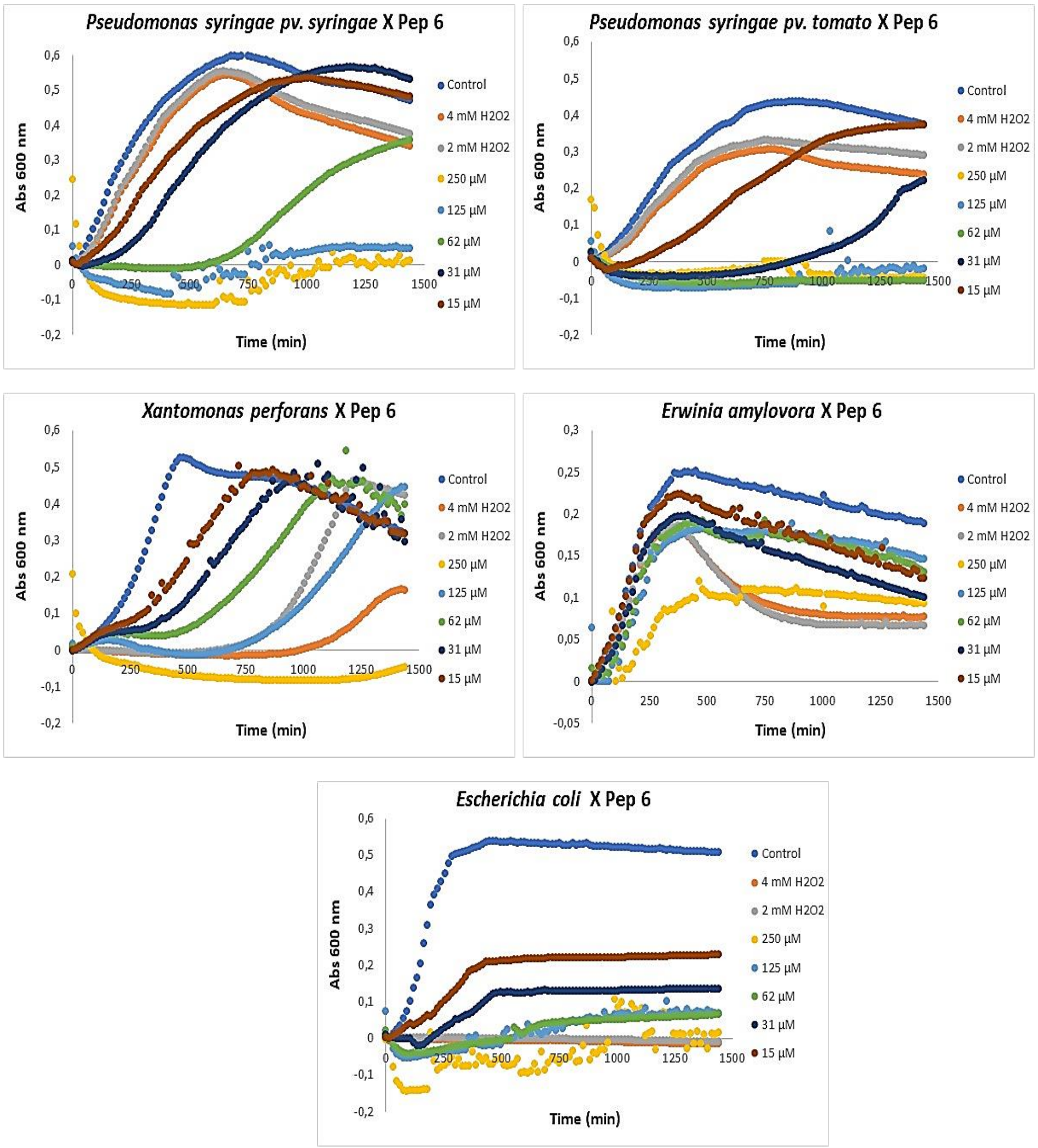
[b] Net charge, hydrophobic ratio, and Boman index were predicted by http://aps.unmc.edu/AP/design/design_improve.php

[c] Potential antifungal and antibacterial activity was predicted using http://cabgrid.res.in:8080/amppred/server.php

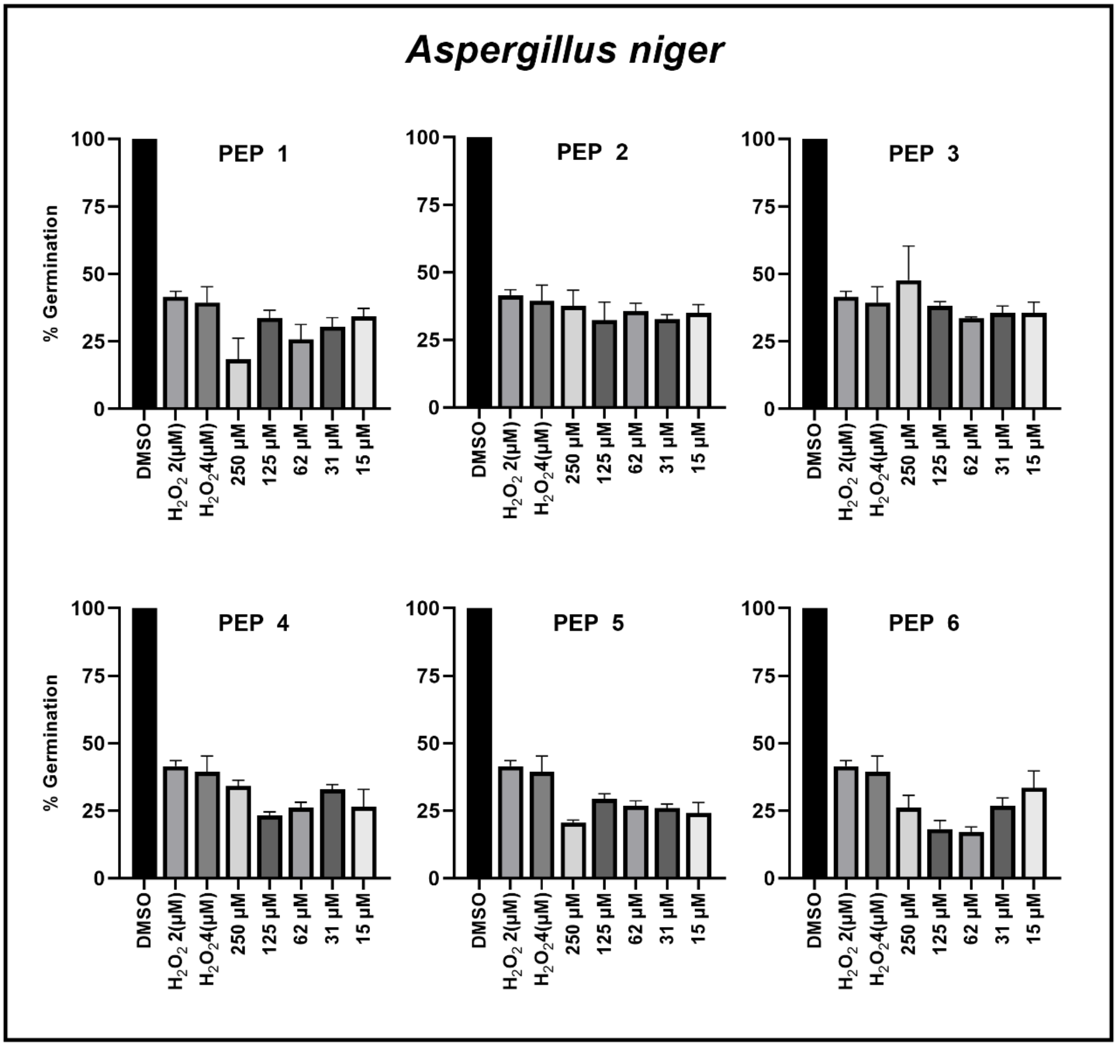
[d] DNA/RNA-binding capacity was predicted using http://biomine.cs.vcu.edu/servers/DNAgenie/



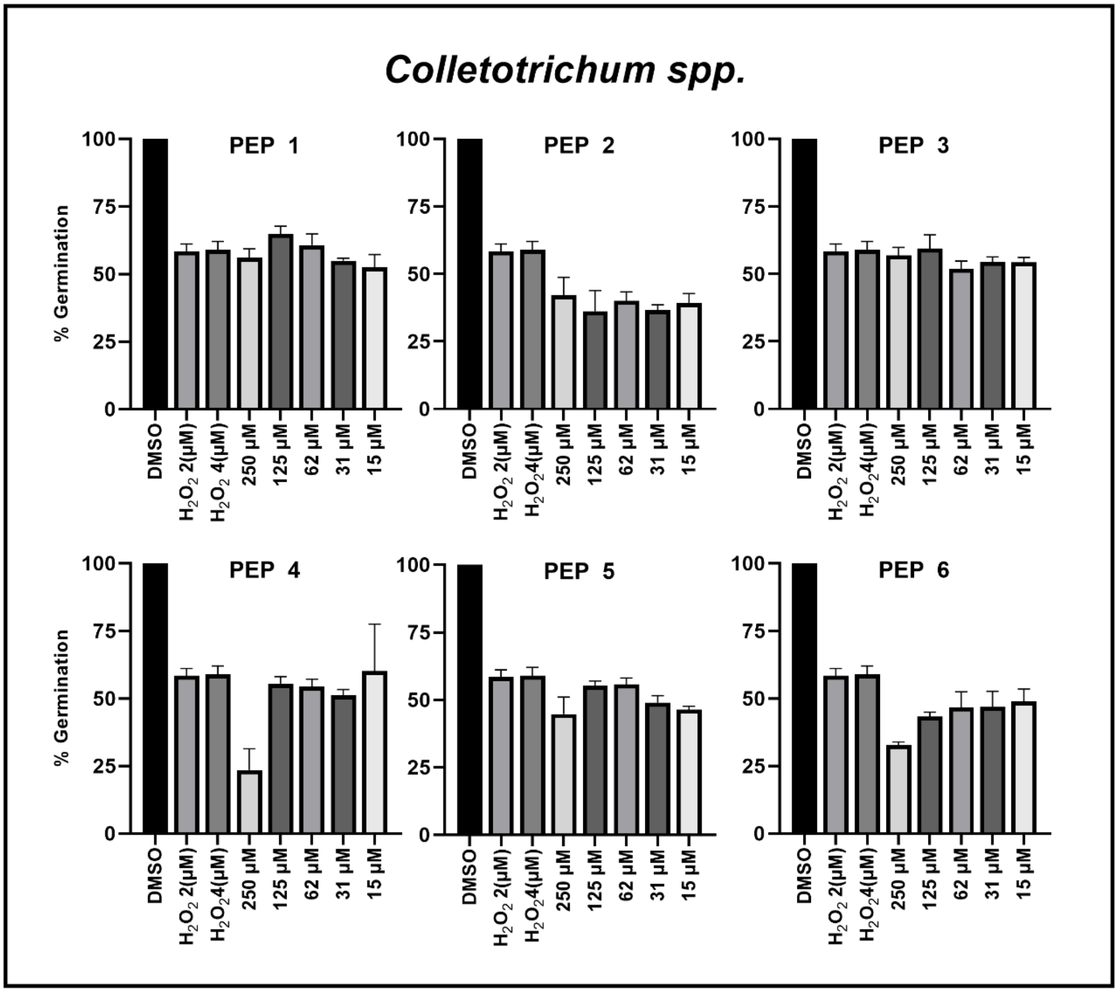
Supplementary Fig. 1. Antibacterial activity of Pep 4 . Sample was tested at different concentration (15-250 µM) and dissolved in 0.9 % NaCl, containing 5 % DMSO, which was used as control. The bacterial growth was monitored by absorbance at 600 nm, for 24 h, 37 °C, using a SpectraMax Multi-Mode Microplate Reader. In addition, H2O2 (at 2 and 4 mM) was used as control.



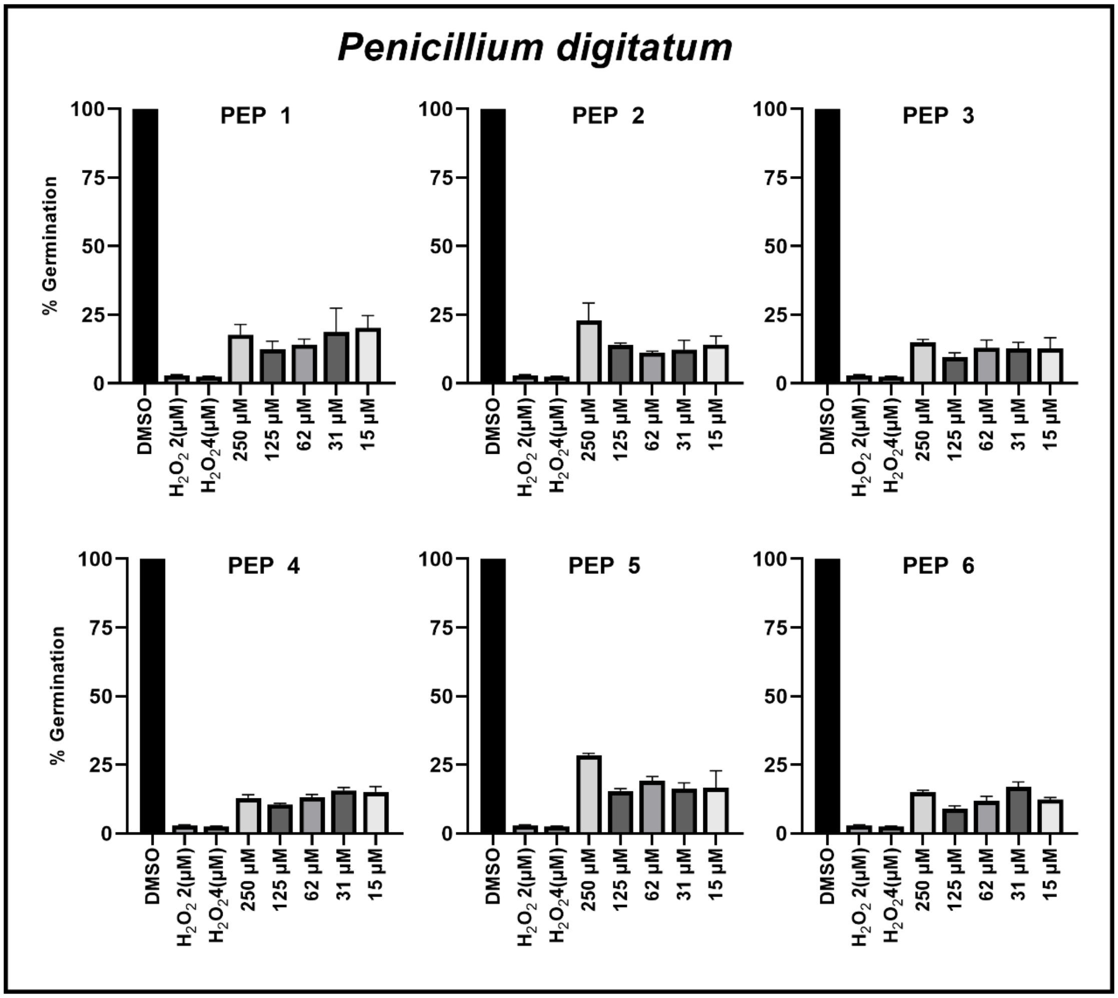
Supplementary Fig. 2. Antibacterial activity of Pep 6. Sample was tested at different concentration (15-250 µM), dissolved in 0.9 % NaCl, containing 5 % DMSO, which was used as control. The bacterial growth was monitored by absorbance at 600 nm, for 24 h, 37 °C, using a SpectraMax Multi-Mode Microplate Reader. In addition, H2O2 (at 2 and 4 mM) was used as control.



Supplementary Fig. 3. Antifungal activity of the six peptides. Samples were tested at different concentrations (15-250 µM), dissolved in 0.9% NaCl containing 5% DMSO, which was used as control. The spores' germination rates were monitored for 48 h at 600 nm, with an automated microplate reader (Model Elx800, Bio-Tek Instruments).



Supplementary Fig. 4. Antifungal activity of the six peptides. Samples were tested at different concentrations (15-250 µM), dissolved in 0.9% NaCl containing 5% DMSO, which was used as control. The spores' germination rates were monitored for 48 h at 600 nm, with an automated microplate reader (Model Elx800, Bio-Tek Instruments).



Supplementary Fig. 5. Antifungal activity of the six peptides. Samples were tested at different concentrations (15-250 µM), dissolved in 0.9% NaCl containing 5% DMSO, which was used as control. The spores' germination rates were monitored for 48 h at 600 nm, with an automated microplate reader (Model Elx800, Bio-Tek Instruments).

Supplementary Table 1. List of nectar peptides and some of their biochemical properties.

[a] BlastP was performed using the website https://blast.ncbi.nlm.nih.gov/Blast.cgi.

[b] Molecular mass and isoelectric point were calculated using https://web.expasy.org/compute_pi/

[c] Net charge, hydrophobic ratio, and Boman index were predicted by http://aps.unmc.edu/AP/design/design_improve.php

[d] Potential antifungal and antibacterial activity was predicted using http://cabgrid.res.in:8080/amppred/server.php

	Peptide	Length	BLASTP best match (Protein/Species/Access number) [a]	Identity (%)	Molecular mass (Da)[b]	Isoelectric point[b]	Net charge[c]	Hydrophobic ratio (%) [c]	Boman Index[c]	Antifungal activity (%)[d]	Antibacterial activity (%)[d]
	RLDDGGYLK	9	Nectarin-3/Nicotiana langsdorffii x Nicotiana sanderae/ Q84UV8.1	100	1036.15	5.96	0	22	+2.92	33	37
1.	CLGFDMCRDGY	11	Probable pectinesterase inhibitor/Nicotiana sylvestris/XP_009798263.1	86	1279.47	4.21	-1	45	+1.61	64	62
2.	FEEVKED	7	Nucleolar protein/Nicotiana tomentosiformis/ XP_009610315.1	100	894.93	4.00	-3	28	+3.95	28	35
3.	LEDDHSPLAP	10	Uncharacterized protein LOC109212631/Nicotiana attenuate/XP_019231843.1	100	1093.16	4.02	-2	30	+2.06	6	10
4.	LCGFDMCRDGY	11	Probable pectinesterase inhibitor/Nicotiana sylvestris/XP_009798263.1	86	1279.47	4.21	-1	45	+1.61	64	62
5.	LEDHDSPL	8	Transcription factor TCP12-like/Nicotiana tabacum/XP_016450579.1.	75	924.96	4.02	-2	25	+2.80	14	31
6.	LENGLVSVPA	10	Uncharacterized protein LOC104089778/Nicotiana tomentosiformis/XP_009593051.1	78	998.14	4.00	-1	50	-0.38	3	6
7.	FCSHVTAL	8	Nuclear pore complex protein NUP98A-like/Nicotiana tabacum/ XP_016449112.1	100	877.03	6.73	+1	62	-0.55	14	77
8.	EFEVKDE	7	Ubiquitin carboxyl-terminal hydrolase/Nicotiana attenuata/XP_019243099.1	100	894.93	4.00	-3	28	+3.95	28	31
9.	KEDEDALR	8	Berberine bridge enzyme-like/Nicotiana attenuata/XP_019238380.1	100	975.02	4.32	-2	25	+5.60	23	23
10.	FYGDSCPCDFGPT	13	Zinc finger protein CONSTANS-LIKE 14-like/Nicotiana tomentosiformis/XP_009631919.1	88	1408.52	3.56	-2	30	+1.01	26	22
11.	WVDDESEFSYDEK	13	Nectarin-3/Nicotiana langsdorffii x Nicotiana sanderae/Q84UV8.1	100	1648.66	3.71	-5	23	+3.82	23	23
12.	SDGDDGGGSTDE	12	Protein argonaute 2/Nicotiana sylvestris/XP_009782518.1	88	1110.95	3.28	-5	0	+3.94	32	54
13.	QEDEWLRLF	9	Plastid movement impaired 1-related 1-like/Nicotiana tomentosiformis/ XP_009594859.1	100	1235.36	4.14	-2	44	+3.07	10	18
14.	PCDGEGRTVK	10	Chaperone protein/Nicotiana sylvestris/XP_009788495.1	86	1061.18	6.45	0	20	+3.13	7	5

15.	KEDEDALLR	9	Vacuolar protein/Nicotiana tabacum/ XP_016505281.1	89	1088.18	4.32	-2	33	+4.43	18	17
16.	KNNDLKVPANK	11	Nectarin-2/Nicotiana langsdorffii x Nicotiana sanderae/ Q84UV8.1	100	1240.43	9.70	+2	27	+3.13	14	18
17.	FYGDACLCDTCTP	13	Cysteine proteinase superfamily protein / Salix suchowensis/ KAG5242440.1	100	1408.58	3.56	-2	42	+0.63	75	37
18.	MCMLCDCTDLLPD	13	ABC transporter G family member / Zostera marina/ KMZ56625.1	100	1472.78	3.42	-3	61	+0.41	65	64
19.	VTVGGVEGNPGRE	13	Miraculin-like/Nicotiana sylvestris/ XP_009782172.1	100	1270.36	4.53	-1	23	+1.68	3	2
20.	PCSVVGSSSSMPA	13	Beta-glucuronosyl transferase/ Actinidia chinensis var. chinensis/ PSR87641.1	100	1208.37	5.91	0	38	+0.19	8	14
21.	AETTPPHCEQAP	12	Kinesin-like protein KIN-7E isoform X1 /Cucurbita maxima/XP_022970361.1	100	1280.37	4.51	-1	25	+2.0	5	18
22.	HGCEHEEGPP	10	Angio-associated migratory cell protein-like / Nicotiana attenuata/ XP_019258193.1	100	1091.12	4.72	-1	10	+2.65	23	62
23.	QEAVHDGFETN	11	Nectarin-2/Nicotiana langsdorffii x Nicotiana sanderae/ Q84UV8.1	100	1246.26	4.13	-2	27	+2.9	2	5
24.	EFGSLTTTGSPMSGDD	16	Hypothetical protein OsJ_10784 / Oryza sativa Japonica Group/ EAZ26865.1	100	1601.66	3.49	-3	18	+1.81	6	9
25.	MPGEDPASPDAHGPR	15	FTSH protease 6 / Actinidia rufa/ GFY87776.1	100	1533.64	4.54	-1	20	+2.62	9	7
26.	FQEDEDALRLF	11	Berberine bridge enzyme-like 28/ Nicotiana attenuata]/ XP_019238380.1	90	1382.49	3.92	-3	45	+3.08	10	15
27.	YEFLDATGDGQVK	13	Probable aspartyl protease At4g16563 / Nicotiana attenuata]/ XP_019252266.1	70	1442.55	4.03	-2	30	+1.72	2	2
28.	QEDEWLRLF	9	Polyphenol oxidase C, chloroplastic /Capsicum annuum/ KAF3659228.1	100	1235.36	4.14	-2	44	+3.07	10	18
29.	VTVGGVEGNPGVW	13	Miraculin-like /Nicotiana sylvestris/ XP_009782172.1	100	1270.41	4.00	-1	38	-0.47	9	25
30.	LENDLKVPANK	11	Bifunctional monodehydroascorbate reductase and carbonic anhydrase nectarin-3 /Nicotiana attenuata/ XP_019224244.1	80	1240.42	6.07	0	36	+2.2	4	5
31.	CPTTPDDPSAAH	12	Probable inactive receptor kinase At5g67200/ Nicotiana tabacum/ XP_016475250.1	70	1211.27	4.20	-1	25	+2.14	18	20
32.	AEGDASNSCAHPAE	14	DNA repair protein UVH3/ Nicotiana attenuata/ XP_019261038.1	77	1358.36	4.13	-2	35	+2.22	8	10
33.	YHGNLRDP	8	Serine/threonine-protein kinase / Pyrus ussuriensis x Pyrus communis/ KAB2600576.1	100	971.04	6.74	+1	12	+3.65	42	30
34.	YSCYCHTL	8	Uncharacterized protein At3g06530 isoform X1/ Nicotiana sylvestris/ XP_009786720.1	67	989.13	6.72	+1	37	+0.42	35	53
35.	LSEPAQPLKGP	11	Uncharacterized GPI-anchored protein At4g28100-like /Nicotiana tabacum/ XP_016456553.1	100	1136.31	6.00	0	27	+0.79	2	1
36.	WALTTPPTFEMEEE	14	mRNA cap guanine-N7 methyltransferase 2-like/Chenopodium quinoa/ XP_021750969.1	100	1680.85	3.58	-4	35	+1.46	10	30

37.	LQEAVHDGFETN	12	Nectarin-2/Nicotiana langsdorffii x Nicotiana sanderae/ Q84UV8.1	100	1359.41	4.13	-2	33	+2.25	1	3
38.	CPTTPDDPSAAH	12	Probable inactive receptor kinase At5g67200 / Nicotiana tomentosiformis/ XP_009599932.1	70	1211.27	4.20	-1	25	+2.14	18	20
39.	GDDPDVYVVPGEGD	14	Vicilin-like seed storage protein At2g18540 isoform X1 /Nicotiana attenuata/ XP_019237371.1	70	1433.45	3.28	-5	21	+1.92	26	40
40.	MTNGNPDPDSLQ	12	Uncharacterized protein LOC109209521 / Nicotiana attenuata/ XP_019228351.1	100	1288.35	3.56	-2	16	+2.83	10	7
41.	MESSTHDHSVE	11	Cannabidiolic acid synthase-like / Nicotiana tabacum/ XP_016462802.1	77	1258.28	4.63	-1	18	+3.45	13	32
42.	YDEDLKPGPGSE	12	Glucan endo-1,3-beta-D-glucosidase isoform X1/ Nicotiana sylvestris/ XP_009804916.1	100	1306.35	3.92	-3	8	+2.77	18	3
43.	NGFELGPKA	9	Uncharacterized protein LOC104087663 / Nicotiana tomentosiformis/ XP_009590498.1	90	932.04	6.00	0	33	+0.82	16	20
44.	PPEYGCSGQ	9	4-coumarate--CoA ligase 2-like / Nicotiana tomentosiformis/ XP_009614283.1	100	936.99	4.00	-1	11	+1.41	22	11
45.	YDEDLAGPGLQE	12	Hypothetical protein CK203_044443 /Vitis vinifera/ RVW88046.1	100	1306.35	3.43	-4	25	+1.93	8	3
46.	EEGEQEEQPPLK	12	Hypothetical protein HPP92_028075 /Vanilla planifolia/ KAG0447942.1	100	1412.47	3.98	-4	8	+3.73	30	28
47.	MFSCCCPLPSAVK	13	Calcium-transporting ATPase 8, plasma membrane-type/ Hordeum vulgare/ KAE8815646.1	100	1385.74	7.73	+1	61	-0.58	88	94
48.	FNEHGGPLR	9	Hypothetical protein /Arabidopsis lyrata subsp. Lyrata/ EFH69312.1	100	1026.12	6.75	+1	22	+2.58	17	36
49.	LSEPAQPLKGP	11	Uncharacterized GPI-anchored protein At4g28100-like /Nicotiana tabacum/ XP_016456553.1	100	1136.31	6.00	0	27	+0.79	2	1
50.	LDKDPDTGGAL	11	Uncharacterized protein LOC107820553 /Nicotiana tabacum/ XP_016502341.1	100	1101.18	3.93	-2	27	+1.88	29	45
51.	SDGDDGGGSTDE	12	Hypothetical protein BUALT_Bualt17G0082600 /Buddleja alternifolia/ KAG8366463.1	100	1110.95	3.28	-5	0	+3.94	32	54
52.	AGASY	5	Hypothetical protein CRG98_027564 /Punica granatum/ PKI52045.1	100	467.48	5.57	0	40	-0.20	34	44
53.	FNESLEEDQN	10	Putative nuclease HARBI1 /Spinacia oleracea/ XP_021854113.1	100	1224.20	3.50	-4	20	+4.34	32	25
54.	TVVGGVEGNPGRET	14	Miraculin-like /Nicotiana tabacum/XP_016475230.1	100	1371.47	4.53	-1	21	+1.74	2	2
55.	FEQAGACNGSAPDAGLP	17	Hypothetical protein MANES_06G077500v8 /Manihot esculenta/ OAY47409.1	90	1604.71	3.67	-2	41	+0.69	8	4
56.	LSTTFGMVPAT	11	Protein COBRA /Striga asiatica/ GER46881.1	100	1124.32	5.52	0	45	-0.53	6	28
57.	LSTTFGMVPTA	11	Pentatricopeptide repeat-containing protein /Carex littledalei/ KAF3330853.1	100	1124.32	5.52	0	45	-0.53	6	28
58.	PCGDASNSMSSCMSGSLQG	19	Unnamed protein product /Miscanthus lutarioriparius/ CAD6333458.1	82	1818.98	3.80	-1	31	+1.28	16	26

59.	SNSHCLDAFDDQP	13	TatD related DNase /Cinnamomum micranthum f. kanehirae/ RWR91706.1	100	1448.48	3.93	-2	30	+2.98	15	9
60.	ACKLCSGDTVV	11	Lysine-specific demethylase JMJ25-like /Nicotiana tabacum/ XP_016499018.1	81	1095.29	5.86	0	54	+0.17	89	94
61.	DAGELPYPH	9	Hypothetical protein HU200_027786 /Digitaria exilis/ KAF8714322.1	100	998.06	4.35	-1	22	+1.40	7	5
62.	VFMGGSGMMGAPSM	14	Transcription factor E2FB-like /Phalaenopsis equestris/ XP_020584517.1	100	1359.65	5.49	0	50	-1.08	64	70
63.	VDHHCCGADHDV	12	Hypothetical protein DCAR_008644 /Daucus carota subsp. sativus/ KZN07807.1	100	1307.38	5.04	0	41	+2.22	41	70
64.	VTSPAHTASG	10	Uncharacterized protein LOC111876449 isoform X1 /Lactuca sativa/ XP_023728743.1	100	926.98	6.71	+1	30	+0.80	5	38
65.	MESSTHDHSVE	11	Cannabidiolic acid synthase-like /Nicotiana tabacum/ XP_016462802.1	77	1258.28	4.63	-1	18	+3.45	13	32
66.	PCTTPFFMLDPNQ	13	15-cis-phytoene desaturase, chloroplastic/chromoplastic /Senna tora/KAF7803690.1	100	1510.74	3.80	-1	38	+0.88	28	48
67.	YSCPEDYL	8	Kinesin-like protein KIN-UC isoform X2 /Nicotiana attenuata/ XP_019248690.1	100	989.06	3.67	-2	25	+1.62	32	24
68.	EVGEDPASPPAQPCH	15	Hypothetical protein CRG98_050252 /Punica granatum/ PKH63838.1	100	1533.63	4.13	-2	26	+1.73	2	1
69.	KEDPFGLTHK	10	Unnamed protein product /Digitaria exilis/ CAB3446761.1	100	1171.32	6.75	+1	20	+2.50	12	21
70.	GDDPDVYHSAGMLG	14	Putative transposase (putative), gypsy type Tanacetum cinerariifolium/GEZ64378.1	100	1433.51	3.93	-2	28	+1.31	14	21
71.	TPYGTTVDGCLSEQD	15	Vignain-like/Nicotiana tomentosiformis/ XP_009617207.1	100	1585.66	3.49	-3	20	+1.92	8	2
72.	KALPYGAPPELE	12	Early nodulin-like protein 1 /Nicotiana tabacum/ XP_016505810.1	77	1284.47	4.53	-1	33	+0.4	3	2
73.	DNNALSPADPDVNN	14	Filament-like plant protein 4 /Nicotiana attenuata/ XP_019258873.1	70	1455.46	3.42	-3	28	+3.11	25	23
74.	FKCTFCGPDVYATGDDPP	18	Hypothetical protein POPTR_019G020500 /Populus trichocarpa/ RQP03299.1	100	1933.14	3.93	-2	33	+1.15	17	12
75.	CVPSGDTDMR	10	Uncharacterized protein LOC109233749 /Nicotiana attenuata/ XP_019255158.1	100	1080.20	4.21	-1	30	+2.97	24	27
76.	DPASTTPGYWTE	12	Hypothetical protein F0562_004612 /Nyssa sinensis/ KAA8548127.1	100	1324.37	3.67	-2	16	+1.80	13	29
77.	VLGSDGMGCGNGLVK	15	Type I inositol polyphosphate 5-phosphatase 13-like isoform X1 /Nicotiana tomentosiformis/ XP_009624818.1	69	1406.63	5.80	0	40	-0.12	65	81
78.	FNESLEDAGFGDS	13	Copia protein /Tanacetum cinerariifolium/ GEW36033.1	100	1387.38	3.43	-4	30	+2.30	16	6
79.	AETTPSCCLTE	11	Hypothetical protein TEA_030013 /Camellia sinensis var. sinensis/ THG02381.1	100	1154.27	3.79	-2	36	+1.40	36	69

80.	PDDGDVCLPSDPG	13	Cell division cycle protein 48 /Zea mays/ PWZ55975.1	100	1286.33	3.32	-4	23	+2.01	23	48
81.	MCMLGHEVDGFCM	13	Hypothetical protein CR513_05736 /Mucuna pruriens/ RDY09845.1	100	1472.79	4.35	-1	61	-0.24	57	69
82.	CASFVGRSQ	9	Uncharacterized protein DS421_18g613890 /Arachis hypogaea/ QHN95919.1	100	954.07	8.25	+1	44	+1.80	31	37
83.	FNESLCGDVTTGQNT	15	Putative polyprotein /Oryza sativa Japonica Group/ AAO37467.1	100	1585.66	3.67	-2	26	+2.02	16	16
84.	CMVSGGDMHEAN	12	Hypothetical protein Lal_00004275 /Lupinus albus/ KAF1855358.1	100	1250.38	4.35	-1	41	+1.37	30	38
85.	HPSDDCYDGMTDGANVP	17	Transposon Ty3-I Gag-Pol polyprotein /Vitis vinifera/ RVW36518.1	89	1793.85	3.77	-3	23	+2.40	16	15
86.	CPGDAHCGNCEALSGSNSP	19	Hypothetical protein MIMGU_mgv1a022380mg /Erythranthe guttata/ EYU26006.1	100	1818.93	4.35	-1	31	+1.49	43	71
87.	HSSVHDGFETNARLTQPQ	18	Alpha carbonic anhydrase 4 isoform X1 /Morus notabilis/ XP_010090219.2	92	2024.14	5.99	+1	22	+3.04	<1	<1
88.	GKGGPGHGQMAP	12	Hypothetical protein CMV_016618 /Castanea molíssima/ KAF3958487.1	100	1093.23	8.76	+2	16	+0.57	59	52
89.	EYFLDATPYPVQ	12	Hypothetical protein A4A49_38845 /Nicotiana attenuata/ OIT26387.1	89	1442.59	3.67	-2	33	+0.84	1	1
90.	QPQGHDGFETNARPTKPQ	18	NO MATCH	-	2008.14	6.75	+1	11	+3.46	2	2
91.	MTNGNPACNGPVN	13	Glutamate-gated kainate-type ion channel receptor subunit GluR5 /Handroanthus impetiginosus/ PIN15248.1	100	1288.42	5.27	0	30	+1.36	12	40
92.	TVSPGTSACSMPA	13	Bromodomain /Arabidopsis suecica/ KAG7536176.1	100	1208.37	5.18	0	38	+0.23	10	22
93.	PVDVHDGFETNARYYP	16	Alpha carbonic anhydrase 4 /Tarenaya hassleriana/ XP_010555357.1	100	1880.00	4.54	-1	25	+2.46	3	1
94.	CMMCCTPNGTCVPLE	15	Hypothetical protein CFC21_052756 /Triticum aestivum/ KAF7043393.1	100	1601.96	4.00	-1	53	-0.07	63	77
95.	TLTPEMAPGQVN	12	Uncharacterized protein LOC104234731 /Nicotiana sylvestris/ XP_009786649.1	88	1257.42	4.00	-1	33	+0.83	1	2
96.	KDKPTGVAGGTEW	13	Hypothetical protein /Oryza sativa Japonica Group/ BAD23381.1	100	1345.47	6.07	0	23	+1.59	9	20
97.	SNHGA	5	Uncharacterized protein LOC109833237 /Asparagus officinalis/ XP_020256424.1	100	484.47	6.46	+1	20	+2.38	32	56
98.	KLEVMSNGVAGWSNF	15	Uncharacterized protein LOC104218945 /Nicotiana sylvestris/ XP_009767874.1	80	1638.86	6.00	0	46	+0.53	7	38
99.	WQESSGDCGQR	11	Unnamed protein product /Arabis nemorensis/ VVA90140.1	100	1252.28	4.37	-1	18	+3.89	22	23
100	VDNVNVGPK	9	Hypothetical protein PHAVU_010G013700g /Phaseolus vulgaris/ XP_007134033.1	100	941.05	5.81	0	33	+1.61	22	46
101	RTLTTPPCCGCTE	13	Uncharacterized protein LOC107784793 /Nicotiana tabacum/ XP_016461461.1	75	1381.60	5.98	0	30	+1.71	58	88
102											

	DVGTASNCSGACCNALSGNRD	21	Non-specific lipid-transfer protein-like protein At5g64080 isoform X2 /Nicotiana attenuata/ XP_019254041.1	80	2015.13	4.21	-1	38	+2.09	85	76
103	NSDSGSLMFGCNGSEM	16	RNA-directed DNA polymerase, eukaryota /Tanacetum cinerariifolium/ GEU87606.1	100	1635.76	3.67	-2	31	+1.60	23	46
104	WALTTPPGYCFEAQP	15	Uncharacterized protein LOC104114470 /Nicotiana tomentosiformis/ XP_009623224.1	80	1680.90	4.00	-1	40	+0.10	7	6
105	SGDGSNPDPDNPV	13	Aspartyl protease family protein 2-like /Nicotiana attenuata/ XP_019229845.1	100	1270.23	3.42	-3	7	+3.10	21	32
106	MNDFHCTDE	9	Hypothetical protein COLO4_37415 /Corchorus olitorius/ OMO52102.1	100	1111.17	4.02	-2	33	+3.50	43	49
107	KELTTPCCPLGYGQ	14	Hypothetical protein GW17_00015739 /Ensete ventricosum/ RWW20170.1	100	1509.76	5.99	0	28	+0.63	37	20
108	PPEGCYSGQ	9	Pentatricopeptide repeat-containing protein At1g06710, mitochondrial /Nicotiana sylvestris/XP_009794459.1	85	936.99	4.00	-1	11	+1.41	23	11
109	ECNGNPDNKGGSP	13	Kinesin-like protein KIN-4A /Helianthus annuus/XP_035840361.1	100	1288.31	4.37	-1	7	+3.09	19	29
110	NGGTCAHDYNEG	12	Unnamed protein product /Digitaria exilis/ CAB3499019.1	100	1237.22	4.35	-1	16	+2.52	63	50
111	YDSTFLACAEGPLAVQ	16	Hypothetical protein CFC21_110980 /Triticum aestivum/ KAF7110917.1	100	1684.88	3.67	-2	50	+0.16	1	<1
112	DLAAGEDYDGAWAVE	15	Calnexin homolog 1-like /Nicotiana tabacum/ XP_016447226.1	85	1581.61	3.33	-5	46	+1.30	10	21
113	NFEHNELPR	9	TMV resistance /Prunus dulcis/ VVA36704.1	100	1155.24	5.40	0	22	+4.28	10	36
114	FNESLTLACGMGENVN	16	Uncharacterized protein LOC108948259 /Nicotiana tomentosiformis/ XP_018632680.1	87	1698.88	3.79	-2	43	+0.95	5	11
115	TDSCTCTLSYDGGQ	14	Hypothetical protein C1H46_015704 /Malus baccata/ TQD98711.1	100	1450.51	3.56	-2	21	+2.01	52	38
116	MFSFAEGTSNAAPGAVK	17	Hypothetical protein C1H46_000681/[Malus baccata/TQE13674.1	100	1684.88	5.75	0	47	+0.40	30	31
117	LSGTPSSSSMPA	12	Hypothetical protein SADUNF_Sadunf14G0021200 /Salix dunnii/ KAF9668607.1	100	1121.23	5.52	0	25	+0.79	10	19
118	FNESLEDATCGGLFVP	16	Uncharacterized protein LOC104231054 /Nicotiana sylvestris/ XP_009782281.1	80	1698.86	3.57	-3	43	+0.63	1	1
119	TPPCYCTEPQA	11	Unnamed protein product /Spirodela intermedia/ CAA7395189.1	100	1209.35	4.00	-1	27	+1.20	47	60
120	NELPYPH	7	Uncharacterized protein LOC107799249 /Nicotiana tabacum/ XP_016477826.1	85	868.94	5.24	0	14	+1.90	21	52
121	WQEEPAPHGAYTSKH	15	Hypothetical protein E3N88_40686 /Mikania micranta/ KAD2393709.1	100	1737.85	6.00	+1	20	+2.21	4	13
122	MCSDDEGLGAPSSTDYSCR	19	Hypothetical protein EJ110_NYTH11555 /Nymphaea thermarum/ KAF3792452.1	100	1994.11	3.84	-3	26	+2.66	31	10
123	EATTPAAQTFCAE	13	Uncharacterized protein LOC107778481 isoform X1 /Nicotiana tabacum/ XP_016454232.1	80	1339.44	3.80	-2	46	+1.18	9	30

124	WQECGYSPPG	10	Hypothetical protein F0562_005537 /Nyssa sinensis KAA8530839.1	100	1123.20	4.00	-1	20	+1.04	22	16
125	MQGGVNGEKM	10	General negative regulator of transcription subunit 3 isoform X1 /Nicotiana sylvestris/XP_009791157.1	100	1050.21	5.75	0	30	+1.29	43	60
126	PDCPTRAYVMMLVV	14	Expansin-like B1 /Hibiscus syriacus/XP_039028729.1	100	1594.97	6.22	0	57	+0.10	18	41
127	KELTTPCCPLGYGQ	14	Hypothetical protein GW17_00015739 /Ensete ventricosum/ RWW20170.1	100	1509.76	5.99	0	28	+0.63	37	20
128	HSSVHDGFETNARPTKQP	18	Full=Bifunctional monodehydroascorbate reductase and carbonic anhydrase nectarin-3; Precursor /Nicotiana langsdorffii x Nicotiana sanderae/ Q84UV8.1	93	2008.14	6.92	+2	16	+3.31	<1	<1
129	TPSMMMSEAGPA	12	Isocitrate lyase-like isoform X1 /Nicotiana attenuata/XP_019223741.1	77	1209.41	4.00	-1	41	+0.38	54	61
130	FSMCCTTAADNQYF	14	Peroxidase 21 /Cucurbita argyrosperma subsp. Argyrosperma/KAG7017352.1	100	1601.78	3.80	-1	50	+1.07	59	44
131	QETFGMALSNCFCNP	15	187-kDa microtubule-associated protein AIR9-like /Nicotiana attenuata/ XP_019225745.1	70	1661.88	4.00	-1	46	+0.87	24	52
132	LDGVSESGPGAL	12	SCAR-like protein 2 isoform X1 /Phalaenopsis equestris/ XP_020587506.1	100	1101.18	3.67	-2	33	+0.31	2	3
133	CPPSPNANPTPW	12	Hypothetical protein Lal_00010843 /Lupinus albus/ KAF1892378.1	100	1280.42	5.52	0	25	+1.15	27	70
134	AEAPVEEPETEKAVFKYS	18	Induced stolen tip protein TUB8-like /Nicotiana tomentosiformis/ XP_009590692.1	82	2024.21	4.33	-3	33	+1.93	2	2
135	FTGCGCGCHEKPA	13	Glycine dehydrogenase /Vigna unguiculata/ QCE10327.1	100	1309.50	6.72	+1	38	+0.62	90	97
136	TTPNCTCEVVECV	13	Uncharacterized protein LOC110737755 isoform X1 /Chenopodium quinoa/ XP_021773792.1	100	1397.60	3.79	-2	46	+0.92	45	84
137	TDSTCCTEAMFGGQ	14	Hypothetical protein Bca52824_064116 /Brassica carinata/ KAG2269561.1	100	1450.57	3.67	-2	35	+1.47	42	42
138	WPSTYAPGTGFEEAPQ	16	Hypothetical protein /Tanacetum cinerariifolium/ GEV83824.1	100	1737.84	3.79	-2	25	+1.06	2	2
139	WVEDPACASWCGKPGR	16	Photoperiod-independent early flowering 1-like isoform X2 /Nicotiana tomentosiformis/ XP_018623798.1	73	1761.99	6.06	0	43	+1.41	12	24
140	WQESAACGQW	10	E3 ubiquitin-protein ligase PRT6 isoform X1 /Cucumis melo var. makuwa/ TYK25045.1	100	1165.25	4.00	-1	50	+1.07	25	55
141	EATTPPDVCGMHTPQA	16	F-box protein PP2-B10-like /Benincasa hispida/ XP_038878692.1	100	1654.83	4.35	-1	31	+1.32	4	5
142	WQESAACGQW	10	E3 ubiquitin-protein ligase PRT6 isoform X1 /Cucumis melo var. makuwa/ TYK25045.1	100	1165.25	4.00	-1	50	+1.07	25	55
143	PCTTPPCGAGPAAEAQP	17	Non-specific lipid-transfer protein C4-like /Triticum dicoccoides/ XP_037463674.1	100	1567.75	4.00	-1	35	+0.34	5	7
144	HCVGVDDGCAPNAP	14	Pentatricopeptide repeat-containing protein At5g47360 /Phoenix dactylifera/ XP_008777828.4	100	1354.47	4.20	-1	42	+0.90	21	59

145	LSGDMAGSCGAQ	12	ATP-dependent DNA helicase PIF1-like /Nicotiana sylvestris/ XP_009805045.1	100	1096.20	3.80	-1	41	+0.50	49	38
146	MALQAAKACDPK	12	Protein STRUBBELIG-receptor FAMILY 3 /Dorcoceras hygrometricum/ KZV14534.1	100	1246.51	7.95	+1	58	+0.79	83	70
147	FEGSLTTCAAEWET	14	Hypothetical protein RchiOBHm_Chr2g0146921 /Rosa chinensis/ PRQ51659.1	100	1544.65	3.67	-3	42	+1.10	6	31
148	GKKTHEEEMLEPPN	14	Probable diphthine synthase /Nicotiana sylvestris/ XP_009783021.1	82	1638.81	4.91	-1	14	+3.14	3	19
149	DLKDPAFMGNTGKYF	15	Hypothetical protein Bca52824_035673 /Brassica carinata/ KAG2299201.1	100	1703.93	5.96	-1	14	+3.14	31	18
150	EAGLGVCYDY	10	Uncharacterized protein LOC107627717 /Arachis ipaensis/ XP_016186023.1	100	1089.18	3.67	-2	40	+0.18	37	18
151	YDAGAAAALEKA	12	Hypothetical protein BRADI_2g09730v3 /Brachypodium distachyon/ KQK03770.1	100	1150.25	4.37	-1	58	+0.37	24	34
152	NYRAGMCAEGDHVHR	15	ER-golgi trafficking TRAPP complex-domain-containing /Salix suchowensis KAG5220519.1	100	1715.88	6.91	+2	33	+3.22	28	38
153	WVWGDGYFPDWW	12	Putative LRR receptor-like serine/threonine-protein kinase /Cinnamomum micranthum f. kanehirae/ RWR91880.1	100	1613.75	3.56	-2	50	-0.05	44	72
154	EGWASNSEGFTCHVSCSSYD	20	Hypothetical protein PAHAL_1G159600 /Panicum hallii/ PVH66144.1	100	2166.23	4.13	-2	30	+1.88	13	59
155	PCTTPPSHLCSEQAP	15	Unnamed protein product /Digitaria exilis CAB3463784.1	100	1567.75	5.25	0	26	+1.31	10	21
156	LPPGSHSSGS	10	WAS/WASL-interacting protein family member 3-like /Nicotiana sylvestris/ XP_009771000.1	80	924.97	6.74	+1	10	+1.14	13	24
157	WFYAYYDSPGNDPWMHWW	18	F-box/kelch-repeat protein SKIP25-like /Nicotiana sylvestris/ XP_009761441.1	73	2421.63	4.20	-1	38	+0.84	35	68
158	NGGTCGHEYNEG	12	Uncharacterized protein LOC110709099 /Chenopodium quinoa/ XP_021743009.1	100	1237.22	4.51	-1	8	+2.43	42	52
159	MGQSGSLCDTFDEGSEM	17	L-type lectin-domain containing receptor kinase VIII.1-like /Nicotiana attenuata/ XP_019264529.1	73	1793.91	3.43	-4	29	+1.92	25	20
160	CPCSGSYTSLCTMGQ	15	Hypothetical protein /Gossypium schwendimanii/ MBA0878728.1	100	1537.76	5.50	0	33	+0.53	59	81
161	ENLAELAAMVV	11	DNA mismatch repair protein MSH4 isoform X1 /Nicotiana tabacum/ XP_016481411.1	78	1159.36	3.80	-2	72	-0.49	12	35
162	FTGDLTTPCGQFGEE	15	Probable glutathione peroxidase 8 /Nicotiana tabacum/ XP_016502397.1	88	1601.70	3.57	-3	26	+1.37	3	6
163	MLELMEEDPALNMNMT	16	Uncharacterized protein LOC107825215 /Nicotiana tabacum/ XP_016507531.1	75	1882.21	3.50	-4	50	+1.18	40	61
164	VPANKKSLTPAVSLGLP	17	Werner syndrome ATP-dependent helicase homolog /Nicotiana sylvestris/ XP_009803231.1	82	1692.03	10.00	+2	41	-0.01	10	13
165	QYHADGYVDPDPGHS	15	Non-specific phospholipase C4 /Oryza sativa Japonica Group/ XP_015615438.1	100	1657.67	4.40	-1	13	+2.46	20	15
166	DLGTVGHRAPADEPPGMNMT	20	Hypothetical protein CFC21_034727 /Triticum aestivum/ KAF7021843.1	100	2066.29	4.54	-1	30	+1.77	2	2

167	SEPTVP	6	Serine/threonine-protein kinase ATM isoform X1 /Capsella rubella/ XP_023639170.1	100	628.68	4.00	-1	16	+1.45	10	18
168	YNRANTFADDHTYQ	14	Hypothetical protein H5410_064824 /Solanum commersonii/ KAG5568159.1	89	1715.76	5.21	0	21	+3.90	46	14
169	NVASAGPLHCSDD	13	Probable lysophospholipase BODYGUARD 4 /Tarenaya hassleriana/ XP_010558692.1	100	1285.35	4.20	-1	38	+1.59	10	13
170	MNAAGGGPDSNPN	13	Hypothetical protein HPP92_000716 /Vanilla planifolia/ KAG0496025.1	100	1201.23	3.80	-1	23	+1.78	20	23
171	DPMGGGSGCACGGPK	15	Protein PFC0760c-like /Erigeron Canadensis/ XP_043639547.1	100	1293.45	5.82	0	26	+0.35	63	69
172	RKGKPKH	7	Filament-like plant protein 7 isoform X1 /Lupinus angustifolius/ XP_019424175.1	100	850.03	11.26	+5	0	+5.04	51	83
173	ENPLGARQVVGADGFNPD	18	Uncharacterized protein LOC110033374 /Phalaenopsis equestris/ XP_020592991.1	100	1855.98	4.03	-2	33	+1.97	2	1
174	PMGVPLSGGCSDPLQ	15	Uncharacterized protein LOC107816792 isoform X1 /Nicotiana tabacum/ XP_016498026.1	100	1457.68	3.80	-1	33	+0.04	6	4
175	RGGCDAEFAPDEGLP	15	DNA polymerase alpha catalytic subunit /Daucus carota subsp. Sativus/ XP_017218227.1	100	1533.63	3.92	-3	33	+2.02	2	1
176	DSPSDGGGPPEAQP	14	Hypothetical protein GQ55_3G080700 /Panicum hallii var. hallii/ PUZ63595.1	100	1310.30	3.49	-3	7	+2.28	8	3
177	WQESNMQW	8	Scarecrow-like protein 33 /Daucus carota subsp. Sativus/ XP_017236188.1	100	1108.19	4.00	-1	37	+2.61	36	63
178	TTPCGGGVGAPHSEPAQ	17	Heat shock factor protein HSF8-like /Nicotiana tomentosiformis/ XP_009619930.2	75	1565.68	5.21	0	23	+0.75	1	1
179	CPTTPGDHGPTEG	13	Uncharacterized protein LOC122594685 /Erigeron canadensis/ XP_043623044.1	100	1268.32	4.35	-1	7	+1.83	12	31
180	TVTTPGVNSGGPDHN	15	Hypothetical protein E2562_026597 /Oryza meyeriana var. granulata/ KAF0903321.1	100	1452.50	5.05	0	13	+1.79	7	17
181	ELTGMELQE	9	Uncharacterized protein LOC104109936 /Nicotiana tomentosiformis/ XP_033515528.1	100	1049.16	3.67	-3	33	+1.71	10	23
182	DDAPGPPAGAAGSGPQLD	18	Hypothetical protein PVAP13_2NG615101 /Panicum virgatum/ KAG2639221.1	90	1592.64	3.42	-3	27	+1.06	7	4
183	TTPGSDESMGV	11	Hypothetical protein /Tanacetum cinerariifolium/ GEX31121.1	100	1080.13	3.67	-2	18	+1.74	4	5
184	LVGGMCGAATAASAVQ	16	Unnamed protein product /Cuscuta campestris/ VFR02526.1	100	1406.63	5.52	0	62	-1.06	34	60
185	REEDDMSSNALGQNVP	16	Hypothetical protein E3N88_08570 /Mikania micranta/KAD6453864.1	100	1761.84	3.92	-3	25	+3.59	2	<1
186	QELTTPCEALGSNF	14	Uncharacterized protein LOC104212348/Nicotiana sylvestris/ XP_009759867.1	100	1509.65	3.79	-2	35	+1.24	2	2
187	MHQSGGEFGDWR	12	GAMETE EXPRESSED 2 isoform X1 /Nicotiana tomentosiformis/ XP_009622174.1	87	1406.49	5.30	0	25	+2.79	22	43
188	SDPCTMGGGTAKG	13	Uncharacterized protein LOC108944582 /Nicotiana tomentosiformis/ XP_033511226.1	100	1181.30	5.55	0	23	+1.04	44	48
189	QDLPYPH	7	Hypothetical protein /Tanacetum cinerariifolium/ GEU28531.1	100	868.94	5.08	0	14	+2.02	25	31

190	EDAGHEGMPG	10	Unnamed protein product /Coffea canephora/ CDP00508.1	100	999.02	4.13	-2	20	+2.00	14	46
191	DPPKAYYDGEYTY	13	Hypothetical protein Leryth_016721 /Lithospermum erythrorhizon/ KAG9132677.1	100	1581.66	4.03	-2	7	+2.32	30	32
192	TQAAPPVKMCATEPA	15	Dof zinc finger protein DOF2.4-like /Nicotiana tomentosiformis/ XP_009620312.1	87	1514.78	5.66	0	46	+0.54	21	25
193	VEQDLPGASYNAPP	14	Beta-amyrin 28-monooxygenase-like /Nicotiana tomentosiformis/ XP_018623627.1	80	1457.56	3.67	-2	28	+1.26	1	<1
194	AWTSHNSLANSGCCNP	16	Purple acid phosphatase 18 /Capsella rubella/ XP_006297698.1	100	1661.78	6.76	+1	37	+1.43	34	70
195	QETTCMALDAQHCPN	15	Hypothetical protein POPTR_013G122300 /Populus trichocarpa/ PNT08006.1	89	1661.84	4.35	-1	40	+1.97	31	10
196	FCNYDTACPLGAVSDDSTD	19	Uncharacterized protein LOC104783616 /Camelina sativa/ XP_010507055.1	80	1994.09	3.32	-4	36	+1.81	34	11
197	DSPHEDVCAEQPA	13	Hhypothetical protein CFC21_068708 /Triticum aestivum/ KAF7062064.1	100	1397.44	3.91	-3	30	+2.74	2	3
198	DHGSDPDSPGGTRSWS	16	Hypothetical protein FNV43_RR25420 /Rhamnella rubrinervis/ KAF3434317.1	100	1657.63	4.41	-1	6	+3.54	7	20
199	SDLDMCAMEAPK	12	Hypothetical protein FNV43_RR08745 /Rhamnella rubrinervis/ KAF3448037.1	100	1310.52	4.03	-2	50	+1.55	34	34
200	YYRANTLYGDHNMF	14	Hypothetical protein G4B88_019072 /Cannabis sativa/ KAF4388795.1	100	1764.93	6.74	+1	28	+2.25	17	18
201	QGSSSCSPGQ	10	Hypothetical protein BAE44_0010586 /Dichanthelium oligosanthes/ OEL28395.1	100	936.95	5.52	0	10	+2.15	16	16
202	PQCQGTGPTGHAPDLPK	17	Uncharacterized protein LOC105116278 /Populus euphratica/ XP_011011856.1	90	1703.89	7.12	+1	17	+1.43	5	3
203	VRDLAHDSVDSDFY	14	Pentatricopeptide repeat-containing protein At5g47360-like /Telopea speciosissima/ XP_043707712.1	100	1638.71	4.13	-2	35	+3.11	15	18
204	WALTTFSCCVGH	12	UNC93-like protein 1 /Nicotiana tomentosiformis/ XP_009629934.1	100	1324.53	6.72	+1	58	-0.53	66	96
205	DSPCGGSAAGHAPQA	15	Hypothetical protein /Tanacetum cinerariifolium/ GEV18685.1	100	1325.38	5.08	0	33	+0.95	7	5
206	DKLAEMAATPL	11	Reverse transcriptase domain-containing protein /Tanacetum cinerariifolium/ GEY19227.1	81	1159.36	4.37	-1	54	+0.54	15	11
207	KGAGTGMAPCYD	12	Subtilisin-like protease /Nicotiana sylvestris/ XP_009800439.1	87	1170.32	5.83	0	33	+0.57	61	38
208	AAPAPAPPAGPGLGRPQ	17	Formin-like protein 5 /Nicotiana sylvestris/ XP_009803708.1	75	1524.74	9.79	+1	35	+0.21	5.7	5
209	YDSAVDGPFLAK	12	Homeobox-DDT domain protein RLT1 isoform X1 /Nicotiana tomentosiformis/XP_018629803.1	87	1282.42	4.21	-1	41	+0.83	7	4
210	EAPSSTPPEETGWRH	15	Hypothetical protein BRADI_3g45206v3 /Brachypodium distachyon/ PNT68781.1	100	1680.75	4.75	-1	13	+3.12	2	7
211	HNDEFCGNHMCCCDYW	16	Mitochondrial ubiquitin ligase activator of nfkb 1-A-like isoform X2 /Nicotiana tabacum/ XP_016473651.1	87	1977.16	4.52	-1	43	+2.07	86	91

212	FPEYAADAPDEEKAAPTM	18	Zinc finger CCCH domain-containing protein 15 homolog /Nicotiana tabacum/ XP_016503198.1	80	1953.11	3.83	-4	38	+1.76	6	5
213	PCTTPPVNPGGCSEPAQ	17	Histone-lysine N-methyltransferase ATX2-like /Nicotiana tomentosiformis/ XP_009589230.1	71	1654.83	4.00	-1	23	+1.01	6	17
214	WHSAAAGADETN	12	Maternal effect embryo arrest 18 /Zea mays/ ONM41244.1	100	1229.23	4.35	-1	41	+1.85	17	55
215	CHAVHDGFETNARSRVPQ	18	Bifunctional monodehydroascorbate reductase and carbonic anhydrase nectarin-3; AltName: Full=Nectarin-III; Contains: RecName: Full=Nectarin-2; Flags/ Nicotiana langsdorffii x Nicotiana sanderae/ Q84UV8.1	100	2024.20	6.91	+2	33	+3.10	1	5
216	LREVSSGGGTTVPGGME	17	Protein FAR1-RELATED SEQUENCE 5-like /Ipomoea nil/ XP_019167884.1	100	1633.79	4.53	-1	23	+1.20	1.1	0.7
217	WGVESMTTASSPVDDNL	17	Hypothetical protein /Tanacetum cinerariifolium/ GEY60842.1	85	1808.93	3.49	-3	35	+1.51	1	2
218	VCPCACCSTPRRV	13	Uncharacterized protein LOC109239433 /Nicotiana attenuata/ XP_019261548.1	65	1394.71	8.56	+2	53	+1.60	87	97
219	PDEGHEEQAP	10	Hypothetical protein DCAR_028685 /Daucus carota subsp. Sativus/ KZM83893.1	100	1108.09	4.00	-3	10	+3.65	10	12
220	WKEACGNMCNPG	12	Uncharacterized protein LOC107806614 /Nicotiana tabacum/ XP_016486286.1	73	1309.50	5.99	0	41	+1.22	29	79
221	VEAADGDFTGCHVLL	15	Probable ubiquitin-like-specific protease 2B isoform X4 /Nicotiana tabacum/ XP_016463539.1	89	1546.71	4.02	-2	53	+0.25	4	11
222	DSAEGECCVRVV	12	Hypothetical protein CMV_010798 /Castanea mollissima/ KAF3964972.1	100	1266.41	4.14	-2	50	+1.93	14	33
223	TCPPEAGCSPNGTDTQ	16	Callose synthase 9 /Nicotiana attenuata/ OIT08780.1	77	1577.66	3.67	-2	18	+2.03	29	44
224	WGPMGPPAHGFTHNVL	16	Hypothetical protein CXB51_000699 /Gossypium anomalum/ KAG8502852.1	100	1717.97	6.92	+2	37	-0.17	9	21
225	AMHVGGYECTCGTDVPA	17	Uncharacterized protein LOC107829855 isoform X3 /Nicotiana tabacum/ XP_016512808.1	77	1710.91	4.35	-1	41	+0.35	24	26
226	WWDHCTCCSPQMTHMD	16	Hypothetical protein Ahy_A03g016304 /Arachis hypogaea/ RYR69753.1	100	1981.24	5.05	0	43	+1.72	61	66
227	TMHDCGMAEVDVV	13	Putative acyl-activating enzyme 5, peroxisomal /Capsicum chinense/ PHU24982.1	100	1406.61	4.02	-2	53	+0.81	24	42
228	YEFLDKALDNSQ	12	Hypothetical protein PVAP13_6KG351900 /Panicum virgatum/ KAG2584833.1	90	1442.54	4.03	-2	33	+2.57	26	4.1
229	ETSGAGMSSCLGLPPW	16	Uncharacterized protein LOC122039969/Zingiber officinale/ XP_042455306.1	100	1592.80	4.00	-1	37	-0.05	3	2
230	RNRHGPFGAPDDCKSHMQY	19	Putative transporter C5D6.04 /Glycine soja/ KHN38858.1	100	2216.44	8.21	+3	21	+3.55	42	22
231	VEGEDPNASDFAKH	14	Uncharacterized protein LOC117276159 /Nicotiana tomentosiformis/ XP_033511370.1	100	1515.56	4.31	-2	28	+2.83	3	6
232	LLAKPPVT	8	Hypothetical protein L484_023970/Morus notabilis/ EXB62674.1	100	838.06	8.75	+1	50	-0.94	22	25

233	HWSHDGPGAVRAFQCP	16	Aconitate hydratase, cytoplasmic-like isoform X2 /Hibiscus syriacus/ XP_039044755.1	87	1764.94	6.91	+2	37	+1.61	7	19
234	LLFEGEFAPDEEVHCF	16	Hypothetical protein BHM03_00049415 /Ensete ventricosum/ RZS17287.1	100	1882.07	3.90	-4	50	+0.86	5	25
235	LCAQGTPPGCQASCDSQ	17	L-type lectin-domain containing receptor kinase IX.1 /Triticum urartu/ EMS49668.1	100	1665.83	3.80	-1	35	+1.20	42	13
236	DSPVHPGMDSEAPQ	14	Unnamed protein product /Digitaria exilis/ CAB3491145.1	100	1466.54	4.02	-2	21	+2.29	3	3
237	CSFSGTDTAEYGDGGA	16	COBRA-like protein 10 /Lupinus angustifolius/ XP_019443094.1	100	1537.53	3.49	-3	25	+1.54	15	9
238	PDGTTTPPGTGRVMMY	16	Nuclear pore complex protein NUP98A-like isoform X3 /Nicotiana tabacum/ XP_016497583.1	91	1680.91	6.26	0	18	+1.40	20	37
239	AAPAPAFANVSAGRPK	16	ENTH/VHS family protein /Actinidia rufa/ GFY81573.1	100	1524.74	11.00	+2	50	+0.73	20	20
240	EREDGHNPAEPSGGGPQV	18	DNA-binding protein HEXBP-like /Nicotiana attenuata/ XP_019237111.1	80	1832.86	4.40	-2	11	+3.03	1	<1
241	VTSTGFTAGS	10	Ribonuclease H-like domain-containing protein /Tanacetum cinerariifolium/ GFA27115.1	100	926.98	5.49	0	30	+0.38	14	71
242	NHETFGFVGGWDEEVLHH	18	Ribonuclease 2-like isoform X2 /Nicotiana tomentosiformis/ XP_009600252.1	100	2110.23	4.78	-1	33	+1.56	17	69
243	YSSLDEA	7	Unnamed protein product /Arabis nemorensis/ VVB08023.1	100	783.79	3.67	-2	28	+2.24	30	10
244	YSGDGADPKGFKVRDR	16	Protein DOWNY MILDEW RESISTANCE 6 isoform X2 /Medicago truncatula/ XP_039684250.1	100	1767.92	8.50	+1	18	+3.68	18	20
245	MALPTRNYQCSLVV	14	Uncharacterized protein LOC104093999 /Nicotiana tomentosiformis/ XP_009598133.2	80	1594.91	7.98	+1	50	+0.70	2	7
246	DSAHGSTTECFR	12	Uncharacterized protein LOC104221975 /Nicotiana sylvestris/ XP_009771439.1	70	1310.36	5.32	0	25	+3.33	3	13
247	WALALEEFSEGLEDE	15	Uncharacterized protein LOC107826936 /Nicotiana tabacum/ XP_016509467.1	83	1737.84	3.40	-6	46	+1.43	6	8
248	MPGDSGSYTPDECLY	15	Uncharacterized protein LOC109241349 /Nicotiana attenuata/ XP_019263628.1	80	1634.75	3.49	-3	20	+1.56	20	6
249	PCGDANGVGGSDAYY	15	DNA replication licensing factor MCM3 homolog 2-like isoform X1 /Nicotiana tabacum/ XP_016460814.1	80	1445.48	3.56	-2	26	+1.00	62	44
250	DTQYCSGGGLDYSQVQ	16	DNA-directed DNA polymerase /Tanacetum cinerariifolium/ GEZ26470.1	100	1720.78	3.56	-2	18	+1.91	20	15
251	DHLPDKGGS	9	Hypothetical protein C3L33_12776 /Rhododendron williamsianum/ KAE9455322.1	100	924.97	5.21	0	11	+2.69	14	39
252	HDGTSGFGFGCMNFVPVDDRA	21	Putative ribonuclease H-like domain-containing protein /Tanacetum cinerariifolium/ GEV72596.1	100	2229.43	4.41	-1	38	+1.53	7	15
253	LVDDSAAYVDPGCTGTYW	18	Non-specific phospholipase C3-like /Prunus avium/ XP_021809098.1	100	1933.08	3.42	-3	38	+0.71	17	7
254	SGCDTQSGPGVGDDPW	16	Hypothetical protein /Gossypium raimondii/ MBA0577971.1	100	1577.60	3.42	-3	18	+1.85	4	15

255	WWMMEADCCDAEHECSWH	18	Hypothetical protein H0E87_020427 /Populus deltoides/ KAF9838999.1	100	2269.50	4.17	-3	55	+1.74	39	66
256	YMFDHAAMGPCQQSYP	16	Uncharacterized protein LOC109240454 isoform X2 /Nicotiana attenuata/ XP_019262651.1	100	1846.08	5.08	0	37	+0.91	45	29
257	KPKGHDGFEHAYAAYFW	17	G-type lectin S-receptor-like serine/threonine-protein kinase RLK1 /Nicotiana tabacum/ XP_016465273.1	85	2024.23	6.92	+2	35	+1.21	42	47
258	DHTAGSCASPAPL	13	Unnamed protein product /Arabis nemorensis/ VVB12156.1	100	1226.33	5.08	0	38	+0.78	4	3
259	QRDASNFCSLDGDGSF	16	Abc subfamily c protein /Thalictrum thalictroides/ KAF5192530.1	100	1718.77	3.93	-2	31	+2.97	20	17
260	THKEDDNKVFEKDTHK	16	Reverse transcriptase domain, reverse transcriptase zinc-binding domain protein /Tanacetum cinerariifolium/ GEW75212.1	100	1971.11	5.96	+1	12	+4.75	14	25
261	WCHDMPEGDPCCFNYE	16	Hypothetical protein /Tanacetum cinerariifolium/ GEW25190.1	100	1946.13	3.91	-3	37	+1.87	53	88
262	WQMHPCAGHG	10	Hypothetical protein Ahy_B05g079486 /Arachis hypogaea/ RYR10993.1	100	1123.27	6.91	+2	40	+0.52	51	55
263	CPCCFGGHDTCLPG	14	WD40 repeat-containing protein smu1-like [Salvia splendens]	100	1409.63	5.08	0	42	+0.00	86	94
264	VCPGAGGCGSRWVQ	14	Hypothetical protein B296_00007283 /Ensete ventricosum/ RRT84829.1	100	1376.57	8.04	+1	42	+0.38	34	37
265	PCNEQGGMPPPPS	13	Hypothetical protein BVRB_2g041450 /Beta vulgaris subsp. Vulgaris/ KMT17091.1	100	1310.46	4.00	-1	15	+1.29	17	45
266	HDGEGHPMVSNHEGCL	16	Hypothetical protein A4A49_09665 /Nicotiana attenuata/ OIT31862.1	77	1718.84	5.17	0	25	+1.93	27	71
267	PRVLPGAK	8	Copper-transporting ATPase RAN1-like /Nicotiana tabacum/ XP_016515405.1	100	837.03	11.01	+2	37	+1.09	10	28
268	EVGCPGGAAGDPKEK	15	Hypothetical protein A4A49_21984 /Nicotiana attenuata/ OIS95845.1	77	1414.55	4.68	-1	26	+1.38	5	6
269	YGGQFDELSEDQ	12	Hypothetical protein E2562_005477 /Oryza meyeriana var. granulata/ KAF0911096.1	100	1387.38	3.43	-4	16	+2.99	19	14
270	TTYSGCAAHETNTAR	15	Cathepsin B-like cysteine proteinase 3 /Nicotiana tomentosiformis/ XP_009598205.1	70	1582.66	6.41	+1	26	+2.61	23	80
271	SDPMDTFMAAPQ	12	Uncharacterized protein LOC107795234 /Nicotiana tabacum/ XP_016473315.1	73	1310.46	3.56	-2	41	+1.47	38	36
272	WWPGSHSGSAEHGATYY	17	Hypothetical protein RchiOBHm_Chr5g0082441 /Rosa chinensis/ PRQ35665.1	100	1892.96	5.98	+1	23	+1.06	24	65
273	HTASVTLPSVDSGCAPFY	18	ERAD-associated E3 ubiquitin-protein ligase /Salix suchowensis/ KAG5219472.1	100	1852.05	5.08	0	38	+0.39	1	3
274	DNSYHAGMTGEGDPAN	16	Unnamed protein product /Triticum turgidum subsp. durum/ VAH43013.1	100	1635.64	4.02	-2	18	+2.46	10	3
275	WMSGGSGGAAAGL	13	Hypothetical protein Bca52824_013231 /Brassica carinata/ KAG2320018.1	100	1121.23	5.52	0	46	-0.99	34	59

276	WWWCSMETPSSACMGFCED	19	Inactive LRR receptor-like serine/threonine-protein kinase BIR2 /Cynara cardunculus var. scolymus/ XP_024975777.1	100	2256.54	3.57	-3	52	+0.72	29	60
277	WYEANATRPACCYSKRH	17	Hypothetical protein F511_43506 /Dorcoceras hygrometricum/ KZV25050.1	100	2056.30	8.86	+3	35	+2.90	75	90
278	KRCAHSTAGECSMD	14	Fimbrin-2-like /Nicotiana tomentosiformis/ XP_009626169.1	87	1495.66	6.73	+1	35	+2.89	64	42
279	YYRAPGPGSVCL	12	Fatty acid amide hydrolase-like /Nicotiana attenuata/ XP_019230443.1	73	1282.48	8.20	+1	33	+0.38	38	38
280	RATGAGLASGGSMDDPAPM	19	AT5G35200 /Arabidopsis thaliana/ BAH20213.1	100	1761.94	4.21	-1	36	+1.11	13	10
281	MKGACSDVVVNGTGSPY	17	Hypothetical protein SASPL_124168 /Salvia splendens/ KAG6416732.1	100	1684.90	5.58	0	35	+0.59	11	29
282	CPCCCTGPGAAGCLPG	16	Uncharacterized protein LOC104244329 /Nicotiana sylvestris/ XP_009798037.1	85	1409.69	5.49	0	50	-1.00	73	75
283	CPYSAGGEANQAQ	13	TRANSPARENT TESTA GLABRA 1-like /Nicotiana tabacum/ NP_001312618.1	73	1295.35	4.00	-1	30	+1.49	35	19
284	NFGLTSGFLGRMD	13	Putative reverse transcriptase domain-containing protein /Tanacetum cinerariifolium/ GEW87094.1	100	1414.60	5.84	0	38	+1.17	27	21
285	FFAVPGACFSGVQAMYWWH	19	Hypothetical protein KK1_050505 /Cajanus cajan/ KYP78676.1	100	2204.55	6.73	+1	63	-0.99	18	54
286	GMPGELPGSGGGMNSCTN	18	Uncharacterized protein LOC111894204 /Lactuca sativa/ XP_023746054.1	91	1665.83	4.00	-1	22	+0.71	17	47
287	KRPAVVVLENPLE	13	Hypothetical protein STAS_07826 /Striga asiatica/ GER31795.1	100	1463.74	6.14	0	46	+1.30	1	4
288	NYTVEHKFL	9	Subtilisin-like protease SBT1.9 /Morus notabilis/ XP_010112177.1	100	1150.30	6.75	+1	33	+1.60	6	27
289	NHTGNCSTTSDGAVFVGPMF	20	Pleiotropic drug resistance protein 1-like /Nicotiana attenuata/ XP_019234268.1	70	2042.23	5.08	0	35	+0.94	8	28
290	PTVKYDSDVGMLDWW	15	Tetratricopeptide repeat protein /Striga asiatica/ GER25614.1	100	1812.03	3.93	-2	40	+1.12	8	36
291	QWGGECGCGAMNGVPSAPPFRY	22	Uncharacterized protein LOC110814328 /Carica papaya/ XP_021897441.1	100	2284.57	5.99	0	36	+0.67	22	28
292	KLEGHLDVCMATFAPVLFY	19	Putative invertase inhibitor /Dioscorea cayenensis subsp. rotundata/ XP_039123611.1	100	2154.57	5.32	0	57	-0.44	3	5
293	EQEHVSGGCGPLQHSR	16	Hypothetical protein /Tanacetum cinerariifolium/ GEW04353.1	100	1720.84	6.01	+1	18	+2.66	14	8
294	KLHVPCGECGMPSPVDYQ	18	Uncharacterized protein LOC109327999 isoform X2 /Lupinus angustifolius/ XP_019416766.1	100	1960.27	5.32	0	33	+0.83	16	23
295	LPKYAKGDDDVGNVH	15	Hypothetical protein TSUD_285430 /Trifolium subterraneum/ GAU43791.1	100	1627.77	5.30	0	26	+2.13	21	31
296	FFADHFAPACLFMMEKPW	18	Hypothetical protein GUJ93_ZPchr0006g41574 /Zizania palustris/ KAG8072541.1	100	2188.61	5.32	0	66	-0.26	48	56
297	KNCCCGMGEEVPDYVHCYAF	20	Hypothetical protein CRG98_010149 /Punica granatum/ PKI69446.1	100	2268.59	4.65	-1	45	+0.86	90	99
298	DEEHVLAPDEKHWYN	15	Uncharacterized protein LOC109218112 /Nicotiana attenuata/ XP_019237975.1	73	1881.98	4.49	-2	26	+3.09	5	23

299	TTPPSETNMSGCMV	14	Hypothetical protein SADUNF_Sadunf05G0007600 /Salix dunnii/ KAF9681498.1	100	1454.65	4.00	-1	28	+1.21	12	34
300	FSAMCNADGVAALTDEVP	18	Homogentisate 1,2-dioxygenase isoform X1 /Carex littledalei/ KAF3337579.1	100	1811.01	3.49	-3	55	+0.50	8	12
301	DSPGSGQANDTYV	13	NADP-dependent malic enzyme-like isoform X1 /Nicotiana attenuata/ XP_019262802.1	77	1310.30	3.56	-2	15	+2.41	6	2
302	DPDSPPDVYFQTNY	14	Hypothetical protein CARUB_v10011150mg /Capsella rubella/ EOA38827.1	100	1657.71	3.42	-3	14	+2.68	22	15
303	LLFPFEATDTAPNRAPGMNCE	21	Tyrosine-specific transport protein 2-like isoform X2 /Daucus carota subsp. sativus/ XP_017254409.1	91	2294.58	4.14	-2	42	+1.42	2	2
304	DWPLGGCAVGPNQHW	15	Two-component system sensor histidine kinase/response regulator /Tanacetum cinerariifolium/ GEU28387.1	100	1636.80	5.08	0	40	+0.40	10	27
305	VAMVVGVAAAVVKLLH	16	Hypothetical protein EJ110_NYTH22707 /Nymphaea thermarum/ KAF3784634.1	100	1577.00	8.73	+2	81	-2.14	58	83
306	WPTLPMLEHGTAFSDH	16	Uncharacterized protein LOC107774114/Nicotiana tabacum/XP_016449069.1	89	1839.06	5.15	0	37	+0.82	2	8
307	DSGVLGFSGS	10	Adenylosuccinate synthetase, chloroplastic-like /Nicotiana tomentosiformis/XP_009593625.1	100	924.96	3.80	-1	30	+0.41	20	38
308	VTMTCGDNQQ	10	Hypothetical protein Csa_009302 /Cucumis sativus/ KGN52102.1	100	1096.20	3.80	-1	30	+2.29	30	32
309	EAPSPGRGGSVCNDDTTE	18	Hypothetical protein SEVIR_9G077600v2 /Setaria viridis/ TKV91185.1	100	1791.82	3.92	-3	16	+3.03	1	<1
310	FVQNSGMADFGGPKERLP	18	Unnamed protein product /Microthlaspi erraticum/ CAA7031689.1	100	1950.20	6.07	0	33	+1.64	7	6
311	WRETCALHGEYELM	14	Hypothetical protein A4A49_60189 /Nicotiana attenuata/ OIT35125.1	100	1737.97	4.75	-1	42	+1.72	6	22
312	KDLSAEPFPDK	11	E3 ubiquitin-protein ligase UPL1 /Medicago truncatula/ XP_013457378.2	100	1246.38	4.56	-1	27	+2.64	13	12
313	AWLTTPCEQCTW	12	Hypothetical protein Ahy_A05g023555 /Arachis hypogaea/ RYR57866.1	100	1438.64	4.00	-1	50	+0.50	50	73
314	YTSAHGVMSCATHM	14	Mitochondrial phosphate carrier /Nicotiana alata/ ATY75539.1	80	1495.71	6.91	+2	42	+0.48	32	40
315	RSGTCAECAHGCV	13	Hypothetical protein H0E87_025803 /Populus deltoides/	100	1293.45	6.72	+1	46	+1.45	62	88
316	RSPKRVLDHLGGFLDPEL	18	Pputative Tetratricopeptide repeat-like superfamily protein /Hibiscus syriacus/ KAE8700444.1	100	2049.36	6.76	+1	33	+2.17	2	2
317	LKEGGPNCTLKGFDHVLYF	19	Uncharacterized protein LOC107935982 isoform X1 /Gossypium hirsutum/ XP_040943244.1	100	2138.47	6.74	+1	36	+0.62	26	22
318	RSACSAGGHK	10	Transcription factor MYC2-like /Nicotiana tabacum/ NP_001312938.1	87	973.07	9.51	+3	30	+2.51	59	64
319	YFVQNGTTTNYGNVHHR	17	Mitogen-activated protein kinase kinase kinase 3-like /Nicotiana attenuata/ XP_019240621.1	72	2008.14	8.60	+3	17	+2.63	22	65

320	MPKDTHATAGGKHTHW	16	Sodium/hydrogen exchanger 8-like /Nicotiana tabacum/ XP_016446545.1	77	1774.97	8.40	+4	25	+1.95	35	58
321	DHGECVCDTSNSVGKPA	17	Retrovirus-related Pol polyprotein from transposon 17.6 /Mucuna pruriens/ RDY05234.1	100	1718.83	4.54	-1	29	+2.12	12	36
322	AERDPAFDVDMPL	13	Patatin-like protein 7 /Eucalyptus grandis/ XP_010052585.2	100	1475.64	3.84	-3	46	+2.30	5	15
323	YMARAGDAMGYMWHW	15	Hypothetical protein PVAP13_3NG040480 /Panicum virgatum/ KAG2615729.1	100	1846.13	6.74	+1	53	+0.63	50	65
324	DHFASNVASCSFSGPFVDDQV	21	Alpha-1,2-L-fucosidase /Nicotiana benthamiana/ QCH41104.1	74	2229.36	3.93	-2	42	+1.41	5	10
325	REEDGVGAFCAALGGAYF	18	Probable L-type lectin-domain containing receptor kinase I.6 /Tarenaya hassleriana/ XP_010541356.1	100	1833.01	4.14	-2	50	+0.56	5	4
326	DSLMAVEFGNPGSCR	15	Hypothetical protein JHK87_007280 /Glycine soja/ KAG5043365.1	100	1582.77	4.37	-1	40	+1.64	6	6
327	DREPPQPLPAFNNHHDKPYCKC	22	Nuclear speckle RNA-binding protein B /Eutrema salsugineum/ XP_006416316.1	100	2606.92	6.90	+2	22	+3.01	14	35
328	DQNVPTHMTDRGSHLC	16	Mediator of RNA polymerase II transcription subunit 33A isoform X1 /Olea europaea subsp. europaea/ CAA2957936.1	100	1810.98	5.98	+1	25	+3.05	9	4
329	GDDPDVMPSAGPE	13	Hypothetical protein GUJ93_ZPchr0006g43676 /Zizania palustris/ KAG8075093.1	100	1286.33	3.37	-4	23	+2.02	12	22
330	QQNDMQCQGGGMVAASQNL	19	Hypothetical protein ZIOFF_046890 /Zingiber officinale/ KAG6491949.1	100	1980.17	3.80	-1	36	+1.66	40	31
331	GPMVNAGMGSGEMAGPLW	18	Hypothetical protein CFC21_067030 /Triticum aestivum/ KAF7060228.1	100	1762.05	4.00	-1	44	-0.54	37	56
332	LHNMMPRALAPDEQHNYW	18	Protein IQ-DOMAIN 32-like /Cucumis melo/ XP_008444783.1	100	2223.51	5.99	+1	38	+2.12	5	6
333	REEDNDMGSTLGPLLD	16	E3 ubiquitin-protein ligase UPL1-like /Nicotiana tomentosiformis/ XP_009606345.1	87	1761.88	3.77	-4	25	+3.01	7	5
334	SRKNWAFSQESGDHVRH	17	Uncharacterized protein LOC107760626 /Nicotiana tabacum/ XP_016434196.1	72	2041.17	8.51	+3	23	+4.14	4	9
335	HCCQCYSENDGYTTCYYW	18	Uncharacterized TPR repeat-containing protein At1g05150-like /Salvia splendens/ XP_042010338.1	100	2239.41	4.35	-1	27	+1.83	62	60
336	SDPDNPGASPDSPAQ	15	Probable helicase CHR10 isoform X5 /Arachis hypogaea/ XP_025606316.1	100	1454.43	3.42	-3	13	+2.93	23	15
337	CPGCEGCCYM	10	Hypothetical protein /Gossypium armourianum/ MBA0837612.1	100	1065.28	4.00	-1	50	-0.24	72	82
338	PCTKHGDPPAWGLP	14	Heme oxygenase (decyclizing) /Trema orientale/ PON54600.1	100	1475.68	7.12	+1	28	+0.66	17	16
339	CPTGNGFTCTMFPFPT	16	Gamma-tubulin complex component 5 isoform X3 /Beta vulgaris subsp. vulgaris/ XP_019103478.1	100	1720.99	5.51	0	37	+0.07	37	71
340	MACSCKLFGFAMTR	14	Protein HIRA isoform X1 /Oryza sativa Japonica group/ XP_015612034.1	100	1565.95	8.94	+2	64	+0.26	93	79

341	WALTVVPWTETTQCC	15	Uncharacterized protein LOC116261421 isoform X2 /Nymphaea colorata/ XP_031496020.1	100	1738.01	4.00	-1	53	+0.04	53	82
342	LWLKHDFGEAGSAVGQASHK	20	Reverse transcriptase domain-containing protein /Tanacetum cinerariifolium/ GFB18900.1	100	2138.37	6.92	+2	40	+1.04	24	71
343	YPHGGPVAVNSDSTGVQS	18	G-type lectin S-receptor-like serine/threonine-protein kinase At2g19130 /Triticum dicoccoides XP_037487574.1 /	100	1771.86	5.08	0	22	+1.20	1	3
344	VLQHVKLHNGAAGVPLE	17	Cyclin-D-binding Myb-like transcription factor 1 /Ipomoea triloba/ XP_031122251.1	100	1782.08	6.89	+2	47	+0.08	35	79
345	LVKFFPGHRNPLGLDPEL	18	Putative F-box protein At1g23770 /Oryza brachyantha/ XP_015690251.2	90	2049.40	6.75	+1	38	+0.87	7	10
346	PCTAPQNCDENM	12	Uncharacterized protein LOC104238968 isoform X1 /Nicotiana sylvestris/ XP_009791794.1	70	1322.45	3.67	-2	33	+2.51	33	41
347	QLWDHACTWCMWN	13	Putative ribonuclease H protein /Trifolium medium/ MCI12807.1	100	1693.93	5.08	0	61	+0.73	34	68
348	RHPDMVDGFGFYE	13	Uncharacterized protein LOC112016091 /Quercus suber/ XP_023904366.1	100	1569.71	4.54	-1	30	+2.28	9	29
349	VLLLFVF	7	Uncharacterized protein LOC104241879 isoform X1 /Nicotiana sylvestris/ XP_009795137.1	85	850.11	5.49	0	0	-4.11	39	54
350	WPKYPCAFADMMSTVNNYELRW	22	Uncharacterized protein LOC109224535 /Nicotiana attenuata/ XP_019244647.1	72	2723.13	6.06	0	45	+1.33	7	35
351	KDPSVAGGAKTEDW	14	Nuclear pore complex protein NUP50A-like /Durio zibethinus/ XP_022714925.1	100	1460.56	4.56	-1	28	+2.10	5	13
352	MNANGASGCYTL	12	Hypothetical protein FH972_008468 /Carpinus fangiana/ KAE8022686.1	100	1201.33	5.27	0	41	+0.44	40	75
353	LKSRHPKAVGNLFKDNP	17	Uncharacterized protein LOC109223605 isoform X3 /Nicotiana attenuata/ XP_019243531.1	77	1921.23	10.29	+4	29	+2.47	27	35
354	AHCVHDGFETNARAVRPQ	18	Full=Bifunctional monodehydroascorbate reductase and carbonic anhydrase nectarin-3; AltName: Full=Nectarin-III; Contains: RecName: Full=Nectarin-2; Flags: Precursor /Nicotiana langsdorffii x Nicotiana sanderae/ Q84UV8.1	74	2008.20	6.95	+2	38	+2.81	2	8
355	YYSPSYTELTPSFTGMFHFT	20	Wall-associated receptor kinase 3 /Hordeum vulgare/ KAE8790748.1	100	2376.62	5.24	0	25	+0.76	2	18
356	KQGTGVCPCYD	11	Gibberellin-regulated protein 6-like /Nicotiana tabacum/ XP_016473209.1	85	1170.32	5.82	0	27	+1.27	82	73
357	WLMDPGLLSSASVEW	15	Hypothetical protein PRUPE_4G135000 /Prunus persica/ ONI11925.1	100	1690.93	3.67	-2	53	-0.18	3	12
358	LVRVNGSAFTTRKRS	15	Hypothetical protein /Tanacetum cinerariifolium/ GEW79156.1	100	1691.95	12.30	+4	33	+3.34	11	8
359	FYLMSPGCHDTHVYSW	16	B3 domain-containing protein REM17-like isoform X1 /Erigeron Canadensis/ XP_043610580.1	100	1943.18	5.97	+1	37	+0.55	13	29
360	NFEDSDRFSTNPKG	14	Hypothetical protein C5167_039968 /Papaver somniferum/ RZC47026.1	100	1613.66	4.56	-1	14	+4.31	14	3

361	WWVRLAGGFMNMDDESGDE VRTD	23	Protein DEHYDRATION-INDUCED 19 homolog 5 isoform X2 /Sesamum indicum/ XP_011071958.1	90	2686.91	3.96	-4	39	+2.65	5	20
362	EDEEWFAPLMEVKMQ	15	Splicing factor 3A subunit 3 /Ananas comosus/ OAY82758.1	100	1882.13	3.91	-4	46	+1.75	17	46
363	YVCDDASFRCYMAYFK	16	Uncharacterized protein LOC120003056 /Tripterygium wilfordii/ XP_038707883.1	89	1982.27	5.94	0	50	+1.45	33	36
364	YYECASSGSYDCEYQYY	17	Uncharacterized protein LOC18446842 isoform X2 /Amborella trichopoda/ XP_020530809.1	100	2094.16	3.57	-3	17	+1.97	27	43
365	MNQYTQTDGGMETVVHH	17	Hypothetical protein E3N88_17362 /Mikania micranta/ KAD5317416.1	100	1948.11	5.14	0	23	+2.10	8	13
366	LRAFEGEENDADEEVRKC	18	Hypothetical protein DM860_008320 /Cuscuta australis/ RAL40180.1	90	2110.24	4.25	-4	33	+4.20	5	4
367	CRHMHGLFYPNSTFSRDTQH	20	Glucan endo-1,3-beta-glucosidase 14 /Carex littledalei/ KAF3332061.1	100	2434.69	8.25	+4	25	+3.06	24	36
368	PDQVGGAVAENGMFNLV	17	Hypothetical protein DEO72_LG3g2066 /Vigna unguiculata/ QCD87530.1	100	1717.91	3.67	-2	47	+0.32	5	15
369	LVQMGPMQCFEPPLQ	15	Hypothetical protein HPP92_018545 /Vanilla planifolia/ KAG0466965.1	100	1718.08	4.00	-1	46	-0.02	39	49
370	FRHAVTMPSCADYLLSNYMM YW	22	Uncharacterized protein LOC107426018 isoform X2 /Ziziphus jujube/ XP_015891598.1	100	2700.16	6.73	+1	50	+0.61	18	27
371	LALKPPVT	8	Protein furry homolog-like isoform X1 /Ipomoea triloba/ XP_031109589.1	100	838.06	8.75	+1	50	-0.94	22	24
372	RQFQLGFFFGHCTYGFEYLCM	21	Putative organic cation/carnitine transporter 4-like /Capsicum annuum/ KAF3623404.1	100	2595.01	6.73	+1	47	+0.37	9	28
373	ESQDTSVAVADPVEFCN	17	Uncharacterized protein LOC110105336 /Dendrobium catenatum/ XP_028555140.1	100	1810.91	3.43	-4	41	+1.91	1	2
374	MYAMNPNMSNVVAYRPSP	18	Hypothetical protein /Gossypium klotzschianum/ MBA0650328.1	100	2042.37	8.34	+1	38	+1.28	20	48
375	WRHGANECDNYLFL	14	Hypothetical protein /Tanacetum cinerariifolium/ GEZ44030.1	100	1737.91	5.32	0	42	+2.09	22	31
376	TTHGAWSSCGAFTE	14	Hypothetical protein CK203_094075 /Vitis vinifera/ RVW41450.1	100	1454.53	5.21	0	35	+0.99	11	84
377	MMCMAFFYAPGGPVAFMGSE NY	22	Putative reverse transcriptase domain-containing protein /Tanacetum cinerariifolium/ GEU37230.1	100	2421.86	4.00	-1	54	-0.67	66	63
378	ESPNAACCSEMNMD	14	Hypothetical protein IFM89_032861 /Coptis chinensis/ KAF9616899.1	100	1501.64	3.57	-3	42	+2.25	25	37
379	RHYTPCNGGTDEFYWT	16	F-box/kelch-repeat protein At3g06240 /Rosa chinensis/ XP_024186413.2	100	1947.07	5.32	0	18	+2.57	19	43
380	WYFFGFEPPGMAFMGMFDYC K	21	Heavy metal-associated isoprenylated plant protein 32-like /Dioscorea cayenensis subsp. Rotundata/ XP_039114904.1	87	2572.03	4.37	-1	52	-0.42	50	54
381	NEKVVEAPTASSTQ	14	Uncharacterized protein LOC104104079 /Nicotiana tomentosiformis/ XP_009610367.1	87	1460.56	4.53	-1	28	+2.25	<1	2
382	WRYDCFPGYEGFFPVLMAYE WY	22	Wall-associated receptor kinase-like 8 /Artemisia annua/ PWA40394.1	100	2840.22	4.14	-2	45	+0.36	8	21

383	RSPNVPRSVDSGCEYW	16	Uncharacterized membrane protein C776.05-like isoform X3 /Nicotiana tomentosiformis/XP_033517306.1	70	1852.01	6.06	0	25	+3.10	2	11
384	THAQHAPPDGLMEYW	15	Hypothetical protein CXB51_006679 /Gossypium anomalum/ KAG8497833.1	9	1752.92	5.14	0	33	+1.26	6	6
385	LSTTPPWTTPFCNC	14	Uncharacterized protein LOC109243087 /Nicotiana attenuata/ XP_019265527.1	80	1567.79	5.51	0	35	+0.53	64	90
386	TCDEVWGSFNMRPFC	15	Ubiquitin carboxyl-terminal hydrolase 14-like /Nicotiana tabacum/ XP_016492598.1	85	1792.03	4.37	-1	46	+1.65	15	65
387	DMHTDGADSGQPPSP	15	COP9 signalosome complex subunit 6a /Nicotiana tomentosiformis/ XP_009613025.1	72	1511.54	3.93	-2	13	+2.64	9	5
388	VCAEGHMGLAGVHN	14	Uncharacterized protein LOC107814608 /Nicotiana tabacum/ XP_016495533.1	85	1394.59	5.98	+1	50	-0.02	48	75
389	PNQCHGDEQAP	11	Uncharacterized protein LOC107792277 /Nicotiana tabacum/ XP_016469956.1	100	1195.23	4.35	-1	18	+3.08	10	9
390	TVVCGHALGAEGYCM	15	Protein FAR1-RELATED SEQUENCE 5-like /Nicotiana tomentosiformis/ XP_033517423.1	100	1510.76	5.21	0	53	-0.67	51	56
391	VHADGSPKGYEGLNVQP	17	Uncharacterized protein LOC111010720 isoform X2 /Momordica charantia/ XP_022139927.1	100	1767.92	5.32	0	23	+1.40	1	3
392	CPNCGSAPGAAPPSP	15	Glycerophosphodiester phosphodiesterase GDPDL4-like /Zingiber officinale/ XP_042407349.1	100	1325.48	5.51	0	33	+0.23	18	17
393	PFGPAVSGVGGGTDSR	16	Hypothetical protein MANES_05G014104v8 /Manihot esculenta/ KAG8653307.1	100	1460.57	6.27	0	25	+0.96	1	<1
394	PMDGTQEHPDECEF	14	Uncharacterized protein LOC109234638 /Nicotiana attenuata/ XP_019256252.1	77	1634.71	3.83	-4	21	+3.07	11	41
395	RWKDCKDGSSGGNHTQWPE	19	Heavy metal-associated isoprenylated plant protein 3-like /Nicotiana attenuata/ XP_019237692.1	100	2188.32	6.75	+1	15	+3.56	5	45
396	SDLASDCSPAVCV	13	Hypothetical protein BUALT_Bualt10G0007600 /Buddleja alternifolia/ KAG8374555.1	100	1266.40	3.56	-2	53	+0.65	19	28
397	QEGPVCNEDCHPLA	14	Hypothetical protein Bca52824_044408 /Brassica carinata/ KAG2297739.1	100	1511.64	4.13	-2	35	+1.77	4	26
398	QTYVESGCEQGFQW	14	Hypothetical protein HU200_020917 /Digitaria exilis/ KAF8724645.1	100	1661.76	3.79	-2	28	+1.70	8	29
399	PMGWAPVGNAGQVLPPM	17	Uncharacterized protein LOC117858928 /Setaria viridis/ XP_034597979.1	100	1722.05	5.96	0	47	-0.84	12	20
400	YYRGPNSCPMTSLSSHPLVPYYL	23	Hypothetical protein Lal_00024085 /Lupinus albus/ KAF1888073.1	100	2646.03	8.16	+2	26	+0.85	3	15
401	TYNVASASSCSSGAQELPGN	20	Pentatricopeptide repeat-containing protein At1g09900 /Nicotiana sylvestris/ XP_009793553.1	80	1943.03	4.00	-1	30	+1.38	12	14
402	WNALAESSVEMDKSE	15	TruB_N domain-containing protein /Cephalotus follicularis/ GAV78696.1	100	1695.82	4.00	-3	40	+2.28	4	6
403	SDYQPVCFDLGPYTNM	16	Uncharacterized protein LOC110030458 /Phalaenopsis equestris/ XP_020588839.1	100	1850.05	3.56	-2	31	+1.21	5	5

404	KLGSKLATPQKPWLSYDCC	19	Peptidyl-prolyl cis-trans isomerase fkbp13 chloroplastic /Phtheirospermum japonicum/ GFP81646.1	100	2138.53	8.82	+2	36	+0.94	71	54
405	WCECDAGGATCSYVSQ	16	Uncharacterized protein LOC110436024 /Sorghum bicolor/ XP_021317883.1	100	1679.81	3.67	-2	43	+0.92	78	79
406	KWSGVCGCEVACGYPVGCLDHT	22	Hypothetical protein /Colocasia esculenta/ MQM17074.1	100	2284.62	5.32	0	45	+0.08	79	90
407	WCSCCGTTMDEECDFMCN	18	Uncharacterized protein LOC104250113 /Nicotiana sylvestris/ XP_009804971.1	100	2078.34	3.43	-4	50	+1.60	85	85
408	WHGFNCPTNCPARSYP	16	Hypothetical protein Acr_04g0004340 /Actinidia rufa/ GFY85696.1	100	1850.06	8.07	+2	31	+1.77	62	94
409	LCDHGDAESGCCL	13	Hypothetical protein GQ55_9G637500 /Panicum hallii var. hallii/ PUZ43130.1	100	1322.45	4.02	-2	46	+1.14	64	78
410	EACKESQGTEYCCSSKRA	18	Molybdenum cofactor sulfurase-like /Hibiscus syriacus/ XP_039001556.1	100	1980.17	6.29	0	27	+3.13	76	67
411	WFVPPAVKEPLAKLP	15	Unnamed protein product /Arabis nemorensis/ VVB04578.1	90	1692.08	8.59	+1	53	-0.59	12	11
412	WHFGFFASMAFHDSEM	16	Hypothetical protein DAI22_06g038550 /Oryza sativa Japonica Group/ KAF2925258.1	100	1947.17	5.15	0	56	+0.50	38	60
413	EYCSAKSAKPGVHCRSCALVNMYK	24	Hypothetical protein F8388_011173 /Cannabis sativa/ KAF4357435.1	100	2646.11	9.03	+4	41	+1.44	88	95
414	EENQPAGFGKYCPVYYRVMDVNQWW	25	Hypothetical protein EJB05_09923 /Eragrostis curvula/ TVU43450.1	100	3080.44	4.68	-1	36	+1.62	6	43
415	NFRALAVASEGCKMT	15	Uncharacterized protein At3g03773 /Spinacia oleracea/ XP_021845467.1	100	1597.87	8.22	+1	53	+1.19	35	30
416	WWDDEFYFYWGSFVVSWMFMWHW	23	Hypothetical protein CK203_039228 /Vitis vinifera/ RVW80336.1	100	3238.65	4.02	-2	60	-0.15	35	72
417	KCPNPAHGANHESEPGNHE	19	Putative pentatricopeptide repeat-containing protein At1g53330 /Nicotiana tabacum/ XP_016455768.1	77	2025.10	5.76	+1	15	+2.97	6	35
418	HCLGHDCTHDTKLAKAEF	18	Zinc finger A20 and AN1 domain-containing stress-associated protein 8-like /Ricinus communis/ XP_015571023.1	100	2026.27	6.26	+2	38	+1.91	35	69
419	WEETPTNPPDESYVEFAQ	18	Hypothetical protein Lal_00032985 /Lupinus albus/ KAF1898219.1	100	2139.22	3.45	-5	22	+2.53	2	3
420	WRCHAADDGESFNW	14	Flavodoxin /Macleaya cordata/ OVA07021.1	100	1693.77	4.54	-1	42	+2.88	11	45
421	RRPAELGGSAGGRKKVYT	18	Eukaryotic translation initiation factor 3 subunit A-like /Nicotiana tabacum/XP_016447681.1	89	1903.17	11.00	+4	22	+2.91	26	17
422	DNFSGNGSAASLVQPE	16	Uncharacterized protein LOC107773821 /Nicotiana tabacum/XP_016448725.1	71	1592.64	3.67	-2	31	+1.69	5	2
423	FHRATNSPGGAACGLDYAYMTMYN	24	Uncharacterized protein LOC104096292 /Nicotiana tomentosiformis/XP_009600942.1	89	2611.90	6.73	+1	37	+1.10	22	16
424	PLSLSVVPKLL	11	Uncharacterized protein LOC101488675 /Cicer arietinum/ XP_012573351.1	100	1165.48	9.18	+1	54	-1.40	26	47

425	MDNSVAGDLYD	11	rho GTPase-activating protein 7-like isoform X1 /Olea europaea var. sylvestris/ XP_022897942.1	100	1199.25	3.42	-3	36	+2.02	28	35
426	LVKNPSKKGHLNFLDPEL	18	Hypothetical protein AXF42_Ash021053 /Apostasia shenzhenica/ PKA48644.1	100	2049.40	8.51	+2	33	+1.43	11	19
427	CGCCSPCMFD	10	Cinnamyl alcohol dehydrogenase 5 /Camelina sativa/ XP_010432445.1	100	1065.28	3.80	-1	60	+0.07	84	85
428	EAVCGHLQAEGNEPG	15	Uncharacterized protein LOC105131193 isoform X2 /Populus euphratica/ XP_011032343.1	100	1510.60	4.24	-2	33	+1.37	3	9
429	MAHASGVCECFR	12	Uncharacterized protein LOC100825465 /Brachypodium distachyon/ XP_010229687.1	100	1310.53	6.49	+1	58	+1.10	66	80
430	LWEAQSNDGDPVTSSWVFW	19	ALTERED PHOSPHATE STARVATION RESPONSE 1-like /Panicum virgatum/ XP_039823540.1	89	2224.37	3.49	-3	42	+1.23	2	24
431	LVKENSTCGHSCEY	14	Putative late blight resistance protein homolog R1A-3 isoform X2 /Nicotiana attenuata/ XP_019246803.1	86	1569.72	5.40	0	28	+1.96	28	83
432	FMFTYDYGVNMAEGYTSSWRW	21	Hypothetical protein HPP92_016433 /Vanilla planifolia/ KAG0471887.1	89	2611.89	4.37	-1	38	+1.25	6	24
433	DEAGCAAATLDY	12	Uncharacterized protein LOC116208260 /Punica granatum/ XP_031397466.1	100	1199.25	3.49	-3	50	+1.04	21	9
434	WACKDGFEHGAWK	13	Endo-1,4-beta-xylanase A-like/[Nicotiana tabacum/ XP_016444878.1	86	1534.71	6.74	+1	46	+1.29	30	84
435	ERPPATPTSGNGTNPSFC	18	Transducin/WD40 repeat-like superfamily protein, putative isoform 3 /Theobroma cacao/ EOY29046.1	100	1832.96	6.09	0	16	+2.30	6	28
436	WRQGGAGYNHYFMAKLQDEY	20	B2 protein /Vitis vinifera/ RVX06931.1	100	2434.67	6.75	+1	30	+1.98	19	19
437	EEEWCDGGCSSSSTDCENMMCEYY	24	IQ-DOMAIN 1-like /Olea europaea subsp. Europaea/ CAA2992873.1	100	2758.90	3.30	-7	29	+2.52	33	55
438	DQACNLGTWLQLRNAGGDQY	20	Uncharacterized protein LOC106424377 /Brassica napus/ XP_013720592.1	100	2223.40	4.21	-1	35	+2.00	20	8.4
439	RSPDLPMLGRLVKLDPEL	18	Uncharacterized protein LOC110785344 isoform X2 /Spinacia oleracea/ XP_021845475.1	100	2049.46	6.12	0	38	+1.72	3	5
440	DTDGDHGTSACSSPTS	16	putative enoyl-CoA hydratase, mitochondrial /Ananas comosus/ OAY70229.1	100	1537.49	3.93	-2	12	+2.94	14	22
441	WRQGSPPAATSLCTGEYNLREPW	23	Hypothetical protein EZV62_010928 /Acer yangbiense/ TXG63934.1	100	2619.89	6.14	0	30	+2.01	2	2
442	SRPKGAAKLFFNPHLTKH	18	Probable prolyl 4-hydroxylase 12 isoform X2 /Nicotiana attenuata/ XP_019224442.1	75	2049.41	11.26	+6	33	+1.84	72	71
443	MHMQYDSYTACCKCTEFEAVKLWWW	25	AAA-ATPase /Vitis vinifera/ RVW75991.1	89	3160.66	5.43	0	52	+0.85	43	74
444	CAPVASWLGCAMDM	14	Uncharacterized protein LOC107818270 /Nicotiana tabacum/ XP_016499741.1	86	1454.76	3.80	-1	71	-0.91	49	44
445	RPEDVAHGCGSANESMNGK	19	Unnamed protein product /Miscanthus lutarioriparius/ CAD6256142.1	100	1959.10	5.45	0	26	+2.81	7	15

446	MFSMSLPNYVQFGPTSFHNMV	21	Uncharacterized protein LOC109236005 /Nicotiana attenuata/ XP_019257786.1	72	2434.83	6.49	+1	42	+0.30	9	22
447	WPDMQSGHCGPCDSHCEHEM	20	Pentatricopeptide repeat-containing protein At1g08070, chloroplastic-like /Asparagus officinalis/ XP_020273495.1	100	2286.49	4.70	-1	30	+2.23	53	65
448	FNEDPFRHDGPGPE	14	Hypothetical protein PVAP13_5NG064481 /Panicum virgatum/ KAG2586636.1	100	1613.66	4.31	-2	14	+3.53	7	14
449	SREAVMGSVLFVSDVDW	17	Hydroquinone glucosyltransferase-like/[Macadamia integrifólia/ XP_042505616.1	100	1897.13	4.03	-2	52	+1.05	2	3
450	DQNPVTPNGTNFPEGHS	17	WRKY transcription factor /Boehmeria nivea/ QQV37190.1	100	1810.85	4.35	-1	11	+2.66	2	4
451	DHNPYAQTGGGSSVAYP	17	WRKY transcription factor /Boehmeria nivea/ QQV37190.1	100	1720.77	5.08	0	17	+1.45	3	1
452	RHAYMYPCAECGGAQTLHRW	20	E3 ubiquitin-protein ligase sina-like protein 4 /Hordeum vulgare/ KAE8821833.1	100	2350.68	8.06	+3	40	+1.74	41	45
453	NYFCHKGEFNPPGNVYARC	19	Probable methionine--tRNA ligase isoform X2 /Cucumis melo/ XP_008456962.1	100	2216.48	8.04	+2	31	+1.88	44	88
454	WNMNKFHATGEESTPYMYPHL	21	Hypothetical protein KY290_028622 /Solanum tuberosum/ KAH0749390.1	89	2553.85	6.00	+1	28	+1.56	3	16
455	MWGGAEGSSMCPRLESAPAHHQY	23	Hypothetical protein PVAP13_6NG090700 /Panicum virgatum/ KAG2577307.1	100	2502.78	5.96	+1	34	+1.40	9	5
456	ETEHFSMYGSCAPQGVYWALYYM	23	Heterogeneous nuclear ribonucleoprotein 1-like isoform X2 /Zingiber officinale/ XP_042398937.1	100	2734.07	4.51	-1	39	+0.34	9	16
457	WYFYYGFSGGYGALSNAYTAHWFSN	25	Dof zinc finger protein DOF3.1-like /Phalaenopsis equestris/ XP_020571739.1	100	2930.14	6.74	+1	36	+0.14	17	30
458	NMQTFDPPDAWFH	13	Uncharacterized protein LOC110939553 /Helianthus annuus/ XP_022036800.1	100	1605.74	4.20	-1	38	+1.87	14	20
459	YYYDCHTGDGNGSCHDWT	18	Pentatricopeptide repeat-containing protein At1g71490-like isoform X2 /Durio zibethinus/ XP_022717502.1	100	2094.13	4.40	-1	16	+2.40	55	51
460	WVVVSPGAMTSCEWC	15	Protein FAR1-RELATED SEQUENCE 5 /Elaeis guineensis/ XP_010908720.1	100	1654.93	4.00	-1	60	-0.55	10	58
461	ARPCVYMFGYWTFRYMNCM	19	Hypothetical protein JHK87_010762 /Glycine soja/ KAG5035852.1	100	2439.93	8.86	+2	52	+0.77	47	73
462	YSRAPADGAQCTDLGDFCT	19	Transcription factor MYB36-like /Pyrus x bretschneideri/ XP_009337136.1	100	1991.13	3.93	-2	36	+1.97	11	1.5
463	CTQTCEVLSWAGSGGY	16	Hypothetical protein PVAP13_6KG124870 /Panicum virgatum/KAG2582271.1	100	1661.82	4.00	-1	37	+0.37	37	52
464	MMNVCEGCLCNMTEYNPRR	19	Hypothetical protein SASPL_119361 /Salvia splendens/ KAG6417208.1	100	2264.67	5.89	0	42	+2.38	15	57
465	GSVPDEKLKGKGLDPNK	17	Hypothetical protein KY290_019432 /Solanum tuberosum/ KAH0763359.1	100	1782.03	8.43	+1	17	+2.34	12	51
466	WRETPPTGEEYLME	14	Zinc finger protein ZAT10-like /Nicotiana attenuata/ XP_019240274.1	80	1737.90	4.09	-3	21	+2.63	7	20
467	WCNGLVQCGQAPYE	14	Nucleotide/sugar transporter family protein /Zea mays/ AQK72607.1	89	1567.75	4.00	-1	42	+0.50	28	50

468	QFCTNAQYCASGQGPEDYRHR	21	Hypothetical protein DKX38_013501 /Salix brachista/ KAB5545389.1	100	2431.60	6.73	+1	23	+3.26	47	34
469	KQKDNYLRNTTDSGGQYW	18	Hypothetical protein BUALT_Bualt17G0015600 /Buddleja alternifolia/ KAG8365858.1	100	2174.31	8.43	+1	11	+3.75	19	27
470	VLLLALRAAPGGGCKRDPN	19	Hypothetical protein C2845_PM03G33900 /Panicum miliaceum/ RLN35531.1	100	1921.29	9.50	+2	47	+0.92	8	13
471	ACDDCMCECMCGDACCQDAPNL	22	Uncharacterized protein LOC104219267 isoform X5 /Nicotiana sylvestris/ XP_009768223.1	77	2314.64	3.28	-5	59	+1.31	83	72
472	DMLPLGAGCTEGSDPLW	17	Hypothetical protein AXF42_Ash020531 /Apostasia shenzhenica/ PKA65601.1	100	1761.98	3.49	-3	41	+0.28	3	3
473	QPSQGPSLAKFCSDWMMMKSGQFW	24	Uncharacterized protein Pyn_33818 /Prunus yedoensis var. nudiflora/ PQQ01536.1	100	2778.23	8.20	+1	41	+0.93	47	43
474	HCGCPDAAGAGPSTWPPS	18	Hypothetical protein PVAP13_8NG256900 /Panicum virgatum/ KAG2557554.1	100	1710.86	5.08	0	33	+0.53	13	11
475	CQVPNSAPFGFPEPYCCEF	19	Hypothetical protein /Gossypium harknessii/ MBA0802613.1	100	2135.41	3.79	-2	42	+0.51	15	71
476	ESEVGGQGCLAVQDCPE	17	Disease resistance protein R3a-like protein /Solanum demissum/ ABV29166.1	100	1720.84	3.50	-4	35	+1.37	6	8
477	WWCHNQACDCCTHMSVWYC	19	Basic 7S globulin-like /Papaver somniferum/ XP_026451696.1	100	2376.72	5.97	+1	57	+0.77	69	87
478	WHPYYSDSNGNCGYYNWC	18	Hypothetical protein CK203_066540 /Vitis vinifera/ RVW61576.1	100	2229.34	5.08	0	22	+1.75	45	64
479	WYVKPGYMACASGGNGHYFAHYY	23	Hypothetical protein SASPL_124831 [Salvia splendens] KAG6412161.1	100	2642.95	8.14	+3	34	+0.14	60	51
480	RKVNFGYCGENTEAYFAYMQ	20	Chitin-binding, type 1 /Corchorus olitorius/ OMO96301.1	100	2391.66	6.13	0	35	+1.83	9	28
481	VNYMLQSDHTTCAFSCW	17	Hypothetical protein SEVIR_8G014400v2 /Setaria viridis/ TKV99051.1	100	2006.25	5.08	0	47	+0.97	24	50
482	MACQFGFSGAWY	12	Uncharacterized protein LOC107767909 isoform X1 /Nicotiana tabacum/ XP_016442505.1	86	1367.56	5.27	0	58	-0.69	41	50
483	DPCSPSEGGSYWPTNEF	17	Uncharacterized protein LOC104219686 /Nicotiana sylvestris/ XP_009768696.1	87	1872.94	3.57	-3	17	+1.96	4	6
484	HWYFDVVCTAPFANNCSWRVD	21	F-box protein /Cucurbita argyrosperma subsp. Sororia/ KAG6576809.1	89	2530.82	5.21	0	52	+1.30	25	62
485	DNPGCHEGGS	10	Mucin-2-like /Nicotiana tabacum/ XP_016444188.1	100	971.95	4.35	-1	10	+2.61	27	55
486	EARPSVYDNLSQDPL	15	Hypothetical protein CR513_05326 /Mucuna pruriens/ RDY10195.1	100	1703.83	4.03	-2	26	+2.83	2	<1
487	CHPTNGYGKWGSYMYVMSGCQKN	23	Histidine-containing phosphotransfer protein 2-like /Triticum dicoccoides/ GEW24004.1	100	2611.97	8.79	+3	26	+1.17	39	81
488	AWLGLHDGFEATAFVPLFY	19	Hypothetical protein HPP92_008259 /Vanilla planifolia/ KAG0486164.1	100	2154.45	4.35	-1	57	-0.76	<1	1
489	MKRDDNRLPAASNYNDWNQN	20	Putative disease resistance RPP13-like protein 1 /Beta vulgaris subsp. Vulgaris/ XP_010670863.1	100	2422.57	5.79	0	25	+4.52	22	12

490	HYETDCDLCWAMSMDMDM	18	Probable cysteine protease RDL5 /Camelina sativa/ XP_010455537.1	100	2197.48	3.71	-4	50	+1.74	45	61
491	FFAYYNKCGFKESYMHTKCW	20	Maturase K /Asteraceae sp. MP 804/ QHB80043.1	100	2553.95	8.76	+3	40	+1.11	35	64
492	WWPGTGSVLFCCMKYRGHSDKDFHWW	26	Probably inactive leucine-rich repeat receptor-like protein kinase IMK2 /Zingiber officinale/ XP_042469099.1	100	3230.69	8.05	+3	42	+1.16	24	80
493	YYEQAGGHNACRLEEAPYNMW	21	Hypothetical protein HU200_000043 /Digitaria exilis/ KAF8784002.1	100	2502.72	4.75	-1	33	+1.95	15	34
494	FVNGNSQEGPED	12	Unnamed protein product /Microthlaspi erraticum/ CAA7046219.1	100	1292.28	3.57	-3	16	+2.97	7	4
495	ALLPVLGVT	9	Hypothetical protein C4D60_Mb10t03460 /Musa balbisiana/THU52387.1	89	882.11	5.57	0	66	-2.55	10	7
496	CHWFDAPVFAAGAAPGLGSGCCC	23	Hypothetical protein /Tanacetum cinerariifolium/ GFD53856.1	100	2240.57	5.08	0	60	-0.80	51	71
497	YYSKDEANLVTMGGSTCADMWWW	23	Beta-hexosaminidase 2-like /Nicotiana tabacum/ XP_016502529.1	75	2715.02	4.03	-2	43	+0.92	14	55
498	EDCHAMGCCHMGCSEHDQHY	20	Receptor-like protein EIX2 /Ziziphus jujuba/ XP_024930060.1	100	2293.50	5.14	0	35	+2.26	79	77
499	WLGDGAWGYSWRVNW	15	Uncharacterized protein LOC104216935 isoform X3 /Nicotiana sylvestris/ XP_009765403.1	87	1853.03	5.84	0	46	+0.72	30	85
500	NHVFFMATFLMDAADPCWQH	20	Uncharacterized protein LOC107780274/[Nicotiana tabacum/ XP_016456293.1	70	2381.73	5.05	0	60	+0.49	20	26
501	EMMDDFDGCYENPYASMCM	19	Protein MODIFIER OF SNC1 1 /Nicotiana tomentosiformis/ XP_009595597.1	80	2252.52	3.33	-5	42	+1.70	39	54
502	EDQVAQCSPGETTQV	15	Transcription factor bHLH143-like /Nicotiana tomentosiformis/ XP_009597068.1	80	1591.67	3.57	-3	26	+2.35	3	3
503	WGHKMYDNLSDKPL	14	Transmembrane 9 superfamily member 12 /Vitis vinifera/ XP_002262879.3	100	1703.93	6.75	+1	28	+1.99	14	26
504	NPVVKMGRGYGWDCNSPK	18	Heterogeneous nuclear ribonucleoprotein 1-like /Nicotiana tomentosiformis/ XP_009588880.1	100	2008.30	9.20	+2	27	+1.92	14	75
505	KAVLLLTKLLRRLV	14	Uncharacterized protein LOC104094522 /Nicotiana tomentosiformis/ XP_009598773.1	80	1636.14	12.02	+4	64	+0.29	40	44
506	LDRSPALVGLMEANMFW	17	Hypothetical protein CDL15_Pgr027025 /Punica granatum/ OWM71374.1	89	1950.30	4.37	-1	58	+0.41	4	6
507	VNYCGSQNYLSYMGRGHKVEHMF	23	Ring-h2 finger protein atl56 /Nicotiana attenuata/ OIS97785.1	100	2721.08	8.15	+3	30	+1.64	25	46
508	WWVLRQCSPNCSQYGSGDEVWW	22	CST complex subunit CTC1 isoform X3 /Cucumis sativus/ XP_031740669.1	100	2686.96	4.37	-1	40	+1.44	15	62
509	FHRAVTQQGFSANSEAYMLMC	21	Hypothetical protein EZV62_000959 /Acer yangbiense/ TXG72380.1	100	2391.72	6.74	+1	47	+1.25	12	15
510	CPPADGNAGGSGFDTNW	17	Hypothetical protein CDL12_10043 /Handroanthus impetiginosus/ PIN17296.1	100	1665.71	3.56	-2	29	+1.33	22	29
511	WVDTGHMEVCGQWY	14	Uncharacterized protein LOC116250854 /Nymphaea colorata/ XP_031480673.1	90	1710.90	4.35	-1	42	+0.72	13	49

512	WQEWHCRDYFGPFTACMFYRP	21	Unnamed protein product /Spirodela intermedia/ CAA2632489.1	100	2741.11	6.73	+1	42	+1.76	20	53
513	PLEEDGPQDMDDRGFLN	17	Hypothetical protein F2Q69_00007008 /Brassica cretica/ KAF3505550.1	100	1948.05	3.66	-5	23	+3.44	10	14
514	CWSCDSACCEEESGSCFEC	19	Hypothetical protein FNV43_RR17798 /Rhamnella rubrinervis/ KAF3439520.1	100	2078.23	3.45	-5	47	+1.77	63	84
515	EFYAVRWGPNLGSQLYFTDGCNDSY	25	Hypothetical protein EJB05_39829 /Eragrostis curvula/ TVU16275.1	100	2903.13	4.03	-2	32	+1.58	4	2
516	WYSWQSQNDECMSNCDQ	17	Uncharacterized protein C2845_PM02G42340 /Panicum miliaceum/ RLN15448.1	100	2124.21	3.49	-3	29	+3.23	25	44
517	FCKGTSQNQYLPMEYDHTTGEVGHWHR	27	Uncharacterized protein LOC122065263 isoform X3 /Macadamia integrifolia/ XP_042484996.1	100	3222.52	6.27	+2	22	+2.41	4	14
518	YRPLKCGGQCSGGQWAPMC	19	Hypothetical protein Prudu_018566 /Prunus dulcis/ BBH06817.1	100	2042.39	8.68	+2	36	+0.84	89	72
519	LVKTAKKEGGDPNLPT	16	Hypothetical protein Leryth_013224 /Lithospermum erythrorhizon/ KAG9133412.1	100	1667.92	8.50	+1	25	+1.64	10	11
520	SEHCGFDACNSCTNGFDEE	19	S-adenosyl-L-methionine-dependent tRNA 4-demethylwyosine synthase-like isoform X2 /Carex littledalei/ KAF3321599.1	100	2065.10	3.83	-4	31	+2.72	50	63
521	RSCTCSVQSNEPS	13	Hypothetical protein IFM89_036966 /Coptis chinensis/ KAF9595077.1	100	1397.50	5.99	0	23	+3.34	17	29
522	YMAYHTLCTSRFGPFTQFEWWD	22	Hypothetical protein CR513_17562 /Mucuna pruriens/ RDX99387.1	100	2787.12	5.32	0	40	+1.23	2	11
523	RWWMAWASHYFMDYGCTPRWHWW	23	ABC transporter C family MRP4-like /Panicum virgatum/ XP_039826103.1	100	3160.60	8.21	+3	52	+1.15	39	78
524	MWWPRTVHMWETCGHPCDCMKYY	23	Integrase, catalytic region, zinc finger, CCHC-type, peptidase aspartic, catalytic /Tanacetum cinerariifolium/ GFB83544.1	100	2961.48	6.68	+2	43	+1.21	50	72
525	ALRFSRNSCGDDGCPNDQ	18	Hypothetical protein Prudu_007133 /Prunus dulcis/ BBG97876.1	100	1955.06	4.43	-1	27	+3.74	37	20
526	YWYQGGNDCFPHMFLRPAVQGHWW	24	CCAAT-binding factor, conserved site-containing protein /Cynara cardunculus var. scolymus/ KVH97331.1	100	2996.37	6.91	+2	41	+0.86	13	42
527	SRLTAWAVKRFKYKVDKPP	19	Hypothetical protein /Gossypium davidsonii/ MBA0629335.1	100	2290.74	10.56	+5	36	+2.36	62	58
528	FMQPRAMYAGDPPDTSAYDWHW	22	Unnamed protein product /Miscanthus lutarioriparius/ CAD6231170.1	100	2642.90	4.41	-1	36	+1.76	11	10
529	KLEMMPPGKEETPVELYF	18	Hypothetical protein AQUCO_03000398v1 /Aquilegia coerulea/ PIA37829.1	100	2138.52	4.49	-2	33	+1.03	8	25
530	RRQGAHCNYRDDFAMYDEC	19	Putative F-box/FBD/LRR-repeat protein At4g03220 /Manihot esculenta/ XP_021602734.1	100	2350.54	5.43	0	31	+4.33	46	28
531	YYRKFAGSASNTHMGYMATALPCCFMWYW	29	Uncharacterized protein LOC109235773 isoform X4 /Nicotiana attenuata/ XP_019257564.1	88	3458.02	8.79	+3	48	+0.34	49	62
532	VNASGSCCDRQFQASSMASW	20	Hypothetical protein G4B88_009439 /Cannabis sativa/ KAF4365716.1	100	2135.33	5.79	0	45	+1.88	25	22

533	MMAHASSSNGMCMGCCCCDEQ	21	Uncharacterized protein LOC110416582 isoform X2 /Herrania umbratica/ XP_021284271.1	100	2199.56	4.35	-1	52	+1.01	65	58
534	ERKGPTCDFTMNPAEH	16	Hypothetical protein GH714_021050 /Hevea brasiliensis/ KAF2291257.1	100	1833.02	5.45	0	25	+3.11	3.5	12
535	WSSTEFETVRCDKVPL	16	Uncharacterized protein LOC109207559 /Nicotiana attenuata/ XP_019226043.1	89	1897.13	4.68	-1	37	+2.19	0.6	2.2
536	VLNAKPPALLGNKFLDPN	18	Unnamed protein product /Digitaria exilis/ CAB3500566.1	100	1921.27	8.56	+1	44	+0.47	22	31
537	DTWPYARKLGTYCGGSFWYY	20	Putative solute carrier family 13 /Helianthus annuus/ KAF5755537.1	100	2434.71	8.14	+1	30	+0.99	35	35
538	FPGASNVTKYRGCVAGWH	18	Probable 2-oxoglutarate-dependent dioxygenase At3g50210 isoform X2 /Nicotiana tomentosiformis/ XP_009611630.1	70	1950.20	9.31	+3	38	+0.93	73	92
539	WFTMLDNEDPQANTGSCDECD	21	Hypothetical protein SADUNF_Sadunf03G0076800 /Salix dunnii/ KAF9685653.1	89	2391.49	3.25	-6	33	+2.76	27	17
540	TPVLLGAVL	9	Putative late blight resistance protein homolog R1A-3 /Nicotiana sylvestris/ XP_009776290.1	89	882.11	5.19	0	66	-2.55	11	7.5
541	WEYAVPHEQPQRH	13	Uncharacterized protein LOC107823884 /Nicotiana tabacum/ XP_016506072.1	88	1676.81	6.00	+1	23	+3.14	13	29
542	CDGRDGYNSLLWFNEDPHVHQ	21	3-phosphoinositide-dependent protein kinase 2 /Lactuca sativa/ XP_023762677.1	100	2502.66	4.64	-1	28	+2.72	5.2	7.7
543	MNDNGPDECDEGQGSMWTYF	20	Hypothetical protein MtrunA17_Chr8g0346791 /Medicago truncatula/ RHN39708.1	90	2296.40	3.33	-5	25	+2.53	20	31
544	KHVYMMCMFQVHSGCGLSWAYEYW	24	Uncharacterized protein LOC107832630 isoform X1 /Nicotiana tabacum/ XP_016515976.1	87	2957.47	6.90	+2	50	+0.02	50	64
545	LALAVVTVPGLL	12	Heat shock protein 70 family /Trema orientale/ PON92857.1	100	1165.48	5.52	0	75	-2.81	12	18
546	SREPKASTFTESGDFEPR	18	Uncharacterized protein LOC109229364 /Nicotiana attenuata/ XP_019250330.1	77	2041.16	4.87	-1	16	+3.95	2	1
547	LSTQTPGELTSCECW	15	Putative glycosyltransferase 7 /Nicotiana tomentosiformis/ XP_009624871.1	82	1654.83	3.79	-2	33	+1.20	22	43
548	MQTAMPPTPQHYMAFKY	17	Hypothetical protein CFC21_037229 /Triticum aestivum/ KAF7024971.1	89	2042.42	8.28	+2	35	+0.76	52	58
549	EYCYTCDPECGCSCGNGDEYC	21	Uncharacterized protein LOC104759515 /Camelina sativa/ XP_010480729.1	82	2314.499	3.39	-5	28	+1.92	88	84
550	DNFWHWCDDEMWFMC	15	ATP-dependent Clp protease proteolytic subunit 4 /Hibiscus syriacus/ KAE8702811.1	100	2065.324	3.84	-3	60	+1.60	40	66
551	NLMDPSNGNWMCWACGAMWY	20	Zinc finger Ran-binding domain-containing protein 2-like /Nicotiana sylvestris/ XP_009773357.1	80	2350.735	3.80	-1	55	+0.25	30	66
552	HHFYPVCACQDGNCVGCEMEDC	22	Uncharacterized protein LOC110617446 [Manihot esculenta] XP_021615906.1	100	2460.785	4.30	-2	45	+1.32	85	97
553	WWMRNHGPGDEGYMYAYFK	19	Hypothetical protein GUJ93_ZPchr0013g36931 /Zizania palustris/ KAG8097884.1	100	2408.704	6.75	+1	31	+1.61	33	56

554	WMNSCCGQELRPTGEMQTFQR	21	Ultraviolet-B receptor UVR8 /Morella rubra/ KAB1217236.1	100	2502.867	6.13	0	33	+2.66	33	51
555	MMDPQPGNAGVAYEDCGCCGSCDHWHC	27	GTPase-activating protein gyp7-like isoform X1 /Nicotiana sylvestris/ XP_009798405.1	70	2887.238	4.21	-2	40	+1.22	80	84
556	GMWWCQSDMEMTPETFCEWEWWH	23	Hypothetical protein Lal_00006362 /Lupinus albus/ KAF1875732.1	100	3036.426	3.90	-4	47	+1.28	32	66
557	LHSGEGSTCYFFKTNPCCCGTWNCT	25	Hypothetical protein ES288_A01G214900v1 /Gossypium darwinii/ TYH31981.1	100	2760.127	6.71	+1	36	+1.00	98	100
558	LWHPSTSGFGPCHVFKP	17	Unnamed protein product /Brassica napus/ CAF2167626.1	100	1897.188	8.24	+3	35	+0.22	28	72
559	RHYTPSCPMCGWRLQSRCHHDMYHN	25	Hypothetical protein KY289_023739 /Solanum tuberosum/ KAH0669246.1	100	3116.572	8.68	+6	28	+3.08	61	66
560	DPEHEALGEWLFYGAFTLGYYQ	22	Hypothetical protein MANES_08G113800v8 /Manihot esculenta/ KAG8649633.1	100	2606.835	4.00	-3	36	+0.58	1	1
561	WLRGYCAEGACYFNQACWWFK	21	Protein kinase-coding resistance protein /Nicotiana repanda/ ACO25602.1	100	2603.005	7.94	+1	57	+0.51	45	79
562	CFWAEPENGQHARVLLEREW	20	Probable protein phosphatase 2C 39 /Hevea brasiliensis/ XP_021682399.1	100	2470.759	4.91	-1	45	+2.32	2	12
563	MFSFFHCQGLTFYSGPMHFHHFFWWH	26	Uncharacterized protein LOC109710698 /Ananas comosus/ XP_020089022.1	100	3362.877	6.95	+5	50	0	45	73
564	WECVANGYWPVTMAKP	16	Protein TIFY 3B-like /Populus euphratica/ XP_011002823.1	100	1852.166	5.99	0	50	+0.04	19	79
565	WYYCDMFSQAPRMLQEYGYNYWWH	24	RNA-binding protein 38 /Helianthus annuus/ XP_021987145.1	100	3238.64	5.32	0	37	+1.38	19	44
566	YNMECFRWWWEETDHTQAVCDR	22	Uncharacterized protein LOC112524783 /Cynara cardunculus var. scolymus/ XP_024990503.1	100	2906.196	4.50	-2	40	+3.14	10	54
567	MAYANMCFFNR	11	Uncharacterized protein LOC104246523 /Nicotiana sylvestris/ XP_009800636.1	100	1367.642	7.98	+1	63	+1.16	40	58
568	WYVRETTFYKECHAMQYDYWHW	22	WAT1-related protein At3g28050-like isoform X2 /Nicotiana tomentosiformis/ XP_018626063.1	100	3043.393	6.01	+1	36	+1.99	22	59
569	AETAQGWSGCGGDSDPVQ	18	Hypothetical protein SASPL_121019 /Salvia splendens/ KAG6418814.1	100	1764.806	3.49	-3	27	+1.64	1	3
570	WKCGSTPAPRKYCTCVAKMW	20	Protein DJ-1 homolog B /Zea mays/ ACN35036.1	100	2316.814	9.42	+4	45	+1.03	96	96
571	RLCFCGLDWFYETDFDVALVVDE	23	Hypothetical protein A4A49_26629 /Nicotiana attenuata/ OIT34153.1	82	2756.116	3.66	-5	56	+0.98	3	5
572	FVGDAHKPNALRTV	14	WD repeat-containing protein 76 /Nicotiana attenuata/ XP_019250418.1	80	1524.742	8.75	+2	42	+1.60	14	12
573	YYRMLMQQGSGPGFAHFVDFYFM	23	Peroxidase 64 /Capsella rubella/ XP_006282231.1	100	2793.251	6.74	+1	43	+0.46	30	38
574	LPWYDCCMSNVTLGSAKAQH	20	Probable polygalacturonase /Nicotiana tabacum/ XP_016472075.1	82	2224.569	6.72	+1	45	+0.74	40	35
575	WWCMECEFPNANGFMCN	17	WD repeat-containing protein 48-like isoform X3 /Zingiber officinale/ XP_042383476.1	100	2082.42	3.79	-2	58	+0.68	31	72
576	MWYTAHAGCPVDMEQGFEDRR	21	Hypothetical protein IFM89_019488 /Coptis chinensis/ KAF9589172.1	100	2499.799	4.75	-1	38	+2.52	8	11

577	DDCDNCNCCGGGHCCEFQDFW	21	Hypothetical protein CK203_045944 /Vitis vinifera/ RVW91772.1	100	2371.56	3.71	-4	42	+2.20	84	90
578	YYALGPDSMNESCMHKL	17	Transposase (putative), gypsy type /Tanacetum cinerariifolium/ GEV99441.1	100	1959.254	5.32	0	35	+1.22	17	16
579	PYNVACGSSNNGWLMAFYHNW	21	traB Domain-containing protein isoform X2 /Nelumbo nucifera/ XP_010278527.1	100	2431.699	7.11	+1	42	+0.59	15	76
580	EFWKAERCVWMDTVFHEMW	19	Hypothetical protein /Tanacetum cinerariifolium/ GEW65934.1	100	2530.937	4.83	-1	57	+1.47	12	60
581	FYQNLQNSFDFMCGPFTDHYWRWL	24	Putative F-box protein PP2-B12 /Phoenix dactylifera/ XP_008789432.1	100	3116.494	5.21	0	41	+1.52	3	8
582	RDWNYCSSDCTGCPDDWH	18	Hypothetical protein M569_06733 /Genlisea aurea/ EPS68039.1	100	2160.271	4.13	-2	27	+3.39	42	76
583	WWRRWLFTYFTCCFTCVMDRHWW	23	Cytochrome c-type biogenesis CcmH-like mitochondrial protein /Nicotiana tomentosiformis/ XP_033512146.1	100	3230.823	8.71	+3	60	+1.31	34	81
584	FYYYVSTFFSFTPSGYTWW	19	Hypothetical protein C3L33_07951 /Rhododendron williamsianum/ KAE9460160.1	100	2449.704	5.52	0	36	-0.16	9	31
585	AYMCQDPGPNSDTFPEFYTTHCKKMFRF	28	Probable membrane-associated kinase regulator 4 /Cucumis melo/ XP_008461610.1	89	3362.836	6.78	0	32	+2.02	28	26
586	KCALHASCHCHHEQMDLDW	19	Zinc finger MYM-type protein 1-like /Nicotiana attenuata/ XP_019250900.1	100	2264.577	5.99	+2	47	+1.86	49	68
587	EQCCCCQDPPDFAMHCNRW	19	Hypothetical protein D1007_32220 /Hordeum vulgare/ KAE8793213.1	100	2286.631	4.54	-1	47	+2.40	94	96
588	TYWTMNYMVCAPCCEQCCC	19	Hypothetical protein Ahy_A03g014026 isoform B /Arachis hypogaea/ RYR67640.1	100	2252.738	4.00	-1	57	+0.20	86	92
589	SPNTGSDFTGTATAHSLEEC	20	Hypothetical protein CXB51_033494 /Gossypium anomalum/ KAG8476579.1	90	2025.096	4.13	-2	25	+1.97	3	13
590	RVPPTTAGPAGDPDMESMDGNYHS	24	Protein RER1B-like /Daucus carota subsp. sativus/ XP_017256393.1	89	2502.686	4.22	-2	20	+2.33	4	2
591	HWFPWVANLPNNHHDPQPDRE	21	Zinc-finger homeodomain protein 9-like /Prunus mume/ XP_008230766.1	89	2606.806	5.73	+1	28	+2.86	8	19
592	HYVQYMFYTYGARSRTGDCKMRYFW	25	Protein FAR1-RELATED SEQUENCE 4-like /Nicotiana attenuata/ XP_019258190.1	100	3230.704	9.43	+4	32	+2.25	28	41
593	YQSFGSMDCGMYHAMQDDHVACMTHWCEN	29	Uncharacterized protein LOC108943744 /Nicotiana tomentosiformis/ XP_033509889.1	73	3398.816	4.62	-1	41	+1.59	54	39
594	SYHHLGTMFQQGPCSRPPDGYGDPEE	26	Uncharacterized protein LOC104235323 /Nicotiana sylvestris/ XP_009787358.1	80	2906.127	4.72	-1	15	+2.33	6	2
595	WHNHFTVSPENCSRMWWWWWWYYYYWDFKMDHKEETKSGYFH	41	NO MATCH	--	5619.239	6.43	+3	36	+1.92	38	61
596	WFDANFTGGPKAVHGS	16	Unnamed protein product /Brassica rapa/ VDD00434.1	100	1690.833	6.74	+1	37	+0.79	16	49
597	HRRWWYTFFSFHSCHGYMY	19	Uncharacterized protein LOC112502498 isoform X9 /Cynara cardunculus var. scolymus/ XP_024962205.1	100	2611.956	9.20	+5	36	+1.86	43	72

598	ARFHFYAFMGYGYGEFGNWNVWHW	24	Probable receptor-like protein kinase At2g23200 /Coffea eugenioides/ XP_027177844.1	100	3043.382	6.96	+2	45	+0.50	26	72
599	KYYGYMAVPGAMFPTECYVWWH	22	Hypothetical protein KY284_005023 /Solanum tuberosum/ KAH0719993.1	100	2700.159	6.74	+1	45	-0.32	34	58
600	FNWLCSGPVSEYCRTNAMYFYY	22	Hypothetical protein FH972_024678 /Carpinus fangiana/ KAB8360946.1	89	2715.089	5.99	0	40	+0.91	6	32
601	KLEGYATAGMGMMETFSGFTHRK	23	Hypothetical protein /Tanacetum cinerariifolium/ GEY06412.1	100	2550.962	8.50	+2	34	+1.31	46	43
602	PPMGTSVVDNEERDSHRV	18	Protein ULTRAPETALA 1-like /Nicotiana tomentosiformis/ XP_018628608.2	80	2025.180	4.75	-1	22	+3.67	<1	<1
603	QLESGGCESWQLPGSVVHKL	20	Hypothetical protein Bca52824_009017 /Brassica carinata/ KAG2326289.1	100	2154.431	5.40	0	35	+0.79	2	5
604	YFHCVRGDGGQLNHEMGFCCERR	23	Hypothetical protein KY289_005485 /Solanum tuberosum/ KAH0722441.1	100	2715.082	6.90	+2	34	+2.77	84	96
605	DWWDFDKVHGYCQHWNFWYQAMCDQCMNAFFNRF	34	NO MATCH	--	4440.981	5.20	0	50	+1.76	22	57
606	VLKFGLGADERHKRQLLRPG	20	Hypothetical protein GQ55_9G637300 /Panicum hallii var. hallii/ PUZ43127.1	100	2290.698	10.90	+4	35	+2.51	25	20
607	LVASLPRL	8	Hypothetical protein F2Q68_00011472 /Brassica cretica/ KAF2599243.1	100	868.09	9.75	+1	62	-0.28	3	3
608	WWVETAHCPGLNEVPT	16	Hypothetical protein A4A49_63951 /Nicotiana attenuata/ OIT20420.1	73	1839.064	4.51	-1	43	+0.52	9	56
609	SMKTVAFSDNYFYSEDPQSNAT	22	Zinc finger CCCH domain-containing protein 18 isoform X2 /Ricinus communis/ XP_002534335.1	89	2502.653	4.03	-2	27	+2.34	3	1
610	SYDFMWRSGGTMFASDDRTWN	21	Hypothetical protein HYC85_023237 /Camellia sinensis/ KAF5938978.1	100	2530.743	4.43	-1	33	+2.81	9	20
611	WYRLADYPDGSDFYGPWHY	19	Hypothetical protein D1007_50498 /Hordeum vulgare/ KAE8776807.1	100	2408.573	4.41	-1	26	+1.76	22	26
612	SLTDGADTDDAEGACPLN	18	Uncharacterized protein DS421_5g159640 /Arachis hypogaea/ QHO43068.1	100	1764.802	3.28	-5	33	+2.13	20	7.9
613	KRSTTFCKTPTQYMYRRWRWWWPVRNYDERGEYGMYELVR	40	NO MATCH	-	5297.057	9.89	+5	27	+3.45	31	67
614	WRCAGYCTGGVANYWW	16	Unnamed protein product /Miscanthus lutarioriparius/ CAD6255579.1	100	1893.14	8.05	+1	50	+0.27	69	90
615	FTQNRMSCYKACCDYRVLYFHHWW	24	Hypothetical protein SORBI_3001G400200 /Sorghum bicolor/ OQU92740.1	100	3158.664	8.64	+4	45	+1.85	54	83
616	CNFHSAPAQRCNPGSSLHW	19	Hypothetical protein I3760_11G039800 /Carya illinoinensis/ KAG2679194.1	100	2112.342	8.09	+3	36	+1.89	13	43
617	EESPSHANTPCMYNHVAYCD	20	Elicitor-responsive protein 3-like isoform X1 /Triticum dicoccoides/ XP_037450168.1	100	2268.453	4.63	-1	30	+2.1	12	39
618	ESDVGDRNDFYSLCEFRPDQS	21	Uncharacterized protein DS421_12g367390 /Arachis hypogaea/ QHO23882.1	100	2479.585	3.96	-4	23	+3.98	8.9	3
619	THVSMARTKNADSPPR	16	Histone H3.3-like /Camellia sinensis/ XP_028126728.1	100	1767.985	10.83	+3	25	+3.58	2	1
620	WCWCTNGMHACCYDNYH	17	Transcription factor MYB108-like /Nicotiana attenuata/ XP_019267622.1	70	2107.387	5.97	+1	47	+1.13	77	89

621	NDDNDCRCSGLGNWHMGCCTGCSSFTC	27	Hypothetical protein BVRB_011770 /Beta vulgaris subsp. Vulgaris/ KMS95166.1	100	2887.194	4.41	-1	37	+2.11	97	99
622	GWYQCGTSNPAYLEGRYF	18	Receptor-like protein 2 /Nicotiana attenuata/ XP_019241406.1	100	2112.312	5.99	0	27	+1.34	16	13
623	HRFSYMCFVAQVLNKDYCSCCKF	23	E3 ubiquitin-protein ligase COP1-like [Olea europaea var. sylvestris]	55	2793.331	8.50	+3	52	+1.19	84	96
624	KHYSCTRHGYCLACYKRWF	19	Uncharacterized protein G2W53_019959 /Senna tora/ KAF7828795.1	89	2422.84	9.36	+6	36	+2.09	93	92
625	LDRKPVAPGVGCRKLFF	17	Hypothetical protein CFC21_037841 /Triticum aestivum/ KAF7025682.1	100	1903.322	10.05	+3	47	+1.22	72	76
626	DPPLTTCAGSWDLETGAFTPNERQ	24	Transcription factor GAMYB-like /Nicotiana attenuata/ XP_019251987.1	71	2606.814	3.92	-3	29	+2.07	1	<1
627	VLWLSMWSCHMSHSMYHFC	19	Ubiquinol-cytochrome-c reductase complex assembly factor 1-like isoform X1 /Nicotiana attenuata/ XP_019246083.1	80	2385.869	6.98	+3	57	-0.17	38	57
628	DWTEYHHTSTGPSAQQCSFDLRMNGYAYEK	30	Hypothetical protein BUALT_Bualt01G0174400 /Buddleja alternifolia/ KAG8391308.1	100	3523.781	5.31	0	23	+2.58	6	4
629	WQNCPAGCTFPS	12	Disease resistance protein TAO1-like /Eucalyptus grandis/ XP_039160603.1	100	1310.478	5.51	0	41	+0.62	56	75
630	RWTWHCQAYGFENTSGCMNRHR	22	Hypothetical protein D1007_38938 /Hordeum vulgare/ KAE8787161.1	100	2741.055	8.96	+4	31	+3.27	32	92
631	FCQVEQEAGGHSAPMQHPFMVSGGPMPWR	29	Hypothetical protein BHM03_00021745 /Ensete ventricosum/ RZR93290.1	100	3199.675	6.00	+1	37	+1.00	22	26
632	DFNMWASGGCNEYRTPMLLGHDDEF	25	Probable pectate lyase 16 /Medicago truncatula/ XP_003629507.2	100	2906.192	4.10	-3	36	+2.00	5	7
633	WMWDFVLGHNLPEYECHSNCGSPMAAMPFYN	31	NO MATCH	-	3648.171	4.63	-1	45	+0.61	8	32
634	DLGADPATAYCLAVRW	16	Uncharacterized protein LOC104216713 /Nicotiana sylvestris/ XP_009765130.1	85	1721.958	4.21	-1	56	+0.58	6	4
635	PDMVFMVTHWYMKTSCFDNCM	21	Hypothetical protein CJ030_MR1G019998 /Morella rubra/ KAB1227542.1	89	2587.108	5.22	0	52	+0.69	47	58
636	SMCFGGTALQEVKSDCTRFWK	21	Cation efflux family protein /Striga asiatica/ GER52782.1	100	2394.777	7.78	+1	42	+1.57	53	60
637	WWCDDTCGPCGAVSFCEYDF	20	Uncharacterized protein LOC104245614 /Nicotiana sylvestris/ XP_009799536.1	100	2304.55	3.37	-4	50	+0.78	43	63
638	MTFFYDAQNVTPMYSPY	17	Hypothetical protein /Antirrhinum hispanicum/ CAC33015.1	100	2075.353	3.80	-1	35	+0.78	6	23
639	NRRNSTEEGSSGCAWWWWWNMYGYECKVWCFE	32	NO MATCH	-	4052.485	4.95	-1	40	+1.99	18	86
640	WHWSMCNTYACFHRWWRWWWWWEFLLGDRSCPSAQTPWY	39	NO MATCH	-	5253.979	7.97	+3	51	+1.21	38	64
641	WWPYFFDMTDGCCTWCDDDYFEWYY	25	Uncharacterized protein LOC104237476 /Nicotiana sylvestris/ XP_009789931.1	75	3358.676	3.21	-6	44	+1.22	31	58
642	FNGCMGHEGMPL	12	Hypothetical protein HHK36_029865 /Tetracentron sinense/KAF8378522.1	100	1292.529	5.24	0	41	+0.11	46	74

643	QRVVCGEQQYSYHWWVRMCE GHYRE	25	Uncharacterized protein LOC104213309 isoform X5 /Nicotiana sylvestris/ XP_009761094.1	78	3230.626	6.91	+2	32	+2.85	51	85
644	QQNGCCSVADCKHALRQNNY FATYWWETEVPSPWHLQ	37	NO MATCH	-	4411.89	6.01	+1	37	+1.84	10	45
645	WWNWCYTHMWSQMFVAAGY DMMWCNSRR	28	Hypothetical protein FXO37_04044 /Capsicum annuum/ KAF3679087.1	100	3648.244	8.05	+2	53	+1.3	26	68
646	PMWLMGMVQYTFHPFNNEGG NYYRY	25	Alpha carbonic anhydrase 8-like /Nymphaea colorata/ XP_031474278.1	100	3116.559	7.16	+1	32	+1.11	10	34
647	YDEDMSCCCSLMSQGYMQW W	20	Hypothetical protein A4A49_61228 /Nicotiana attenuata/ OIT36359.1	77	2466.827	3.49	-3	45	+1.21	44	53
648	DWAVSSSGDKVTYMMAYWKF NSFHWW	26	Hypothetical protein COLO4_17480 /Corchorus olitorius/ OMO92567.1	100	3230.627	6.74	+1	46	+0.91	10	61
649	FFGCTEFDFGPDHGNRPTHEFQ E	23	Uncharacterized protein LOC115690741 /Syzygium oleosum/ XP_030473067.1	81	2714.876	4.49	-2	26	+2.62	6	21
650	WPFPAVSAGLYNCAGRSLDPS CCNYT	26	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial-like /Nicotiana tabacum/ XP_016456219.1	75	2793.161	5.81	0	42	+0.75	58	69
651	HWYDCNGQAGLGPGLHRWW WFWWWWWWWWWFYLNGY NGDDDSWWW	45	NO MATCH	-	6182.785	4.54	-1	51	+0.48	43	64
652	WYQFMAQDVWYYAGAELRD VP	21	Hypothetical protein FXO37_27845 /Capsicum annuum/ KAF3631639.1	100	2608.921	4.03	-2	47	+1.01	5	11
653	MYNCRGNACGCERPFTFKRWE FA	23	Protein SGS3 isoform D /Glycine soja/ RZC13323.1	100	2787.227	8.66	+2	43	+2.47	64	88
654	PDRAMGLHMNNNYFSSSTTLW ED	23	Hypothetical protein BT93_C1686 /Corymbia citriodora subsp. variegata/ KAF8035734.1	100	2686.926	4.54	-1	30	+2.46	2	2
655	YWFYFWETFQMSSPSYYWME TTFHCKGYFSHWW	33	NO MATCH	-	4460.999	6.00	+1	39	+0.68	18	59
656	LWHPAASLFMYWYASPGSRFY	21	Protease Do-like 8, chloroplastic isoform X2 /Rhodamnia argentea/ XP_030513218.1	100	2550.928	8.50	+2	47	+0.04	10	13
657	RVYYWEVYPLFHNRGYWCW WWYYYHWAHQMSPNYWW	36	NO MATCH	-	5124.771	8.11	+4	41	+0.91	41	64
658	FNTLGDACRAEEPNAA	16	Hypothetical protein C4D60_Mb07t11350 /Musa balbisiana/ THU60315.1	100	1678.804	4.14	-2	43	+2.23	10	3
659	MYAMNQRCGLGKNFTQCHW WH	21	Ran-binding 10 /Olea europaea subsp. europaea/ CAA3029827.1	100	2612.04	8.89	+4	42	+1.58	32	71
660	WYQTVLTHSLGGRGFTALSW WWWWWWWWKVCDGCCHC VNFEYYW	44	NO MATCH	-	5721.537	6.88	+2	54	+0.07	37	70
661	LLKTLVKRHGGNCRDPNK	18	BAG family molecular chaperone regulator 8 like /Actinidia chinensis var. chinensis/ PSS30496.1	100	2049.423	10.31	+5	27	+2.98	56	72
662	DKRHAGNGPAAMWDMEDYY GNT	22	Hypothetical protein M569_13668 /Genlisea aurea/ EPS61131.1	100	2499.683	4.66	-1	27	+2.67	19	17
663	YYPTCPQVPPPEEQRFMTEYSM YRW	25	NAC domain-containing protein 41-like /Nicotiana attenuata/ XP_019224265.1	87	3199.644	4.79	-1	24	+2.2	20	43

664	EFYSPGGPDRNNLWNTFAMYPMWTDD	26	Pentatricopeptide repeat-containing protein At4g13650/Rosa chinensis/ XP_024199561.1	100	3125.41	3.84	-3	30	+2.02	8	14
665	PMCPACASEPPVANVSMTDSQ	21	Increased DNA methylation 1-like /Ipomoea nil/ XP_019150222.1	100	2135.453	3.67	-2	42	+0.93	9	8
666	YTYFEVNPGPCFRDHHWNEGTCSPRW	26	Hypothetical protein /Tanacetum cinerariifolium/ GEY82793.1	100	3199.5	6.01	+1	26	+2.48	35	86
667	AFPMHTPVRDNMEDENEPSNAT	22	Cyclic dof factor 3-like /Nicotiana sylvestris/ XP_009761438.1	80	2502.687	4.17	-3	27	+3.2	2	4
668	MFSYKDVLFTYFFSFYDCCKWWFR	24	Unnamed protein product /Cuscuta campestris/ VFQ99269.1	90	3230.78	7.78	+1	54	+0.7	8	15
669	HYRAWAQTADDCMRTAALAYMAFE	24	Peptidyl-prolyl cis-trans isomerase FKBP42 /Sorghum bicolor/ XP_002448986.1	100	2793.165	5.38	0	54	+1.7	17	12
670	MNYGSSGHDWGENDSDCMQY	20	Uncharacterized protein LOC105634626 isoform X2 /Jatropha curcas/ XP_012072896.1	100	2296.376	3.84	-3	20	+2.78	24	32
671	WNGHFCYMFQWQAFMY	16	Hypothetical protein ES332_D11G365400v1 /Gossypium tomentosum/ TYH46809.1	100	2159.505	6.73	+1	56	+0.02	24	64
672	WMQHGDAEDVYSDFAGRGTQKLP	23	Hypothetical protein CQW23_32643 /Capsicum baccatum/ PHT27757.1	100	2608.831	4.66	-1	30	+2.27	2	1.0
673	WWGRGSHNTDMSAMDPAWWMWWWWWWWWRRLWMTYHADDVVPQFMH	46	NO MATCH	-	6197.077	6.26	+2	54	+1.14	43	64
674	WHSYESWEKYQMWEQFLVPFHWW	23	Putative disease resistance RPP13-like protein /Arachis hypogaea/ QHO22223.1	89	3230.613	5.33	0	43	+1.06	24	72
675	DWDHLQEWYDFCMMEYYCC	19	Uncharacterized protein DS421_17g583160 /Arachis hypogaea/ QHN92374.1	100	2580.91	3.77	-4	47	+1.54	42	61
676	FMYAGCSDANTRSLWCAFL	19	Cysteine-rich repeat secretory protein 15 isoform X2 /Daucus carota subsp. sativus/ XP_017234126.1	100	2156.498	5.82	0	57	+0.54	27	17
677	NVYVVTSCMSFMYGHSNGEMWNTC	24	Hypothetical protein FRX31_018797 /Thalictrum thalictroides/ KAF5191616.1	100	2761.16	5.24	0	41	+0.75	7	50
678	LKESNGPSGSRFENRKSAGHWCC	23	TMV resistance protein N-like /Eucalyptus grandis/ XP_039164560.1	100	2550.816	8.90	+3	26	+2.98	35	60
679	WWSGDHNRQYVMMRTCNTCCMDSYCCYNM	29	Uncharacterized protein LOC117275369 /Nicotiana tomentosiformis/ XP_033510557.1	70	3603.179	6.70	+1	41	+2.21	61	81
680	CMQWTGMECVQCHHQVCHSVWRLTFV	26	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 homolog isoform X1 /Ananas comosus/ XP_020081632.1	100	3149.748	6.99	+3	53	+0.82	32	72
681	MWRLDCNGSYLTFSDVLWWMWYRYWWKWRHYFMMCQMPDHVPQTWQ	46	NO MATCH	-	6197.24	7.83	+3	47	+1.27	40	60
682	RRPQRCGAMPNACWWWWYWWWWWWWYWHPDRFTQLMCNQY	40	NO MATCH	-	5655.518	9.11	+4	52	+1.42	42	65
683	EKQNGHQYGTVFMTGQNTPHWW	22	Hypothetical protein FNV43_RR07551 /Rhamnella rubrinervis/ KAF3451456.1	100	2646.883	7.01	+2	22	+1.93	7	48

684	WGSDAFVPEYWESSMASW	18	Serine-threonine protein kinase, plant-type, putative /Ricinus communis/ EEF44112.1	89	2135.299	3.57	-3	44	+0.84	8	39
685	QCPRAEVYNQSCEGVETERCNRRNQ	25	Hypothetical protein GW17_00051041 /Ensete ventricosum/ RWV87010.1	100	2970.244	6.27	0	24	+4.59	22	55
686	EMYFCMAGSMSSNGNECMEF	20	Uncharacterized protein LOC105649867 /Jatropha curcas/ XP_012092075.1	100	2268.604	3.67	-3	45	+1.12	38	58
687	WYMDDLEANKNSCMTTVPCGHCMMRW	26	Cysteine/Histidine-rich C1 domain family protein, putative /Theobroma cacao/ EOY24253.1	100	3123.678	5.38	0	46	+1.60	37	49
688	EWMACAMPFARPHWYVWWWWWWWWRWNYAQGQMGHACHKWYE	42	NO MATCH	-	5732.596	8.13	+4	57	+0.6	42	62
689	HWNYRKAPTSTLANGMWCDWRHYYDWFWEFNMSYCRPFDVYW	42	NO MATCH	-	5531.206	6.9	+2	40	+1.93	19	73
690	PYEDNESGCCVQDNVPREARMVLM	24	Hypothetical protein JCGZ_25077 /Jatropha curcas/ KDP24513.1	100	2756.122	4.18	-3	37	+2.62	5	18
691	RFKWTCRDAPGEQEHNYYYWCMEMMMCQQTCHTYW	35	NO MATCH	-	4558.236	6.03	+1	37	+2.23	52	77
692	WWGWPDGEMPTYMDCQCCFHMDPQESPYY	29	Putative ubiquitin-conjugating enzyme E2 18 /Populus alba/ TKS10123.1	100	3604.048	3.77	-4	34	+1.35	35	49
693	QFMMYGSNCGGGQLDDHAHGQFW	23	Putative glycine-rich cell wall structural protein 1 isoform X5 /Malus domestica/ XP_028953947.1	100	2586.835	5.05	0	34	+1.21	42	46
694	DHMMSPMYAMGPGYFPYFLYKKWWWWYWLEMAWLTSWDQTACYR	43	NO MATCH	-	5539.475	6.74	+1	46	+0.42	28	53
695	LVAGSLVPL	9	Hypothetical protein ES332_D03G001800v1 /Gossypium tomentosum/ TYH78623.1	100	868.087	5.52	0	66	-2.46	16	32
696	WWMNCTPCPDYEDMWWWFWWWWFWWKKLAAKHTWACDDREW	41	NO MATCH	-	5701.519	4.89	-1	58	+1.01	43	64
697	YYYDQHRTNGNRSVMYYWLWWWWFERHDCSACGGQKYTLVWWW	43	NO MATCH	-	5729.408	8.01	+3	39	+1.67	31	73
698	RPNTDVGFNGLNALDACTTGWQ	22	Glycoside hydrolase, family 19, catalytic /Corchorus olitorius/ OMP09563.1	100	2350.558	4.21	-1	36	+1.75	21	10
699	WYYYMTGYTEMHFSMDPWWWNFSSYAECGWFRWW	34	NO MATCH	-	4602.157	4.65	-1	44	+0.80	28	72
700	WLCVTGAGDPGCVGQGDAFE	20	Lipoyl synthase 2, mitochondrial-like /Nicotiana tabacum/ NP_001312765.1	100	1982.186	3.49	-3	45	+0.15	5	15
701	YEYEFEVQPFMPWVHQSNDG	20	Exocyst complex component EXO70A1-like /Camelina sativa/ XP_010426049.1	100	2502.707	4.00	-3	30	+1.77	2	17
702	WHKWMQCGFTGHDNLNTYMMTVTSMSCPTDMMEE	34	NO MATCH	-	4044.674	4.72	-1	38	+1.45	32	40

703	FQWWTKVGDGTPEFPGYTYFYMHWW	25	Hypothetical protein F3Y22_tig00111427pilonHSYRG00684 /Hibiscus syriacus/ KAE8678387.1	100	3230.61	5.32	0	36	+0.47	12	54
704	YWRNYQCYSSFMYYWSEEYTGSNSDRVYYWW	31	NO MATCH	-	4184.512	4.68	-1	25	+2.28	22	43
705	EERACPQNNGDSGQDEPSWGMMCCMDWCF	29	Hypothetical protein Bca52824_016370 /Brassica carinata/ KAG2323157.1	86	3327.693	3.71	-5	37	+2.35	42	58
706	YWHTSLVCSGTTSNGYDLRKMYFWFTWPHWEWWMSSHNLYVPYPDWY	47	NO MATCH	-	6026.753	6.26	+2	36	+1.00	13	65
707	WWQDWRTLFFGHANHWRWWWWWWWWWWWPMLSNDMDKNWWMR	42	NO MATCH	-	6198.064	8.76	+3	59	+1.23	43	65
708	MECWWWNSCFDFTCCTYY	18	Protein DA1-related 5-like /Quercus lobata/ XP_030973502.1	100	2388.736	3.67	-2	55	+0.58	54	82
709	WWNNGMNCCLCTQFRDKRYWQWWKWEWYKVEANTSWPVEFWY	42	NO MATCH	-	5656.411	7.92	+1	45	+1.74	15	87
710	WQFLVATFCMYSFWWWYWWWWWWWNQYWMCSTTFQVQPWY	40	NO MATCH	-	5732.605	5.51	0	62	-0.51	43	64
711	LPSGLLGLL	9	Hypothetical protein F2P56_011920 /Juglans regia/ KAF5467689.1	100	882.114	5.52	0	55	-2.56	46	76
712	HFWNFVNYSPMYMYWWMWLCEHVNCHYY	28	Hypothetical protein /Tanacetum cinerariifolium/ GEW00999.1	100	3851.46	6.25	+2	50	+0.24	30	68
713	WWLTCVTKLDDCNCPWWQWWWRWWSWYERAMMAGAVWTWHWW	42	NO MATCH	-	5721.607	6.73	+1	61	+0.53	42	66
714	RWPMCALYHSHQWMRYGQ	18	F-box protein SKIP23-like /Nicotiana tomentosiformis/ XP_009629323.1	100	2350.742	9.31	+4	38	+1.97	38	46
715	FHCYANANYFMCTMHCQNGLDCDDEEYY	28	transcription factor MYB8-like /Cucurbita moschata/ XP_022959319.1	100	3401.75	4.10	-3	39	+1.87	58	58
716	EAPCMLPPGGLEQNFGYYQY	20	Hypothetical protein TRIUR3_29153 /Triticum urartu/ EMS54330.1	100	2277.568	3.80	-2	30	+0.53	7	9
717	YEANPQDPGSMKSEFFL	17	Uncharacterized protein LOC115742110 /Rhodamnia argentea/ XP_030532084.1	100	1960.151	4.14	-2	29	+1.82	6	4
718	YYNQESHYMQNCMTCAWMWRRMKEYWWW	28	Pentatricopeptide repeat-containing protein /Arachis hypogaea/ QHN85336.1	88	3912.521	8.02	+2	42	+2.11	30	68
719	WMFDGYRKGPAGQDYTYWYYFWWFWWMYSKALAKCDWDHERF	42	NO MATCH	-	5589.296	6.75	+1	42	+1.37	33	56
720	FFWHWYFPGQWLGRWRWNWHFYMYYRDHQFGPDMAMFDWWF	41	NO MATCH	-	5729.508	7.02	+3	48	+1.14	23	68

721	WWTPSLECTHMGMRYWWWWPEWEYWWYWPRPWVEPLFDWY	40	NO MATCH	-	5656.443	4.57	-2	47	+0.69	47	79
722	WWERNGPASCWMSGCCQCCWDNHMTHYY	28	Hypothetical protein BHE74_00008879 /Ensete ventricosum/ RWW82651.1	73	3455.917	5.99	+1	42	+1.57	62	91
723	WNHQWPYYTTHFAVTECKPWWFYWHYSQGMFCELPWFYW	39	NO MATCH	-	5253.942	6.26	+2	43	+0.45	25	77
724	WRFEAYSTGLYWWPMCTDPNMWDCE	25	Putative reverse transcriptase domain-containing protein /Tanacetum cinerariifolium/ GEZ30465.1	100	3188.599	3.92	-3	44	+1.36	18	61
725	WYCGNTYSGKSARNSGPTDPAEFFCSFR	28	Hypothetical protein C4D60_Mb01t16100 /Musa balbisiana/ THU63472.1	89	3149.43	8.03	+1	28	+2.24	46	47
726	YWEFMRTYGYSDPGANAVVQQPVMW	25	Leucine--tRNA ligase, cytoplasmic-like /Nicotiana tomentosiformis/ XP_018627656.1	73	2996.381	4.37	-1	40	+0.98	4	16
727	GRYRDSHWCEAPYYMYGDNCSW	22	Hypothetical protein HYC85_024073 /Camellia sinensis/ KAF5936567.1	100	2760.005	5.38	0	27	+2.70	56	56
728	WFTDAEAPASGVRMELVWAWKWWYTWWWFVPNPKEEKVLR	40	NO MATCH	-	5083.85	6.31	0	52	+0.91	8	76
729	WEHHLHLSANVCNNMCPTTDLDYGYSGSNEMWW	33	NO MATCH	-	3912.3	4.70	-1	36	+1.52	8	39
730	FYMQNALMDGGHWHYVFWMWWWHMLRHFPWGSCAPHAEQDY	41	NO MATCH	-	5257.004	6.15	+3	48	+0.68	24	59
731	WWCFPNETSNQHSCSYYYRCWMMNVHPWYY	30	Unnamed protein product /Brassica napus/ CAF2103076.1	100	3983.492	6.89	+2	36	+1.50	27	79
732	CFQVCSAPRGVRLWPECPMCMQSMPRW	27	hypothetical protein Zm00014a_031301 /Zea mays/ PWZ04748.1	100	3199.918	8.57	+2	51	+1.25	41	50
733	DMYLFDGSRSERCLLMCTDLTMSLWCMWWW	30	Hypothetical protein E2562_030593 /Oryza meyeriana var. granulata/KAF0927147.1	100	3780.506	4.23	-2	56	+0.90	30	49
734	WEWRLCYALNGTHMRWFWERWWWWYAYRECGFARCPYPDWY	41	NO MATCH	-	5628.422	7.93	+2	48	+1.65	32	78
735	TLMSCRNGGESPCWTATNVCMHMH	24	DNAj homolog subfamily C member 17 /Sorghum bicolor/ XP_021307132.1	100	2667.118	6.61	+2	41	+1.37	27	45
736	EETDPDYWNRTQYFCYCKWNPF	22	Hypothetical protein KK1_004972 /Cajanus cajan/ KYP72384.1	100	2906.164	4.32	-2	27	+2.85	28	50
737	HWNKKCMDPSPTGHYSEWYWWTWCCVMWRDYFTMNFPFVDYW	42	NO MATCH	-	5532.314	6.01	+1	42	+1.22	23	80
738	MRYKHVNDMAWMMYWNMHQFSHLVCSYDY	29	Cation/H(+) antiporter 4-like /Hibiscus syriacus/ XP_039034277.1	80	3788.421	6.80	+3	44	+1.46	34	49
739	WMHSPVLCCSGYCMWWWVWKWWWEEQEEWERFMWW	35	NO MATCH	-	4914.704	4.64	-2	60	+0.52	41	72
740	ENYFKSYMGAAVREQFHWWWEWCYWEFCRVDNQECGFYFQNYW	43	NO MATCH	-	5734.359	4.70	-2	44	+1.73	11	70

741	HEEVCMMSEACHWCSDHSSYSTHNQEHYW	29	CBL-interacting serine/threonine-protein kinase 12-like /Durio zibethinus/ XP_022720390.1	100	3554.826	5.19	0	31	+2.49	30	70
742	KRKSVFPTGGPVSRAMERYKMSYFFDQQCFWYKDLFSNSDVWY	43	NO MATCH	-	5297.037	9.30	+3	34	+2.12	8	8
743	RKTGRFPPSQGMDKWHYTHWFWWWHCRPRAVCAPHDEPYWR	41	NO MATCH	-	5297.025	9.69	+8	34	+2.64	39	76
744	WYYYVMYHFSSQNLQDLEWWQWWWYMWFGFWFREHHFW	37	NO MATCH	-	5341.009	5.75	+1	51	+0.71	39	64
745	MYELVRPSEQGGQPDSRNWWRMCMCWYMFQPCKRYVRDEYWRF	43	NO MATCH	-	5616.514	8.59	+2	37	+2.79	27	62
746	DRSWNCALEHFNDRKHVFLY	20	Mitochondrial substrate carrier family protein C /Herrania umbratica/ XP_021295252.1	90	2550.843	6.91	+2	40	+3.02	10	13
747	DEYTEEMWCAVGFYCMPEYMYVMQVVHPAMRC	32	NO MATCH	-	3913.633	4.25	-3	50	+0.70	43	63
748	FCWWWKWGNHEEHEYYWQHYWACPCAEVMMSNW	33	NO MATCH	-	4424.978	5.29	0	48	+0.99	28	81
749	YKCYNKEHVHAVHQTSSLYWYWHYWWYKWYHFTCAYWCNFW	41	NO MATCH	-	5616.323	8.52	+7	41	+0.87	39	63
750	LKPRNLARHAEETNLWCC	18	Unnamed protein product /Lactuca saligna/ CAB4110305.1	100	2154.505	8.07	+2	44	+2.56	4	10
751	VLKAGGVAVLPRVYMNGAPH	20	Probable pectinesterase 15 /Nicotiana sylvestris/ XP_009780329.1	70	2049.472	9.99	+3	50	-0.23	28	59
752	HCLRMYSAYNHVAYMGHCGRMW	22	Hypothetical protein F511_30301 /Dorcoceras hygrometricum/ KZV44597.1	100	2687.179	8.86	+5	45	+1.26	51	58
753	CDFYETPWYKVHQQSCFYYYRGQVWWW	27	Putative F-box protein At1g65770 /Nicotiana attenuata/ XP_019228459.1	73	3670.106	6.73	+1	37	+1.37	25	48
754	MDYYYPMTSSSHYTQWFYMDTSSMNVVWFQW	31	NO MATCH	-	3983.457	4.20	-1	35	+1.12	11	34
755	WWTWMYRWCVNCYCYEFYHYTYGRGYHLFDWWH	33	NO MATCH	-	4623.228	6.99	+3	42	+1.06	49	73
756	YFWFRWDMNQFCHMWFKFYWWMWWRKLHFWCWGAHWWH	38	NO MATCH	-	5591.554	9.31	+7	63	+0.52	42	64
757	HWNYGVFVAGPCETFMMDMHMQYNSHRQRAWKNHHNSNRFVDYW	44	NO MATCH	-	5530.208	8.20	+6	36	+2.44	12	35
758	FWRGHRSFFVCYVYMWCWWWWWWWMWFAWATCWQLGQWHM	40	NO MATCH	-	5655.667	8.68	+4	70	-0.37	43	64
759	EYYYWLMNGCWMMWWWLWFYSFDSMDFWFFFW	32	NO MATCH	-	4602.352	3.49	-3	65	-0.61	41	65

760	RRRNMLLGPSGTCMCDYQCFGPYWWWFLMEREDEQWQQQY	40	NO MATCH	-	5139.871	4.94	-1	37	+2.36	19	41
761	RWKMRLPLSCQGCTATVWWWYYWWWWWWWYWQGDRYMGPYYYEW	44	NO MATCH	-	6198.115	8.70	+2	47	+0.69	43	64
762	RWWWPKTMNMEFMMDDCQTYFMHQWMYYCW	30	NO MATCH	-	4176.932	5.38	0	50	+1.27	41	66
763	CKCWWTNEGYWSKVRYFYYWWWWWRWLWYYSDYSTMDYW	39	NO MATCH	-	5631.335	7.96	+1	43	+1.15	43	64
764	YHHYGLLYACCGQVQLSQKFKDYEDMMWRTRWSWMQDEPLFDWY	44	NO MATCH	-	5656.432	5.38	0	38	+1.78	9	14
765	NYYSRHFFWDFSCRAHWWWCFMQYYKSYEEYYE	33	NO MATCH	-	4623.109	6.03	+1	36	+2.09	22	50
766	FWYHMVSNSSHQRHQYMFCWSYFWEYDW	28	Protein-tyrosine-phosphatase PTP1-like isoform X2 /Punica granatum/ XP_031391674.1	100	3852.272	6.26	+2	39	+1.71	19	56
767	WCHSYYYMTDDVYDVEWWWRWWWWWDELEALMLLYGLWWW	40	NO MATCH	-	5655.407	3.90	-5	57	+0.30	42	65
768	QMDDWHDACQMSLCFHCMC	19	Laccase-4-like isoform X2 /Senna tora/ KAF7800900.1	100	2304.71	4.40	-1	57	+1.35	69	58
769	WYWYAKTVMTFDMWWWWWWYRYWWRWPPNWAHCFVWYW	38	NO MATCH	-	5644.522	8.99	+3	60	+0.13	43	65
770	EWYHSMCACQFEYFWYSDAYPTNSCYY	27	Hypothetical protein /Oryza sativa Japonica Group/ BAD45135.1	100	3458.796	4.13	-2	37	+1.19	12	24
771	WYWFVVCCMFYCMDYFYHMAWSTRNVVWEMW	31	NO MATCH	-	4184.978	5.32	0	64	-0.11	32	74
772	YYYMYWASPYMNWECSMDWEPYNWESGASNVMYERW	36	NO MATCH	-	4690.195	3.91	-4	36	+1.51	22	58
773	YYRHDTQACERCYTWWYWWFYQYRGYWCPRLLEWWQY	37	NO MATCH	-	5256.911	7.91	+2	37	+1.99	42	64
774	WAECWDYGCVCQMYQSGSQGCYCCWYM	27	Uncharacterized protein LOC104243743/Nicotiana sylvestris/ XP_009797291.1	77	3254.748	3.67	-2	48	+0.42	72	76
775	VWWWLAYECFTSCYHTYWYYWPHMWWCLCFMDTWRFWRKW	40	NO MATCH	-	5655.609	7.85	+3	57	+0.35	42	81
776	WDVWMMRDYWWWWWWWWWWWWWWWWWWWWLDNQYEGAHK	39	NO MATCH	-	6181.992	4.66	-1	69	+0.07	43	64
777	CWWDETKPHDNNGVMDYWRYDRWWNEWKNRMVGYRWSHSWHW	42	NO MATCH	-	5701.27	7.02	+3	33	+3.15	18	79

778	YWDQLYGNQEQNMAPQHFMMWYYYRNWTYRRGSCGNYFVDWY	42	NO MATCH	-	5533.138	6.74	+1	30	+2.19	18	46
779	WDWDERMFECARMWYKWPWWWRFHFYVFDPPHMYNGWMWF	40	NO MATCH	-	5654.52	6.03	+1	52	+1.32	26	76
780	WHCFRTNYSYDYLRCNPTWFYCMNMYWW	28	Uncharacterized protein LOC116029213 /Ipomoea triloba/ XP_031126982.1	85	3851.417	7.93	+2	42	+1.55	34	78
781	TRTGPGWSSVWCEQWWWYMDWWWWHSYDEWDHH	33	NO MATCH	-	4513.88	4.77	-1	39	+1.72	43	76
782	RRFRRMDDGYDYYHRWYNFRWWACQSQWCDQWW	33	NO MATCH	-	4668.171	8.82	+3	36	+3.89	32	65
783	WWGKHTGYSNAKLFFKRWWWWMWWARFWKLAAMNDFGNLW	40	NO MATCH	-	5297.16	10.56	+6	57	+0.66	41	63
784	CWLYELTAQNSRGFQDHWPDWALWFWHCTMYFQMYFTEW	39	NO MATCH	-	5125.794	4.72	-1	48	+0.96	7	44
785	WTWYQQMATLGGLMAASEHMEWE	23	Uncharacterized protein LOC104228010 isoform X1 /Nicotiana sylvestris/ XP_009778694.1	100	2757.127	4.24	-2	47	+0.59	19	39
786	WESSKCAEFGNLHRWMWQRWWWHRNYKWWYNCYGKHDWMWY	41	NO MATCH	-	5729.474	9.14	+6	41	+2.15	31	83
787	DLHFDGVCVVVAMWMHWCLGSYGWR	25	Hypothetical protein BRADI_2g47560v3 /Brachypodium distachyon/ PNT72669.1	100	2957.127	5.89	+1	60	-0.10	14	52
788	YYWWDRYKMWNMYWWCSTYSCMMYFFYWWY	30	Hypothetical protein CR513_50505 /Mucuna pruriens/ RDX70271.1	85	4441.166	7.97	+1	50	+0.40	41	65
789	RWGWMPSYCLYRWWWWWEEYNTVRRQNQYCMYMR	34	NO MATCH	-	4815.56	9.24	+3	41	+2.45	35	69
790	NDDWFEQGGDWCEDDMWWAACHWYYE	26	Hypothetical protein B296_00019713 /Ensete ventricosum/ RRT62436.1	100	3358.529	3.54	-7	42	+2.15	26	64
791	HWNYRRDHDAHQYHFWRHMWRFYRFEMYWSTPFCHHW	37	NO MATCH	-	5254.87	9.11	+9	35	+3.21	46	75
792	WRMWAQVFLMYFHSWWMWWFGWKWRHMFHENYGHKFMMWW	40	NO MATCH	-	5702.73	9.99	+7	60	+0.43	36	72

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