UNIVERSIDADE DE RIBEIRÃO PRETO – UNAERP

DOUTORADO EM BIOTECNOLOGIA

Luciano Pereira Carvalho

DataNature - Sistema para armazenamento de dados de projetos genômicos: Estudo de caso *Solanum lycocarpum* (Lobeira).

Ribeirão Preto

2015

UNIVERSIDADE DE RIBEIRÃO PRETO – UNAERP

DOUTORADO EM BIOTECNOLOGIA

DataNature - Sistema para armazenamento de dados de projetos genômicos: Estudo de caso *Solanum lycocarpum* (Lobeira).

Tese apresentada ao Programa de Pós-Graduação *Stricto Sensu* - Doutorado em Biotecnologia da Universidade de Ribeirão Preto para obtenção do título de Doutor em Biotecnologia.

Orientadora: Orientadora: Profª. Dra. Suzelei de Castro França
Co-Orientador: Profº. Dr. Mozart de Azevedo Marins

Ribeirão Preto

2015

Ficha catalográfica preparada pelo Centro de Processamento Técnico da
Biblioteca Central da UNAERP

- Universidade de Ribeirão Preto -

Carvalho, Luciano Pereira, 1989-
C331d DataNature - Sistema para armazenamento de dados de projetos genômicos: Estudo de caso *Solanum lycocarpum* (Lobeira) / Luciano Pereira Carvalho. - - Ribeirão Preto, 2015.
112 f.: il. color.

Orientadora: Profª. Drª. Suzelei de Castro França.

Tese (doutorado) - Universidade de Ribeirão Preto, UNAERP, Biotecnologia. Ribeirão Preto, 2015.

1. *S. lycocarpum*. 2. Glicoalcaloides. 3. Banco de Dados.
I. Título.

CDD 660

LUCIANO PEREIRA CARVALHO

DATANATURE – PLATAFORMA ON-LINE PARA ARMAZENAMENTO DE DADOS GENÔMICOS DE PRODUTOS NATURAIS: MODELO *SOLANUM LYCOCARPUM* (LOBEIRA)

Tese de Doutorado apresentada ao Programa de Pós-Graduação em Biotecnologia da Universidade de Ribeirão Preto, para obtenção do título de Doutor em Biotecnologia.

Área de Concentração: Biotecnologia Aplicada à Saúde

Data da defesa: 22 de outubro de 2015

Resultado: Aprovado

BANCA EXAMINADORA

Profa. Dra. Suzelei de Castro França
Universidade de Ribeirão Preto - UNAERP

Profa. Dra. Sandra Regina Costa Fantinato
Universidade de Ribeirão Preto - UNAERP

Prof. Dr. Edilson Carlos Caritá
Universidade de Ribeirão Preto - UNAERP

Prof. Dr. Joaquim Cezar Felipe
Faculdade de Filosofia Ciências e Letras de Ribeirão Preto - USP

Prof. Dr. Mozart de Azevedo Marins
Universidade de Ribeirão Preto - UNAERP

RIBEIRÃO PRETO - SP
2015

DEDICATÓRIA

Ao meu pai Joaquim Carvalho, que sentiria muito orgulho ao ver a conclusão dessa etapa. À minha mãe Cristina Reis, que com amor, exemplo de vida e trabalho me inspirou na profissão. Aos meus filhos Tiago e Taís e a minha esposa Kellen.

AGRADECIMENTOS

Agradeço em primeiro lugar ao Grande Arquiteto do Universo que iluminou meu caminho até aqui.

Ao Instituto Federal de Educação, Ciência e Tecnologia do Sul de Minas Gerais – IFSULDEMINAS, *Campus* Machado, pela oportunidade concluir meus estudos, principalmente nas pessoas dos Diretores Gerais: Prof. Walner José Mendes e Prof. Dr. Carlos Henrique Rodrigues Reinato.

Agradeço minha orientadora Profª Drª Suzelei de Castro França, por sua atenção, paciência e responsabilidade direta na construção da Tese.

Ao Prof. Dr. Mozart de Azevedo Marins, pela co-orientação e instruções nos primeiros contatos com a biotenologia e bioinformática.

Aos meus colegas Prof. Dr. Matheus Eloy Franco, Profª Drª Sandra Fantinato e Prof. Danilo Fernandes pelo apoio.

Aos colegas professores do IFSULDEMINAS – *Campus* Machado, pelo companheirismo.

Agradeço a minha família pela compreensão nos momentos de ausência.

RESUMO

Solanum lycocarpum conhecida popularmente como lobeira ou fruta-do-lobo, encontrada no cerrado brasileiro, é uma espécie da família Solanaceae, com uso medicinal no tratamento de diabetes melitus, obesidade, taxa de colesterol ruim elevada, asma, doenças hepáticas e inflamações. Tais atividades foram validadas em diversos estudos farmacológicos e várias delas estão correlacionadas com metabólitos secundários acumulados nesta espécie, dentre estes os glicoalcalóides estereoidais (SGAs) e polifenóis. Alguns glicoalcalóides esteroidais são úteis na síntese de hormônios esteroidais, como os contraceptivos, e como precursores para a síntese de outros fármacos. A biossíntese destes metabólitos é catalisada por enzimas cuja produção é regulada em nível transcricional, ou seja, por expressão gênica. Apesar do interesse pelos metabólitos de *S. lycocarpum*, não existe até o presente nenhuma informação sobre genes expressos em órgãos específicos desta planta, relacionados à biossíntese de metabólitos secundários bioativos. Diante do potencial da aplicação de metabólitos de S. lycocarpum, objetivou-se nesse trabalho o estudo de bibliotecas de genes expressos. Após clonagem e sequenciamento o conjunto de transcritos similares foi agrupado constituindo os chamados *contigs* e os demais, designados como *Singlets*. O conjunto de dados obtidos foi armazenado em uma base de dados para suporte à realização de buscas *in sílico*. Um *pipeline* de buscas foi implementado para acesso à base de dados existente, viabilizando a realização de anotação, categorização de genes conhecidos e determinação do índice de novidade das bibliotecas. Ferramentas computacionais adicionais foram acessadas para rastreamento *in sílico* de genes da via de biossíntese de metabólitos de interesse, com foco em genes codificadores de enzimas chaves na biossíntese de SGAs, inclusive com o uso de primers desenhados a partir de sequências conservadas em outras espécies de Solanum ou outros gêneros de Solanaceae. A integração de aplicativos adequados à análise da espécie em estudo resultou na estruturação do sistema computacional DataNature, para armazenagem, consulta e tratamento de dados oriundos de pesquisas em projetos de transcriptomas de espécies diversas.

Palavras-chave: *S. lycocarpum*, glicoalcaloides, Solamargina, Solasodina, transcriptoma, ESTs, Banco de Dados.

ABSTRACT

Solanum lycocarpum known as lobeira or fruit-of-wolf, is a Solanaceae found in the Brazilian cerrado popularly used in the treatment of diabetes mellitus, obesity, asthma, inflammations, liver disease and for the reduction of LDL cholesterol (bad cholesterol) levels. Numerous studies have been carried out with *S. lycocarpum* and the pharmacological activities attributed to this species have been correlated to the secondary metabolites produced by the plant, among them the steroidal glycoalkaloids (SGAs) and polyphenols. Some steroidal glycoalkaloids are useful in the synthesis of steroid hormones which are contraceptive drugs and also as precursors for the synthesis of other pharmaceuticals. The biosynthesis of those metabolites is catalyzed by enzymes whose production is regulated at transcriptional level, i.e. by gene expression. Despite of the relevance of *S. lycocarpum* bioactives, there is no information about organ specific gene expression related to the biosynthesis of secondary metabolites of this plant species. Considering the potential of genetic manipulation of the production of SGAs by cultured cells and tissues of *S. lycocarpum* an experimental molecular work was carried out to construct cDNA organ specific libraries. After cloning and sequencing the similar transcripts were assembled into contigs and sole reads were assigned as singletons.

Collected data were stored in a database to implement in silico analyses. A pipeline system was designed for mining the structured database, allowing annotation and categorization of known genes and also the determination of the redundancy index of libraries. Additional application software were accessed for in silico screening of genes of the biosynthetic pathway of the metabolites of interest, focusing on genes coding for key enzymes of the SGAs biosynthesis. Furthermore primers designed from conserved sequences of those genes in other *Solanum* species or in other genders of Solanaceae were used to track homolog sequences in the constructed libraries. The integration of computational programs appropriate for the analysis of the plant species under study lead to the development of the DataNature a computer system for storage, mining and analysis of data generated from transcriptome studies of different species.

Keywords: S. lycocarpum, glycoalkaloids, solamargine, solasodine, transcriptome, EST, Database.

LISTA DE FIGURAS

LISTA DE TABELAS

LISTA DE GRÁFICOS

LISTA DE ABREVIATURAS

cDNA	Clones de Ácido Desoxiribonucleico
CLR	Common Language Runtime
CP	CHROMAS PRO
ESTs	Expressed Sequence Tags
GAME	Galactosiltransferase
HMG-CoA	hidroximetilglutaril coenzima A
HS	Heat Shock
IFSULDEMINAS	Instituto Federal de Educação, Ciência e Tecnologia do Sul de Minas Gerais
KEGG	Kyoto Encyclopedia of Genes and Genomes
Kg	quilograma
mg	miligrama
MS	manuscrito
MT	Metalotioneina
NCBI	National Center for Biotechonology Information
PIN	Puroindolinas
RNA	Ácido Ribonucleico
RNAs	Ácido Ribonucleico mensageiro
RNA-seq	Tecnologia de sequênciamento de nova geração para revelar o perfil transcricional de RNA a partir de um genoma em um determinado momento ou condição
SGA	Steroidal Glycosylated Alkaloids
SQS	Squalene synthase
TRX	Tioredoxina
tSMS	Heliscope True Single Molecule Seq
WEB	Rede Mundial de Computadores
XLS	Extensão de arquivo tipo planilha eletrônica

SUMÁRIO

1. INTRODUÇÃO

As plantas descritas popularmente como medicinais são uma fonte rica de moléculas com amplo espectro de atividade biológica. Devido à demanda crescente pela validação de eficácia e segurança no uso destas moléculas de origem natural, existe um forte interesse no estudo das plantas medicinais brasileiras, as quais possuem enorme diversidade biológica e química (BARBOSA-FILHO *et al*., 2006a).

As plantas produzem uma grande variedade de metabólitos especializados que não só são essenciais para o crescimento e desenvolvimento, mas também desempenham papéis importantes na adaptação às variáveis ambientais. Além disso, muitos metabólitos de plantas são elementos nutrientes essenciais para os seres humanos, além de servir como medicamentos naturais. No entanto, o estudo da biossíntese de produtos naturais ainda está no início, porque mais de 90% dos metabolitos de plantas são desconhecidos e apenas um pequeno número de genes/enzimas envolvidas no metabolismo são identificados (Qi, X. and ZHANG, D., 2014).

Neste sentido, buscas etnofarmacológicas (conhecimento popular sobre atividades terapêuticas de plantas), etnobotânicas (conhecimento popular sobre a planta), quimiotaxonômicas (estudo dos componentes químicos da planta) e mais recentemente a genômica funcional, têm sido as principais estratégias metodológicas para a escolha de plantas medicinais como fonte renovável de produtos naturais com propriedades bio/farmacológicas. Estudos multidisciplinares permitem obter o maior número de informações sobre determinado organismo, estes estudos demandam um menor tempo e baixo custo podendo assim viabilizar descobertas de bioativos inovadores (ELISABETSKY, 2003; ALBUQUERQUE & HANAZAKI, 2006). Atualmente, plantas com diferentes atividades farmacológicas têm sido estudadas, principalmente com base em dados etnofarmacológicos, como é o caso de espécies da família *Solanaceae* que é cosmopolita e apresenta maior concentração nas regiões tropicais.

No Brasil, o gênero *Solanum* possui cerca de 1800 espécies das quais muitas são de grande interesse econômico como é o caso da batata (*Solanum tuberosum*), tomate (*Solanum lycopersycum*), berinjela (*Solanum melongena*) e pimentão (*Capsicum sp*) (SOUZA & LORENZI, 2008). Nesse sentido, a *Solanum lycocarpum St. Hill*, um arbusto ou árvore pequena com até 4m de altura (CORREA, 1984), conhecida popularmente como lobeira ou fruta-do-lobo por ser o alimento preferido do lobo-guará (OLIVEIRA JR *et al*., 2004), encontrada no bioma cerrado é de grande interesse pela sua utilização no tratamento de diabetes mellitus, obesidade, aumento das taxas de colesterol, asma, doenças hepáticas, inflamações (CRUZ, 1982) dentre outras atividades farmacológicas.

Várias espécies da família *Solanaceae*, produzem metabólitos secundários, como os glicoalcalóides esteroidais (compostos nitrogenados análogos de saponinas esteroidais e estão presentes como glicosídeos) e polifenóis, importantes para proteger a planta de ataques de animais e insetos, pois apresentam toxicidade (PEREIRA *et al*, 2008; ALMEIDA & ROCCA, 1995). Os principais glicoalcalóides encontrados em *S. lycocarpum* são solamargina e solasonina (figura 1).

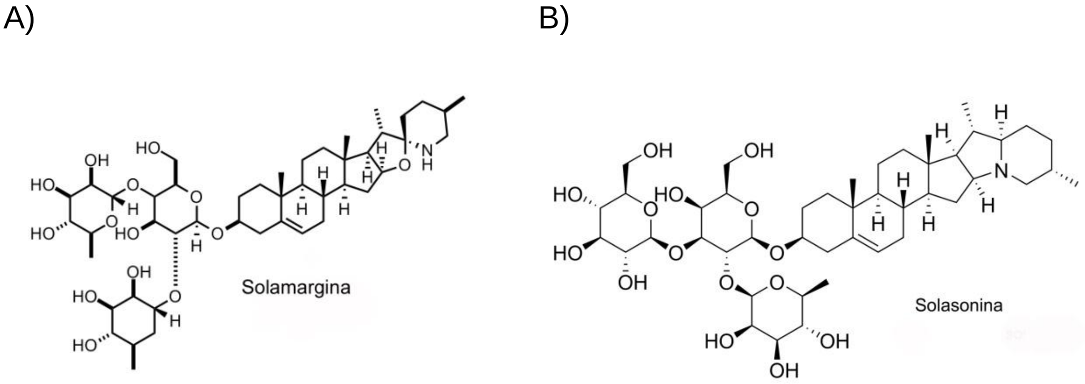


Figura 1 - Estrutura química dos glicoalcalóides Solamargina (A) e Solasonina (B).

O glicoalcalóide solamargina (Figura 1A) é um constituinte químico muito importante, pois tem sido atribuído a ele a atividade de inibir o crescimento de células tumorais humanas (cólon de útero, mama, hepatoma (fígado) e próstata) (KUO *et al*, 2000; MARUO *et al*, 2003). Outros estudos demonstram que glicoalcalóides são precursores para a síntese de fármacos e por isso são utilizados em medicamentos para combater o câncer e também possuem atividade antifúngica (EANES *et al*, 2008; ESTEVES-SOUZA *et al*, 2002).

Alcaloides esteroidais e glicosídeos ocorrem em numerosas espécies do gênero *Solanum* e possuem estruturas semelhantes aos hormônios sexuais

(CALTAGIRONE et al, 2000; DEWICK, 1998). Sabe-se que a solasodina (figura 2) pode ser utilizada como um composto importante na síntese de hormônios esteroidais como os contraceptivos sendo fundamental para a produção de progesterona, de cortisona (MOLA *et al*., 1997; HARAGUCHI, *et al*., 1978) e de andrógeno (GOSWANI *et al*., 2003) por ser um análogo da sapogenina.

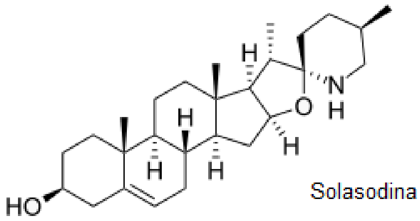


Figura 2 - Estrutura química do glicoalcalóide Solasodina.

De acordo com Weissenberg (2001), a solasodina, além de ser precursora para a síntese de esteróides, também apresenta atividades como: fungicida; inibidora do ciclo de desenvolvimento de insetos; atua ainda como inibidor enzimático; exibe efeito anti-inflamatório (EMMANUEL *et al*., 2006) e outros efeitos farmacológicos como a atividade citotóxica contra alguns tumores (CHAM, 2007).

Nas plantas, em resposta à herbivoria ou ao mecanismo adaptativo em diferentes condições, são produzidas substâncias ligadas à ativação de vias metabólicas específicas. Algumas das defesas químicas dos vegetais a ataques por insetos são, geneticamente, expressas constitutivamente, enquanto outras possuem uma atividade modulada por danos, situação de estresse, sejam eles causados por agentes físicos ou químicos, sofridos pela planta.

Após uma análise detalhada sobre pesquisas já realizadas em *S. lycocarpum*, obteve-se os seguintes dados que demonstram as principais atividades Botânico-Agronômicas, Farmacológicas e Químicas, já comprovadas. Tabelas 1, 2 e 3.

Tabela 1 - Estudos botânicos e agronômicos realizados com a espécie *S. lycocarpum*

AUTOR/ANO	**ATIVIDADE ENCONTRADA**
ARAUJO, *et.al.*, 2010	Com base nos estudos realizados, apesar da grande semelhança morfológica entre as espécies estudadas, destacaram-se como parâmetros distintivos: a morfologia do pecíolo, a base do limbo, o indumento da face adaxial, a anatomia do mesófilo, os tipos de estômatos e a morfologia do bordo foliar.
GONZAGA, *et.al.*, 2009	Foram observadas diferenças para o número de folhas e no tratamento ácido sulfúrico para o diâmetro. Assim, a escarificação com lixa é o método mais adequado para tratamento das sementes de S.Lycocarpum.

PINTO, *et.al.*, 2007	Concluiu-se que o mecanismo de germinação de S. lycocarpum apresenta semelhanças com sementes de tomate e café. No entanto, diferenças quantitativas estavam relacionadas com taxas de germinação entre as três espécies.
ZELANDI, *et.al.*, 2006	Devido a sua potencial importância medicinal e a comprovada importância ambiental, a estrutura genética de populações de *S. lycocarpum* foi investigada utilizando-se marcadores moleculares microssatélites desenvolvidos exclusivamente para esta espécie.
OLIVEIRA, *et.al.*, 2005	Os resultados mostram que as propriedades alelopáticas de *S. lycocarpum* se manifestam no substrato solo em ampla faixa de temperatura.
MOREIRA & DEL-CLARO, 2005	Os resultados permitiram verificar que formigas se beneficiam de uma fonte alimentar rica e previsível no tempo e espaço, enquanto que os membracídeos atendidos por formigas sobreviveram melhor. Os resultados mostram também que o benefício da relação pode se estender sobre a fecundidade dos membracídeos. A presença da associação formiga-hemíptero teve um impacto significativo sobre a redução da herbivoria por mastigadores na planta hospedeira.
ELIAS, *et.al.*, 2003	Observa-se que a epiderme é unisseriada e o mesofilo é dorsiventral. O parênquima paliçádico é uniestratificado e o parênquima voltado para a face abaxial é formado por três a cinco camadas de células com disposição compacta.
CHAVES FILHO & STACCIARINI-SERAPHIN, 2001	A análise dos resultados mostrou que as plantas de *S. lycocarpum* apresentaram redução significativa nos valores de potencial osmótico em resposta ao estresse hídrico. O aumento no teor de carboidratos solúveis foi verificado em plantas sob condições estressantes em casa de vegetação, em particular o de carboidratos redutores. Os resultados obtidos sugerem que essa espécie apresenta mecanismo de ajustamento osmótico, nas condições de estresse hídrico, adaptando-a a sobrevivência nessa condição.
STEFANI, *et.al.*, 2000	Foi concluído que *E. brasiliensis* - *S. lycocarpum* - é um interessante sistema para o estudo de três interações tróficas com a presença da relação durante todas as estações, pela abundância forte da planta e da infestação em cerrados , pela diversidade de formigas e pela facilidade de manipulação do sistema.
VIDAL, *et.al.*, 1999	Os resultados apontam para uma característica adaptativa da espécie para sobrevivência em condições de baixa disponibilidade de água.

Tabela 2 - Estudos farmacológicos realizados com constituintes de S. lycocarpum

AUTOR/ANO	**ATIVIDADE ENCONTRADA**
BORBA, *et.al.*, 2010	Com os resultados obtidos, pode-se especular que o efeito anti-helmíntico de *S. lycocarpum* foi notado, devido à concentração de esteroides oligoglycosides alcaloide e de cadeia curta de ácidos graxos.
XAVIER, *et.al.*, 2010	Observação da influência dos extratos de *S. lycocarpum* nos parâmetros mortalidade dos caramujos sobreviventes.
SOARES, *et.al.*, 2010	Diferenças em relação ao crescimento/perda de peso em animais (machos) estudados.
ALMEIDA, *et.al.*, 2010	Apresenta efeito mutagênico
SCHWARZ, *et.al.*, 2009	Alteração no trânsito espermático.
COSTA, *et.al.*, 2008	Atividade anti-helmíntico relacionada à ação dos alcaloides esteroidais.
EANES *et al*, 2008	Glicoalcalóides de *S. lycocarpum* apresentaram atividade antifúngica.

CHAM, 2007	Solasodina possui atividade citotóxica contra alguns tumores
EMMANUEL *et al*., 2006	Solasodina possui efeito anti-inflamatório e inibidor enzimático
SILVA *et al*, 2006	Solasodina inibiu o crescimento do Trypanosoma cruzi, é capaz de curar feridas na pele causadas por Herpes, tem efeito anti-hepatotóxico em ratos, propriedades letais contra o molusco *Biomphalaria glabrata.*
SCHWARZ, *et.al.*, 2005	Efeito estrógeno a longo prazo.
MARUO, *et.al.*, 2003	O consumo de *S. lycocarpum* em 3%, na dieta durante a gravidez de ratos causou ligeiros efeitos toxicológicos.
MARUO, *et.al.*, 2003	Os resultados mostram diferenças relacionadas à toxidade em relação ao sexo. Efeito tóxico apenas em ratos machos.
OLIVEIRA, *et.al.*, 2003	Estudos demonstraram que o amido da fruta de *S. lycocarpum* não é um agente hipoglicêmico.
RODOVALHO, *et.al.*, 2003	O extrato etanólico bruto do fruto de *S. lycocarpum* possui efeito anti-inflamatório.
VIEIRA, *et.al.*, 2003	Efeito anti-inflamatório de *S. lycocarpum.*
FERREIRA, *et.al.*, 2002	Apresenta ação gastroprotetora das folhas de *S. lycocarpum*.
MOTTA, *et.al.*, 2002	Não apresentou efeito tóxico.
REIS, *et.al.*, 2002	Verificação de efeito fetotóxico de *S. lycocarpum*.
GRASSELLI, *et.al.*, 2001	Redução da glicemia quando consumiam o amido obtido dos frutos de *S. lycocarpum* como parte da dieta.
PETERS, *et.al.*, 2001	Não causou toxicidade.
SÁ, *et.al.*, 2001	O polvilho do fruto apresenta toxicidade na próstata ventral.
WEISSENBERG, 2001	O alcaloide Solasodina apresenta atividade como fungicida e controla o crescimento de inseto.
CALTAGIRONE *et al*., 2000	Possui alcaloides esteroidais semelhantes a hormônios sexuais.
Kuo, *et al*, 2000	O alcaloide solamargina inibiu o crescimento de células tumorais de cólon de útero, mama, hepatoma (fígado) e próstata.
SÁ, *et.al.*, 2000	Efeito tóxico de *S. lycocarpum* no sistema reprodutor masculino do rato Swiss (atividade antiandrogênica), mas não apresentou atividade antifertilidade nas doses analisadas.
GUERRA, *et.al.*, 1997	A solução aquosa do polvilho de *S. lycocarpum*, administrado durante o período de organogênese, afeta o desenvolvimento de fetos do sexo masculino.
MOLA *et al*., 1997; HARAGUCHI, *et al*., 1978; GOSWANI *et al*., 2003	Solasodina pode ser utilizada como um composto importante na síntese de hormônios esteroidais como os contraceptivos, fundamental para a produção de progesterona, cortisona e de andrógeno por ser um análogo da sapogenina.
KANWAR *et al*., 1990	Solasodina em testes *in vitro* com humanos e bovinos demonstraram redução da mobilidade dos espermatozoides também efeito tóxico na gestação e lactação em ratas e um aumento do fígado
DIXIT *et al*., 1989	Solasodina apresentou atividade antiespermatogênica em macacos na dose de 150mg/kg por 150 dias

CRUZ, 1982	*S. lycocarpum* é utilizada no tratamento de diabetes mellitus, obesidade, altas taxas de colesterol, asma, doenças hepáticas, inflamações.
DIXIT & GUPTA, 1982	Solasodina controla os níveis de colesterol em coelhos, efeito hipotensivo em gatos e atividade antiespermatogênica na dose de 20 mg/kg por 30 dias em cães.

Tabela 3 - Estudos químicos realizados com extratos/frações de *S. lycocarpum*

AUTOR/ANO	**ATIVIDADE ENCONTRADA**
MARTINS, *et.al.*, 2011	Dispersão de sementes por estradas de terra pode ser crucial na preservação da diversidade *S. lycocarpum* genética em paisagens fragmentadas.
ARAÚJO, *et.al.*, 2010	Os testes fitoquímicos demonstraram a presença de fenóis, taninos, saponinas, alcaloides e esteroides e triterpenos livres. O extrato foi fracionado em diferentes solventes para a avaliação da toxicidade frente à A. salina, apresentando considerável citotoxicidade encontrada na fração hidroalcoólica.
ARAÚJO, *et.al.*, 2010	Os glicoalcalóides solamargine e solasonine foram identificados através de TLC e GC / MS. Os níveis de fenóis totais e taninos foram quantificados no extrato.
MARTINS, *et.al.*, 2006	A amostragem deve incluir o maior número possível de populações em uma área ampla para permitir a maior manutenção possível da diversidade.
OLIVEIRA JUNIOR, *et.al.*, 2004	Observou-se diminuição dos teores de polifenóis e das atividades das enzimas peroxidase e polifenoloxidase e consequente diminuição do escurecimento da polpa do fruto.
OLIVEIRA JUNIOR, *et.al.*, 2003	Os teores encontrados na fruta-de-lobo de vitamina C, açúcares solúveis totais, sacarose, fósforo e ferro, comparados aos de outros frutos como abacaxi, banana, laranja, manga e outros, são equivalentes ou superiores aos dos frutos em questão, podendo-se concluir que o fruto da lobeira representa mais uma alternativa como fonte desses nutrientes.
CHAVES FILHO, *et.al.*, 2001	Os resultados obtidos sugerem que *S. lycocarpum* apresenta mecanismo de ajustamento osmótico, nas condições de estresse hídrico, adaptando-a a sobrevivência nessa condição.

Alcaloides esteroidais glicosilados (SGA) são metabólitos especializados derivados de triterpenos, encontrados na família Solanaceae, que exibem atividade como barreira química contra vasto número de patógenos. A biossíntese destes compostos envolve a ação de enzimas chaves como 3-hidroxi-3-metilglutaril coenzimaA redutase; esqualeno sintase; metiltransferases e glicotransferases. Estudos já realizados mostraram que a síntese de SGAs propriamente dita começa com a formação de colesterol, no entanto, a regulação gênica das etapas metabólicas posteriores da biossíntese destes alcaloides ainda não está totalmente elucidada (Idit *et al*., 2012). Figura 3.

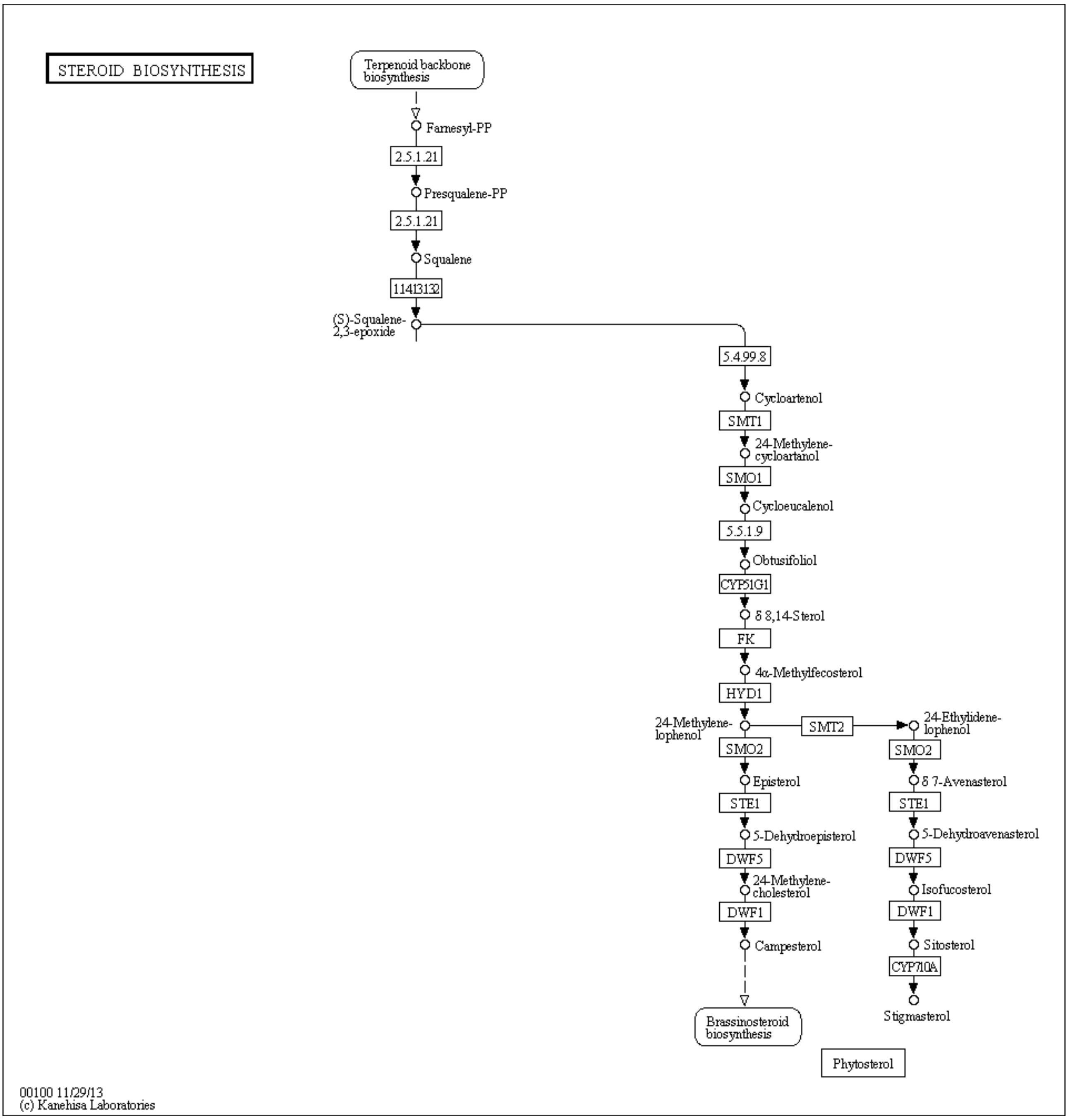


Figura 3 – Via da biossíntese de esteroides
Fonte: Kegg Pathway (http://www.genome.jp/kegg/pathway.html), adaptado pelo autor

Investigações conduzidas por Krits e col. (2007), mostraram correlação entre o nível de alcaloides glicosilados e a abundância de genes codificantes de HMG-CoA redutase (HMG1) e esqualeno sintase (SQS1) em tecidos de batata e em genótipos de batata apresentando diferentes conteúdos de SGA. Resultados sugerem que essas enzimas participam da regulação coordenada do metabolismo de isoprenóides e no metabolismo dos SGAs. Adicionalmente, foi demonstrado que a biossíntese dos SGAs em *Lycopersicum* também envolve a participação da enzima galactosiltransferase (GAME 1) responsável pela glicosilação do principal alcaloide biossintetizado por esta espécie, o α-tomatine (ITKIN e col.,2011).

Etapas da via de biossíntese dos glicoalcalóides esteroidais solamargina, solanina e solasodina, ainda não estão totalmente elucidadas e especialmente a sua regulação em nível transcricional. Estudos até então realizados para a identificação de genes codificadores de enzimas reguladoras da síntese de solamargina, solasonina e solasodina são poucos. Nesse sentido, abordagens de genômica funcional e transcriptômica em *S. lycocarpum* poderão contribuir para a identificação e compreensão da funcionalidade de genes envolvidos nos processos de biossíntese dessa classe de micromoléculas. O perfil de expressão desses genes poderá ser estudado com metodologias como o sequenciamento em larga escala de clones de cDNA, gerados a partir de amostras de RNA mensageiro obtidos da planta submetida a diferentes condições ambientais. O emprego de macroarranjos para a configuração de expressão diferencial de genes é de grande importância, pois permitem analisar simultaneamente a expressão de milhares de genes, embora outras técnicas forneçam novas estratégias de estudo (MITRA *et al*., 2003). Mais recentemente a identificação de genes expressos por meio de técnicas de RNA Seq.

As novas tecnologias de sequenciamento, denominadas de tecnologias de sequenciamento de nova geração, promovem o sequenciamento de DNA em plataformas capazes de gerar informação sobre milhões de pares de bases em uma única corrida. Dentre essas pode-se destacar: a plataforma 454 FLX da Roche, a Solexa da Illumina, a plataforma da Applied Biosystems, denominada SOLiD System, e o Heliscope True Single Molecule Sequencing (tSMS), da Helicos. Essas plataformas possuem como características comuns, gerar informações muitas vezes maior que o sequenciamento de Sanger, com uma grande economia de tempo e custo por base para o sequenciamento. Essa maior eficiência advém do uso da clonagem *in vitro* e de sistemas de suporte sólido para as unidades de sequenciamento, não precisando mais do intensivo trabalho laboratorial de produção de clones bacterianos, da montagem das placas de sequenciamento e da separação dos fragmentos em géis. A clonagem *in vitro* em suporte sólido permite que milhares de leituras possam ser produzidas de uma só vez. As novas plataformas de sequenciamento apresentam a grande vantagem de permitir um sequenciamento altamente representativo de genomas e/ou transcritomas em um único passo, o que é extremamente relevante, em razão da grande redução de custo alcançada com essas metodologias. Seu emprego tem revolucionado a transcritômica com a geração de dados altamente reprodutíveis e informativos e com precisão na quantificação de transcritos. Em função do problema da montagem das leituras curtas produzidas por essas tecnologias, seu uso na genômica de plantas tem sido direcionado para o sequenciamento dos genomas plastidiais, sequências expressas, clones de interesse, ressequenciamento e detecção de variantes genotípicas. Uma combinação de alguma dessas tecnologias à tecnologia de Sanger poderia associar o baixo custo e a alta representatividade da primeira à facilidade de montagem do genoma da segunda, facilitando seu emprego no sequenciamento genômico de plantas (CARVALHO, 2010).

Um dos objetivos principais do avanço científico na área de biologia molecular é a análise dos genomas dos seres vivos. As ESTs – *Expressed Sequence Tags*, ou Etiquetas de Sequências Expressas, correspondem a pedaços de genes expressos, derivados de RNAs mensageiros, que são utilizados na análise de transcriptomas de organismos. A denominação etiquetas é em razão de que correspondem apenas a pedaços dos genes que um organismo expressa quando em uma determinada situação. Essas etiquetas permitem identificar quais genes estão sendo induzidos ou reprimidos produzidos por uma célula determinada condição e permitem também a realização de estudos comparativos (PROSDOCIMI, 2007). De acordo com Lesk (2008), há diversos bancos de dados de ESTs. Em sua maioria, as entradas contém campos que indicam os tecidos de origem e/ou a localização subcelular, a fase do desenvolvimento, o crescimento e a quantificação dos níveis de expressão.

O NCBI – Centro Nacional para Informação Biotecnológica dos EUA, é considerado o banco de dados central sobre informações genômicas. Vários outros bancos de dados similares estão distribuídos por países da Europa e Japão, mas todos trocam dados com o NCBI diariamente (MOREIRA, 2012).

O GenBank é o principal banco de dados do NCBI e armazena todas sequências disponíveis publicamente de DNA, RNA e proteínas. Além do GenBank, que coleta todas as entradas de sequências, outros bancos do NCBI apresentam as informações organizadas de diferentes maneiras.

Um dos desafios encontrados pela bioinformática é a busca por uma boa maneira para armazenar, consultar e tratar dados oriundos de pesquisas em projetos transcriptomas, em bancos de dados, para que se consiga, futuramente, compartilhar a informação, contida nesses bancos de dados, da melhor maneira possível (WIECZOREK; LEAL, 2002). Lifschitz (2006) ainda justifica a importância da utilização de banco de dados na bioinformática citando a quantidade de dados que alguma dessas bases de dados possuem.

Prosdocimi et.al. (2003) descreve que devido ao grande volume de dados que esses bancos armazenam, o acesso a esses dados são disponibilizados na Internet para acesso *online*. Esses bancos de dados, que envolvem sequências de nucleotídeos, aminoácidos, ou estrutura de proteínas, podem ser classificados como primários e secundários. Os bancos de dados primários possuem como característica o depósito de sequências de nucleotídeos, aminoácidos ou estruturas proteicas, sem que essas passem por análises ou algum processamento.

Os bancos de sequências também podem ser classificados em bancos estruturais ou bancos funcionais. Sequências de nucleotídeos, de aminoácidos e estruturas de proteínas apresentam informações diferentes, apesar de representarem o produto de um gene, e devem ser armazenados em bancos específicos. Nos bancos de dados estruturais são mantidos apenas dados relativos à estrutura de proteínas, já em bancos funcionais, são fornecidos *links* para mapas metabólicos de organismos com genoma parcialmente ou totalmente elucidados. As buscas são realizadas a partir de palavras-chave ou de sequências. O principal banco funcional é o Kyoto Encyclopedia of Genes and Genomes conhecido como KEGG (PROSDOCIMI et.al., 2003 *apud* FANTINATO, 2015).

O estudo do transcriptoma de *S. lycocarpum* poderá contribuir na elucidação das vias genéticas envolvidas com a biossíntese de SGAs e outros metabólitos com atividades de interesse biotecnológico, a exemplo da solamargina e solasonina. A partir da identificação dos genes dessas vias, poderão ser desenvolvidos trabalhos de engenharia genética para expressão heteróloga em organismos que comportem a produção destas substâncias ou ainda poderão ser úteis no sentido de manipulação genética de culturas *in vitro de S. lycocarpum,* voltadas ao aumento da produção de tais substâncias. Dessa forma, nesse trabalho foi feita a construção de um banco de ESTs obtidas de células em cultura, órgãos e tecidos de *S. lycocarpum*. A análise deste banco permitirá o acompanhamento dos níveis de expressão coordenada dos genes potenciais identificados e relacionados à regulação de vias de biossíntese de metabólitos secundários e outras em resposta a agentes causadores de estresse físico, químico ou biológico. Para essa finalidade, foram integradas ferramentas computacionais já disponíveis, como as exemplificadas na tabela 4 e foi desenvolvida ferramenta de pesquisa no banco de dados para identificação automática de dados de sequências, facilitar a exploração de outras características e viabilizar uma análise rápida para preconização da funcionalidade dos genes expressos sob as condições ambientais a que a espécie medicinal modelo está exposta em seu habitat.

A prospecção de genes relacionados a vias de biossíntese específicas pode ser realizada por meio uso de oligos (*primers*) desenhados com base em regiões conservadas de genes codificadores de enzimas chaves. Nesse sentido é possível realizar varreduras *in sílico* em bibliotecas de genes expressos, buscando identificar homólogos.

A construção, análise de um banco de sequências e o uso *in sílico* de *primers* na investigação do transcriptoma de *S. lycocarpum*, justifica-se pela possibilidade de identificar genes relacionados com a biossíntese de glicoalcaloides e outros metabólitos com atividades de interesse biotecnológico.

A análise de sequência expressa é trabalhosa e demorada, segundo Villas-Bôas e Gombert (2006), existem diversas ferramentas computacionais correlatas disponíveis no mercado e na Internet, que permitem realizar tratamentos de dados gerados a partir de amostras de dados multivariados. Não há um único método para tratamento dos dados multivariados. Em alguns casos, pesquisadores analisam as imagens obtidas utilizando-se de programas específicos (vide tabela 4), e os arquivos gerados pelos programas são exportados para um *software* tipo planilha eletrônica, para posterior análise estatística.

Propõe-se integrar e aplicar ferramentas computacionais já disponíveis bem como desenvolver um *software* para identificação automática de dados de sequências para facilitar a exploração de outras características e viabilizar uma análise rápida para preconização de funcionalidade de genes expressos sob as condições ambientais a que a espécie medicinal modelo está exposta em seu habitat. Pretende-se ainda criar uma estrutura de banco de dados para armazenamento e manipulação de sequências e disponibilizar em um sistema *web* para validação das referidas sequências e posterior comunicação com outras bases internacionais.

Tabela 4 – Relação de programas computacionais úteis para análise de perfil de expressão gênica
Fonte: Felix *et al.* (Biotecnologia Ciência & Desenvolvimento : 24,2002), adaptada pelo autor

***Softwares* para Banco de Dados**	
MAExplorer Padrões de DataMining e Expressão Gênica	http://www.lecb.ncifcrf.gov/MAExplorer/
MGED Grupo de Banco de dados de expressão gênica em Microarrays	http://www.mged.org/
Exemplos de Banco de Dados para Expressão Gênica	
Multi Experiment Viewer; Aplicação Java que permite análise de dados de Microarrays para identificar padrões de expressão e genes diferencialmente expressos	http://www.tigr.org/softlab/
NIH Banco de dados de expressão gênica, Molecular Pharmacology of Cancer	http://discover.nci.nih.gov/nature2000/naturemain.html
MGV Visão global sobre Microarray de levedura	http://transcriptome.ens.fr/ymgv/
***Softwares* para Análises**	
ArrayViewer Visualização e análise de dados de Microarrays . Gratuito	http://www.tigr.org/softlab/
Chromas Pro; Technelysium Pty Ltd	http:// http://technelysium.com.au
Cluster Software de clusterização; Michael Eisen, Eisen Lab, University of California, Berkeley – gratuito	http://rana.lbl.gov/EisenSoftware.htm
Expresssion Profiler Ferramenta para clusterização, análise e visualização de expressão gênica. Análises online. Gratuito	http://ep.ebi.ac.uk/
SAM Análise de Significância de Microarrays . Gratuito	http://www-stat.stanford.edu/~tibs/SAM/
Spotfinder Detecta e quantifica spots. Gratuito	http://www.tigr.org/softlab/
Treeview Visualização e clusterização de dados provindos do software Cluster; Michael Eisen, Eisen Lab, University of California, Berkeley. Gratuito	http://rana.lbl.gov/EisenSoftware.htm

A construção de um banco de dados de genes expressos de *S. lycocarpum* foi motivada pela importância biotecnológica dos produtos naturais da planta modelo. A identificação de genes destas vias, permitirá futuramente, a manipulação genética para induzir aumento na biosíntese de SGAs em culturas de células e tecidos de *S. lycocarpum* ou por expressão heteróloga em outros organismos.

A construção e análise de um banco de sequências do transcriptoma de *S. lycocarpum*, possibilitará a identificação de novos genes e a busca *in sílico* com *primers* desenhados para o rastreamento de genes relacionados à regulação de SGAs.

2. OBJETIVOS

2.1 Objetivos gerais

Implementar um sistema computacional para armazenamento de dados de sequências de genes expressos relacionados à biossíntese de produtos naturais bioativos, tendo como modelo a espécie *Solanum lycocarpum*.

2.2 Objetivos específicos

- Estruturar um banco de genes relacionados à produção de metabólitos secundários bioativos em *S. lycocarpum;*
- Realizar buscas *in sílico* para categorizar genes expressos em órgãos específicos de *S. lycocarpum*;
- Subsidiar a preconização de funcionalidade de genes expressos com potencial interesse biotecnológico;
- Utilizar ferramentas computacionais para o desenho de *primers* nucleotídicos, visando o rastreamento de bibliotecas de cDNA, na busca de genes do metabolismo secundário.

3. MATERIAIS E MÉTODOS

Para o desenvolvimento do DataNature, foram utilizadas algumas técnicas para identificar o perfil de expressão gênica de metabólitos bioativos em *S. lycocarpum*. A sequência representada na figura 4, demonstra o *pipeline* utilizado.

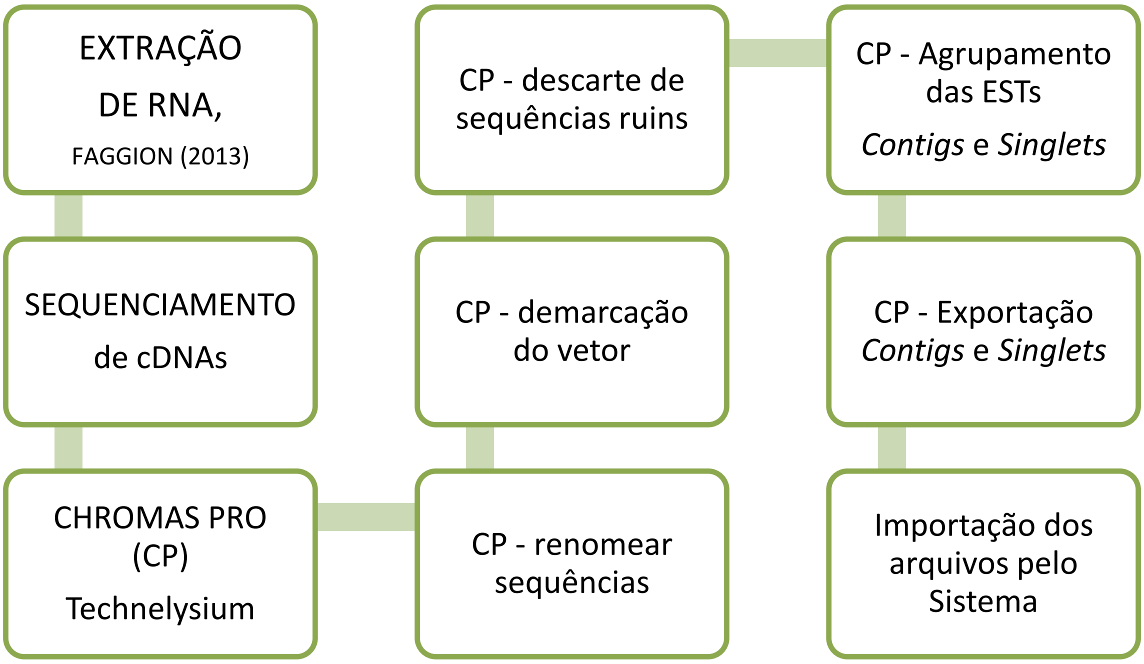


Figura 4 – *Pipeline* para manipulação de dados e alimentação do Sistema

3.1 Obtenção de biblioteca de sequências expressas

O trabalho de extração do RNA total, obtenção do conjunto de RNA mensageiros e construção de biblioteca de cDNA de diferentes órgãos de *S. lycocarpum* foi realizado pelo grupo de trabalho da Unidade de Biotecnologia da UNAERP. Após obtenção de clones e extração plasmidial foi realizado o sequenciamento randômico de genes expressos em sementes, folhas e calos de *S. lycocarpum*, através do método Sanger. O resultado do sequenciamento são as sequências fasta de nucleotídeos, designadas como expressed sequence tags (ESTs), que fornecem informações valiosas que podem ser usadas para prever a funcionalidade de genes envolvidos na síntese de metabólitos, primários e secundários. Os resultados repassados em arquivo digital com a extensão ab1. A partir do sequenciamento do material de *S. lycocarpum*, foram identificadas 1248 ESTs brutas.

3.2 Trabalho *in sílico*

A partir da conversão dos cromatogramas em sequências fasta, inicia-se o trabalho de bioinformatica com o uso do *software* Chromas Pro (versão 1.7.6), desenvolvido pela Technelysium (2009) para plataforma Windows, e assim esses arquivos digitais foram importados gerando um novo projeto. Cada uma das sequências ao ser importada para o Chromas Pro deve ser renomeada seguindo um padrão, como por exemplo: SLSEPL01A01, em que SL indica que são de *S. lycocarpum*, SE indica que se trata desses extraídos da semente, PL01 indica o número da placa e A01 indica a posição da EST na placa de 96 poços; para as sequências de folhas utilizou-se a codificação FL e para sequência de calos utilizou-se a codificação CA.

Na etapa *in vitro* de extração do RNA, foi utilizado o vetor pGEM-T Easy, portanto todas as EST brutas sequenciadas contêm no início e no fim das sequências, resquícios do vetor que devem ser retirados. Essa etapa é possível, inserindo o arquivo digital com a sequência FASTA contendo o vetor no *software* Chromas Pro. É feita uma análise visual de cada sequência e respeitando-se a marcação das bases do vetor no início e no fim da sequência, para o corte do vetor. Ainda nessa análise visual deve-se retirar também, parte das sequências cuja leitura está danificada, deixando somente sequências visivelmente boas. Outro ponto importante é a exclusão/descarte das sequências ruins.

Após as etapas anteriores em que são retirados fragmentos do vetor e, faz-se a exclusão/descarte de sequências ruins, partimos para a análise *in sílico*, onde utilizando as configurações padrões (*default settings*) do Chromas Pro para realização do Assembly, é alterado o mínimo de identidade (Minimum identity) para 90%. Todas as sequências são selecionadas e um comando Assembler é ativado. O comando Assembler possui um algoritmo que analisa todas as sequências selecionadas e as compara, fazendo um agrupamento das ESTs redundantes, criando os chamados *Contigs*, e as EST não redundantes que não se agruparam são mantidas isoladas e denominadas de *Singlets*. A exportação dos *Contigs* e *Singlets* no formato FASTA resulta na geração de 2 arquivos digitais no formato FASTA (um com as sequências de *Contigs* e outro com as sequências de *Singlets*), para cada órgão específico (sementes, folhas e calos).

Com a formação dos *Contigs* e dos *Singlets*, os mesmos foram comparados com a base de dados não redundantes do National Center for Biotechnology Information – NCBI, para verificação se os *Contigs* e *Singlets* possuem homologia com sequências de algum organismo já identificado e categorizado. A plataforma *on-line* do NCBI possui vários *softwares* que fazem diversos tipos de análises e comparações. A análise *in sílico* foi feita para cada biblioteca construída: 1ª. analisando as ESTs de sementes, 2ª. analisando as ESTs de folhas e a 3ª. analisando as ESTs de calos de *S. lycocarpum*.

A partir dos primeiros dados, observou-se que a análise e comparação com a base de dados do NCBI já poderia ser integrada ao sistema computacional desenvolvido e os resultados armazenados em base de dados própria. Iniciou-se então a estruturação e confecção do sistema computacional com a finalidade de integrar e aplicar ferramentas adequadas para identificação automática de sequências. Adicionalmente a exploração de outras características estruturais voltadas para preconização de funcionalidade de genes de *S. lycocarpum* já identificados, pode ser agilizada. Criou-se uma estrutura de banco de dados para armazenamento e manipulação de sequências, conforme pode ser visto na Figura 5. Essas sequências estão disponíveis no sistema para consulta de usuários, validação e integração com bases nacionais e internacionais já existentes.

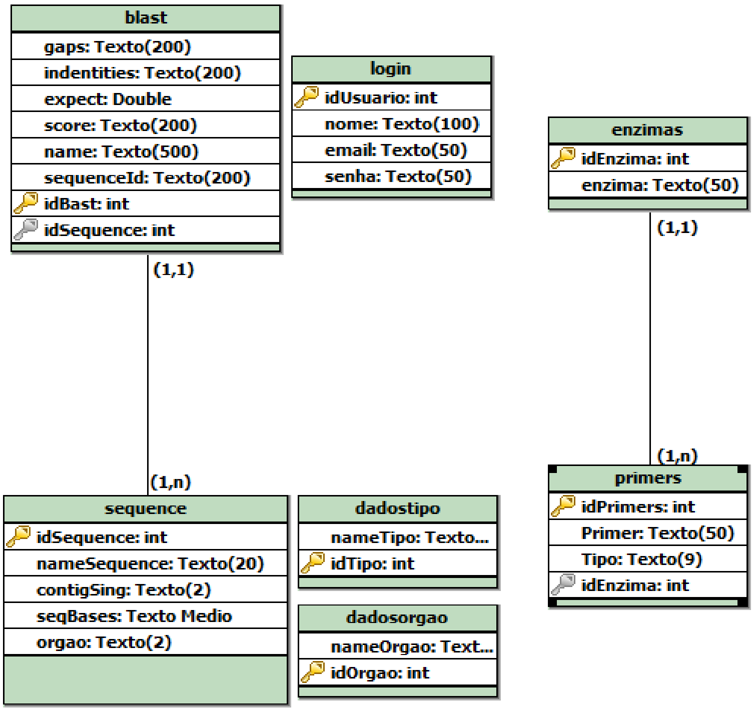


Figura 5 – Estrutura do banco de dados do DataNature

3.3 Critérios de alinhamento de sequências

Na análise dos resultados, foram consideradas 3 respostas possíveis: 1ª. No *significant similarity found*, que indica que a EST verificada não possui semelhança com nada depositado na base de dados não redundante do NCBI; 2ª. *No Hits*, indica que apesar de apresentar similaridade com sequências já depositadas, o grau de confiabilidade é relativamente baixo, ou seja, com e-Value > e^{-10}; e a 3ª. resposta seriam as ESTs com e-Value < e^{-10}, com similaridade a sequências de plantas e outros organismos de interesse.

3.4 Desenho de *primers*

Para a definição dos *primers* foram utilizados *softwares* já existentes, onde em um *pipeline* (Figura 21) desses, chega-se ao resultado esperado.

- Através da descoberta da via metabólica de cada enzima, no Keeg Pathway– Steroid biosynthesis (http://www.genome.jp/kegg/pathway), são verificadas e anotadas informações úteis, sobre a enzima de interesse;
- De posse dessas informações, recorre-se ao NCBI – Nucleotide (http://www.ncbi.nlm.nih.gov/nuccore), onde é pesquisado pelo nome e código de cada enzima, para obtenção da sequência Fasta da mesma;
- Com a sequência Fasta, faz-se a pesquisa e desenho de oligos degenerados através do aplicativo Primer3 (http://simgene.com/Primer3), obtendo-se então o conjunto de *primers* úteis para o rastreamento *in sílico* de bibliotecas de cDNA e para experimentos laboratoriais de validação de expressão de genes por qPCR.

4. RESULTADOS E DISCUSSÃO

4.1 Resultados Obtidos - Transcriptoma

Os dados a seguir são resultado do sequenciamento randômico das bibliotecas de cDNA, após realização do *pipeline*, descrito na figura 4. Foram clonados 1248 cDNAs de sementes, folhas e calos, de *S. lycocarpum*. Desse total de ESTs obteve-se os seguintes dados:

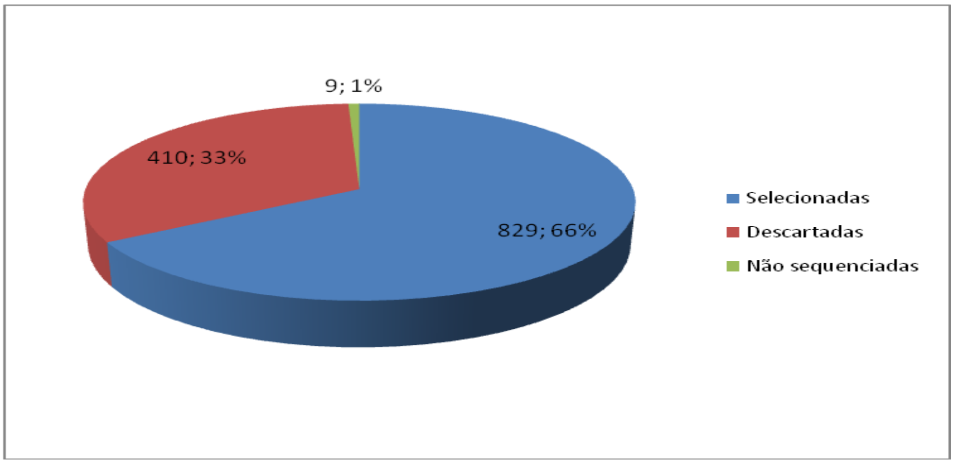


Gráfico 1 - Sequências identificadas de sementes, folhas e calos de *S. lycocarpum*

Fonte: Elaborado pelo autor.

Com a analise do gráfico 1, conclui-se que, dos 1248 clones contendo cDNAs de sementes, folhas e calos foram descartadas 410 sequências, que equivalem a 33%, por apresentarem baixa qualidade e 9 ESTs, que equivalem a 1%, não foram sequenciadas.

O gráfico 2 mostra a distribuição das ESTs selecionadas de sementes, folhas e calos. Neste estão representados dois conjuntos: ESTs que se agruparam em *Contigs* e sequências isoladas que foram designadas como *Singlets*.

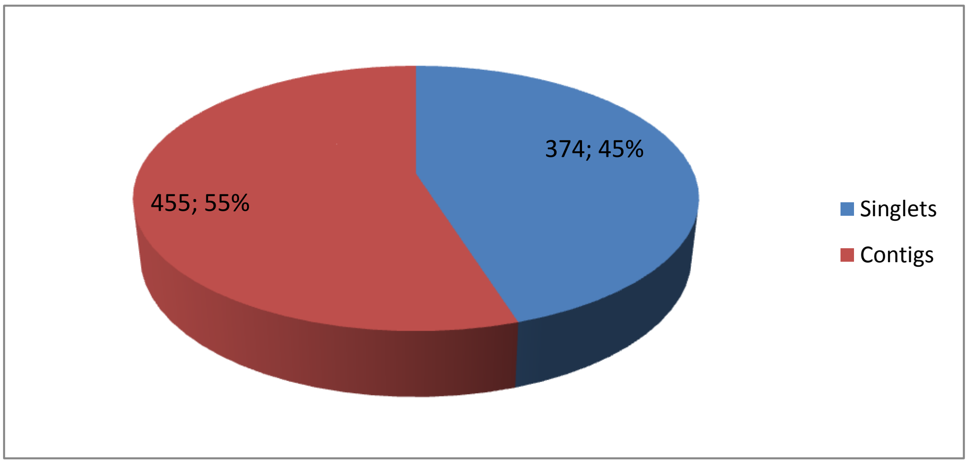


Gráfico 2 - ESTs de sementes, folhas e calos isoladas e identificadas: *Singlets* e *Contigs*

Fonte: Elaborado pelo autor.

Nota-se que 55% (455) das ESTs identificadas possuem algum tipo de homologia e formaram 85 *Contigs* (18 de sementes, 36 de folhas e 32 de calos) e 45% (374) das ESTs não se agruparam e foram designadas como *Singlets* (140 de sementes, 92 de folhas e 142 de calos).

As tabelas contidas no apêndice A e B (sementes), C e D (folhas) e E e F (calos), mostram os resultados, após a realização de uma pesquisa no NCBI, utilizando o pacote BlastX. Já a tabela apêndice G mostra a partir da seleção de proteínas de interesse uma busca *in sílico* na base de dados do NCBI. Para todas as tabelas foram adotados como parâmetros:

- Sequence ID: Código do Gene homólogo encontrado na base de dados não redundante do NCBI;
- Name: Nome da sequência conhecida/depositada que apresenta homologia com a sequência em análise;
- Score: Número de sinais analisados;
- Expect ou eValue: Índice de confiabilidade dos resultados;
- Identities: Quantidade (%) de aminoácidos idênticos no intervalo (cobertura) de sequência analisada;
- Gaps: Falhas no comparativo.

4.2 Desenvolvimento do DataNature

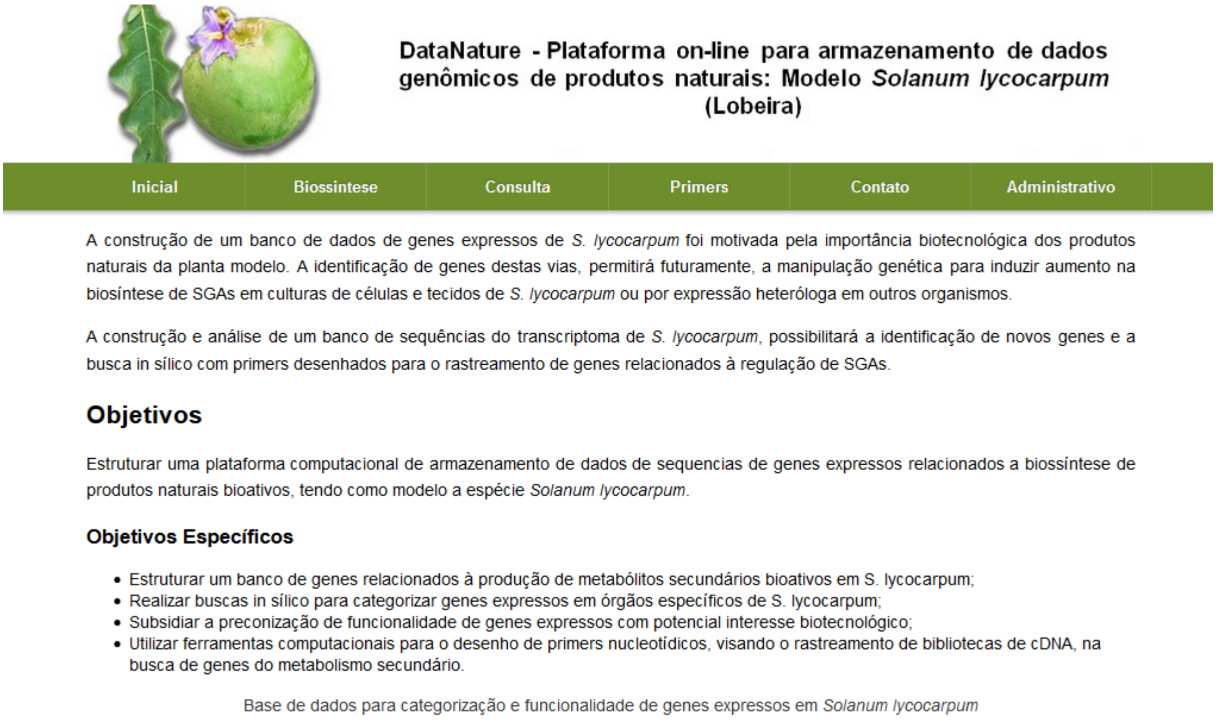
O sistema DataNature foi desenvolvido na tecnologia ASP.NET, uma plataforma para a Rede Mundial de Computadores (WEB), que fornece todos os serviços necessários para construir aplicações web profissionais baseadas em servidor. A tecnologia ASP.NET é baseada em .NET Framework, assim o sistema desenvolvido é dotado de todos os recursos dessa modelagem Os aplicativos podem ser escritos em qualquer linguagem compatível com o Common Language Runtime (CLR), incluindo Visual Basic e C#. No sistema foi utilizado a linguagem C#, que é uma linguagem de programação criada para o desenvolvimento de uma variedade de aplicações que são executadas em .NET Framework . C# é uma linguagem simples, poderosa, com tipagem segura e orientada a objetos. As várias inovações no C# permitem o desenvolvimento rápido de aplicações, mantendo o estilo das linguagens C. Foi utilizada também a biblioteca .NET Bio que é um kit de ferramentas de bioinformática, inicialmente voltado para a área de pesquisa Genomica, desenvolvido em linguagem neutra, construído como uma extensão para o Microsoft .NET Framework. Atualmente, implementa uma série de analisadores para formatos de arquivo de bioinformática comum; uma variedade de algoritmos para manipulação de DNA, RNA e sequências de proteínas; e um conjunto de conectores para serviços web biológicos, tais como NCBI BLAST. No sistema foi utilizado o BlastX, que permite a pesquisa em base de dados não redundante de sequências de proteínas usando sequências de nucleotídeos convertidas. Para armazenamento dos dados optou-se pelo sistema gerenciador de banco de dados MySQL, que é um banco de dados de código aberto, que possibilita processamento ágil de aplicativos de banco de dados confiáveis, de alto desempenho e escaláveis.

O sistema é composto pelas seguintes páginas: Página Inicial, Biossíntese, Consulta, *Primers*, Contato e Administrativo. A página Administrativo, ainda se subdivide em: Inserir Dados, Exportar para XLS, Inserir Usuário, Altera Dados, Acessar Busca e Novo Primer. Ainda na área administrativa, têm-se as seguintes opções:

- Exportar para XLS, que tem a finalidade de exportar os dados que estão no banco de dados para um arquivo tipo planilha eletrônica com a extensão XLS. Para isso basta selecionar o tipo e o órgão específico que deseja ser exportado;
- Altera Dados, que permite mudar as informações sobre o tipo de ESTs e o órgão fonte da sequência salva no banco. Essas informações são as únicas susceptíveis a engano no armazenamento da sequência. Para alterar, é necessário informar o tipo, órgão específico e etiqueta da sequência armazenada. após a busca ser realizada aparecerá uma tabela com os identificadores, basta selecionar a sequência que deseja alterar e, abaixo da tabela selecionar, as novas informações para aquela sequência. Pode-se também apagar dados armazenados.

4.3 Apresentação do DataNature

A aplicação foi hospedada inicialmente em um dos servidores de arquivos e aplicação do Instituto Federal de Educação, Ciência e Tecnologia do Sul de Minas Gerais (IFSULDEMINAS), *Campus* Machado, devido à facilidade para administração e atualização dos dados. A figura 6 demonstra a tela inicial do sistema, onde temos já disponíveis informações sobre o software, objetivos gerais e específicos do projeto, botão de consulta à via de biossíntese, botão de consulta ao banco de dados, botão de consulta aos *primers* armazenados, contato e acesso à área administrativa.



DataNature - Plataforma on-line para armazenamento de dados genômicos de produtos naturais: Modelo *Solanum lycocarpum* (Lobeira)

A construção de um banco de dados de genes expressos de *S. lycocarpum* foi motivada pela importância biotecnológica dos produtos naturais da planta modelo. A identificação de genes destas vias, permitirá futuramente, a manipulação genética para induzir aumento na biosíntese de SGAs em culturas de células e tecidos de *S. lycocarpum* ou por expressão heteróloga em outros organismos.

A construção e análise de um banco de sequências do transcriptoma de *S. lycocarpum*, possibilitará a identificação de novos genes e a busca in sílico com primers desenhados para o rastreamento de genes relacionados à regulação de SGAs.

Objetivos

Estruturar uma plataforma computacional de armazenamento de dados de sequencias de genes expressos relacionados a biossíntese de produtos naturais bioativos, tendo como modelo a espécie *Solanum lycocarpum*.

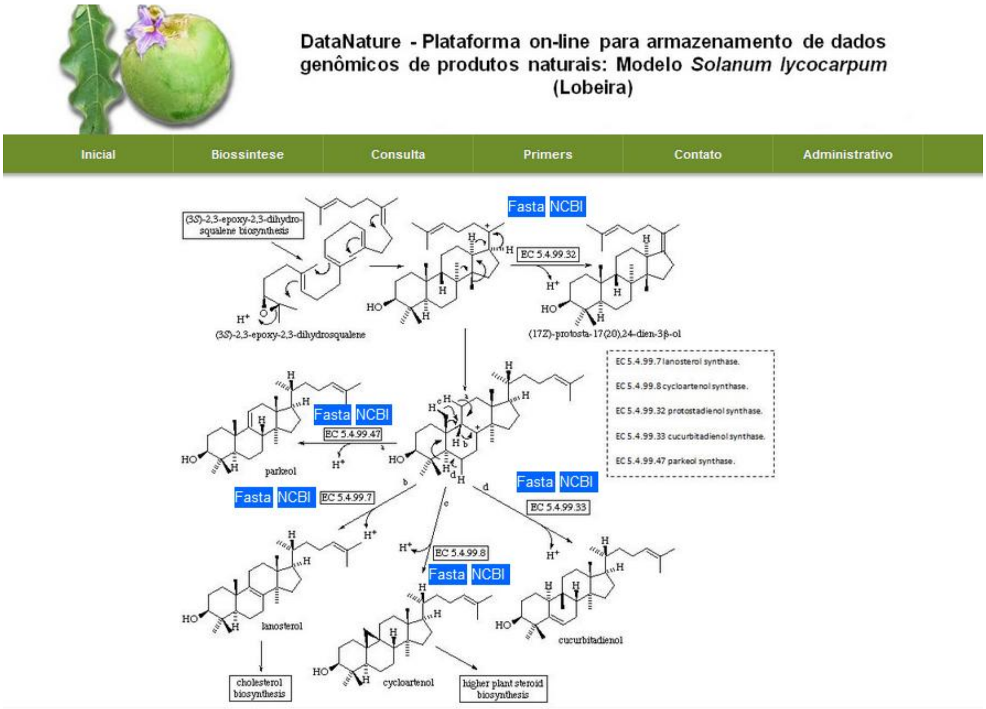
Objetivos Específicos

- Estruturar um banco de genes relacionados à produção de metabólitos secundários bioativos em S. lycocarpum;
- Realizar buscas in sílico para categorizar genes expressos em órgãos específicos de S. lycocarpum;
- Subsidiar a preconização de funcionalidade de genes expressos com potencial interesse biotecnológico;
- Utilizar ferramentas computacionais para o desenho de primers nucleotídicos, visando o rastreamento de bibliotecas de cDNA, na busca de genes do metabolismo secundário.

Base de dados para categorização e funcionalidade de genes expressos em *Solanum lycocarpum*

Figura 6 – Tela inicial do sistema
Disponível em: http://compserver.mch.ifsuldeminas.edu.br/geneluciano/Default.aspx

A figura 7 apresenta a via de biossíntese, escolhida inicialmente como roteiro de pesquisa, para elucidação de novas vias e conhecimento completo da via já existente.



DataNature - Plataforma on-line para armazenamento de dados genômicos de produtos naturais: Modelo *Solanum lycocarpum* (Lobeira)

Figura 7 – Via de Biossíntese

A figura 8 apresenta a opção consulta, onde temos acesso as informações armazenadas na base de dados, referentes as ESTs já analisadas, categorizadas bem como comparadas com a base do NCBI.

DataNature - Plataforma on-line para armazenamento de dados genômicos de produtos naturais: Modelo *Solanum lycocarpum* (Lobeira)

Pesquisar por: ○ Name ○ Sequence ID ○ Fasta ○ Primers ○ Todos

Órgão: Todos

Tipo: Todos

Reverse:

cForward:

Descrição:

Base de dados para categorização e funcionalidade de genes expressos em *Solanum lycocarpum*

Figura 8 – Tela Consulta

Pode-se observar além do layout padrão para as outras telas, a caixa de seleção para as pesquisas na base de dados, em que temos as seguintes opções: caixa de seleção, pesquisar por: onde o usuário define se a pesquisa vai ser por

Name, Sequence ID, Fasta, *Primers* ou Todos (deve-se obrigatoriamente marcar uma das opções); a caixa de seleção órgão: na qual o usuário escolhe sobre que órgão específico deseja obter resultados; a caixa de seleção tipo: onde o usuário define se a pesquisa vai ser na base de *contigs*, *singlets* ou todos; a caixa de texto reverse ou forward: que é habilitada somente quando a pesquisa for por *primers*; a caixa de texto descrição: em que o usuário digita a enzima de interesse; o botão buscar: que inicia a pesquisa; e botão manual de utilização que trará um manual descritivo de como operar as pesquisas.

Como demonstração de uma pesquisa na base de dados, temos a figura 9. Nesse exemplo foi feita uma pesquisa por Name, buscando todos os *Contigs* de Semente que tenham relação com *solanum*. Nota-se que logo abaixo do botão buscar, aparece uma tabela, com os resultados da pesquisa. Nesse caso foram encontrados 4 resultados para a pesquisa. Em cada um dos resultados, temos a opção de selecionar, que nos leva para outra tela (figura 10), já com os resultados.

DataNature - Plataforma on-line para armazenamento de dados genômicos de produtos naturais: Modelo *Solanum lycocarpum* (Lobeira)

Pesquisar por: ● Name ○ Sequence ID ○ Fasta ○ Primers ○ Todos

Órgão: Sementes

Tipo: Contig

Reverse:

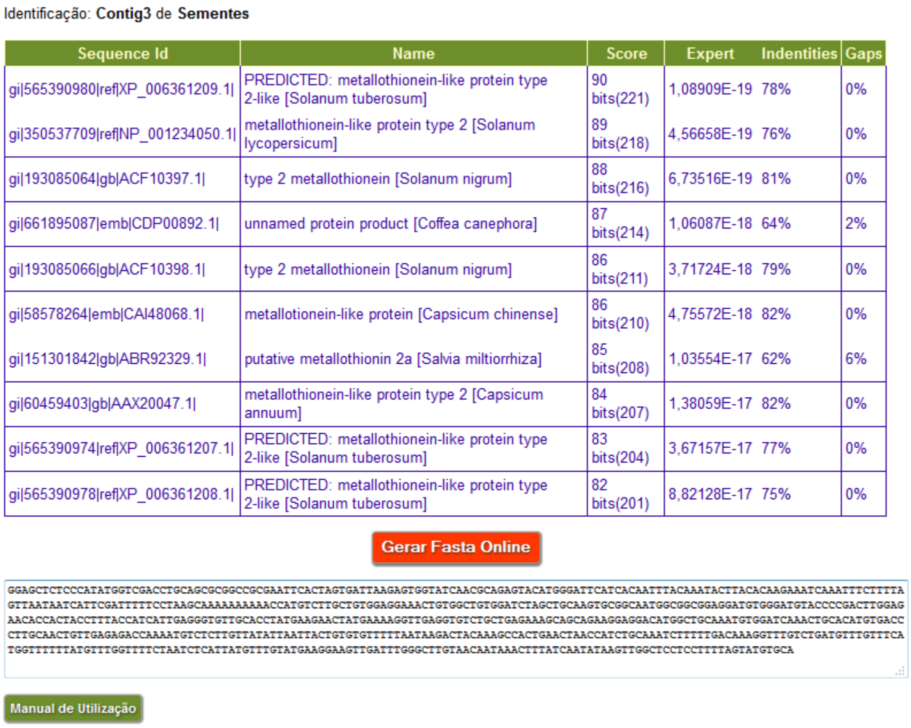
cForward:

Descrição: solanum

	nameSequence	Orgao
Selecionar	Contig3	Sementes
Selecionar	Contig6	Sementes
Selecionar	Contig10	Sementes
Selecionar	Contig13	Sementes

Base de dados para categorização e funcionalidade de genes expressos em *Solanum lycocarpum*

Figura 9 – Tela de exemplo de uma consulta a base de dados



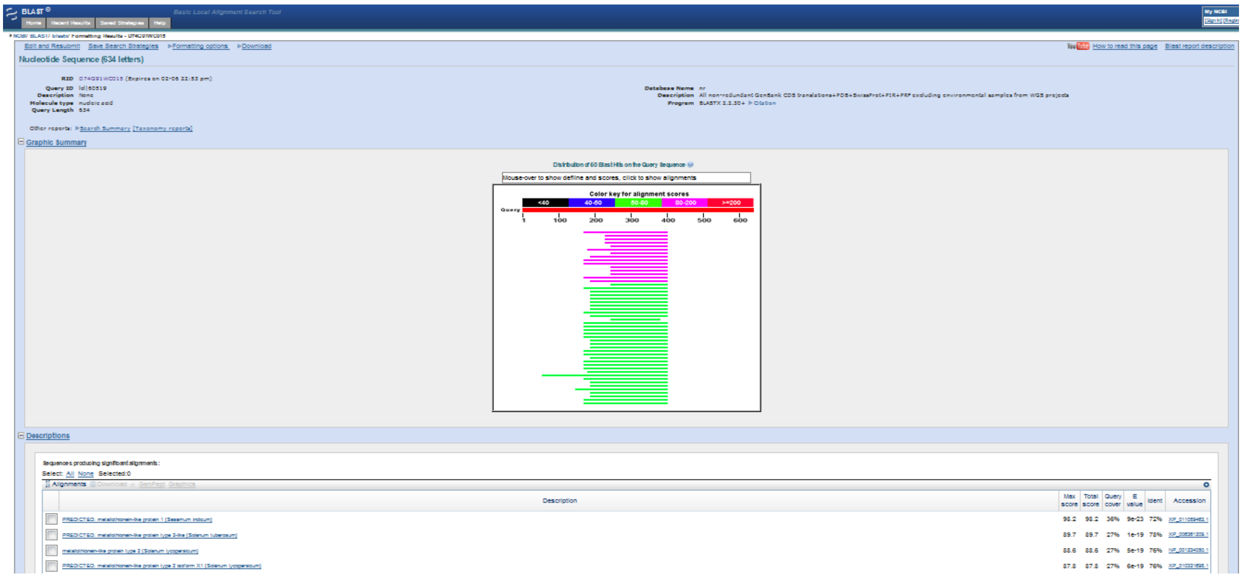
Identificação: **Contig3** de **Sementes**

Sequence Id	Name	Score	Expert	Indentities	Gaps
gi|565390980|ref|XP_006361209.1|	PREDICTED: metallothionein-like protein type 2-like [Solanum tuberosum]	90 bits(221)	1,08909E-19	78%	0%
gi|350537709|ref|NP_001234050.1|	metallothionein-like protein type 2 [Solanum lycopersicum]	89 bits(218)	4,56658E-19	76%	0%
gi|193085064|gb|ACF10397.1|	type 2 metallothionein [Solanum nigrum]	88 bits(216)	6,73516E-19	81%	0%
gi|661895087|emb|CDP00892.1|	unnamed protein product [Coffea canephora]	87 bits(214)	1,06087E-18	64%	2%
gi|193085066|gb|ACF10398.1|	type 2 metallothionein [Solanum nigrum]	86 bits(211)	3,71724E-18	79%	0%
gi|58578264|emb|CAI48068.1|	metallotionein-like protein [Capsicum chinense]	86 bits(210)	4,75572E-18	82%	0%
gi|151301842|gb|ABR92329.1|	putative metallothionin 2a [Salvia miltiorrhiza]	85 bits(208)	1,03554E-17	62%	6%
gi|60459403|gb|AAX20047.1|	metallothionein-like protein type 2 [Capsicum annuum]	84 bits(207)	1,38059E-17	82%	0%
gi|565390974|ref|XP_006361207.1|	PREDICTED: metallothionein-like protein type 2-like [Solanum tuberosum]	83 bits(204)	3,67157E-17	77%	0%
gi|565390978|ref|XP_006361208.1|	PREDICTED: metallothionein-like protein type 2-like [Solanum tuberosum]	82 bits(201)	8,82128E-17	75%	0%

```
GGAGCTCTCCCATATGGTCGACCTGCAGCGCGGCCGCGAATTCACTAGTGATTAAGAGTGGTATCAACGCAGAGTACATGGGATTCATCACAATTTACAAATACTTACACAAGAAATCAAATTTCTTTTA
GTTAATAATCATTCGATTTTTCCTAAGCAAAAAAAAAAACCATGTCTTGCTGTGGAGGAAACTGTGGCTGTGGATCTAGCTGCAAGTGCGGCAATGGCGGCGGAGGATGTGGGATGTACCCCGACTTGGAG
AACACCACTACCTTTACCATCATTGAGGGTGTTGCACCTATGAAGAACTATGAAAAGGTTGAGGTGTCTGCTGAGAAAGCAGCAGAAGGAGGACATGGCTGCAAATGTGGATCAAACTGCACATGTGACC
CTTGCAACTGTTGAGAGACCAAAATGTCTCTTGTTATATTAATTACTGTGTGTTTTTAATAAGACTACAAAGCCACTGAACTAACCATCTGCAAATCTTTTTGACAAAGGTTTGTCTGATGTTTGTTTCA
TGGTTTTTTATGTTTGGTTTTCTAATCTCATTATGTTTGTATGAAGGAAGTTGATTTGGGCTTGTAACAATAAACTTTATCAATATAAGTTGGCTCCTCCTTTTAGTATGTGCA
```

Figura 10 – Tela de exemplo com o resultado de uma consulta a base de dados

Nota-se na figura 10, que, após selecionarmos o Contig3, o software nos retorna os resultados armazenados após realização do BlastX. Para compor a tabela de armazenamento, foram considerados os seguintes campos de retorno do BlastX: Sequence ID, que é o código do gene homólogo encontrado na base de dados não redundante do NCBI; Name, que é o nome da sequência conhecida/depositada que apresenta homologia com a sequência em análise; Score, que é o número de sinais analisados; Expect ou eValue, que é o índice de confiabilidade dos resultados; Identities, que é a Quantidade (%) de aminoácidos idênticos no intervalo (cobertura) de sequência analisada; e os Gaps, que são falhas no comparativo. Há ainda nessa tela, a sequência fasta relacionada ao Contig3 e o botão Gerar fasta on-line, que faz uma consulta em tempo real à base de dados do NCBI, onde podem-se obter mais detalhes sobre os resultados. A figura 11 demonstra o resultado da consulta ao NCBI.



Nucleotide Sequence (634 letters)

RID D74G91WC015 (Expires on 02-06 22:53 pm)
Query ID lcl|60519
Description None
Molecule type nucleic acid
Query Length 634

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTX 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports]

Sequences producing significant alignments:
Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: metallothionein-like protein 1 [Sesamum indicum]	98.2	98.2	36%	9e-23	72%	XP_011069462.1
☐	PREDICTED: metallothionein-like protein type 2-like [Solanum tuberosum]	89.7	89.7	27%	1e-19	78%	XP_006361209.1
☐	metallothionein-like protein type 2 [Solanum lycopersicum]	88.6	88.6	27%	5e-19	76%	NP_001234050.1
☐	PREDICTED: metallothionein-like protein type 2 isoform X1 [Solanum lycopersicum]	87.8	87.8	27%	6e-19	76%	XP_010321696.1

Figura 11 – Tela de exemplo com o resultado do NCBI

A pesquisa segue o mesmo padrão de resultados, tanto para *Contigs* e *Singlets*. A caixa de seleção descrição consegue tratar termos inteiros ou partes de um texto, tanto na pesquisa por name, quanto por *sequence ID*. A opção buscar todos mostra todos os *Contigs* ou *Singlets* de um determinado órgão específico escolhido ou todos, seguindo a partir daí a mesma lógica de abertura dos resultados.

Existe a opção de pesquisa por sequência fasta, onde o usuário pode selecionar qualquer conjunto de dados que compoeem uma sequência fasta. Marcando a opção fasta e na descrição inserindo a sequência a ser pesquisada.

A pesquisa por *primers* segue a mesma lógica. A diferença está que ao marcar a opção *Primers* em pesquisar por, habilita as caixas de texto reverse e forward. O usuário deve inserir um primer utilizando da lógica: *reverse* x *cfoward* ou *creverse* x *forward*. A pesquisa retornará se há na base alguma sequência armazenada que possui esse primer escolhido. A figura 12 demonstra tal ação, onde o resultado foi um primer pesquisado e encontrado em um Contig de Calos.

Pesquisar por: ○ Name ○ Sequence ID ○ Fasta ● Primers ○ Todos

Órgão: Todos

Tipo: Todos

Reverse: TCGCATGCTCCCGGC

cForward: GTCCACCGACAGCCGAC

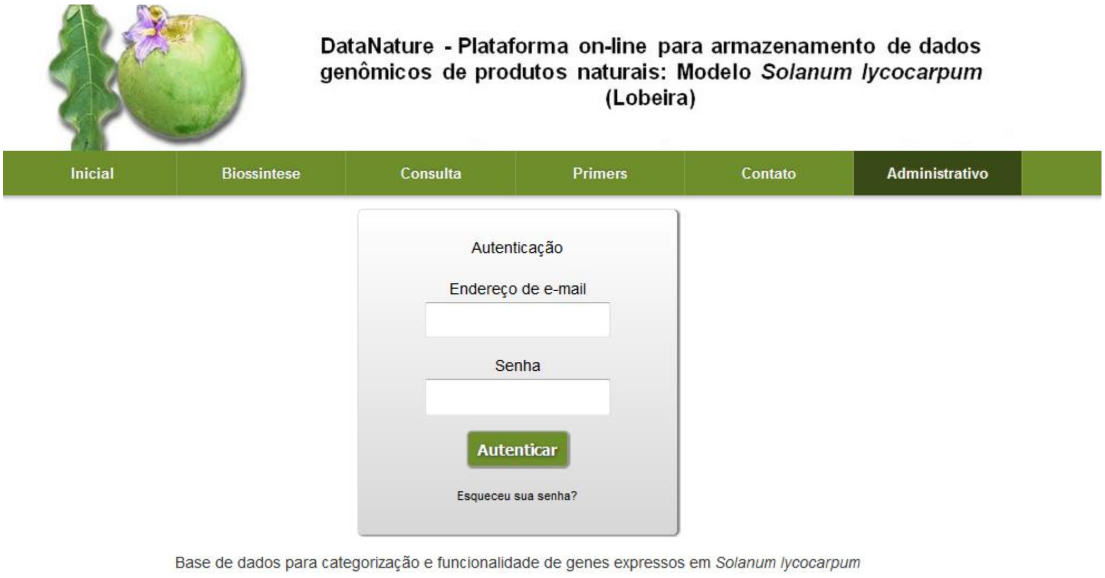
Descrição:

	nameSequence	Orgao
Selecionar	Contig0	Calos

Base de dados para categorização e funcionalidade de genes expressos em *Solanum lycocarpum*

Figura 12 – Tela de exemplo de uma consulta a *primers* na base de dados

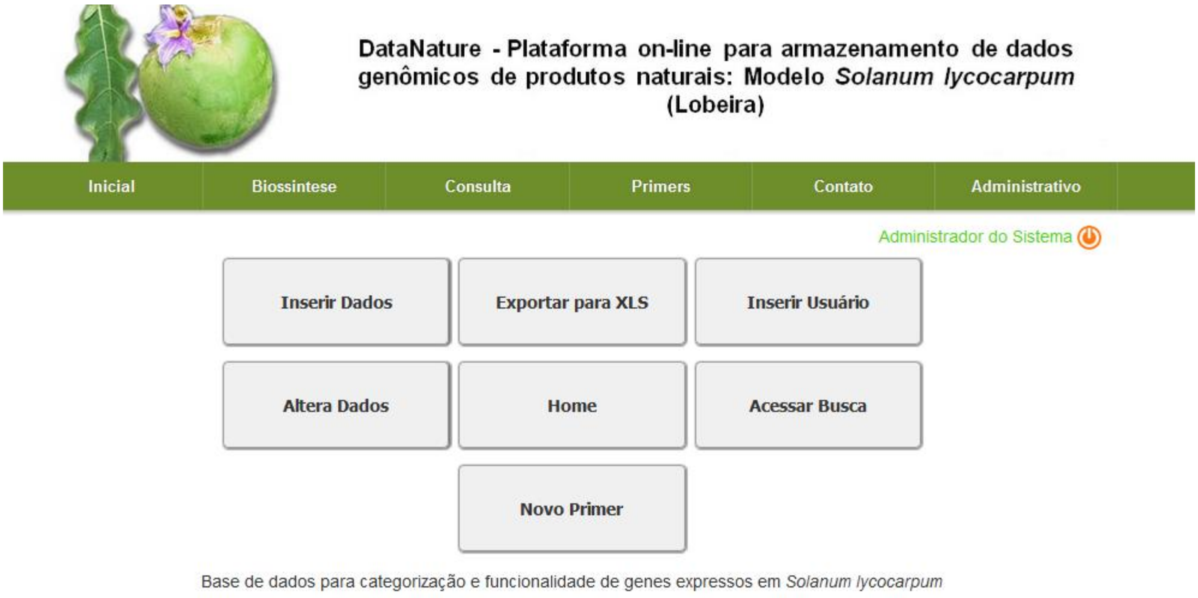
As telas de consulta são somente de visualização e estão disponíveis a qualquer usuário, sem restrições. Na área administrativa é que podemos fazer inserções, alterações e até apagar a base de dados. Ela deve estar disponível somente a usuários que participem do projeto e por isso seu acesso é restrito e depende de login e senha. O cadastro de usuários com permissão de acesso a área administrativa é feito única e exclusivamente pelo administrador do sistema.



Base de dados para categorização e funcionalidade de genes expressos em *Solanum lycocarpum*

Figura 13 – Tela de acesso à área administrativa

Na figura 13, tem-se a tela que demonstra o acesso à área administrativa. A área administrativa é restrita e há alguns utilizadores que poderão ser criados apenas pelo administrador principal do sistema. Nessa área ficam as páginas de inserção, exportação dos dados, alteração de dados, inserção de novo primer, acesso a busca e existe também a página de criação de novos usuários e um local onde o usuário poderá alterar a senha, conforme apresentado na figura 14. Tem-se a opção de digitar o endereço de *e-mail* que é o *login*, a opção para digitar senha criada no momento do cadastro do usuário e o botão autenticar, que faz a verificação da permissão do usuário. No caso de não autenticação do usuário, como login ou senha errados, retorna-se a mensagem de “usuário inexistente ou senha inválida”. Em caso de esquecimento de senha, tem-se ainda a opção de lembrete de senha e, assim ao clicar em “esqueceu sua senha?”, um *e-mail* é enviado com uma nova senha ao *e-mail* cadastrado.



DataNature - Plataforma on-line para armazenamento de dados genômicos de produtos naturais: Modelo *Solanum lycocarpum* (Lobeira)

Base de dados para categorização e funcionalidade de genes expressos em *Solanum lycocarpum*

Figura 14 – Tela da área administrativa

A figura 14 apresenta no canto superior direito o tipo de usuário (Administrador do Sistema) e um botão de *logoff*, que faz com que o usuário saia com segurança da área administrativa. Nas próximas figuras serão detalhadas as opções mais importantes.

A figura 15 apresenta a opção insere dados. A etapa insere dados é responsável pela inserção de novas sequências no banco de dados do sistema. Para adicionar novos dados é necessário fazer *upload* de arquivo com a extensão fasta (arquivo criado pelo ChromasPro) contendo o identificador e a sequência. A primeira opção é escolher que tipo de EST (contig ou singlet) e de órgão a ser armazenado. Ainda nessa opção tem-se a possibilidade de criar novos órgãos que deverão ser armazenados. Na sequência faz-se o *upload* do arquivo fasta. Depois de enviado o arquivo, será preenchido o campo identificador que possibilita a escolha de qual sequência se deseja salvar, há também a necessidade de informar a quantidade de resultados Blast que o sistema do NCBI deverá retornar para a inserção no banco de dados. Os campos base de dados e programa são preenchidos automaticamente. Concluído os preenchimentos acima, e executando a aplicação, a caixa “Dados Retornados” irá exibir os dados encontrados para aquela sequência no banco de dados do NCBI.

Base de dados para categorização e funcionalidade de genes expressos em *Solanum lycocarpum*

Insere Dados

Tipo: Contig Órgão: Sementes

Selecione o arquivo Fasta:

Identificador: Contig0 Quantidade de Blast:

Sequência:

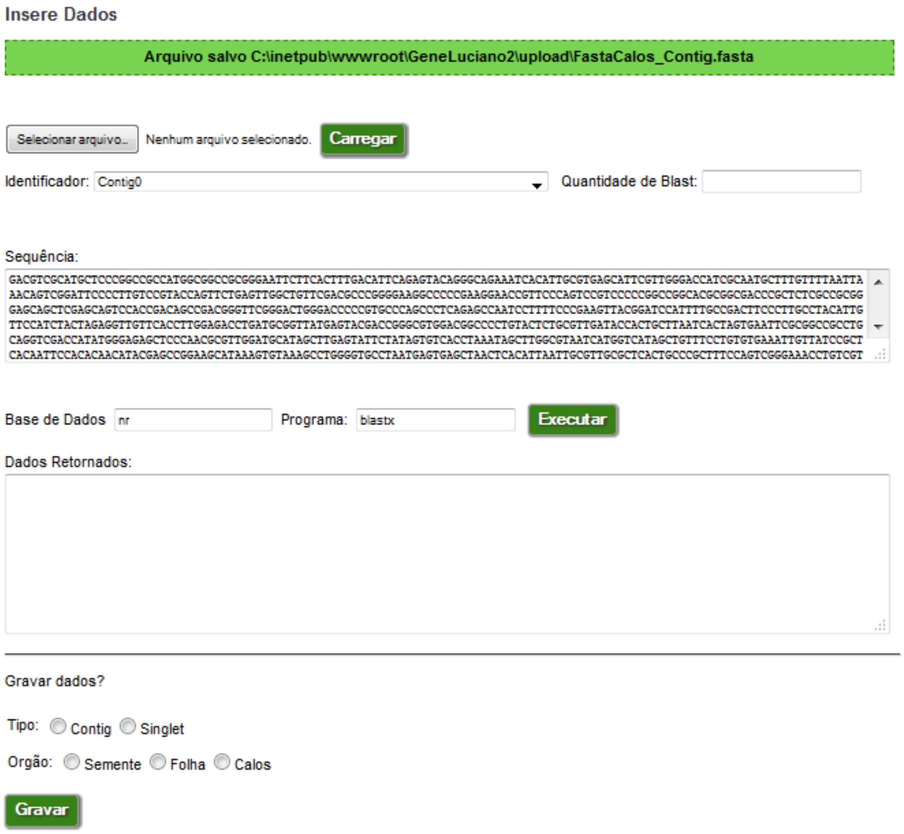
```
TTTTTTTTTTTTTAGCTGGGCAAGAGAAGAACTATTATAAATACGAATGTCGAAATTGAAGGGAGAATTATAACCTAACATCGAAAAAGAACAACATTAAGTCGACCCTATCACATATTGTTCTGAAG
GGGTAAAACATAACTAACAAAAACTAGAGAATAATTAGTAAGGGAACACCATAAGATATCAACCATTAACGGTTAACTTAATCAACCTCCTCCATTTTGCTGCCCTCAGCTTCAGCTTCCCCTGTACT
CTGCGTTGATACCACTGCTTAATCACTAGTGAATTCGCGGCCGCCTGCAGGTCGACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTATAGTGTCACCTAAATAGCTTGGCG
TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGC
GTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTG
```

Base de Dados: nr Programa: blastx

Base de dados para categorização e funcionalidade de genes expressos em *Solanum lycocarpum*

Figura 15 – Tela de inserção de dados

A figura 16 demonstra o *software* após a seleção de um arquivo fasta de *contigs* de calos. O sistema faz um tratamento nas extensões de arquivo e somente aceita arquivo com a extensão .fasta. Após o carregamento do arquivo o usuário que está alimentando o banco de dados, deve escolher o identificador (exemplo da tela com o contig0) e determinar a quantidade de resultados blastx. Na sequência clica-se no botão Executar e a comparação com a base de dados do NCBI é feita.



Arquivo salvo C:\inetpub\wwwroot\GeneLuciano2\upload\FastaCalos_Contig.fasta

Identificador: Contig0

Quantidade de Blast:

Sequência:

```
GACGTCGCATGCTCCCGGCCGCCATGGCGGCCGCGGGAATTCTTCACTTTGACATTCAGAGTACAGGGCAGAAATCACATTGCGTGAGCATTCGTTGGGACCATCGCAATGCTTTGTTTTAATTA
AACAGTCGGATTCCCCTTGTCCGTACCAGTTCTGAGTTGGCTGTTCGACGCCCGGGGAAGGCCCCCGAAGGAACCGTTCCCAGTCCGTCCCCCGGCCGGCACGCGGCGACCCGCTCTCGCCGCGG
GAGCAGCTCGAGCAGTCCACCGACAGCCGACGGGTTCGGGACTGGGACCCCCGTGCCCAGCCCTCAGAGCCAATCCTTTTCCCGAAGTTACGGATCCATTTTGCCGACTTCCCTTGCCTACATTG
TTCCATCTACTAGAGGTTGTTCACCTTGGAGACCTGATGCGGTTATGAGTACGACCGGGCGTGGACGGCCCCTGTACTCTGCGTTGATACCACTGCTTAATCACTAGTGAATTCGCGGCCGCCTG
CAGGTCGACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTATAGTGTCACCTAAATAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCT
CACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGT
```

Base de Dados: nr

Programa: blastx

Dados Retornados:

Gravar dados?

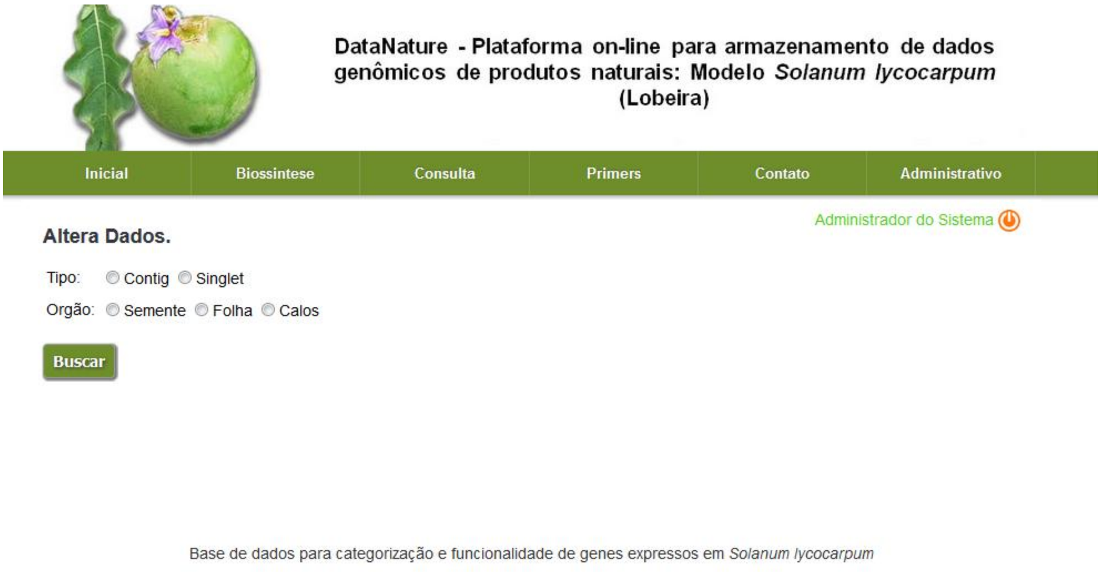
Tipo: ○ Contig ○ Singlet

Orgão: ○ Semente ○ Folha ○ Calos

Figura 16 – Tela de inserção de dados, após *upload* de arquivo fasta

Após a finalização do executar, a caixa "dados retornados" é preenchida com os resultados encontrados e o usuário deve marcar a opção tipo e órgão para gravar os dados. No caso demonstrado seria Contig e Calos. Habilita-se ainda o botão "Ver Resultado" que aparece no base inferior da tela para que o usuário possa visualizar os dados que retornam do NCBI antes da gravação, conforme já mostrado na figura 12.

As figuras 17 e 18 apresentam a opção altera dados. Sua função é alterar e apagar dados já armazenados no banco de dados. Para tanto, marca-se o tipo e órgão que se quer alterar e após clicar no botão buscar, é apresentado ao usuário a lista, conforme escolha. Feito isso, basta selecionar o contig ou singlet desejado e alterar ou apagar.



DataNature - Plataforma on-line para armazenamento de dados genômicos de produtos naturais: Modelo *Solanum lycocarpum* (Lobeira)

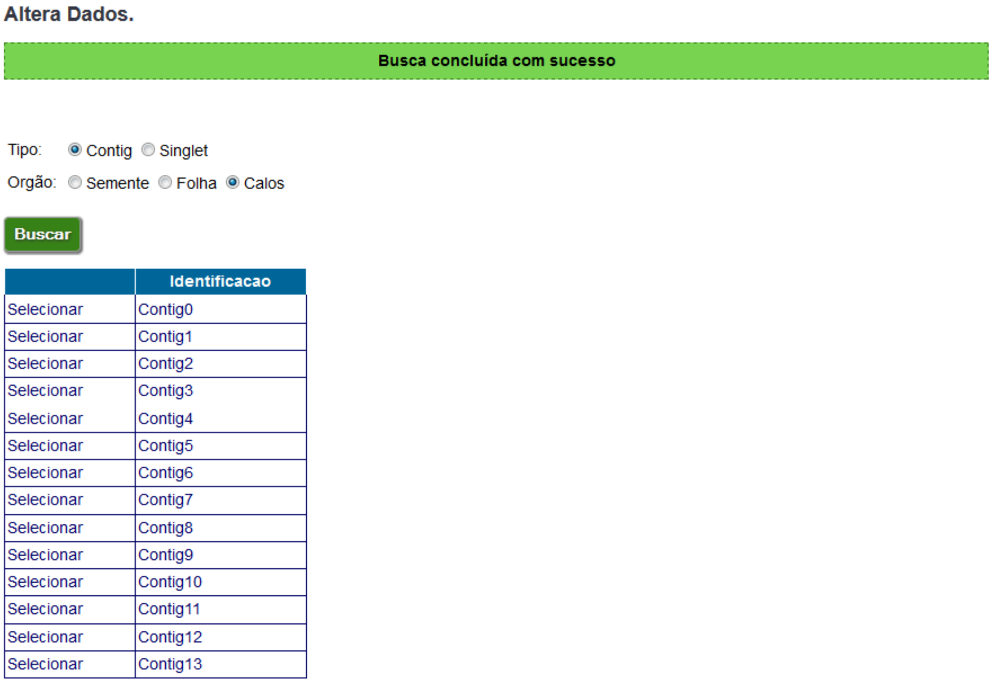
Altera Dados.

Tipo: ○ Contig ○ Singlet

Orgão: ○ Semente ○ Folha ○ Calos

Base de dados para categorização e funcionalidade de genes expressos em *Solanum lycocarpum*

Figura 17 – Tela de alteração de dados



Altera Dados.

Busca concluída com sucesso

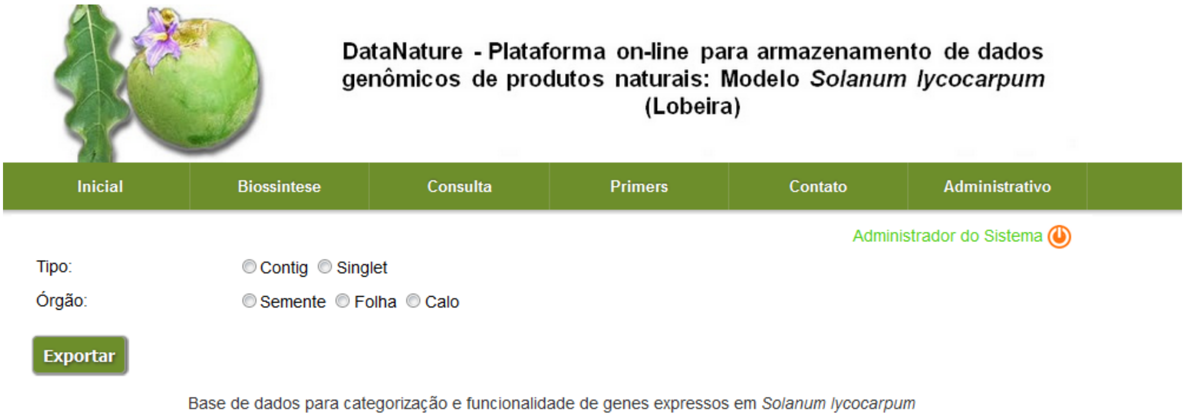
Tipo: ● Contig ○ Singlet

Orgão: ○ Semente ○ Folha ● Calos

	Identificacao
Selecionar	Contig0
Selecionar	Contig1
Selecionar	Contig2
Selecionar	Contig3
Selecionar	Contig4
Selecionar	Contig5
Selecionar	Contig6
Selecionar	Contig7
Selecionar	Contig8
Selecionar	Contig9
Selecionar	Contig10
Selecionar	Contig11
Selecionar	Contig12
Selecionar	Contig13

Figura 18 – Tela de alteração de dados, após escolha do tipo e órgão

Outra opção da área administrativa é “Exportar dados”. Essa opção permite ao usuário a exportação da base de dados em formato de planilha eletrônica no formato .xls. Para exportação o usuário deve selecionar o tipo e o órgão desejado e clicar no botão exportar. Automaticamente é gerado um arquivo do tipo planilha que deverá ser salvo ou aberto no computador. A figura 19 demonstra tal ação.



DataNature - Plataforma on-line para armazenamento de dados genômicos de produtos naturais: Modelo *Solanum lycocarpum* (Lobeira)

Tipo: ○ Contig ○ Singlet

Órgão: ○ Semente ○ Folha ○ Calo

Base de dados para categorização e funcionalidade de genes expressos em *Solanum lycocarpum*

Figura 19 – Tela de exportar dados

Ainda na área administrativa, existe a opção insere usuário. Essa opção permite que o administrador faça a inserção de outros usuários que também terão acesso à área administrativa. A inserção é simples e contém os seguintes campos: nome, *e-mail* (*login*), senha e confirmação de senha, além do botão cadastrar. A figura 20 demonstra a opção insere usuário.

DataNature - Plataforma on-line para armazenamento de dados genômicos de produtos naturais: Modelo *Solanum lycocarpum* (Lobeira)

Insere Usuário

Nome:

E-mail:

Senha:

Confirme a Senha:

Base de dados para categorização e funcionalidade de genes expressos em *Solanum lycocarpum*

Figura 20 – Tela insere usuário

Os dois últimos botões da área administrativa têm a função de voltar para a página inicial (figura 6) e consulta ao banco de dados (figura 8).

A figura 21 descreve através de um diagrama de caso de uso o passo-a-passo do sistema e suas possibilidades a nível de usuário e administrador.

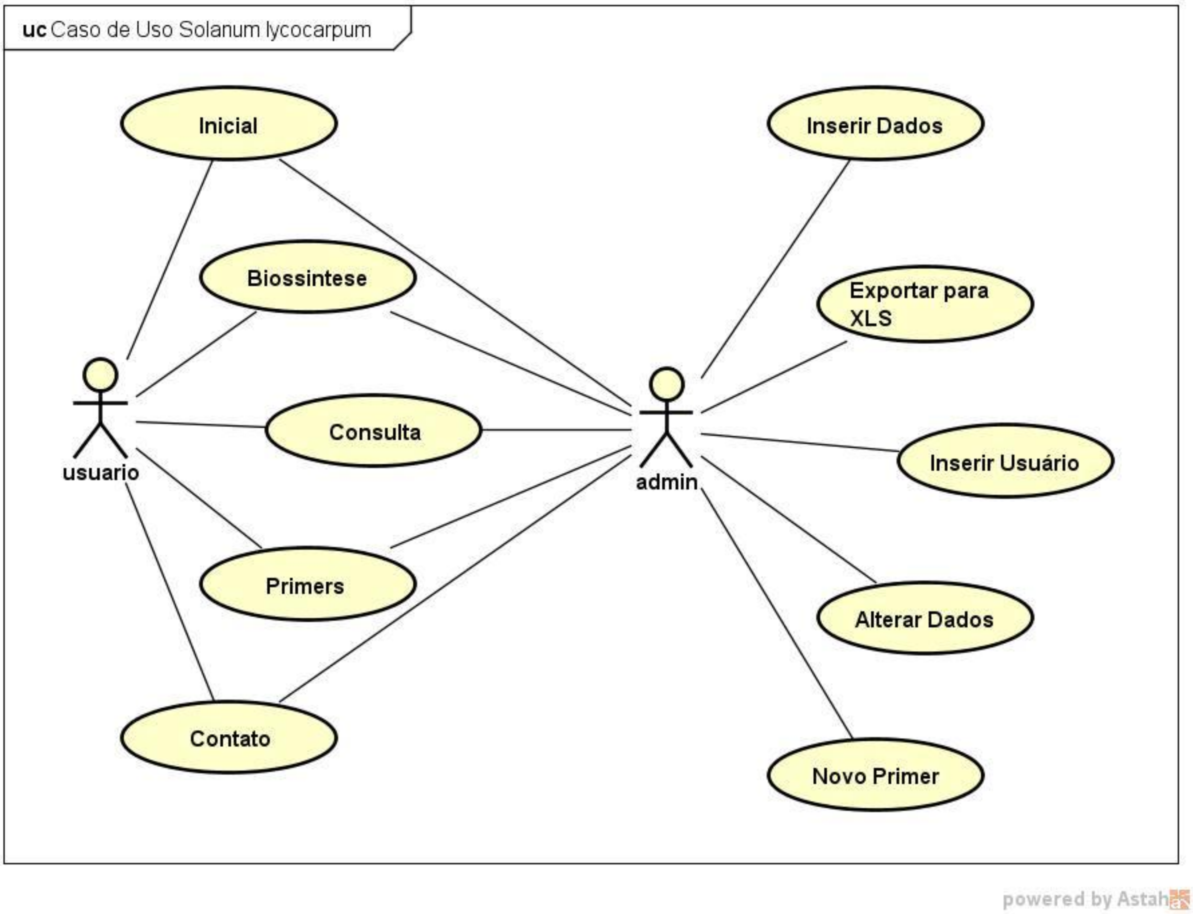


Figura 21 – Diagrama de caso de uso
Elaborado pelo autor

4.4 – Enzimas alvo

Foi realizada uma seleção de genes que representam um catálogo de enzimas reguladoras de diversas vias metabólicas de plantas e, sobretudo dos genes candidatos que podem regular a via de biossíntese de glicoalcalóides esteroidais de *S. lycocarpum*.

Com os resultados obtidos através dos *Contigs* e *Singlets* de sementes, folhas e calos de *S. lycocarpum* foram indentificadas enzimas bem representadas, que estão destacadas na figura 22.

Biossíntese de esteróides	Peptídeos	Proteínas de defesa	Fenilpropanóides
• cytochrome P450 • zinc finger • laccase-14 • cytochrome c oxidase • superoxide dismutase • steroid 5beta-reductase • lipid-transfer protein	• actin • profilin-1-like • thioredoxin reductase • calmodulin-like	• metallothionein-like • heat shock protein	• 4-coumarate • phenylalanine amônia-lyase (PAL)

Figura 22 – Enzimas selecionadas
Elaborada pelo autor

A seleção natural resultou na escolha de um conjunto relativamente pequeno de proteínas potencialmente úteis aos organismos vivos, inclusive para o homem. Assim, a descoberta de características críticas, específicas de proteínas, a partir do entendimento do processo de evolução dos genes que as codificam torna-se uma poderosa ferramenta para abordar a funcionalidade destas enzimas quando presentes em muitas espécies diversas (BASHFORD *et al.* 1987).

Steroid-5-beta-redutase ou Progesterona 5-beta-reductase – Catalisa a conversão estéreo específica de progesterona a 5-beta-pregnano-3,20-diona. Essa enzima pode usar como substrato progesterona, testosterona, 21-acetil cortexona, 2-ciclohexenona, but-1-en-3-ona, acrilato de etila, etilmetilacrilato, cortisona e canarigenona. Pode estar envolvida na formação de 5-beta fitoecdysteróides. Fonte: UNIProt.

Metalotioneinas (MTs) – Metalotioneinas são proteínas de baixa massa molecular, ricas em resíduos de enxofre e capazes de sequestrar quantidades excessivas de íons metálicos por meio da formação de complexos do tipo tiolatos. Assim, essas proteínas desempenham importante papel na detoxificação de metais e na homeostasis. Membros típicos dessa família de proteínas apresentam duas regiões ricas em cisteínas contendo de seis a oito resíduos Cys, separados por uma região constituída por 41 aminoácidos. A expressão de genes relacionados a metaloproteínas de plantas sujeitas a estresses ambientais demonstra que essas proteínas com seu amplo numero de resíduos de cisteina podem funcionar segundo dois tipos de mecanismos: na segregação de metais pesados e no sequestro de moléculas oxigênio reativas, protegendo as plantas de danos oxidativos.

Puroindolinas PINA e PINB são proteínas membros da família de inibidores de proteases/proteínas de transporte de lipídeos (PF00234) (FINN *et al.* 2008), ricas em cisteínas e únicas a terem também em sua estrutura um domínio rico em resíduos de triptofano (BLOCHET *et al*.1993), ambos domínios responsáveis por compor o locus que confere dureza ao grão de trigo, "the wheat *Hardness* (*Ha*) locus" (GIROUX and MORRIS 1998; WANJUGI *et al*. 2007a). Segundo Massa e Morris (2006), até então, PINs foram encontradas apenas em trigo hexaplóide e espécies a ele relacionadas. Como parte deste trabalho, identificamos na biblioteca de cDNAs de semente de *S. lycocarpum* vários transcritos candidatos a genes codificadores de puroindolinas.

Tioredoxinas - TRXs são proteínas da classe das oxidoreductases com aproximadamente 12 - kD contendo um sitio ativo ditiol – bissulfeto, dois resíduos Cys vicinais, o motivo CXXC. Funcionam como antioxidantes promovendo a redução de resíduos Cys de outras proteínas. Seis tipos bem definidos de tioredoxinas de plantas já foram descritos: TRXs F, M, X, Y, H e O, que se localizam em diferentes compartimentos celulares e funcionam em uma variedade de processos biológicos de plantas que vão desde a fotossíntese para o crescimento, a floração, o desenvolvimento e a germinação de sementes. Mais recentemente, também foi demonstrado que tioredoxinas estão envolvidas na comunicação célula-célula (Meng et al , 2010) e desempenham um papel crucial na regulação de respostas celulares tais como expressão gênica, proliferação celular e apoptose (Nishinaka et al, 2001). As TRXs são mantidas no estado reduzido pela flavoenzima tioredoxina redutase, numa reação dependente de NADPH (MUSTACICH e POWIS, 2000). Tioredoxinas atuam como doadores de elétrons para as peroxidases e a ribonucleotideo redutase (Arner e Holmgren, 2000). As glutaredoxinas são estruturalmente relacionadas às tioredoxinas compartilhando muitas das funções de tioredoxinas, porém são reduzidas pela glutationa redutase. TRXs são induzidas por uma variedade de estímulos oxidativos, incluindo a irradiação UV, citocinas inflamatórias e substâncias químicas cancerígenas. Superexpressão de trx protege as células de citotoxicidade provocada pelo estresse oxidativo em modelos in vitro e in vivo. Assim, a modulação das funções TRX pode ser uma nova estratégia terapêutica para o tratamento de doenças mediadas por estresse oxidativo (VICTOR & ROCHA, 2007).

Peptídeos biossintetizados em plantas, assim como aqueles de células animais, desempenham importantes papeis na resposta a agentes causadores de estresse biológico, químico ou físico-químico. Em geral, esses peptídeos são codificados por famílias de genes cujos membros apresentam diversificados padrões temporais de expressão de modo a realizarem a regulação de processos metabólicos ligados ao desenvolvimento e defesa das plantas.

Aquaporinas pertencem à grande família das proteínas intrínsecas de membrana (MIP) as quais formam poros na membrana de células biológicas. A membrana plasmática de uma variedade de células animais e também de células vegetais contém aquaporinas por meio das quais o fluxo de água para dentro da célula pode ocorrer mais rapidamente do que por difusão, através da bicamada fosfolipídica, que forma uma contínua barreira ao redor de todas as células. Defeitos genéticos envolvendo genes codificadores de aquaporinas têm sido associados a várias doenças humanas. Aquaporinas do hospedeiro funcionam como peptídeos de defesa ativos contra bactérias, fungos e muitos vírus envelopados (fáceis de matar) e não envelopados (difíceis de matar).

Calmodulin é um peptídeo que atua como parte da via de sinalização de cálcio e se liga a proteínas alvo para alterar suas funções. Recentemente, Jia e col. (2014) investigaram o papel de Calmodulin na tolerância térmica e demonstraram que existe uma interação entre oxido nitroso (NO) e peróxido de hidrogênio (H202), elementos chaves na via de sinalização de choque térmico (heat shock – HS) e canais de cálcio Ca (2+), de modo que a ativação de Calmodulin estimula a atividade DNA-binding de fatores de transcrição, bem como o acúmulo de proteínas HS e a decorrente tolerância térmica

Na área de saúde, uma abordagem que vem ganhando destaque é a busca de novos ativos anti arritmia cardíaca e dentre os alvos para controle da mobilidade de cálcio intracelular está a proteína kinase II (CaMKII),Ca(2+)/Calmodulin-dependente.

Utilizando o DataNature, foram feitas análises *in sílico*, a fim de verificar a funcionalidade potencial de produtos de genes alvos, além de responder algumas questões, como por exemplo: número de genes codificadores de cada enzima? Sequências com mesma funcionalidade putativa, cobrem diferentes partes de um mesmo gene? Na tabela 5 encontram-se respostas a essas questões.

Tabela 5 – Resultado de análise *in sílico* para predicção de funcionalidade do produto gênico
Fonte: DataNature. Elaborado pelo autor.

1. Quantos genes de cytochrome P450 há na biblioteca?		
Contig/Singlet	**Órgão**	**ESTs**
Contig26	Folha	SLFLPL04B03, SLFLPL03F02, SLFLPL01D10, SLFLPL03G08
Contig0	Calos	SLCAPL01B02, SLCAPL04F05, SLCAPL01B11, SLCAPL04E09, SLCAPL05A06
Contig7	Calos	SLCAPL02E01, SLCAPL01A09, SLCAPL05E04, SLCAPL04H08, SLCAPL03G06, SLCAPL01B07, SLCAPL01E07, SLCAPL05G09, SLCAPL05H05, SLCAPL05E08, SLCAPL05D03, SLCAPL05H03, SLCAPL05C09, SLCAPL03D03, SLCAPL01F06, SLCAPL04C02, SLCAPL05D12, SLCAPL02G02, SLCAPL01G01, SLCAPL01A02
Contig26	Calos	SLCAPL05B12, SLCAPL03F07, SLCAPL04C11, SLCAPL05E07
Os *contigs* cobrem diferentes partes de um mesmo gen?		
Contig/Singlet	**Órgão**	**Codificação/Cobertura**
Contig26	Folha	ref|XP_003614400.1| 13 to 58
Contig0	Calos	dbj|BAA10929.1| 134 to 296 pir||T02955 135 to 266
Contig7	Calos	ref|XP_003614380.1| 367 to 412, 414 to 444, 442 to 519 ref|XP_003614400.1| 421 to 466, 468 to 498, 495 to 552, 547 to 577
Contig26	Calos	dbj|BAA10929.1| 91 to 230
R: Genes codificadores de proteínas similares a cytochrome P450. Quantidade de genes putativos = 4		

2. Quantos genes de zinc finger há na biblioteca?		
Contig/Singlet	**Órgão**	**ESTs**
SLSEPL04G10	Semente	SLSEPL04G10
Contig31	Calos	SLCAPL03B12, SLCAPL03H04
SLCAPL05F03	Calos	SLCAPL05F03
Os *contigs* cobrem diferentes partes de um mesmo gen?		
Contig/Singlet	**Órgão**	**Codificação/Cobertura**
SLSEPL04G10	Semente	ref|XP_006363144.1| 432 to 525 ref|XP_003517239.1| 423 to 516
Contig31	Calos	ref|XP_007031126.1| 3 to 73, 78 to 152, 186 to 202 ref|XP_004158724.1| 1 to 73, 78 to 152, 186 to 202 ref|XP_008453709.1| 1 to 73, 78 to 152, 186 to 202 ref|XP_004144761.1| 1 to 73, 78 to 152, 186 to 202
SLCAPL05F03	Calos	ref|XP_007051260.1| 32 to 122
R: Genes codificadores de proteínas similares a zinc finger. Quantidade de genes transcritos = 3		

3. Quantos genes de laccase-14 há na biblioteca?		
Contig/Singlet	**Órgão**	**ESTs**
SLCAPL01D01	Calos	SLCAPL01D01
Os *contigs* cobrem diferentes partes de um mesmo gen?		
Contig/Singlet	**Órgão**	**Codificação/Cobertura**
SLCAPL01D01	Calos	ref|XP_004237852.1 359 to 567 ref|XP_002269593.2| 357 to 565 ref|XP_002264702.1| 358 to 565 ref|XP_002264394.2| 355 to 563
R: Gene codificador de proteína similar a laccase-14. Quantidade de transcritos = 1		

4. Quantos genes de cytochrome c oxidase há na biblioteca?		
Contig/Singlet	**Órgão**	**ESTs**
SLCAPL01D05	Calos	SLCAPL01D05
Os *contigs* cobrem diferentes partes de um mesmo gen?		
Contig/Singlet	**Órgão**	**Codificação/Cobertura**
SLCAPL01D05	Calos	ref|XP_004231959.1| 5 to 100 ref|XP_006357740.1| 5 to 100 ref|XP_002531993.1| 6 to 101 ref|XP_002264013.1| 7 to 97
R: Gene codificador de proteína similar a cytochrome c oxidase. Quantidade de transcritos = 1		

5. Quantos genes de superoxide dismutase há na biblioteca?		
Contig/Singlet	**Órgão**	**ESTs**
SLCAPL01E01	Calos	SLCAPL01E01
Os *contigs* cobrem diferentes partes de um mesmo gen?		
Contig/Singlet	**Órgão**	**Codificação/Cobertura**
SLCAPL01E01	Calos	sp|P11796.1|SODM_NICPL 70 to 228 ref|XP_006358755.1| 70 to 228 ref|XP_004240868.1| 70 to 228 sp|Q9SM64.1|SODM_PRUPE 70 to 228
R: Gene codificador de proteína similar a superoxidase dismutase. Quantidade de transcritos = 1		

6. Quantos genes de steroid 5beta-reductase há na biblioteca?		
Contig/Singlet	**Órgão**	**ESTs**
SLCAPL01H07	Calos	SLCAPL01H07
Os *contigs* cobrem diferentes partes de um mesmo gen?		
Contig/Singlet	**Órgão**	**Codificação/Cobertura**
SLCAPL01H07	Calos	gb|AEX31544.1| 344 to 387 ref|XP_006353962.1| 345 to 388 ref|NP_001266103.1| 344 to 387
R: Gene codificador de proteína similar a steroid 5beta-reductase. Quantidade de transcritos = 1		

7. Quantos genes de steroid lipid-transfer protein há na biblioteca?		
Contig/Singlet	**Órgão**	**ESTs**
SLCAPL03H11	Calos	SLCAPL03H11
Os *contigs* cobrem diferentes partes de um mesmo gen?		
Contig/Singlet	**Órgão**	**Codificação/Cobertura**
SLCAPL03H11	Calos	ref|XP_003624386.1| 52 to 94 ref|XP_007033193.1| 76 to 118 ref|XP_002284213.1| 50 to 92 ref|XP_004492965.1| 50 to 92
R: Gene codificador de proteína similar a lipid-transfer protein. Quantidade de transcritos = 1		

8. Quantos genes de actin há na biblioteca?		
Contig/Singlet	**Órgão**	**ESTs**
SLFLPL03D04	Folhas	SLFLPL03D04
SLCAPL03F09	Calos	SLCAPL03F09
Os *contigs* cobrem diferentes partes de um mesmo gen?		
Contig/Singlet	**Órgão**	**Codificação/Cobertura**
SLFLPL03D04	Folhas	ref|XP_004246462.1| 76 to 139 gb|ACB32233.1| 76 to 139 ref|XP_006341057.1| 76 to 139 emb|CAJ38388.1| 76 to 139
SLCAPL03F09	Calos	gb|AEM46061.1| 6 to 100 gb|AAW31852.1| 37 to 131 gb|AFY06656.1| 116 to 210

		gb|ADZ73581.1| 74 to 168

R: Genes codificadores de proteínas similares a actin. Quantidade de genes transcritos = 2

9. Quantos genes de profilin-1-like há na biblioteca?

Contig/Singlet	**Órgão**	**ESTs**
SLCAPL05D01	Calos	SLCAPL05D01

Os *contigs* cobrem diferentes partes de um mesmo gen?

Contig/Singlet	**Órgão**	**Codificação/Cobertura**
SLCAPL05D01	Calos	ref|XP_004251645.1| 1 to 131 ref|XP_006353502.1| 1 to 131

R: Gene codificador de proteína similar a profilin-1-like. Quantidade de transcritos = 1

10. Quantos genes de thioredoxin reductase há na biblioteca?

Contig/Singlet	**Órgão**	**ESTs**
SLCAPL05E10	Calos	SLCAPL05E10

Os *contigs* cobrem diferentes partes de um mesmo gen?

Contig/Singlet	**Órgão**	**Codificação/Cobertura**
SLCAPL05E10	Calos	ref|XP_006343316.1| 268 to 328 ref|XP_004234501.1| 268 to 328 gb|AAA33376.1| 59 to 117 ref|XP_006364831.1| 309 to 367

R: Gene codificador de proteína similar a thioredoxin reductase. Quantidade de transcritos = 1

11. Quantos genes de calmodulin-like há na biblioteca?

Contig/Singlet	**Órgão**	**ESTs**
SLCAPL05F07	Calos	SLCAPL05F07

Os *contigs* cobrem diferentes partes de um mesmo gen?

Contig/Singlet	**Órgão**	**Codificação/Cobertura**
SLCAPL05F07	Calos	ref|XP_004251249.1| 1 to 151 ref|XP_004249098.1| 1 to 149 ref|XP_006369409.1| 1 to 149 ref|XP_004251248.1| 1 to 149, 85 to 153

R: Gene codificador de proteína similar a calmodulin-like. Quantidade de transcritos = 1

12. Quantos genes de metallothionein-like há na biblioteca?

Contig/Singlet	**Órgão**	**ESTs**
Contig3	Sementes	SLSEPL01G08, SLSEPL01E08, SLSEPL01F08
Contig5	Calos	SLCAPL01H04, SLCAPL03A11

Os *contigs* cobrem diferentes partes de um mesmo gen?

Contig/Singlet	**Órgão**	**Codificação/Cobertura**
Contig3	Sementes	ref|XP_006361209.1| 19 to 76 ref|NP_001234050.1| 19 to 76 gb|ACF10397.1| 25 to 77 gb|ACF10398.1| 25 to 77 emb|CAI48068.1| 7 to 77
Contig5	Calos	gb|ACF10397.1| 25 to 77 ref|XP_006361209.1| 19 to 76 ref|NP_001234050.1| 19 to 76 emb|CAI48068.1| 9 to 77 gb|AAX20047.1| 9 to 77

R: Genes codificadores de proteínas similares a metallothionein-like. Quantidade de genes transcritos = 2

13. Quantos genes de heat shock protein há na biblioteca?

Contig/Singlet	**Órgão**	**ESTs**
Contig6	Sementes	SLSEPL02D04, SLSEPL02C04
SLSEPL04F05	Sementes	SLSEPL04F05
Contig34	Folhas	SLFLPL04G10, SLFLPL04C07

SLCAPL02F07	Calos	SLCAPL02F07
Os *contigs* cobrem diferentes partes de um mesmo gen?		
Contig/Singlet	**Órgão**	**Codificação/Cobertura**
Contig6	Sementes	ref|XP_006355458.1| 111 to 211 ref|NP_001233872.1| 110 to 210 gb|ADJ57588.1| 105 to 211 ref|XP_004172503.1| 111 to 212
SLSEPL04F05	Sementes	ref|NP_001234439.1| 579 to 699 gb|ADU04386.1| 579 to 699 gb|AAF31705.1|AF221856_1 200 to 320 ref|XP_006344905.1| 579 to 699
Contig34	Folhas	ref|XP_002517081.1| 54 to 132, 17 to 153
SLCAPL02F07	Calos	ref|XP_004236689.1| 62 to 145 ref|XP_006346757.1| 62 to 145 ref|NP_001238444.1| 72 to 144 ref|XP_008383146.1| 108 to 183
R: Genes codificadores de proteínas similares a heat shock protein. Quantidade de genes transcritos = 4		

14. Quantos genes de 4-coumarate há na biblioteca?		
Contig/Singlet	**Órgão**	**ESTs**
Contig6	Calos	SLCAPL01H06, SLCAPL03H01
Contig8	Calos	SLCAPL02G06, SLCAPL01F01
Os *contigs* cobrem diferentes partes de um mesmo gen?		
Contig/Singlet	**Órgão**	**Codificação/Cobertura**
Contig6	Calos	gb|AAD40664.1|AF150686_1 501 to 545 gb|AHJ78613.1| 501 to 545 sp|P31685.1|4CL2_SOLTU 501 to 545
Contig8	Calos	dbj|BAA07828.1| 503 to 542 sp|O24146.1|4CL2_TOBAC 503 to 542 ref|XP_006366277.1| 509 to 548
R: Genes codificadores de proteínas similares a 4-coumarate. Quantidade de genes transcritos = 2		

15. Quantos genes de phenylalanine amônia-lyase (PAL) há na biblioteca?		
Contig/Singlet	**Órgão**	**ESTs**
Contig17	Calos	SLCAPL04A10, SLPLCA04C06
Os *contigs* cobrem diferentes partes de um mesmo gen?		
Contig/Singlet	**Órgão**	**Codificação/Cobertura**
Contig17	Calos	ref|XP_004249558.1| 671 to 711 gb|ABG75910.1| 662 to 717 sp|P45733.1|PAL3_TOBAC 672 to 712 sp|P35513.2|PAL2_TOBAC 672 to 712 ref|XP_004234632.1| 409 to 449
R: Gene codificador de proteína similar a phenylalanine amônia-lyase (PAL). Quantidade de transcritos = 1		

4.5 – Rastreamento de enzimas

A partir da via de biossíntese de esteroides (figura 3), foram selecionadas enzimas chaves. Suas respectivas funcionalidades estão representadas a partir da tabela 6.

Tabela 6 – Descrição funcional de enzimas chaves na via de biossíntese de SGAs
Fonte: Kegg Pathway Database

Entry	**EC 2.5.1.21**
Name	squalene synthase; farnesyltransferase; presqualene-diphosphate synthase; presqualene synthase; squalene synthetase; farnesyl-diphosphate farnesyltransferase;
Class	Transferases; Transferring alkyl or aryl groups, other than methyl groups; Transferring alkyl or aryl groups, other than methyl groups (only sub-subclass identified to date)
Sysname	(2E,6E)-farnesyl-diphosphate:(2E,6E)-farnesyl-diphosphate farnesyltransferase
Reaction	2 (2E,6E)-farnesyl diphosphate + NAD(P)H + H+ = squalene + 2 diphosphate + NAD(P)+ (overall reaction) [RN:R06223]; (1a) 2 (2E,6E)-farnesyl diphosphate = diphosphate + presqualene diphosphate [RN:R00702]; (1b) presqualene diphosphate + NAD(P)H + H+ = squalene + diphosphate + NAD(P)+ [RN:R02872]
Product	squalene [CPD:C00751]; diphosphate [CPD:C00013]; NAD+ [CPD:C00003]; NADP+ [CPD:C00006]; presqualene diphosphate [CPD:C03428]
Comment	This microsomal enzyme catalyses the first committed step in the biosynthesis of sterols. The enzyme from yeast requires either Mg2+ or Mn2+ for activity. In the absence of NAD(P)H, presqualene diphosphate (PSPP) is accumulated. When NAD(P)H is present, presqualene diphosphate does not dissociate from the enzyme during the synthesis of squalene from farnesyl diphosphate (FPP) [8]. High concentrations of FPP inhibit the production of squalene but not of PSPP [8].
History	EC 2.5.1.21 created 1976, modified 2005, modified 2012
Pathway	ec00100 Steroid biosynthesis ec00909 Sesquiterpenoid and triterpenoid biosynthesis ec01100 Metabolic pathways ec01110 Biosynthesis of secondary metabolites
References	1. Tansey TR, Shechter I. Structure and regulation of mammalian squalene synthase. Biochim. Biophys. Acta. 1529 (2000) 49-62. 2. Pandit J, Danley DE, Schulte GK, Mazzalupo S, Pauly TA, Hayward CM, Hamanaka ES, Thompson JF, Harwood HJ Jr. Crystal structure of human squalene synthase. A key enzyme in cholesterol biosynthesis. J. Biol. Chem. 275 (2000) 30610-7. 3. Radisky ES, Poulter CD. Squalene synthase: steady-state, pre-steady-state, and isotope-trapping studies. Biochemistry. 39 (2000) 1748-60.
Entry	**EC 1.14.13.132**
Name	squalene monooxygenase; squalene epoxidase; squalene-2,3-epoxide cyclase; squalene 2,3-oxidocyclase; squalene hydroxylase; squalene oxydocyclase; squalene-2,3-epoxidase
Class	Oxidoreductases; Acting on paired donors, with incorporation or reduction of molecular oxygen; With NADH or NADPH as one donor, and incorporation of one atom of oxygen into the other donor
Sysname	squalene,NADPH:oxygen oxidoreductase (2,3-epoxidizing)

Reaction	squalene + NADPH + H+ + O2 = (3S)-2,3-epoxy-2,3-dihydrosqualene + NADP+ + H2O [RN:R02874]
Product	(3S)-2,3-epoxy-2,3-dihydrosqualene [CPD:C01054]; NADP+ [CPD:C00006]; H2O [CPD:C00001]
Comment	A flavoprotein (FAD). This enzyme, together with EC 5.4.99.7 lanosterol synthase, was formerly known as squalene oxidocyclase. The electron donor, NADPH, is coupled via EC 1.6.2.4, NADPH---hemoprotein reductase [5,7].
History	EC 1.14.13.132 created 1961 as EC 1.99.1.13, transferred 1965 to EC 1.14.1.3, part transferred 1972 to EC 1.14.99.7, transferred 2011 to EC 1.14.13.132
Pathway	ec00100 Steroid biosynthesis ec00909 Sesquiterpenoid and triterpenoid biosynthesis ec01100 Metabolic pathways ec01110 Biosynthesis of secondary metabolites
References	1. He F, Zhu Y, He M, Zhang Y Molecular cloning and characterization of the gene encoding squalene epoxidase in Panax notoginseng. DNA. Seq. 19 (2008) 270-3. 2. Chugh A, Ray A, Gupta JB Squalene epoxidase as hypocholesterolemic drug target revisited. Prog. Lipid. Res. 42 (2003) 37-50. 3. Satoh T, Horie M, Watanabe H, Tsuchiya Y, Kamei T Enzymatic properties of squalene epoxidase from Saccharomyces cerevisiae. Biol. Pharm. Bull. 16 (1993) 349-52.
Entry	**EC 5.4.99.8**
Name	cycloartenol synthase; 2,3-epoxysqualene cycloartenol-cyclase; squalene-2,3-epoxide-cycloartenol cyclase; 2,3-epoxysqualene-cycloartenol cyclase; 2,3-oxidosqualene-cycloartenol cyclase; (S)-2,3-epoxysqualene mutase (cyclizing, cycloartenol-forming)
Class	Isomerases; Intramolecular transferases; Transferring other groups
Sysname	(3S)-2,3-epoxy-2,3-dihydrosqualene mutase (cyclizing, cycloartenol-forming)
Reaction	(3S)-2,3-epoxy-2,3-dihydrosqualene = cycloartenol [RN:R03200]
Product	cycloartenol [CPD:C01902]
History	EC 5.4.99.8 created 1972
Pathway	ec00100 Steroid biosynthesis ec01100 Metabolic pathways ec01110 Biosynthesis of secondary metabolites
References	1. Rees HH, Goad LJ, Goodwin TW. 2,3-oxidosqualene cycloartenol cyclase from Ochromonas malhamensis. Biochim. Biophys. Acta. 176 (1969) 892-4

Foi realizado o rastreamento dessas enzimas com a utilização de sondas (nucleotídeos) específicas. A figura 23 demonstra o *pipeline* utilizado para se chegar a esses resultados.

Figura 23 – *Pipeline* rastreamento de *primers*

A partir de sequências conservadas de enzimas reguladoras das várias etapas da via de biossintese de esteróides foram desenhados *primers* para rastreamento de homólogos nas bibliotecas de cDNA de *S. lycocarpum*. (tabela 7).

Tabela 7 – Oligonucleotídeos sondas de genes codificadores de enzimas da via da biossíntese de esteroides

1. squalene synthase								
Primer 1	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	ATGGCACTTTGCATGTGGTA	Plus	20	314	59.99	45.00	4.00	4.00
Reverse primer	AAATTTTGCCATTCCTGCAC	Minus	20	462	59.94	40.00	6.00	6.00
Product length	148							
Primer 2	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	AATGAAGTACCCAAGTGCCG	Plus	20	652	59.99	50.00	4.00	4.00
Reverse primer	GATGGAAGGATCACGCAAAT	Minus	20	844	59.90	45.00	4.00	4.00
Product length	192							
2. squalene monooxygenase								
Primer 1	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	CTCTGCTTGAAGAAAACGGG	Plus	20	760	59.98	50.00	5.00	5.00
Reverse primer	TGATGGATCAGCCAAAATGA	Minus	20	993	60.00	40.00	6.00	6.00
Product length	233							
Primer 2	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	CCAGCTGCTCCTCATCCTAC	Plus	20	1197	59.97	60.00	6.00	6.00
Reverse primer	GCTTGATCAGGTGAAGCACA	Minus	20	1466	59.99	55.00	7.00	7.00
Product length	269							
3. cycloartenol synthase								
Primer 1	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	CAGAACAGTGATGGTGGGTG	Plus	20	596	59.99	55.00	3.00	3.00
Reverse primer	CATCATTAGCTCCTTCCCCA	Minus	20	705	60.02	50.00	4.00	4.00
Product length	109							
Primer 2	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	TGGGGAAGGAGCTAATGATG	Plus	20	685	60.02	50.00	4.00	4.00
Reverse primer	ACTGTTGGCGTGATAGGACC	Minus	20	967	59.99	55.00	3.00	3.00
Product length	282							

Utilizando-se da mesma metodologia, também foi feita a pesquisa por *primers* das enzimas alvo, listadas na figura 22. Vide apêndice H.

5. CONCLUSÕES

Tendo em vista os levantamentos realizados sobre a planta modelo, os aplicativos computacionais já existentes e suas possibilidades de utilização no *pipeline* desenvolvido, obteve-se êxito e eficiência no objetivo proposto.

Os estudos realizados a cerca de sequências de genes expressos relacionados a biossíntese de produtos naturais bioativos, tendo como modelo a espécie *S. lycocarpum*, foram pano de fundo para a construção de uma plataforma computacional de armazenamento de dados.

O DataNature contempla um banco de dados de genes relacionados à produção de metabólitos secundários bioativos em *S. lycocarpum*, onde pode-se realizar buscas *in sílico*, visando a categorização de genes expressos em órgãos específicos. É importante também por subsidiar a preconização de funcionalidade de genes expressos com potencial interesse biotecnológico. A partir da informação obtida foi possível também o desenho de *primers* nucleotídicos, que visam o rastreamento de bibliotecas de cDNA, na busca de genes do metabolismo secundário e regulação de SGAs.

A plataforma pode ser utilizada para inserção de dados genômicos de outros organismos, constituindo-se em um poderosa ferramenta on-line para consulta de dados genômicos de produtos naturais, subsidiando o trabalho de pesquisadores.

6. REFERÊNCIAS BIBLIOGRÁFICAS

AIRES, S. S.; FERREIRA, A. G.; BORGHETTI, F.. Efeito alelopático de folhas e frutos de Solanum lycocarpum A. St.-Hil.(Solanaceae) na germinação e crescimento de Sesamun indicum L.(Pedaliaceae) em solo sob três temperaturas. **Acta Botanica Brasilica**, v. 19, n. 2, p. 339-344, 2005.

ALBUQUERQUE, U. P. de; HANAZAKI, N.. As pesquisas etnodirigidas na descoberta de novos fármacos de interesse médico e farmacêutico: fragilidades e pespectivas. **Rev Bras Farmacogn**, v. 16, n. sSupl, 2006.

ALMEIDA, A.E. *et al.* Mutagenic activity of glycoalkaloids from Solanum palinacanthum Dunal (Solanaceae) found in the Brazilian cerrado. **Acta Farmaceutica Bonaerense**, [S.l.], v. 29, p. 122-126, 2010.

ALMEIDA, A.E.; ROCCO, M.A. Glicoalcaloides dos frutos do Solanum Flaccidum Vell. **Revista de Ciências Farmacêuticas**, [S.l.], v. 16, p. 111-118, 1995.

ARAÚJO, M. G. F. *et al.* Pharmacognostical evaluation of fruits of Solanum lycocarpum A. St.-Hill.(Solanaceae). **Pharmacognosy Journal**, v. 2, n. 9, p. 248-253, 2010.

ARNÉR, E; HOLMGREN A. Physiological functions of thioredoxin and thioredoxin reductase. **European Journal Biochemistry**, [S.l.], v. 267, n. 20, p. 6102- 6109, 2000.

BARBOSA-FILHO J.M. *et al.* Natural products inhibitors of the enzyme acetylcholinesterase. **Rev Bras Farmacogn** 16: 258-285.

BASHFORD, D.; CHOTHIA C.; LESK, A. M. Determinants of a protein fold: unique features of the globin amino acid sequence. **Journal Molecular Biology**, [S.l.], v.196, p. 199–216, 1987.

BLOCHET, J. E. *et al.* Complete amino acid sequence of Puroindoline, a new basic and cystine-rich protein with a unique tryptophan-rich domain, isolated from wheat endosperm by Triton X-114 phase partitioning. **FEBS Letters**., [S.l.], v. 329, p.336–340, 1993.

BORBA, H. R. *et al.* Anthelmintic comparative study of Solanum lycocarpum St. Hill extracts in mice naturally infected with Aspiculuris tetraptera. **Nature and science**, v. 8, n. 4, p. 94-100, 2010.

CALTAGIRONE, S. *et al.* Flavonoids apigenin and quercetin inhibit melanoma growth and metastatic potential**. International Journal of Cancer**, [S.l.], v. 87, p. 595, 2000.

CARVALHO, M. C. C. G.; SILVA, D. C. G. S. DNA de nova geração e suas aplicações na genômica de plantas. **Ciência Rural,** vol.40, n.3, p. 735-744, 2010. Disponível em: <http://dx.doi.org/10.1590/S0103-84782010000300040>. Acesso em: 1. abr. 2015.

CHANG, C.V.*et al.* Fetal toxicity of Solanum lycocarpum (Solanaceae) in rats. **Journal of Ethnopharmacology**, New York, v.81, p. 265-269,2002.

CHAVES FILHO, J. T.; STACCIARINI-SERAPHIN, E. Alteração no potencial osmótico e teor de carboidratos solúveis em plantas jovens de lobeira (Solanum lycocarpum St.-Hil.) em resposta ao estresse hídrico. **Revista brasileira de Botânica**, v. 24, n. 2, p. 199-204, 2001.

COSTA, D.P.C. *et al.* Effect of Solanum lycocarpum aqueous extracts in helminth parasites of conventionally maintained laboratory mice. **Research Journal of Parasitology**, v. 3, p. 12-19, 2008.

DE ARAÚJO, M. G. F.; CUNHA, W. R.; VENEZIANI, R. C. S.. Estudo fitoquímico preliminar e bioensaio toxicológico frente a larvas de Artemia salina Leach. de extrato obtido de frutos de Solanum lycocarpum A. St.-Hill (Solanaceae). **Revista de Ciências Farmacêuticas Básica e Aplicada**, p. 205-209, 2010.

DEWICK, P.M. **Medicinal natural products**: a Biosynthetic Approach. West Sussex: John Willey & Sons Ltda, 1998.

DIXIT, V.P.; GUPTA, R.S. Antiespermatogenic antiandrogenic properties of solasodine ($C_{27}H_{43}O_2N$) obtained from Solanum xanthocarpum berries on the male genital tract of dog (Canis familiars). **International Journal of Andrology**, v. 5, n. 3, p. 295-307, 1982.

DIXIT, V.P.; GUPTA, R.S.; GUPTA, S. Antifertility plant products: testicular cellpopulation dynamics following solasodine ($C_{27}H_{43}O_2N$) administration in rhesus monke (Macaca mulatta). **Andrologia**, [S.l.], v. 21, n. 6, p. 542-546, 1989.

DRIESSEN H. E, *et al.* New antiarrhythmic targets to control intracellular calcium handling. **Neth Heart Journal**, [S.l.], v. 22, n.5, p. 198-213, 2014.

EANES, R.C. *et al.* Development of practical HPLC methods for separation and determination of eggplant steroidal glycoalkaloids and their aglycones. **Journal of Liquid Chomatography e Related Technologies**, [S.l.], v. 31, p. 984-1000, 2008.

ESTEVES-SOUZA, A.E. *et al.* Mutagenic activity of Glycoallkaloids from Solanum palinacanthum Dunal (Solanaceae) found in the Brazilian cerrado. **Brazilian Chemichal Society**, [S.l.], v. 13, p. 838-842, 2002.

FACELI, K. *et al.* **Inteligência artificial**: uma abordagem de aprendizado de máquina. Rio de Janeiro: LTC, 2011.

FANTINATTO, S. R. C.. **Sistema de tratamento e caracterização da expressão de genes de fenilpropanoides em folhas de Myracrodruon urundeuva (Aroeira-do-Sertão)**. Tese de Doutorado. Universidade de Ribeirão Preto, 2015.

FERREIRA, P.M. *et al.* Ação gastroprotetora do extrato etanólico das folhas de Solanum lycocarpum St. Hil. (Lobeira). **Revista Brasileira de Plantas Medicinais**, Brasil, v. 4, n. 2, p. 60-64, 2002.

FINN, R. D. *et al.* The pfam protein families database. **Nucleic Acids Research**, [S.l.], v. 36, p. 281–288,2008.

GALLA, G. *et al.* Computational annotation of genes differentially expressed along olive fruit development. **BMC Plant Biology**, [S.l.], 2009.

GINZBERG, I. *et al.* Induction of potato steroidal glycoalkaloid biosynthetic pathway by overexpression of cDNA encoding primary metabolism HMG-CoA reductase and squalene synthase. **Planta**, v. 235, n. 6, p. 1341-1353, 2012.

GIROUX, M. J.; MORRIS, C.F. Wheat grain hardness results from highly conserved mutations in the friabilin components puroindoline a and b. **Proceedings of the National Academy of Sciences**, USA, v. 95, p. 6262–6266, 1998.

GOSWANI, A. *et al.* A One-pott efficient process for 16-dehydropregnenolone acetate. **Organic Process Research and Development**, [S.l.], v. 7, n. 7, p. 306-308, 2003.

GONZAGA, A. P. D. *et al.* GERMINAÇÃO DE SEMENTES E ESTABELECIMENTO DE PLÂNTULAS DE SOLANUM LYCOCARPUM ST. HILL (SOLANACEAE) SUBMETIDAS A ESCARIFICAÇÃO MECÂNICA, QUÍMICA E TÉRMICA. In: **CONGRESSO DE ECOLOGIA DO BRASIL**. 2007. p. 1-2.

GRASSELLI, C.S.M. Uso do Amido dos Frutos da Lobeira - Solanum lycocarpum St. Hill - por indivíduos diabéticos: relatos de casos. **Revista Brasileira de Nutrição Clínica,** [S.l.], v. 16, p. 34-37, 2001.

GUERRA, M.O. *et al.* Avaliação do potencial teratogênico do fruto da lobeira (Solanum grandiflorum) administrado no período de organogênese do rato. **Boletim do Centro da Biologia da Reprodução**, Juiz de Fora, v. 16, p. 52-56, 1997.

HARAGUCHI, M. *et al.* Aproveitamento dos esteróides dos frutos da lobeira. **Ciência e Cultura**, [S.l.], v. 32, p. 81-82, 1978.

JUNIOR, O. *et al.* EN de *et al.* Alterações pós-colheita da “Fruta-de-Lobo”(Solanum lycocarpum St. Hil.) durante o amadurecimento: análises físico-químicas, químicas e enzimáticas. **Revista Brasileira de Fruticultura**, v. 26, n. 3, p. 410-413, 2004.

JUNIOR, E. N. O. *et al.* Análise nutricional da fruta-de-lobo (Solanum lycocarpum St. Hil.) durante o amadurecimento. **Ciência e Agrotecnologia**, v. 27, p. 846-851, 2003.

ITKIN, M. L. *et al.* Glycoalkaloid Metabolism is required for steroidal alkaloid glycosylation and prevention of phytotoxicity in tomato. **Plant Cell**, [S.l.], v. 23, n. 12, p. 4507- 4525, 2011.

KANWAR, U. *et al.* Glycolytic enzyme activities of human and bovine spermatozoa treated in vitro with solasodine. **Journal of Ethnopharmacology**, [S.l.], v. 28, n. 2, p. 249-254, 1990.

KRITS, P.L.; FOGELMAN, E; GINZBERG, I. Potato steroidal glycoalkaloid levels and the expression of key isoprenoid metabolic genes. **Planta**, [S.l.], v. 227, n. 1, p. 143-50, 2007.

KUO, K.W. *et al.* Anticance activity evaluation of Solanum glycoalcaloid solamargina: triggering apoptosis in human hepatoma cells. **Biochemichal Pharmacology**, [S.l.], v. 60, p. 1865-1873, 2000.

LIFSCHITZ, S. Algumas pesquisas em banco de dados e bioinformática. In: CONGRESSO DA SBC, n. 26, 2006, Campo Grande. **Anais...** Porto Alegre: Editora da SBC, 2006, p. 44-53, 2006.

MARTINS, K. *et al.* Genetic structure based on nuclear and chloroplast microsatellite loci of Solanum lycocarpum A. St. Hil.(Solanaceae) in Central Brazil. **Genet. Mol. Res**, v. 10, p. 665-677, 2011.

MARTINS, K. *et al.* Mating system and fine-scale spatial genetic structure of Solanum lycocarpum St. Hil.(Solanaceae) in the Brazilian Cerrado. **Conservation Genetics**, v. 7, n. 6, p. 957-969, 2006.

MARUO, V.M.; BERNARDI, M.M.; SPINOSA, H.S. Toxicological evaluations of long-term consumption of Solanum lycocarpum St. Hill fruits in male and female adult rats. **Phytomedicine**, [S.l.], v. 10, p. 48-52, 2003.

MASSA, A. N.; MORRIS, C. F. Molecular evolution of the puroindoline-a, puroindoline-b, and grain softness protein-1 genes in the tribe Triticeae**. Journal Molecular Evolution**, [S.l.], v. 63, p. 526–536, 2006.

MATSUOKA, M. Protective effects of humanin and calmodulin-like skin protein in alzheimer's disease and broad range of abnormalities. **Molecular Neurobiology**, [S.l.], v. 27, p. 1232-1239, 2014.

MCDOWELL, P. **Biologically inspired learning system**. [S.l.] : Louisiana State University, 2005.

MENG, L. *et al.* A membrane-associated thioredoxin required for plant growth moves from cell to cell, suggestive of a role in intercellular communication. **Proceedings of the National Academy of Sciences of the USA**, [S.l.], v. 107, n. 8, p. 3900–3905, 2010.

MIKKILINENI, V. *et al.* Digital quantitative measurements of gene expression. **Biotechnology and Bioenergy**, [S.l.], v. 86, p. 117-124, 2004.

MITRA, R.D.*et al.* Fluorescent in situ sequencing on polymerase colonies. **Analls of Biochemistry**, [S.l.], v. 320, p. 55-65, 2003.

MOREIRA, V. S.S.; DEL-CLARO, K.. The outcomes of an ant-treehopper association on Solanum lycocarpum St. Hill: increased membracid fecundity and reduced damage by chewing herbivores.**Neotropical Entomology**, v. 34, n. 6, p. 881-887, 2005.

MOREIRA, S. **Desenvolvimento de um sistema original simplificado para análise do poliformismo relacionado ao gene IL28B**. 2012. Dissertação (Mestrado saúde e meio ambiente) - Universidade da Região de Joinville, Joinville, 2012.

MOTTA, S. *et al.* Administração de polvilho de lobeira a ratas lactando: desenvolvimento físico das crias. **LECTA**, Bragança Paulista, v. 20, p. 53-59, 2002.

MUSTACICH, D; POWIS, G. Thioredoxin reductase. **Biochemichal Journal**, [S.l.], v. 346, p. 1–8, 2000.

NISHINAKA, Y. *et al.* Redox control of cellular function by thioredoxin: a new therapeutic direction in host defence. **Archives Immunology Therapy Experimental**, [S.l.], v. 49, n. 4, p. 285-292, 2001.

OLIVEIRA JUNIOR, E.N. *et al.* Análise nutricional da fruta-de-lobo (Solanum lycocarpum St. Hil.) durante o amadurecimento. **Ciência e Agrotecnologia**, Lavras, v. 27, n. 4, p. 846-851, 2003.

OLIVEIRA JUNIOR, E.N. *et al.* Alterações pós-colheita da "fruta-de-lobo" (Solanum lycocarpum St. Hil.) durante o amadurecimento: análises físico-químicas, químicas e enzimáticas. **Revista Brasileira de Fruticultura**, Jaboticabal, v. 26, n.3, p. 410-413, 2004.

PEREIRA, A.C. *et al.* [Inserir aqui nome do artigo sem destaque em negrito]. **Anais da Academia Brasileira de Ciências**, [S.l.], v. 80, p. 427-32, 2008. Faltando o nome do artigo!

PINTO, L. V. A. *et al.* Mechanism and control of Solanum lycocarpum seed germination. **Annals of botany**, v. 100, n. 6, p. 1175-1187, 2007.

PROSDOCIMI, F et.al. Bioinformática: manual do usuário. **Biotecnologia Ciência e Desenvolvimento**, [S.l.], n. 29, p. 18-31, 2003.

PROSDOCIMI, F.; SANTOS, F. R. Sobre bioinformática, genoma e Ciência. **Ciência Hoje**, [S.l.], v. 35, n. 209, p. 54-57, 2004.

PROSDOCIMI, F. Curso Online: introdução a bioinformática. **Instituto de Química da Universidade de São Paulo**, São Paulo, 2007. Disponível em: <http://www.iq.usp.br/setubal/bmc/2013/FProsdocimi07_CursoBioinfo.pdf>. Acesso em: 05 abr. 2015.

QI, X.; ZHANG, D. Plant metabolomics and metabolic biology. **Journal of Integrative Plant Biology**, [S.l.], v. 56, p. 814–815, 2014.

RECHE, P. A. Prediction of methylated CpGs in DNA sequences using a support vector machine. **FEBS Letters**, [S.l.], v. 579, p. 4302–4308, 2005.

RIBEIRO, A. O.. Análise anatômica e quantificação de taninos de Stryphnodendron adstringens (Mart.) Coville em diferentes estratos da copa e entre períodos de coleta. 2011.

RODOVALHO, W.; FERRI, P.H.; FERREIRA, E.C. Anti-inflammatory effects of solanum lycocarpum Fruits Phytotherapy Research. **Phytotherapy Research**, [S.l.], v. 17, n.8, p. 892-896, 2003.

RODRIGUES, T. S. **Codificação de seqüências de aminoácidos e sua aplicação na classificação de proteínas com redes neurais artificiais**. 2007. Tese (Doutorado) - PGBIOINFO, Universidade Federal de Minas Gerais, Belo Horizonte, 2007.

SÁ, R.C.S.E *et al.* Evaluation of the toxicity of Solanum lycocarpum in the reproductive system of male mice and rats. **Journal of Ethnopharmacology.** [S.l.], v. 73, p. 283-287, 2000.

SÁ, R.C.S.E.; REIS, J.E.P.; GUERRA, M.O. Avaliação do potencial tóxico do extrato aquoso de Solanum lycocarpum (St.Hil) administrado durante o ciclo espermatogênico de camundongos suícos. **Boletim do Centro da Biologia da Reprodução**, Juiz de Fora, v. 20, p. 19-27, 2001.

SOARES, M.R. *et al.* Toxicological evaluation of 10% Solanum lycocarpum St.Hill frui tconsumption in the diet of growing rats: hematological, biochemical and histopathological effects. **Experimental and Toxicologic Pathology**, [S.l.], v. 62, n. 5, p. 549-553, 2010.

SOUZA, V.; LORENZI, H.. **Botânica sistemática: guia ilustrado para identificação das famílias de fanerógamas nativas e exóticas no Brasil**, baseado em APG II. 2008.

STEFANI, V. *et al.* Development of Enchenopa brasiliensis Strümpel (Homoptera, Membracidae) in plants of Solanum lycocarpum St. Hill.(Solanaceae) in the cerrado and associated ants. **Revista Brasileira de Zoociências**, v. 2, n. 1, p. 21-30, 2000.

VICTOR, V. M; ROCHA, M. Targeting antioxidants to mitochondria: a potential new therapeutic strategy for cardiovascular diseases. **Current Pharmaceutical Design**, [S.l.], v. 13, n. 8, p. 845-863, 2007.

VIDAL, M. C.; STACCIARINI-SERAPHIN, E.; CÂMARA, H. H. L. L. Crescimento de plântulas de Solanum lycocarpum St. Hil.(Lobeira) em casa de vegetação. **Acta Botanica Brasilica**, v. 13, n. 3, p. 271-274, 1999.

VIEIRA, G. *et al.* Antiinammatory effect of Solanum lycocarpum fruits. **Phytotherapy Research**, [S.l.], v. 17, n. 8, p. 892-896, 2003.

VILLAS-BÔAS, S.G.; GOMBERT, A.K. Análise do Metaboloma**. Biotecnologia Ciência & Desenvolvimento**, [S.l.], v. 9, n. 36, 2006.

XAVIER, V. B.; BORBA, H. R.; BRANDOLINI, S. V. P. B.. Atividade biológica de Solanum lycocarpum (Solanaceae) procedente de regiões fitogeográficas distintas sobre Biomphalaria glabrata (Planorbidae). **Revista Brasileira de Zoociências**, v. 12, n. 1, 2011.

WANJUGI, H. W. *et al.* The role of puroindoline A and B individually and in combination on grain hardness and starch association. **Crop Science**. [S.l.], v. 47, p. 67–76, 2007.

WEISSENBERG, M. Isolation of solasodine and other esteroidal alkaloids and sapogenins by direct hidrolysis-extraction of Solanum plants or glycosides there from. **Phytochemistry**, [S.l.], v. 58, p. 501-508, 2001.

WIECZOREK, E. M; LEAL, E. M. **Caminhos e tendências do uso do banco de dados em bioinformática.** In: ENCONTRO DE ESTUDANTES DE INFORMÁTICA DO ESTADO DO TOCANTINS, n.4, 2002, Palmas. Anais. Palmas 2002. p. 89-98.

ZELANDI, E. M.. **Estrutura de populações naturais de Solanum lycocarpum St Hil (Solanaceae)**. 2006. Tese de Doutorado. Universidade Estadual Paulista. Instituto de Biociências de Botucatu.

Apêndice A – Resultado da busca *in sílico* da funcionalidade hipotética em Contigs, da biblioteca de sementes de *Solanum lycocarpum*
Fonte de dados: BlastX/NCBI
Elaborada pelo autor

Name Sequence	**Sequence**	**Name**	**score**	**expert**	**indentities**	**gaps**
Contig0	gi|188593505|emb|CAQ53852.1|	putative reverse transcriptase maturase protein [bacterium AK-MB19]	82 bits(202)	1,03E-15	74%	0%
	gi|44894084|gb|AAS48583.1|	lacZa [Mammalian expression vector pTargeT]	67 bits(162)	4,04E-11	70%	1%
	gi|407227153|emb|CCM44347.1|	CcdB toxin fusion [Cloning vector pSAWloxP-K]	71 bits(173)	4,40E-12	89%	0%
	gi|2950220|emb|CAA71575.1|	fused-ccdB [Cloning vector pZeRO-2T]	70 bits(169)	1,86E-11	82%	0%
	gi|190361707|gb|ACE77052.1|	LacZ alpha peptide [Cloning vector pSMARTGC Blue]	70 bits(170)	4,92E-12	79%	0%
	gi|2664255|emb|CAA67127.1|	ccdB [synthetic construct]	70 bits(169)	1,81E-11	82%	0%
	gi|45861223|gb|AAS78488.1|	LacZ alpha & ccdB lethal fusion protein [Cloning vector pZero++ Amp]	71 bits(172)	7,89E-12	89%	0%
Contig1	gi|190361707|gb|ACE77052.1|	LacZ alpha peptide [Cloning vector pSMARTGC Blue]	124 bits(311)	2,40E-32	84%	3%
	gi|147724741|gb|ABQ45977.1|	lacZ alpha peptide [Linear cloning vector pJAZZ-OC]	119 bits(298)	4,50E-31	90%	0%
	gi|184991891|emb|CAQ43070.2|	putative puroindoline b protein [Triticum macha]	153 bits(384)	4,30E-42	95%	0%
	gi|45861223|gb|AAS78488.1|	LacZ alpha & ccdB lethal fusion protein [Cloning vector pZero++ Amp]	126 bits(316)	5,13E-32	83%	3%
	gi|3402817|emb|CAA07704.1|	lacZ' [Cloning vector pGreen]	121 bits(301)	4,68E-31	98%	0%
	gi|2950220|emb|CAA71575.1|	fused-ccdB [Cloning vector pZeRO-2T]	125 bits(313)	8,92E-32	81%	3%
	gi|155733602|gb|ABU39928.1|	beta-galactosidase [Cloning vector pGreenII 0029]	121 bits(301)	4,73E-31	98%	0%
	gi|407227153|emb|CCM44347.1|	CcdB toxin fusion [Cloning vector pSAWloxP-K]	127 bits(317)	1,41E-32	83%	3%
	gi|89158283|gb|ABD62894.1|	lacZ alpha [Cloning vector pJAZZ-KA]	119 bits(298)	4,50E-31	90%	0%
	gi|62945802|gb|AAS77687.2|	LacZ-alpha [Shuttle vector pLPV111]	135 bits(338)	1,38E-36	98%	0%
Contig2	gi|595780|gb|AAA56741.1|	lacZ alpha peptide [unidentified cloning vector]	112 bits(279)	3,75E-61	90%	0%
	gi|605702959|gb|EYU61585.1|	hypothetical protein CI00_06105 [Leptospira interrogans serovar Manilae]	146 bits(367)	2,26E-40	97%	0%
	gi|510843006|ref|WP_016211909.1|	putative beta-D-galactosidase [Piscirickettsia salmonis]	132 bits(331)	3,25E-34	91%	0%
	gi|62945802|gb|AAS77687.2|	LacZ-alpha [Shuttle vector pLPV111]	162 bits(408)	8,07E-46	99%	0%
	gi|4884787|gb|AAD31805.1|AF128862_1	LacZ [Cloning vector pHIND2.2]	143 bits(359)	7,24E-39	99%	0%
	gi|184991891|emb|CAQ43070.2|	putative puroindoline b protein [Triticum macha]	154 bits(388)	1,30E-41	95%	0%
	gi|152144113|gb|EDN71582.1|	lacZ alpha peptide [Beggiatoa sp. SS]	141 bits(355)	1,45E-38	100%	0%
	gi|595775|gb|AAA56738.1|	lacZ alpha peptide [unidentified cloning vector]	113 bits(281)	1,81E-61	90%	0%
	gi|190361707|gb|ACE77052.1|	LacZ alpha peptide [Cloning vector pSMARTGC Blue]	151 bits(380)	1,61E-41	87%	3%
	gi|7208800|emb|CAB76939.1|	alpha-peptide [Cloning vector pPW78]	141 bits(354)	3,40E-38	97%	0%
Contig3	gi|661895087|emb|CDP00892.1|	unnamed protein product [Coffea canephora]	87 bits(214)	1,06E-18	64%	2%
	gi|60459403|gb|AAX20047.1|	metallothionein-like protein type 2 [Capsicum annuum]	84 bits(207)	1,38E-17	82%	0%
	gi|565390980|ref|XP_006361209.1|	PREDICTED: metallothionein-like protein type 2-like [Solanum tuberosum]	90 bits(221)	1,09E-19	78%	0%
	gi|193085066|gb|ACF10398.1|	type 2 metallothionein [Solanum nigrum]	86 bits(211)	3,72E-18	79%	0%
	gi|565390974|ref|XP_006361207.1|	PREDICTED: metallothionein-like protein type 2-like [Solanum tuberosum]	83 bits(204)	3,67E-17	77%	0%
	gi|350537709|ref|NP_001234050.1|	metallothionein-like protein type 2 [Solanum lycopersicum]	89 bits(218)	4,57E-19	76%	0%
	gi|58578264|emb|CAI48068.1|	metallotionein-like protein [Capsicum chinense]	86 bits(210)	4,76E-18	82%	0%
	gi|565390978|ref|XP_006361208.1|	PREDICTED: metallothionein-like protein type 2-like [Solanum tuberosum]	82 bits(201)	8,82E-17	75%	0%
	gi|193085064|gb|ACF10397.1|	type 2 metallothionein [Solanum nigrum]	88 bits(216)	6,74E-19	81%	0%
	gi|151301842|gb|ABR92329.1|	putative metallothionin 2a [Salvia miltiorrhiza]	85 bits(208)	1,04E-17	62%	6%
Contig4	gi|108864390|gb|ABG22487.1|	40S ribosomal protein S5, putative, expressed [Oryza sativa Japonica Group]	113 bits(281)	1,66E-28	98%	0%
	gi|413947079|gb|AFW79728.1|	hypothetical protein ZEAMMB73_326578 [Zea mays]	112 bits(280)	4,92E-28	98%	0%
	gi|645271910|ref|XP_008241140.1|	PREDICTED: 40S ribosomal protein S5-like [Prunus mume]	114 bits(283)	6,40E-28	98%	0%
	gi|658047699|ref|XP_008359536.1|	PREDICTED: 40S ribosomal protein S5-like [Malus domestica]	111 bits(277)	2,84E-28	96%	0%
	gi|596187545|ref|XP_007223418.1|	hypothetical protein PRUPE_ppa011314mg [Prunus persica]	114 bits(284)	4,98E-28	98%	0%
	gi|573962596|ref|XP_006663445.1|	PREDICTED: 40S ribosomal protein S5-like, partial [Oryza brachyantha]	112 bits(278)	3,42E-28	96%	0%
	gi|595820939|ref|XP_007204730.1|	hypothetical protein PRUPE_ppa011341mg [Prunus persica]	114 bits(284)	5,59E-28	98%	0%
	gi|223974323|gb|ACN31349.1|	unknown [Zea mays]	112 bits(278)	1,37E-28	98%	0%
	gi|645225812|ref|XP_008219748.1|	PREDICTED: 40S ribosomal protein S5 [Prunus mume]	114 bits(284)	4,58E-28	98%	0%
	gi|255640594|gb|ACU20582.1|	unknown [Glycine max]	111 bits(277)	5,63E-28	96%	0%
Contig5	No Hits.					
Contig6	gi|565378014|ref|XP_006355458.1|	PREDICTED: small heat shock protein, chloroplastic-like [Solanum tuberosum]	170 bits(429)	1,39E-48	93%	0%
	gi|659095978|ref|XP_008448861.1|	PREDICTED: small heat shock protein, chloroplastic-like isoform X2 [Cucumis melo]	151 bits(381)	1,98E-41	74%	0%

<table>
<tr><td></td><td>gi|645266293|ref|XP_008238549.1|</td><td>PREDICTED: heat shock 22 kDa protein, mitochondrial [Prunus mume]</td><td>138 bits(346)</td><td>2,51E-36</td><td>66%</td><td>2%</td></tr>
<tr><td></td><td>gi|350539261|ref|NP_001233872.1|</td><td>mitochondrial small heat shock protein [Solanum lycopersicum]</td><td>169 bits(428)</td><td>2,14E-48</td><td>93%</td><td>0%</td></tr>
<tr><td></td><td>gi|659095976|ref|XP_008448860.1|</td><td>PREDICTED: small heat shock protein, chloroplastic-like isoform X1 [Cucumis melo]</td><td>151 bits(381)</td><td>2,08E-41</td><td>74%</td><td>0%</td></tr>
<tr><td></td><td>gi|224074141|ref|XP_002304270.1|</td><td>hypothetical protein POPTR_0003s07360g [Populus trichocarpa]</td><td>137 bits(344)</td><td>6,09E-36</td><td>63%</td><td>5%</td></tr>
<tr><td></td><td>gi|299891471|gb|ADJ57588.1|</td><td>mitochondrial small heat shock protein [Capsicum annuum]</td><td>165 bits(417)</td><td>9,89E-47</td><td>87%</td><td>5%</td></tr>
<tr><td></td><td>gi|661886590|emb|CDP09954.1|</td><td>unnamed protein product [Coffea canephora]</td><td>140 bits(352)</td><td>4,54E-37</td><td>74%</td><td>0%</td></tr>
<tr><td></td><td>gi|449531055|ref|XP_004172503.1|</td><td>PREDICTED: small heat shock protein, chloroplastic-like [Cucumis sativus]</td><td>152 bits(383)</td><td>8,44E-42</td><td>74%</td><td>0%</td></tr>
<tr><td></td><td>gi|595848808|ref|XP_007209602.1|</td><td>hypothetical protein PRUPE_ppa011466mg [Prunus persica]</td><td>139 bits(348)</td><td>1,16E-36</td><td>66%</td><td>2%</td></tr>
<tr><td>Contig7</td><td>gi|11344886|gb|AAG34526.1|</td><td>beta-galactosidase [Cloning vector pUG26]</td><td>116 bits(289)</td><td>2,89E-55</td><td>97%</td><td>2%</td></tr>
<tr><td></td><td>gi|7384996|gb|AAF61634.1|</td><td>lacZ [Cloning vector pTG8]</td><td>115 bits(287)</td><td>6,73E-55</td><td>97%</td><td>2%</td></tr>
<tr><td></td><td>gi|31415494|gb|AAP44986.1|</td><td>LacZalpha [Shuttle vector pNG168]</td><td>115 bits(287)</td><td>3,04E-55</td><td>97%</td><td>2%</td></tr>
<tr><td></td><td>gi|2440160|emb|CAA75108.1|</td><td>beta-galactosidase [Phagemid cloning vector pTZ19U]</td><td>113 bits(282)</td><td>4,36E-51</td><td>92%</td><td>0%</td></tr>
<tr><td></td><td>gi|510843006|ref|WP_016211909.1|</td><td>putative beta-D-galactosidase [Piscirickettsia salmonis]</td><td>115 bits(287)</td><td>4,37E-56</td><td>97%</td><td>2%</td></tr>
<tr><td></td><td>gi|113473484|gb|ABI35978.1|</td><td>LacZ alpha peptide [Cloning vector pYESW29']</td><td>116 bits(288)</td><td>3,74E-55</td><td>97%</td><td>2%</td></tr>
<tr><td></td><td>gi|567893|gb|AAA53120.1|</td><td>beta-galactosidase-complementation protein [unidentified cloning vector]</td><td>113 bits(282)</td><td>6,88E-51</td><td>92%</td><td>0%</td></tr>
<tr><td></td><td>gi|11344916|gb|AAG34547.1|</td><td>beta-galactosidase [Cloning vector pUG7]</td><td>116 bits(289)</td><td>2,73E-55</td><td>97%</td><td>2%</td></tr>
<tr><td></td><td>gi|38385703|gb|AAR19394.1|</td><td>modified lacZ' [Cloning vector pTA6]</td><td>115 bits(287)</td><td>4,37E-55</td><td>97%</td><td>2%</td></tr>
<tr><td></td><td>gi|567890|gb|AAA53118.1|</td><td>beta-galactosidase-complementation protein [unidentified cloning vector]</td><td>110 bits(274)</td><td>7,35E-50</td><td>90%</td><td>0%</td></tr>
<tr><td>Contig8</td><td>No Hits.</td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Contig9</td><td>No Hits.</td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Contig10</td><td>gi|661891931|emb|CDP04157.1|</td><td>unnamed protein product [Coffea canephora]</td><td>97 bits(240)</td><td>6,39E-20</td><td>68%</td><td>2%</td></tr>
<tr><td></td><td>gi|672133880|ref|XP_008790577.1|</td><td>PREDICTED: chromatin assembly factor 1 subunit FSM-like [Phoenix dactylifera]</td><td>87 bits(213)</td><td>2,21E-16</td><td>63%</td><td>0%</td></tr>
<tr><td></td><td>gi|296080865|emb|CBI18795.3|</td><td>unnamed protein product [Vitis vinifera]</td><td>92 bits(228)</td><td>1,61E-19</td><td>68%</td><td>1%</td></tr>
<tr><td></td><td>gi|657993130|ref|XP_008388834.1|</td><td>PREDICTED: chromatin assembly factor 1 subunit FAS1-like isoform X2 [Malus domestica]</td><td>86 bits(210)</td><td>4,58E-16</td><td>58%</td><td>3%</td></tr>
<tr><td></td><td>gi|317106648|dbj|BAJ53153.1|</td><td>JHL23J11.8 [Jatropha curcas]</td><td>83 bits(203)</td><td>4,54E-15</td><td>50%</td><td>1%</td></tr>
<tr><td></td><td>gi|565373398|ref|XP_006353261.1|</td><td>PREDICTED: chromatin assembly factor 1 subunit FAS1-like [Solanum tuberosum]</td><td>143 bits(358)</td><td>7,90E-36</td><td>88%</td><td>2%</td></tr>
<tr><td></td><td>gi|359496944|ref|XP_002268317.2|</td><td>PREDICTED: uncharacterized protein LOC100261350, partial [Vitis vinifera]</td><td>92 bits(227)</td><td>7,20E-19</td><td>68%</td><td>1%</td></tr>
<tr><td></td><td>gi|645223145|ref|XP_008218490.1|</td><td>PREDICTED: chromatin assembly factor 1 subunit FAS1 [Prunus mume]</td><td>82 bits(201)</td><td>7,50E-15</td><td>61%</td><td>2%</td></tr>
<tr><td></td><td>gi|460409299|ref|XP_004250076.1|</td><td>PREDICTED: chromatin assembly factor 1 subunit FAS1-like [Solanum lycopersicum]</td><td>129 bits(324)</td><td>3,39E-31</td><td>83%</td><td>2%</td></tr>
<tr><td></td><td>gi|590633373|ref|XP_007028094.1|</td><td>Chromatin assembly factor 1 subunit A, putative [Theobroma cacao]</td><td>92 bits(228)</td><td>2,15E-18</td><td>64%</td><td>2%</td></tr>
<tr><td>Contig11</td><td>gi|62945802|gb|AAS77687.2|</td><td>LacZ-alpha [Shuttle vector pLPV111]</td><td>163 bits(411)</td><td>6,88E-48</td><td>100%</td><td>0%</td></tr>
<tr><td></td><td>gi|7208800|emb|CAB76939.1|</td><td>alpha-peptide [Cloning vector pPW78]</td><td>142 bits(357)</td><td>4,27E-40</td><td>99%</td><td>0%</td></tr>
<tr><td></td><td>gi|3402817|emb|CAA07704.1|</td><td>lacZ' [Cloning vector pGreen]</td><td>134 bits(337)</td><td>9,05E-37</td><td>100%</td><td>0%</td></tr>
<tr><td></td><td>gi|190361707|gb|ACE77052.1|</td><td>LacZ alpha peptide [Cloning vector pSMARTGC Blue]</td><td>152 bits(383)</td><td>1,58E-43</td><td>88%</td><td>3%</td></tr>
<tr><td></td><td>gi|45826070|gb|AAS77680.1|</td><td>LacZ-alpha [Shuttle vector pELS100]</td><td>141 bits(355)</td><td>1,84E-39</td><td>97%</td><td>1%</td></tr>
<tr><td></td><td>gi|155733607|gb|ABU39931.1|</td><td>beta-galactosidase [Cloning vector pGreenII 0179]</td><td>134 bits(337)</td><td>1,83E-36</td><td>100%</td><td>0%</td></tr>
<tr><td></td><td>gi|184991891|emb|CAQ43070.2|</td><td>putative puroindoline b protein [Triticum macha]</td><td>154 bits(388)</td><td>3,28E-43</td><td>95%</td><td>0%</td></tr>
<tr><td></td><td>gi|9294789|gb|AAF86672.1|AF178450_1</td><td>beta-galactosidase alpha peptide [Integration vector pCD11PSK]</td><td>137 bits(343)</td><td>1,25E-37</td><td>96%</td><td>2%</td></tr>
<tr><td></td><td>gi|4884787|gb|AAD31805.1|AF128862_1</td><td>LacZ [Cloning vector pHIND2.2]</td><td>147 bits(370)</td><td>6,26E-42</td><td>100%</td><td>0%</td></tr>
<tr><td></td><td>gi|155733602|gb|ABU39928.1|</td><td>beta-galactosidase [Cloning vector pGreenII 0029]</td><td>134 bits(337)</td><td>8,73E-37</td><td>100%</td><td>0%</td></tr>
<tr><td>Contig12</td><td>gi|147724741|gb|ABQ45977.1|</td><td>lacZ alpha peptide [Linear cloning vector pJAZZ-OC]</td><td>119 bits(297)</td><td>2,05E-31</td><td>92%</td><td>0%</td></tr>
<tr><td></td><td>gi|407227153|emb|CCM44347.1|</td><td>CcdB toxin fusion [Cloning vector pSAWloxP-K]</td><td>126 bits(316)</td><td>5,54E-33</td><td>84%</td><td>3%</td></tr>
<tr><td></td><td>gi|3402817|emb|CAA07704.1|</td><td>lacZ' [Cloning vector pGreen]</td><td>120 bits(299)</td><td>2,10E-31</td><td>100%</td><td>0%</td></tr>
<tr><td></td><td>gi|190361707|gb|ACE77052.1|</td><td>LacZ alpha peptide [Cloning vector pSMARTGC Blue]</td><td>124 bits(310)</td><td>9,77E-33</td><td>86%</td><td>3%</td></tr>
<tr><td></td><td>gi|229620414|gb|ACQ84163.1|</td><td>truncated LacZ [BAC cloning vector attB-P[acman]-CmR-BW-F-2-attB-BW3]</td><td>120 bits(299)</td><td>1,05E-31</td><td>100%</td><td>0%</td></tr>
<tr><td></td><td>gi|184991891|emb|CAQ43070.2|</td><td>putative puroindoline b protein [Triticum macha]</td><td>151 bits(379)</td><td>4,47E-42</td><td>95%</td><td>0%</td></tr>
<tr><td></td><td>gi|45861223|gb|AAS78488.1|</td><td>LacZ alpha & ccdB lethal fusion protein [Cloning vector pZero++ Amp]</td><td>126 bits(315)</td><td>2,06E-32</td><td>84%</td><td>3%</td></tr>
<tr><td></td><td>gi|2664253|emb|CAA67126.1|</td><td>ccdB [synthetic construct]</td><td>122 bits(305)</td><td>1,84E-31</td><td>98%</td><td>0%</td></tr>
<tr><td></td><td>gi|62945802|gb|AAS77687.2|</td><td>LacZ-alpha [Shuttle vector pLPV111]</td><td>134 bits(336)</td><td>6,75E-37</td><td>100%</td><td>0%</td></tr>
<tr><td></td><td>gi|2950220|emb|CAA71575.1|</td><td>fused-ccdB [Cloning vector pZeRO-2T]</td><td>125 bits(312)</td><td>3,11E-32</td><td>82%</td><td>3%</td></tr>
<tr><td>Contig13</td><td>gi|350535016|ref|NP_001234171.1|</td><td>thioredoxin peroxidase 1 [Solanum lycopersicum]</td><td>90 bits(222)</td><td>1,01E-19</td><td>90%</td><td>0%</td></tr>
<tr><td></td><td>gi|629117733|gb|KCW82408.1|</td><td>hypothetical protein EUGRSUZ_C03812 [Eucalyptus grandis]</td><td>86 bits(212)</td><td>1,45E-18</td><td>86%</td><td>0%</td></tr>
<tr><td></td><td>gi|568214762|ref|NP_001275255.1|</td><td>peroxiredoxin-2B-like [Solanum tuberosum]</td><td>90 bits(222)</td><td>1,07E-19</td><td>90%</td><td>0%</td></tr>
<tr><td></td><td>gi|629117732|gb|KCW82407.1|</td><td>hypothetical protein EUGRSUZ_C03812 [Eucalyptus grandis]</td><td>87 bits(213)</td><td>1,72E-18</td><td>86%</td><td>0%</td></tr>
<tr><td></td><td>gi|40287562|gb|AAR83895.1|</td><td>thioredoxin peroxidase CATP [Capsicum annuum]</td><td>91 bits(224)</td><td>8,29E-21</td><td>92%</td><td>0%</td></tr>
<tr><td></td><td>gi|511774226|gb|AGN92481.1|</td><td>peroxiredoxin 2B [Nicotiana benthamiana]</td><td>89 bits(219)</td><td>2,45E-19</td><td>90%</td><td>0%</td></tr>
</table>

	gi|645274937|ref|XP_008242575.1|	PREDICTED: peroxiredoxin-2B [Prunus mume]	84 bits(207)	1,29E-17	84%	0%
	gi|18654477|gb|AAL35363.2|AF442385_1	thioredoxin peroxidase [Capsicum annuum]	92 bits(228)	1,55E-20	92%	0%
	gi|674810460|gb|AIL30482.1|	thioredoxin peroxidase 1 [Nicotiana tabacum]	89 bits(219)	2,69E-19	90%	0%
	gi|595807897|ref|XP_007202687.1|	hypothetical protein PRUPE_ppa012586mg [Prunus persica]	84 bits(207)	1,30E-17	84%	0%
Contig14	gi|595775|gb|AAA56738.1|	lacZ alpha peptide [unidentified cloning vector]	113 bits(281)	2,08E-53	90%	0%
	gi|190361707|gb|ACE77052.1|	LacZ alpha peptide [Cloning vector pSMARTGC Blue]	151 bits(380)	7,35E-42	87%	3%
	gi|45826070|gb|AAS77680.1|	LacZ-alpha [Shuttle vector pELS100]	140 bits(351)	9,61E-38	96%	1%
	gi|595780|gb|AAA56741.1|	lacZ alpha peptide [unidentified cloning vector]	112 bits(279)	3,91E-53	90%	0%
	gi|605702959|gb|EYU61585.1|	hypothetical protein CI00_06105 [Leptospira interrogans serovar Manilae]	144 bits(361)	9,92E-40	96%	0%
	gi|9294789|gb|AAF86672.1|AF178450_1	beta-galactosidase alpha peptide [Integration vector pCD11PSK]	136 bits(340)	5,48E-36	95%	2%
	gi|62945802|gb|AAS77687.2|	LacZ-alpha [Shuttle vector pLPV111]	162 bits(408)	3,56E-46	99%	0%
	gi|4884787|gb|AAD31805.1|AF128862_1	LacZ [Cloning vector pHIND2.2]	143 bits(359)	3,41E-39	99%	0%
	gi|184991891|emb|CAQ43070.2|	putative puroindoline b protein [Triticum macha]	154 bits(388)	6,06E-42	95%	0%
	gi|7208800|emb|CAB76939.1|	alpha-peptide [Cloning vector pPW78]	141 bits(354)	1,61E-38	97%	0%
Contig15	gi|655432281|gb|KED02449.1|	hypothetical protein P820_00010, partial [Klebsiella pneumoniae UCI 17]	299 bits(764)	1,50E-100	100%	0%
	gi|486147410|ref|WP_001517795.1|	hypothetical protein [Escherichia coli]	299 bits(764)	2,83E-100	100%	0%
	gi|660299543|gb|KEN88941.1|	transposase DDE domain protein, partial [Escherichia coli 2-222-05_S3_C1]	299 bits(764)	1,64E-100	100%	0%
	gi|485764543|ref|WP_001389360.1|	hypothetical protein, partial [Escherichia coli]	298 bits(762)	2,91E-100	100%	0%
	gi|691549278|ref|WP_032073034.1|	hypothetical protein [Vibrio sp. 04Ya090]	314 bits(803)	5,33E-103	92%	0%
	gi|485803586|ref|WP_001424208.1|	transposase, partial [Escherichia coli]	299 bits(765)	2,41E-100	100%	0%
	gi|660310426|gb|KEN98699.1|	transposase DDE domain protein, partial [Escherichia coli 2-222-05_S3_C2]	299 bits(763)	3,44E-100	100%	0%
	gi|545174715|ref|WP_021528775.1|	hypothetical protein, partial [Escherichia coli]	299 bits(765)	1,49E-100	100%	0%
	gi|485803989|ref|WP_001424561.1|	transposase, IS4 family, IS10, partial [Escherichia coli]	299 bits(763)	2,61E-100	100%	0%
	gi|660303169|gb|KEN92147.1|	transposase DDE domain protein, partial [Escherichia coli 2-222-05_S3_C2]	298 bits(762)	3,47E-100	100%	0%
Contig16	gi|190361707|gb|ACE77052.1|	LacZ alpha peptide [Cloning vector pSMARTGC Blue]	146 bits(366)	1,27E-40	91%	0%
	gi|45826070|gb|AAS77680.1|	LacZ-alpha [Shuttle vector pELS100]	130 bits(326)	8,52E-35	88%	3%
	gi|1132426|gb|AAA84370.1|	beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	124 bits(311)	2,12E-32	71%	2%
	gi|7208800|emb|CAB76939.1|	alpha-peptide [Cloning vector pPW78]	140 bits(352)	5,27E-39	76%	7%
	gi|9294789|gb|AAF86672.1|AF178450_1	beta-galactosidase alpha peptide [Integration vector pCD11PSK]	126 bits(314)	5,95E-33	87%	4%
	gi|155733602|gb|ABU39928.1|	beta-galactosidase [Cloning vector pGreenII 0029]	124 bits(310)	2,50E-32	90%	2%
	gi|62945802|gb|AAS77687.2|	LacZ-alpha [Shuttle vector pLPV111]	140 bits(352)	1,09E-38	93%	0%
	gi|510843006|ref|WP_016211909.1|	putative beta-D-galactosidase [Piscirickettsia salmonis]	125 bits(312)	1,53E-32	88%	0%
	gi|4884787|gb|AAD31805.1|AF128862_1	LacZ [Cloning vector pHIND2.2]	136 bits(342)	1,96E-37	96%	0%
	gi|3402817|emb|CAA07704.1|	lacZ' [Cloning vector pGreen]	124 bits(310)	2,04E-32	90%	2%
Contig17	No Hits.					
Contig18	gi|485803990|ref|WP_001424562.1|	transposase [Escherichia coli]	145 bits(364)	4,29E-42	97%	0%
	gi|485720736|ref|WP_001352060.1|	tnpR protein, partial [Escherichia coli]	144 bits(362)	4,57E-42	97%	0%
	gi|660299104|gb|KEN88510.1|	putative tnpA transposase of IS10, partial [Escherichia coli 2-222-05_S3_C1]	144 bits(362)	5,17E-42	97%	0%
	gi|24052025|gb|AAN43271.1|	iso-IS10R ORF [Shigella flexneri 2a str. 301]	145 bits(364)	4,44E-42	97%	0%
	gi|487670518|ref|WP_001755850.1|	hypothetical protein, partial [Escherichia coli]	144 bits(362)	4,86E-42	97%	0%
	gi|652155586|gb|KDY67120.1|	transposase DDE domain protein, partial [Escherichia coli 2-460-02_S4_C3]	146 bits(368)	4,89E-42	97%	0%
	gi|485805156|ref|WP_001425577.1|	putative transposase, partial [Escherichia coli]	144 bits(363)	4,44E-42	97%	0%
	gi|6685159|gb|AAF23820.1|AF219140_1	gastric cancer-related protein GCYS-20 [Homo sapiens]	152 bits(382)	9,85E-43	97%	0%
	gi|1196996|gb|AAA88658.1|	unknown protein, partial [Transposon Tn10]	144 bits(363)	5,06E-42	97%	0%
	gi|485764311|ref|WP_001389156.1|	hypothetical protein, partial [Escherichia coli]	144 bits(362)	4,48E-42	97%	0%

Apêndice B – Resultado da busca *in silico* da funcionalidade hipotética em Singlets, da biblioteca de sementes de *Solanum lycocarpum*
Fonte de dados: Blastx/NCBI
Elaborada pelo autor

Name Sequence	Sequence	Name	score	expert	indentities	gaps
SLSEPL01A04	No Hits.					
SLSEPL01A05	No Hits.					
SLSEPL01A07	No Hits.					
SLSEPL01A10	No Hits.					
SLSEPL01A11	No Hits.					
SLSEPL01A12	No Hits.					
SLSEPL01B03	No Hits.					
SLSEPL01B07	gi|595813648|ref|XP_007203612.1|	hypothetical protein PRUPE_ppa002880mg [Prunus persica]	163 bits(411)	2,38E-43	71%	2%
	gi|470102058|ref|XP_004287476.1|	PREDICTED: uncharacterized protein LOC101296509 [Fragaria vesca subsp. vesca]	166 bits(419)	1,69E-44	74%	2%
	gi|470105031|ref|XP_004288892.1|	PREDICTED: LOW QUALITY PROTEIN: uncharacterized tRNA/rRNA methyltransferase slr0955-like [Fragaria vesca subsp. vesca]	161 bits(407)	4,97E-43	72%	2%
	gi|567918590|ref|XP_006451301.1|	hypothetical protein CICLE_v10007826mg [Citrus clementina]	163 bits(411)	1,61E-43	77%	0%
	gi|565352483|ref|XP_006343172.1|	PREDICTED: rRNA methyltransferase 1, mitochondrial-like [Solanum tuberosum]	199 bits(505)	1,16E-57	90%	1%
	gi|255546313|ref|XP_002514216.1|	rRNA methylase, putative [Ricinus communis]	161 bits(407)	3,50E-43	75%	2%
	gi|641847696|gb|KDO66575.1|	hypothetical protein CISIN_1g007847mg [Citrus sinensis]	164 bits(414)	5,99E-44	78%	2%
	gi|661893446|emb|CDP03255.1|	unnamed protein product [Coffea canephora]	181 bits(459)	1,75E-50	80%	2%
	gi|590576712|ref|XP_007013032.1|	TRNA/rRNA methyltransferase family protein [Theobroma cacao]	162 bits(409)	3,38E-43	74%	4%
	gi|460387763|ref|XP_004239543.1|	PREDICTED: uncharacterized tRNA/rRNA methyltransferase slr0955-like [Solanum lycopersicum]	165 bits(416)	1,80E-44	89%	1%
SLSEPL01B08	No Hits.					
SLSEPL01B11	No Hits.					
SLSEPL01C01	No Hits.					
SLSEPL01C02	No Hits.					
SLSEPL01C03	No Hits.					
SLSEPL01C07	No Hits.					
SLSEPL01C11	No Hits.					
SLSEPL01C12	No Hits.					
SLSEPL01D02	No Hits.					
SLSEPL01D08	No Hits.					
SLSEPL01D12	No Hits.					
SLSEPL01E05	No Hits.					
SLSEPL01E06	No Hits.					
SLSEPL01E07	No Hits.					
SLSEPL01E09	No Hits.					
SLSEPL01E12	No Hits.					
SLSEPL01F01	No Hits.					
SLSEPL01F02	No Hits.					
SLSEPL01F03	No Hits.					
SLSEPL01F06	No Hits.					
SLSEPL01F07	No Hits.					
SLSEPL01F10	No Hits.					
SLSEPL01G06	No Hits.					
SLSEPL01G12	gi|184991891|emb|CAQ43070.2|	putative puroindoline b protein [Triticum macha]	154 bits(387)	4,06E-44	100%	0%
	gi|4884787|gb|AAD31805.1|AF128862_1	LacZ [Cloning vector pHIND2.2]	136 bits(340)	1,30E-38	98%	0%
	gi|155733607|gb|ABU39931.1|	beta-galactosidase [Cloning vector pGreenII 0179]	132 bits(332)	8,35E-37	98%	0%
	gi|7208800|emb|CAB76939.1|	alpha-peptide [Cloning vector pPW78]	133 bits(333)	1,40E-37	97%	0%
	gi|45826070|gb|AAS77680.1|	LacZ-alpha [Shuttle vector pELS100]	132 bits(330)	9,69E-37	96%	1%
	gi|62945802|gb|AAS77687.2|	LacZ-alpha [Shuttle vector pLPV111]	153 bits(386)	3,45E-45	99%	0%
	gi|3402817|emb|CAA07704.1|	lacZ' [Cloning vector pGreen]	133 bits(333)	3,23E-37	98%	0%
	gi|157165877|gb|ABV25015.1|	beta-galactosidase a-peptide [Cloning vector pTriplEx2]	131 bits(329)	1,47E-36	98%	0%
	gi|190361707|gb|ACE77052.1|	LacZ alpha peptide [Cloning vector pSMARTGC Blue]	142 bits(356)	1,71E-40	85%	3%
	gi|155733602|gb|ABU39928.1|	beta-galactosidase [Cloning vector pGreenII 0029]	133 bits(333)	3,58E-37	98%	0%
SLSEPL01H01	No Hits.					

SLSEPL01H05	No Hits.					
SLSEPL01H06	No Hits.					
SLSEPL02A01	No Hits.					
SLSEPL02A04	No Hits.					
SLSEPL02A08	gi|184991891|emb|CAQ43070.2|	putative puroindoline b protein [Triticum macha]	71 bits(172)	7,04E-13	97%	0%
SLSEPL02A10	No Hits.					
SLSEPL02A12	No Hits.					
SLSEPL02B01	No Hits.					
SLSEPL02B04	No Hits.					
SLSEPL02B05	No Hits.					
SLSEPL02B06	No Hits.					
SLSEPL02B07	No Hits.					
SLSEPL02B12	No Hits.					
SLSEPL02C01	No Hits.					
SLSEPL02C05	No Hits.					
SLSEPL02C06	No Hits.					
SLSEPL02C07	No Hits.					
SLSEPL02C08	No Hits.					
SLSEPL02C10	No Hits.					
SLSEPL02C11	No Hits.					
SLSEPL02C12	gi|371486150|gb|AEX31051.1|	polyprotein 2, partial [uncultured virus]	89 bits(219)	1,69E-19	57%	2%
	gi|628872199|gb|AHY82851.1|	coat protein, partial [Arabis mosaic virus]	73 bits(177)	9,38E-12	26%	7%
	gi|50511901|ref|YP_054438.1|	capsid protein [Arabis mosaic virus]	72 bits(175)	1,69E-11	28%	7%
	gi|194021637|gb|ACF32435.1|	polyprotein 2 [Arabis mosaic virus]	76 bits(186)	1,21E-12	28%	9%
	gi|60663|emb|CAA39108.1|	coat protein [Arabis mosaic virus]	73 bits(177)	1,05E-11	26%	7%
	gi|221018|dbj|BAA00982.1|	polyprotein [Arabis mosaic virus]	72 bits(176)	1,73E-11	27%	5%
	gi|167861136|gb|ACA05287.1|	polyprotein P2 [Arabis mosaic virus]	75 bits(183)	1,77E-12	27%	5%
	gi|628872203|gb|AHY82853.1|	coat protein, partial [Arabis mosaic virus]	73 bits(177)	1,06E-11	25%	7%
	gi|157679074|dbj|BAF35851.2|	polyprotein P2 123KDa [Arabis mosaic virus]	75 bits(182)	4,37E-12	27%	5%
	gi|130397|sp|P24819.1|POL2_ARMV	RecName: Full=RNA2 polyprotein; AltName: Full=P2; Contains: RecName: Full=Movement protein; AltName: Full=2B-MP; Contains: RecName: Full=Coat protein; AltName: Full=2C-CP, partial [Arabis mosaic virus]	73 bits(177)	1,06E-11	26%	7%
SLSEPL02D01	No Hits.					
SLSEPL02D02	No Hits.					
SLSEPL02D05	No Hits.					
SLSEPL02D06	No Hits.					
SLSEPL02D09	No Hits.					
SLSEPL02D10	No Hits.					
SLSEPL02D11	No Hits.					
SLSEPL02E01	No Hits.					
SLSEPL02E02	No Hits.					
SLSEPL02E03	No Hits.					
SLSEPL02E05	No Hits.					
SLSEPL02E06	No Hits.					
SLSEPL02E07	No Hits.					
SLSEPL02E10	No Hits.					
SLSEPL02F01	No Hits.					
SLSEPL02F02	No Hits.					
SLSEPL02F03	No Hits.					
SLSEPL02F04	No Hits.					
SLSEPL02F05	gi|45861223|gb|AAS78488.1|	LacZ alpha & ccdB lethal fusion protein [Cloning vector pZero++ Amp]	124 bits(311)	3,85E-33	83%	3%
	gi|2664253|emb|CAA67126.1|	ccdB [synthetic construct]	120 bits(300)	7,72E-32	97%	0%
	gi|184991891|emb|CAQ43070.2|	putative puroindoline b protein [Triticum macha]	148 bits(372)	2,91E-42	100%	0%
	gi|62945802|gb|AAS77687.2|	LacZ-alpha [Shuttle vector pLPV111]	132 bits(330)	3,17E-37	98%	0%
	gi|2950220|emb|CAA71575.1|	fused-ccdB [Cloning vector pZeRO-2T]	123 bits(308)	7,19E-33	82%	3%
	gi|3402817|emb|CAA07704.1|	lacZ' [Cloning vector pGreen]	117 bits(293)	1,31E-31	98%	0%
	gi|407227153|emb|CCM44347.1|	CcdB toxin fusion [Cloning vector pSAWloxP-K]	125 bits(312)	1,14E-33	83%	3%

	gi|147724741|gb|ABQ45977.1|	lacZ alpha peptide [Linear cloning vector pJAZZ-OC]	117 bits(293)	5,88E-32	90%	0%
	gi|190361707|gb|ACE77052.1|	LacZ alpha peptide [Cloning vector pSMARTGC Blue]	123 bits(307)	1,82E-33	84%	3%
	gi|89158283|gb|ABD62894.1|	lacZ alpha [Cloning vector pJAZZ-KA]	117 bits(292)	6,62E-32	90%	0%
SLSEPL02F06	No Hits.					
SLSEPL02F07	No Hits.					
SLSEPL02F07	No Hits.					
SLSEPL02F08	No Hits.					
SLSEPL02F10	No Hits.					
SLSEPL02F11	No Hits.					
SLSEPL02G01	No Hits.					
SLSEPL02G04	No Hits.					
SLSEPL02G07	No Hits.					
SLSEPL02G11	No Hits.					
SLSEPL02H01	No Hits.					
SLSEPL02H03	No Hits.					
SLSEPL02H04	No Hits.					
SLSEPL02H05	No Hits.					
SLSEPL02H06	No Hits.					
SLSEPL02H08	No Hits.					
SLSEPL02H09	No Hits.					
SLSEPL02H10	No Hits.					
SLSEPL03A08	No Hits.					
SLSEPL03B01	No Hits.					
SLSEPL03B02	No Hits.					
SLSEPL03B03	No Hits.					
SLSEPL03B04	No Hits.					
SLSEPL03B06	No Hits.					
SLSEPL03B07	No Hits.					
SLSEPL03B08	No Hits.					
SLSEPL03B09	No Hits.					
SLSEPL03B10	No Hits.					
SLSEPL03C09	No Hits.					
SLSEPL03C10	No Hits.					
SLSEPL03C12	No Hits.					
SLSEPL03D01	No Hits.					
SLSEPL03D06	No Hits.					
SLSEPL03E03	No Hits.					
SLSEPL03E12	No Hits.					
SLSEPL03F07	gi|407227153|emb|CCM44347.1|	CcdB toxin fusion [Cloning vector pSAWloxP-K]	124 bits(310)	4,64E-33	83%	3%
	gi|2664253|emb|CAA67126.1|	ccdB [synthetic construct]	121 bits(302)	8,59E-32	97%	0%
	gi|190361707|gb|ACE77052.1|	LacZ alpha peptide [Cloning vector pSMARTGC Blue]	122 bits(304)	8,01E-33	84%	3%
	gi|3402817|emb|CAA07704.1|	lacZ' [Cloning vector pGreen]	119 bits(296)	9,00E-32	98%	0%
	gi|184991891|emb|CAQ43070.2|	putative puroindoline b protein [Triticum macha]	145 bits(364)	9,16E-41	99%	0%
	gi|45861223|gb|AAS78488.1|	LacZ alpha & ccdB lethal fusion protein [Cloning vector pZero++ Amp]	124 bits(309)	1,65E-32	83%	3%
	gi|155733602|gb|ABU39928.1|	beta-galactosidase [Cloning vector pGreenII 0029]	119 bits(296)	1,03E-31	98%	0%
	gi|62945802|gb|AAS77687.2|	LacZ-alpha [Shuttle vector pLPV111]	129 bits(323)	7,74E-36	97%	0%
	gi|2950220|emb|CAA71575.1|	fused-ccdB [Cloning vector pZeRO-2T]	122 bits(306)	2,92E-32	81%	3%
	gi|155733607|gb|ABU39931.1|	beta-galactosidase [Cloning vector pGreenII 0179]	118 bits(295)	2,21E-31	98%	0%
SLSEPL03F08	No Hits.					
SLSEPL03G01	No Hits.					
SLSEPL03G12	No Hits.					
SLSEPL03H02	No Hits.					
SLSEPL03H03	No Hits.					
SLSEPL03H04	No Hits.					
SLSEPL03H08	No Hits.					
SLSEPL04A05	No Hits.					

SLSEPL04B04	gi|297743530|emb|CBI36397.3|	unnamed protein product [Vitis vinifera]	399 bits(1025)	2,24E-136	98%	0%
	gi|790475|emb|CAA58699.1|	inorganic pyrophosphatase [Nicotiana tabacum]	401 bits(1030)	1,83E-134	99%	0%
	gi|641854643|gb|KDO73437.1|	hypothetical protein CISIN_1g004159mg [Citrus sinensis]	403 bits(1034)	5,08E-133	99%	0%
	gi|14149007|emb|CAC39165.1|	vacuolar-type H+-pyrophosphatase [Solanum lycopersicum]	396 bits(1016)	7,03E-135	99%	0%
	gi|525313901|ref|NP_001265905.1|	vacuolar-type H+-pyrophosphatase [Solanum lycopersicum]	406 bits(1042)	1,40E-133	100%	0%
	gi|359482390|ref|XP_003632767.1|	PREDICTED: pyrophosphate-energized vacuolar membrane proton pump 1-like [Vitis vinifera]	392 bits(1006)	7,15E-133	97%	0%
	gi|297598707|ref|NP_001046107.2|	Os02g0184200 [Oryza sativa Japonica Group]	396 bits(1016)	7,21E-135	97%	0%
	gi|565387417|ref|XP_006359496.1|	PREDICTED: pyrophosphate-energized vacuolar membrane proton pump-like [Solanum tuberosum]	406 bits(1041)	2,32E-133	100%	0%
	gi|359482767|ref|XP_003632833.1|	PREDICTED: pyrophosphate-energized vacuolar membrane proton pump 1-like [Vitis vinifera]	398 bits(1020)	1,31E-134	98%	0%
	gi|413935926|gb|AFW70477.1|	hypothetical protein ZEAMMB73_398917 [Zea mays]	395 bits(1013)	3,59E-133	97%	0%
SLSEPL04C04	No Hits.					
SLSEPL04C05	gi|576095874|gb|AHH11882.1|	hypothetical protein BCO_0900160 [Borrelia coriaceae Co53]	131 bits(327)	8,91E-36	98%	0%
	gi|491608269|ref|WP_005465829.1|	beta-lactamase TEM, partial [Vibrio parahaemolyticus]	111 bits(277)	8,28E-28	100%	0%
	gi|499390617|ref|WP_011078084.1|	hypothetical protein [Erwinia amylovora]	163 bits(411)	6,45E-48	99%	0%
	gi|553724178|gb|ESE38970.1|	hypothetical protein HMPREF1622_00175 [Escherichia coli A35218R]	125 bits(313)	9,52E-34	94%	0%
	gi|485893553|ref|WP_001485324.1|	beta-lactamase TEM domain protein, partial [Escherichia coli]	109 bits(272)	1,12E-27	100%	0%
	gi|694075581|ref|WP_032421365.1|	hypothetical protein, partial [Klebsiella pneumoniae]	155 bits(390)	3,98E-45	100%	0%
	gi|491122707|ref|WP_004981147.1|	hypothetical protein, partial [Streptomyces ghanaensis]	118 bits(294)	7,29E-31	100%	0%
	gi|636314395|gb|KDK92099.1|	beta-lactamase TEM, partial [Klebsiella pneumoniae CHS 75]	109 bits(272)	1,13E-27	100%	0%
	gi|491128575|ref|WP_004987004.1|	hypothetical protein, partial [Streptomyces ghanaensis]	145 bits(364)	5,84E-41	91%	0%
	gi|493329074|ref|WP_006286292.1|	beta-lactamase TEM [Corynebacterium crenatum]	112 bits(279)	4,96E-28	100%	0%
SLSEPL04C07	gi|184991891|emb|CAQ43070.2|	putative puroindoline b protein [Triticum macha]	79 bits(194)	1,17E-14	100%	0%
SLSEPL04C08	No Hits.					
SLSEPL04D01	No Hits.					
SLSEPL04D03	gi|184991891|emb|CAQ43070.2|	putative puroindoline b protein [Triticum macha]	82 bits(200)	4,42E-17	98%	0%
	gi|62945802|gb|AAS77687.2|	LacZ-alpha [Shuttle vector pLPV111]	69 bits(168)	5,04E-13	100%	0%
SLSEPL04D04	No Hits.					
SLSEPL04D08	No Hits.					
SLSEPL04E09	No Hits.					
SLSEPL04F03	No Hits.					
SLSEPL04F05	gi|350535224|ref|NP_001234439.1|	heat shock cognate protein 80 [Solanum lycopersicum]	240 bits(610)	1,64E-71	98%	0%
	gi|565356086|ref|XP_006344905.1|	PREDICTED: heat shock cognate protein 80-like [Solanum tuberosum]	232 bits(591)	1,03E-68	93%	0%
	gi|449524954|ref|XP_004169486.1|	PREDICTED: heat shock cognate protein 80-like [Cucumis sativus]	213 bits(540)	2,07E-67	88%	0%
	gi|171854657|dbj|BAG16518.1|	putative Hsp90-2 [Capsicum chinense]	236 bits(602)	2,49E-70	96%	0%
	gi|350535174|ref|NP_001234436.1|	molecular chaperone Hsp90-1 [Solanum lycopersicum]	232 bits(590)	1,21E-68	93%	0%
	gi|38154485|gb|AAR12194.1|	molecular chaperone Hsp90-2 [Nicotiana benthamiana]	227 bits(578)	6,80E-67	91%	0%
	gi|315307966|gb|ADU04386.1|	heat shock protein 90-1 [Nicotiana attenuata]	236 bits(600)	4,50E-70	95%	0%
	gi|565371920|ref|XP_006352548.1|	PREDICTED: heat shock cognate protein 80-like [Solanum tuberosum]	230 bits(586)	5,46E-68	93%	0%
	gi|6934298|gb|AAF31705.1|AF221856_1	heat-shock protein 80 [Euphorbia esula]	225 bits(572)	1,38E-69	91%	0%
	gi|315307968|gb|ADU04387.1|	heat shock protein 90-2 [Nicotiana attenuata]	230 bits(584)	1,07E-67	93%	0%
SLSEPL04F09	No Hits.					
SLSEPL04F11	gi|76163167|gb|AAX30965.2|	SJCHGC09657 protein [Schistosoma japonicum]	92 bits(228)	4,81E-22	71%	2%
SLSEPL04G01	gi|82394572|gb|ABB72375.1|	seed maturation protein [Glycine tomentella]	89 bits(219)	4,09E-20	60%	3%
	gi|82394566|gb|ABB72372.1|	seed maturation protein [Glycine tomentella]	87 bits(214)	2,05E-19	59%	3%
	gi|82394634|gb|ABB72406.1|	seed maturation protein [Glycine canescens]	87 bits(213)	2,93E-19	57%	7%
	gi|643717537|gb|KDP29011.1|	hypothetical protein JCGZ_19500 [Jatropha curcas]	88 bits(217)	7,88E-20	66%	0%
	gi|82394652|gb|ABB72415.1|	seed maturation protein [Glycine tomentella]	87 bits(214)	2,42E-19	52%	18%
	gi|82394632|gb|ABB72405.1|	seed maturation protein [Glycine canescens]	87 bits(213)	3,44E-19	57%	7%
	gi|82394648|gb|ABB72413.1|	seed maturation protein [Glycine tabacina]	87 bits(215)	1,78E-19	52%	18%
	gi|82394646|gb|ABB72412.1|	seed maturation protein [Glycine tabacina]	87 bits(213)	2,75E-19	57%	7%
	gi|82394658|gb|ABB72418.1|	seed maturation protein [Glycine tomentella]	87 bits(214)	1,93E-19	52%	18%
	gi|82394586|gb|ABB72382.1|	seed maturation protein [Glycine tomentella]	87 bits(213)	2,88E-19	59%	3%
SLSEPL04G10	gi|356496771|ref|XP_003517239.1|	PREDICTED: zinc finger protein MAGPIE-like [Glycine max]	122 bits(306)	3,30E-29	66%	0%
	gi|9858780|gb|AAG01127.1|AF273333_12	BAC19.12 [Solanum lycopersicum]	171 bits(431)	2,27E-46	91%	0%
	gi|643721914|gb|KDP31793.1|	hypothetical protein JCGZ_12254 [Jatropha curcas]	121 bits(303)	8,56E-29	69%	0%

	gi|460373151|ref|XP_004232386.1|	PREDICTED: uncharacterized protein LOC101252546 [Solanum lycopersicum]	171 bits(431)	2,58E-46	91%	0%
	gi|565360357|ref|XP_006346936.1|	PREDICTED: uncharacterized threonine-rich GPI-anchored glycoprotein PJ4664.02-like [Solanum tuberosum]	127 bits(318)	3,76E-30	77%	0%
	gi|156070761|gb|ABU45176.1|	unknown [Solanum melongena]	178 bits(451)	2,72E-49	98%	0%
	gi|565395015|ref|XP_006363144.1|	PREDICTED: zinc finger protein MAGPIE-like [Solanum tuberosum]	169 bits(427)	7,43E-46	90%	0%
	gi|460375430|ref|XP_004233509.1|	PREDICTED: uncharacterized protein LOC101262076 [Solanum lycopersicum]	125 bits(313)	1,24E-29	76%	0%
	gi|156070798|gb|ABU45210.1|	unknown [Solanum bulbocastanum]	171 bits(432)	1,51E-46	90%	0%
	gi|156070783|gb|ABU45196.1|	unknown [Petunia integrifolia subsp. inflata]	151 bits(381)	2,50E-39	84%	4%

Apêndice C – Resultado da busca *in silico* da funcionalidade hipotética em Contigs, da biblioteca de folhas de *Solanum lycocarpum*
Fonte de dados: Blastx/NCBI
Elaborada pelo autor

Name Sequence	Sequence	Name	score	expert	indentities	gaps
Contig0	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	85 bits(209)	2,83E-18	100%	0%
	gi|27475622|emb|CAD59768.1|	putative reverse transcriptase [Cicer arietinum]	74 bits(180)	2,90E-14	100%	0%
	gi|485748338|ref|WP_001374558.1|	lac repressor [Escherichia coli]	73 bits(177)	6,36E-12	97%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	85 bits(208)	4,71E-18	100%	0%
	gi|571207123|emb|CDK78388.1|	Transcriptional repressor of the lac operon [Klebsiella pneumoniae IS22]	74 bits(181)	1,99E-13	100%	0%
	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	7,17E-11	100%	0%
	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	88 bits(216)	1,97E-17	98%	0%
	gi|27475620|emb|CAD59767.1|	putative reverse transcriptase [Cicer arietinum]	68 bits(165)	3,76E-12	94%	0%
	gi|330752400|emb|CBL87351.1|	hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]	77 bits(188)	9,80E-15	97%	0%
	gi|330752561|emb|CBL87507.1|	hypothetical protein S18_873_0002 [uncultured Flavobacteriia bacterium]	69 bits(168)	4,13E-12	100%	0%
Contig1	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	82 bits(200)	3,16E-15	97%	0%
	gi|330752561|emb|CBL87507.1|	hypothetical protein S18_873_0002 [uncultured Flavobacteriia bacterium]	69 bits(168)	4,83E-12	100%	0%
	gi|330752400|emb|CBL87351.1|	hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]	77 bits(187)	1,19E-14	97%	0%
	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	7,43E-11	100%	0%
	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	78 bits(191)	1,15E-15	100%	0%
	gi|27475622|emb|CAD59768.1|	putative reverse transcriptase [Cicer arietinum]	74 bits(180)	3,66E-14	100%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	78 bits(191)	1,20E-15	100%	0%
	gi|27475620|emb|CAD59767.1|	putative reverse transcriptase [Cicer arietinum]	68 bits(164)	4,81E-12	94%	0%
Contig2	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	6,80E-11	100%	0%
Contig3	gi|357510405|ref|XP_003625491.1|	hypothetical protein MTR_7g099720 [Medicago truncatula]	75 bits(182)	3,63E-14	78%	1%
	gi|224098382|ref|XP_002311160.1|	hypothetical protein POPTR_0008s05340g [Populus trichocarpa]	78 bits(191)	1,07E-15	90%	0%
	gi|460401911|ref|XP_004246459.1|	PREDICTED: dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 4A-like isoform 2 [Solanum lycopersicum]	75 bits(183)	1,31E-14	97%	0%
	gi|460401909|ref|XP_004246458.1|	PREDICTED: dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 4A-like isoform 1 [Solanum lycopersicum]	76 bits(186)	4,84E-15	92%	0%
	gi|218200034|gb|EEC82461.1|	hypothetical protein OsI_26901 [Oryza sativa Indica Group]	75 bits(183)	1,61E-14	79%	1%
	gi|568854297|ref|XP_006480767.1|	PREDICTED: dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 4A-like [Citrus sinensis]	75 bits(183)	1,09E-14	97%	0%
	gi|672117993|ref|XP_008782193.1|	PREDICTED: dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 4A [Phoenix dactylifera]	75 bits(182)	1,68E-14	95%	0%
	gi|297740396|emb|CBI30578.3|	unnamed protein product [Vitis vinifera]	82 bits(202)	4,40E-17	85%	1%
	gi|566192018|ref|XP_006378723.1|	hypothetical protein POPTR_0010s21410g, partial [Populus trichocarpa]	75 bits(184)	1,30E-14	78%	6%
	gi|595823590|ref|XP_007205093.1|	hypothetical protein PRUPE_ppa014550mg [Prunus persica]	74 bits(180)	2,75E-14	95%	0%
Contig4	gi|290790838|gb|ADD63094.1|	photosystem II protein M [Microlaena stipoides]	69 bits(167)	8,50E-12	87%	0%
	gi|290488068|gb|ADD30418.1|	photosystem II protein M (chloroplast) [Aucuba japonica]	66 bits(159)	6,52E-11	97%	0%
	gi|290790770|gb|ADD63027.1|	photosystem II protein M [Potamophila parviflora]	71 bits(173)	1,08E-12	70%	0%
	gi|651514776|ref|YP_009040786.1|	photosystem II protein M (chloroplast) (chloroplast) [Centaurea diffusa]	67 bits(162)	2,84E-11	97%	0%
	gi|114329962|ref|YP_740644.1|	photosystem II protein M [Nandina domestica]	66 bits(159)	6,52E-11	97%	0%
	gi|150251454|ref|YP_001312187.1|	photosystem II M protein [Cycas taitungensis]	71 bits(173)	2,01E-12	55%	7%
	gi|357470667|ref|XP_003605618.1|	Photosystem II reaction center protein M [Medicago truncatula]	70 bits(169)	2,89E-11	97%	0%
	gi|556927073|ref|YP_008757427.1|	photosystem II reaction center protein M (chloroplast) [Oryza rufipogon]	70 bits(170)	3,33E-12	90%	0%
	gi|7525027|ref|NP_051053.1|	photosystem II protein M [Arabidopsis thaliana]	67 bits(161)	3,68E-11	100%	0%
Contig5	gi|659113393|ref|XP_008456551.1|	PREDICTED: uncharacterized protein LOC103496471 isoform X2 [Cucumis melo]	114 bits(283)	7,92E-28	88%	0%
	gi|567888052|ref|XP_006436548.1|	hypothetical protein CICLE_v10032582mg [Citrus clementina]	114 bits(284)	4,00E-27	83%	0%
	gi|567888056|ref|XP_006436550.1|	hypothetical protein CICLE_v10032582mg [Citrus clementina]	113 bits(281)	1,52E-27	83%	0%
	gi|449441832|ref|XP_004138686.1|	PREDICTED: uncharacterized protein SYNPCC7002_A1590-like [Cucumis sativus]	114 bits(283)	5,09E-27	88%	0%
	gi|565358060|ref|XP_006345847.1|	PREDICTED: uncharacterized protein LOC102602810 [Solanum tuberosum]	122 bits(306)	1,83E-30	98%	0%
	gi|659113391|ref|XP_008456550.1|	PREDICTED: uncharacterized protein LOC103496471 isoform X1 [Cucumis melo]	114 bits(285)	2,54E-27	88%	0%
	gi|470145987|ref|XP_004308612.1|	PREDICTED: uncharacterized protein SYNPCC7002_A1590-like [Fragaria vesca subsp. vesca]	113 bits(282)	5,65E-27	88%	0%
	gi|460388111|ref|XP_004239713.1|	PREDICTED: uncharacterized protein SYNPCC7002_A1590-like [Solanum lycopersicum]	122 bits(304)	3,42E-30	98%	0%
	gi|449493277|ref|XP_004159242.1|	PREDICTED: uncharacterized protein SYNPCC7002_A1590-like [Cucumis sativus]	114 bits(284)	3,33E-27	88%	0%
	gi|645252294|ref|XP_008232056.1|	PREDICTED: uncharacterized protein LOC103331217 isoform X3 [Prunus mume]	111 bits(276)	8,29E-27	85%	0%
Contig6	No Hits.					
Contig7	gi|27475620|emb|CAD59767.1|	putative reverse transcriptase [Cicer arietinum]	68 bits(164)	5,41E-12	94%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	72 bits(175)	2,22E-13	100%	0%

	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	72 bits(175)	2,30E-13	100%	0%
	gi|330752561|emb|CBL87507.1|	hypothetical protein S18_873_0002 [uncultured Flavobacteriia bacterium]	69 bits(168)	6,03E-12	100%	0%
	gi|27475622|emb|CAD59768.1|	putative reverse transcriptase [Cicer arietinum]	72 bits(174)	2,61E-13	100%	0%
	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	9,78E-11	100%	0%
	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	75 bits(184)	6,82E-13	97%	0%
	gi|330752400|emb|CBL87351.1|	hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]	77 bits(187)	1,69E-14	97%	0%
Contig8	gi|460381722|ref|XP_004236592.1|	PREDICTED: zeatin O-glucosyltransferase-like [Solanum lycopersicum]	200 bits(506)	4,28E-58	81%	0%
	gi|565377107|ref|XP_006355031.1|	PREDICTED: zeatin O-glucosyltransferase-like [Solanum tuberosum]	194 bits(491)	3,56E-56	78%	0%
	gi|565367208|ref|XP_006350268.1|	PREDICTED: zeatin O-glucosyltransferase-like [Solanum tuberosum]	191 bits(483)	9,44E-55	79%	0%
	gi|565383387|ref|XP_006357999.1|	PREDICTED: zeatin O-glucosyltransferase-like [Solanum tuberosum]	199 bits(505)	6,20E-58	83%	0%
	gi|460382368|ref|XP_004236911.1|	PREDICTED: zeatin O-glucosyltransferase-like [Solanum lycopersicum]	193 bits(490)	7,53E-56	79%	0%
	gi|565383636|ref|XP_006358040.1|	PREDICTED: zeatin O-xylosyltransferase-like [Solanum tuberosum]	191 bits(485)	6,23E-58	81%	0%
	gi|460381724|ref|XP_004236593.1|	PREDICTED: zeatin O-glucosyltransferase-like [Solanum lycopersicum]	193 bits(488)	1,69E-55	80%	0%
	gi|565377117|ref|XP_006355036.1|	PREDICTED: zeatin O-glucosyltransferase-like [Solanum tuberosum]	201 bits(511)	1,80E-58	82%	0%
	gi|460382796|ref|XP_004237122.1|	PREDICTED: zeatin O-glucosyltransferase-like [Solanum lycopersicum]	195 bits(494)	1,57E-56	80%	0%
	gi|460382756|ref|XP_004237102.1|	PREDICTED: zeatin O-glucosyltransferase-like [Solanum lycopersicum]	186 bits(470)	6,12E-55	77%	0%
Contig9	No Hits.					
Contig10	gi|254729136|gb|ACT79685.1|	petB [Circaea alpina subsp. alpina]	151 bits(380)	1,66E-41	100%	0%
	gi|372000347|gb|AEX65250.1|	cytochrome b6, partial (chloroplast) [Portulaca oleracea]	152 bits(383)	5,87E-41	100%	0%
	gi|254729205|gb|ACT79731.1|	petB [Circaea canadensis subsp. quadrisulcata]	151 bits(380)	1,70E-41	100%	0%
	gi|587840353|gb|EXB30985.1|	Cytochrome b6 [Morus notabilis]	151 bits(379)	6,31E-41	99%	0%
	gi|674962251|emb|CDX71257.1|	BnaC07g05360D [Brassica napus]	152 bits(382)	3,03E-42	83%	0%
	gi|254729293|gb|ACT79789.1|	petB [Fuchsia pachyrrhiza]	151 bits(380)	1,85E-41	100%	0%
	gi|309322149|ref|YP_003934064.1|	cytochrome b6/f complex subunit II [Geranium palmatum]	152 bits(383)	6,39E-41	100%	0%
	gi|254729314|gb|ACT79803.1|	petB [Fuchsia thymifolia]	151 bits(381)	1,59E-41	100%	0%
	gi|254729281|gb|ACT79781.1|	petB [Fuchsia excorticata]	151 bits(379)	2,83E-41	99%	0%
	gi|164597830|ref|NP_084723.2|	cytochrome b6 [Oenothera elata subsp. hookeri]	152 bits(383)	6,39E-41	100%	0%
Contig11	gi|460413951|ref|XP_004252338.1|	PREDICTED: translation machinery-associated protein 7-like [Solanum lycopersicum]	112 bits(279)	7,31E-28	98%	0%
	gi|413934615|gb|AFW69166.1|	hypothetical protein ZEAMMB73_278211, partial [Zea mays]	96 bits(237)	3,78E-21	85%	0%
	gi|247421936|gb|ACS96448.1|	unknown protein [Jatropha curcas]	90 bits(222)	1,24E-19	80%	1%
	gi|53748433|emb|CAH59409.1|	hypothetical protein [Plantago major]	96 bits(237)	8,01E-22	86%	0%
	gi|195618088|gb|ACG30874.1|	hypothetical protein [Zea mays]	94 bits(231)	5,89E-21	85%	0%
	gi|413943299|gb|AFW75948.1|	hypothetical protein ZEAMMB73_554206, partial [Zea mays]	91 bits(225)	1,95E-19	82%	0%
	gi|413943298|gb|AFW75947.1|	hypothetical protein ZEAMMB73_554206, partial [Zea mays]	97 bits(240)	1,31E-21	85%	0%
	gi|195655819|gb|ACG47377.1|	hypothetical protein [Zea mays]	93 bits(229)	9,64E-21	84%	0%
	gi|242096814|ref|XP_002438897.1|	hypothetical protein SORBIDRAFT_10g027860 [Sorghum bicolor]	94 bits(233)	3,18E-21	85%	0%
	gi|674858490|emb|CDY70031.1|	BnaAnng32380D [Brassica napus]	93 bits(230)	5,05E-20	80%	1%
Contig12	gi|460394437|ref|XP_004242809.1|	PREDICTED: ABC transporter F family member 4-like [Solanum lycopersicum]	129 bits(322)	6,94E-31	98%	0%
	gi|568822020|ref|XP_006465438.1|	PREDICTED: ABC transporter F family member 4-like [Citrus sinensis]	115 bits(286)	6,33E-26	86%	0%
	gi|658017059|ref|XP_008343888.1|	PREDICTED: ABC transporter F family member 4-like isoform X2 [Malus domestica]	112 bits(280)	3,66E-25	84%	0%
	gi|586751918|ref|XP_006852125.1|	hypothetical protein AMTR_s00049p00049960 [Amborella trichopoda]	117 bits(291)	1,17E-26	87%	0%
	gi|567868965|ref|XP_006427104.1|	hypothetical protein CICLE_v10025010mg [Citrus clementina]	115 bits(286)	6,45E-26	86%	0%
	gi|658003492|ref|XP_008394261.1|	PREDICTED: ABC transporter F family member 4 [Malus domestica]	112 bits(280)	3,91E-25	84%	0%
	gi|565393585|ref|XP_006362455.1|	PREDICTED: ABC transporter F family member 4-like [Solanum tuberosum]	129 bits(322)	6,80E-31	98%	0%
	gi|643738578|gb|KDP44499.1|	hypothetical protein JCGZ_16332 [Jatropha curcas]	115 bits(287)	4,02E-26	87%	0%
	gi|565385563|ref|XP_006358671.1|	PREDICTED: ABC transporter F family member 4-like [Solanum tuberosum]	129 bits(322)	6,80E-31	98%	0%
	gi|641839255|gb|KDO58187.1|	hypothetical protein CISIN_1g048654mg [Citrus sinensis]	115 bits(286)	6,27E-26	86%	0%
Contig13	gi|356560959|ref|XP_003548753.1|	PREDICTED: uncharacterized protein LOC100805680 [Glycine max]	104 bits(258)	4,88E-23	85%	0%
	gi|661882103|emb|CDP14328.1|	unnamed protein product [Coffea canephora]	103 bits(256)	9,13E-23	83%	0%
	gi|590643104|ref|XP_007030711.1|	NDH-dependent cyclic electron flow 1 [Theobroma cacao]	104 bits(257)	6,39E-23	85%	0%
	gi|224145977|ref|XP_002325834.1|	hypothetical protein POPTR_0019s04970g [Populus trichocarpa]	103 bits(255)	1,19E-22	83%	0%
	gi|565402862|ref|XP_006366888.1|	PREDICTED: uncharacterized protein LOC102593344 [Solanum tuberosum]	109 bits(271)	8,98E-25	91%	0%
	gi|356571694|ref|XP_003554009.1|	PREDICTED: putative glucose-6-phosphate 1-epimerase-like [Glycine max]	104 bits(257)	6,79E-23	85%	0%
	gi|593797792|ref|XP_007161934.1|	hypothetical protein PHAVU_001G110100g [Phaseolus vulgaris]	103 bits(255)	1,27E-22	83%	0%
	gi|460378079|ref|XP_004234806.1|	PREDICTED: uncharacterized protein LOC101263383 [Solanum lycopersicum]	108 bits(269)	1,49E-24	89%	0%
	gi|470134744|ref|XP_004303198.1|	PREDICTED: uncharacterized protein LOC101312554 [Fragaria vesca subsp. vesca]	103 bits(256)	8,37E-23	85%	0%

	gi|595937516|ref|XP_007215595.1|	hypothetical protein PRUPE_ppa007725mg [Prunus persica]	102 bits(254)	1,75E-22	85%	0%
Contig14	gi|460400000|ref|XP_004245524.1|	PREDICTED: uncharacterized protein LOC101259182 [Solanum lycopersicum]	190 bits(482)	7,65E-57	68%	26%
	gi|565353923|ref|XP_006343868.1|	PREDICTED: uncharacterized protein LOC102590834 [Solanum tuberosum]	110 bits(274)	1,79E-26	69%	4%
Contig15	No Hits.					
Contig16	gi|460400320|ref|XP_004245683.1|	PREDICTED: nudix hydrolase 14, chloroplastic-like [Solanum lycopersicum]	156 bits(394)	1,05E-42	97%	0%
	gi|225426698|ref|XP_002281806.1|	PREDICTED: nudix hydrolase 14, chloroplastic [Vitis vinifera]	136 bits(341)	6,56E-35	82%	0%
	gi|567895954|ref|XP_006440465.1|	hypothetical protein CICLE_v10021310mg [Citrus clementina]	133 bits(333)	2,20E-34	81%	0%
	gi|661886484|emb|CDP09848.1|	unnamed protein product [Coffea canephora]	147 bits(369)	6,59E-39	90%	0%
	gi|223974585|gb|ACN31480.1|	unknown [Zea mays]	133 bits(334)	1,02E-34	79%	0%
	gi|297742638|emb|CBI34787.3|	unnamed protein product [Vitis vinifera]	137 bits(344)	1,23E-35	82%	0%
	gi|255537175|ref|XP_002509654.1|	ADP-ribose pyrophosphatase, putative [Ricinus communis]	135 bits(338)	1,53E-34	83%	0%
	gi|568214519|ref|NP_001274884.1|	nudix hydrolase 14, chloroplastic-like [Solanum tuberosum]	157 bits(396)	5,95E-43	96%	0%
	gi|659073654|ref|XP_008437180.1|	PREDICTED: nudix hydrolase 14, chloroplastic [Cucumis melo]	136 bits(341)	6,19E-35	82%	0%
	gi|413953401|gb|AFW86050.1|	putative NUDIX hydrolase family protein [Zea mays]	133 bits(333)	2,07E-34	79%	0%
Contig17	No Hits.					
Contig18	No Hits.					
Contig19	gi|565386328|ref|XP_006358972.1|	PREDICTED: FK506-binding protein 4-like [Solanum tuberosum]	67 bits(161)	1,35E-11	86%	1%
Contig20	gi|565372958|ref|XP_006353052.1|	PREDICTED: photosystem I reaction center subunit III, chloroplastic-like [Solanum tuberosum]	102 bits(254)	6,58E-23	96%	0%
	gi|6635336|gb|AAF19787.1|AF162201_1	photosystem I subunit III [Lactuca sativa]	92 bits(226)	9,57E-20	88%	0%
	gi|460374804|ref|XP_004233199.1|	PREDICTED: photosystem I reaction center subunit III, chloroplastic-like [Solanum lycopersicum]	104 bits(259)	1,02E-23	98%	0%
	gi|604299126|gb|EYU19061.1|	hypothetical protein MIMGU_mgv1a013112mg [Erythranthe guttata]	101 bits(249)	2,56E-22	92%	0%
	gi|1172664|sp|P46486.1|PSAF_FLATR	RecName: Full=Photosystem I reaction center subunit III, chloroplastic; AltName: Full=Light-harvesting complex I 17 kDa protein; AltName: Full=PSI-F; Flags: Precursor	91 bits(225)	6,58E-19	84%	0%
	gi|460374802|ref|XP_004233198.1|	PREDICTED: photosystem I reaction center subunit III, chloroplastic-like [Solanum lycopersicum]	104 bits(259)	1,05E-23	98%	0%
	gi|30013659|gb|AAP03872.1|	putative photosystem I subunit III precursor [Nicotiana tabacum]	97 bits(241)	3,25E-21	92%	0%
	gi|413968524|gb|AFW90599.1|	photosystem I subunit III precursor (chloroplast) [Solanum tuberosum]	102 bits(254)	6,32E-23	96%	0%
	gi|565372960|ref|XP_006353053.1|	PREDICTED: photosystem I reaction center subunit III, chloroplastic-like [Solanum tuberosum]	102 bits(254)	6,51E-23	96%	0%
	gi|527191774|gb|EPS62468.1|	hypothetical protein M569_12323 [Genlisea aurea]	98 bits(242)	3,91E-21	92%	0%
Contig21	No Hits.					
Contig22	gi|260222396|emb|CBA31918.1|	Uncharacterized protein TC_0114 [Curvibacter putative symbiont of Hydra magnipapillata]	105 bits(260)	1,59E-24	57%	0%
	gi|491721707|ref|WP_005563231.1|	hydrolase [Aggregatibacter actinomycetemcomitans]	101 bits(250)	7,53E-23	56%	0%
	gi|491852495|ref|WP_005633968.1|	hydrolase [Parabacteroides merdae]	104 bits(259)	4,42E-24	56%	0%
	gi|261412306|gb|ACX81677.1|	cell wall-associated hydrolase [Aggregatibacter actinomycetemcomitans D11S-1]	101 bits(250)	7,61E-23	56%	0%
	gi|661254397|ref|WP_029949898.1|	RNAase [Parvimonas micra]	99 bits(245)	1,61E-22	59%	0%
	gi|511039265|ref|WP_016293279.1|	hypothetical protein [Lachnospiraceae bacterium 28-4]	44 bits(102)	6,29E-24	71%	0%
	gi|491567972|ref|WP_005425556.1|	RNAase [[Ruminococcus] obeum]	100 bits(247)	8,73E-23	58%	0%
	gi|490424962|ref|WP_004297142.1|	hydrolase [Bacteroides ovatus]	111 bits(275)	4,22E-26	50%	5%
	gi|491564249|ref|WP_005421835.1|	RNAase [[Ruminococcus] obeum]	103 bits(255)	6,41E-24	62%	0%
	gi|496309627|ref|WP_009018805.1|	hydrolase [Parabacteroides sp. D13]	100 bits(248)	1,57E-22	54%	0%
Contig23	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	92 bits(226)	2,07E-20	100%	0%
	gi|571207123|emb|CDK78388.1|	Transcriptional repressor of the lac operon [Klebsiella pneumoniae IS22]	75 bits(184)	1,11E-13	88%	3%
	gi|330752561|emb|CBL87507.1|	hypothetical protein S18_873_0002 [uncultured Flavobacteriia bacterium]	69 bits(168)	6,58E-12	100%	0%
	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	92 bits(228)	1,16E-18	98%	0%
	gi|485748338|ref|WP_001374558.1|	lac repressor [Escherichia coli]	77 bits(187)	4,92E-13	88%	0%
	gi|330752400|emb|CBL87351.1|	hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]	77 bits(187)	1,96E-14	97%	0%
	gi|9652070|gb|AAF91388.1|AF263243_1	SocE [Myxococcus xanthus]	75 bits(182)	4,46E-12	51%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	103 bits(255)	1,41E-24	100%	0%
	gi|27475622|emb|CAD59768.1|	putative reverse transcriptase [Cicer arietinum]	74 bits(180)	4,82E-14	100%	0%
	gi|27475620|emb|CAD59767.1|	putative reverse transcriptase [Cicer arietinum]	68 bits(164)	6,35E-12	94%	0%
Contig24	gi|620730798|gb|KAK89041.1|	hypothetical protein L499_A3769 [Bordetella holmesii CDC-H635-BH]	260 bits(664)	1,20E-81	100%	0%
	gi|321919|pir||JQ1541	hypothetical 16.9K protein - Salmonella typhimurium plasmid NTP16	253 bits(645)	1,15E-78	91%	0%
	gi|487657862|ref|WP_001750129.1|	hypothetical protein [Escherichia coli]	285 bits(729)	7,64E-91	85%	5%
	gi|499390615|ref|WP_011078082.1|	hypothetical protein [Erwinia amylovora]	260 bits(663)	1,87E-81	100%	0%
	gi|544695983|ref|WP_021127222.1|	hypothetical protein, partial [[Clostridium] sordellii]	253 bits(644)	2,35E-78	99%	0%
	gi|327408611|emb|CCA30004.1|	hypothetical protein NCLIV_068840 [Neospora caninum Liverpool]	283 bits(722)	3,29E-90	100%	0%
	gi|194380874|dbj|BAG64005.1|	unnamed protein product [Homo sapiens]	268 bits(685)	6,19E-81	100%	0%

	gi|501390216|ref|WP_012421782.1|	hypothetical protein [Shigella boydii]	236 bits(602)	1,64E-72	98%	0%
	gi|487657863|ref|WP_001750130.1|	hypothetical protein [Escherichia coli]	281 bits(718)	3,62E-89	84%	5%
	gi|504871937|ref|WP_015059039.1|	hypothetical protein [Escherichia coli]	256 bits(652)	1,08E-79	93%	0%
Contig25	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	8,42E-11	100%	0%
Contig26	gi|303291414|ref|XP_003064992.1|	senescence-associated protein [Micromonas pusilla CCMP1545]	105 bits(260)	2,38E-26	98%	0%
	gi|657371000|gb|KEH17031.1|	hypothetical protein MTR_0052s0170 [Medicago truncatula]	96 bits(237)	5,42E-21	96%	0%
	gi|403333060|gb|EJY65597.1|	hypothetical protein OXYTRI_14248 [Oxytricha trifallax]	92 bits(226)	3,30E-19	96%	0%
	gi|678336953|emb|CDW75723.1|	UNKNOWN [Stylonychia lemnae]	99 bits(245)	1,23E-21	96%	0%
	gi|630364069|ref|XP_007871309.1|	hypothetical protein GLOTRDRAFT_50878, partial [Gloeophyllum trabeum ATCC 11539]	86 bits(212)	4,51E-20	98%	0%
	gi|646383637|gb|KDQ49118.1|	hypothetical protein JAAARDRAFT_143849, partial [Jaapia argillacea MUCL 33604]	84 bits(207)	5,66E-19	95%	0%
	gi|357488225|ref|XP_003614400.1|	Cytochrome P450 likeTBP [Medicago truncatula]	97 bits(240)	2,56E-21	96%	0%
	gi|357488193|ref|XP_003614384.1|	hypothetical protein MTR_5g051010 [Medicago truncatula]	74 bits(181)	2,86E-13	78%	0%
	gi|170048439|ref|XP_001852902.1|	GLP_748_1200_211 [Culex quinquefasciatus]	89 bits(219)	3,32E-21	82%	0%
	gi|403334965|gb|EJY66653.1|	hypothetical protein OXYTRI_13058 [Oxytricha trifallax]	92 bits(226)	3,06E-19	96%	0%
Contig27	gi|21491|emb|CAA27989.1|	unnamed protein product [Solanum tuberosum]	240 bits(611)	5,54E-77	90%	4%
	gi|588295538|gb|AHK23268.1|	chloroplast photosystem II subunit R [Gossypium hirsutum]	228 bits(579)	3,37E-72	84%	5%
	gi|350537547|ref|NP_001234042.1|	photosystem II 10 kDa polypeptide, chloroplastic [Solanum lycopersicum]	238 bits(607)	1,76E-76	89%	4%
	gi|661882615|emb|CDP13618.1|	unnamed protein product [Coffea canephora]	226 bits(574)	2,26E-71	83%	4%
	gi|3914472|sp|Q40519.1|PSBR_TOBAC	RecName: Full=Photosystem II 10 kDa polypeptide, chloroplastic; Short=PII10; Flags: Precursor	246 bits(626)	2,83E-79	90%	0%
	gi|645239765|ref|XP_008226285.1|	PREDICTED: photosystem II 10 kDa polypeptide, chloroplastic [Prunus mume]	231 bits(588)	1,60E-73	82%	3%
	gi|595876424|ref|XP_007212214.1|	hypothetical protein PRUPE_ppa013107mg [Prunus persica]	225 bits(573)	3,30E-71	81%	3%
	gi|568214281|ref|NP_001275173.1|	photosystem II 10 kDa polypeptide, chloroplastic [Solanum tuberosum]	243 bits(620)	2,29E-78	91%	4%
	gi|1418984|emb|CAA99757.1|	photosystem II 10 kD polypeptide [Solanum lycopersicum]	230 bits(586)	2,28E-73	89%	1%
	gi|83776786|gb|ABC46708.1|	chloroplast photosystem II 10 kDa protein [Arachis hypogaea]	224 bits(569)	8,35E-71	84%	0%
Contig28	gi|645239765|ref|XP_008226285.1|	PREDICTED: photosystem II 10 kDa polypeptide, chloroplastic [Prunus mume]	231 bits(588)	1,60E-73	82%	3%
	gi|3914472|sp|Q40519.1|PSBR_TOBAC	RecName: Full=Photosystem II 10 kDa polypeptide, chloroplastic; Short=PII10; Flags: Precursor	246 bits(626)	2,83E-79	90%	0%
	gi|595876424|ref|XP_007212214.1|	hypothetical protein PRUPE_ppa013107mg [Prunus persica]	225 bits(573)	3,30E-71	81%	3%
	gi|1418984|emb|CAA99757.1|	photosystem II 10 kD polypeptide [Solanum lycopersicum]	230 bits(586)	2,28E-73	89%	1%
	gi|568214281|ref|NP_001275173.1|	photosystem II 10 kDa polypeptide, chloroplastic [Solanum tuberosum]	243 bits(620)	2,29E-78	91%	4%
	gi|83776786|gb|ABC46708.1|	chloroplast photosystem II 10 kDa protein [Arachis hypogaea]	224 bits(569)	8,35E-71	84%	0%
	gi|21491|emb|CAA27989.1|	unnamed protein product [Solanum tuberosum]	240 bits(611)	5,54E-77	90%	4%
	gi|588295538|gb|AHK23268.1|	chloroplast photosystem II subunit R [Gossypium hirsutum]	228 bits(579)	3,37E-72	84%	5%
	gi|350537547|ref|NP_001234042.1|	photosystem II 10 kDa polypeptide, chloroplastic [Solanum lycopersicum]	238 bits(607)	1,76E-76	89%	4%
	gi|661882615|emb|CDP13618.1|	unnamed protein product [Coffea canephora]	226 bits(574)	2,26E-71	83%	4%
Contig29	gi|297838541|ref|XP_002887152.1|	hypothetical protein ARALYDRAFT_894553 [Arabidopsis lyrata subsp. lyrata]	66 bits(160)	3,80E-11	57%	4%
	gi|604318628|gb|EYU30120.1|	hypothetical protein MIMGU_mgv1a017329mg [Erythranthe guttata]	66 bits(159)	5,57E-11	52%	11%
	gi|565377172|ref|XP_006355063.1|	PREDICTED: uncharacterized protein LOC102579558 [Solanum tuberosum]	111 bits(276)	9,30E-28	85%	4%
	gi|224099549|ref|XP_002311528.1|	hypothetical protein POPTR_0008s13370g [Populus trichocarpa]	65 bits(158)	7,99E-11	59%	5%
	gi|18408896|ref|NP_564914.1|	uncharacterized protein [Arabidopsis thaliana]	67 bits(162)	1,99E-11	58%	4%
Contig30	gi|225434704|ref|XP_002280988.1|	PREDICTED: uncharacterized protein LOC100258718 [Vitis vinifera]	91 bits(223)	2,86E-19	62%	0%
	gi|356566203|ref|XP_003551324.1|	PREDICTED: uncharacterized protein LOC100811254 isoform X1 [Glycine max]	81 bits(199)	6,64E-16	58%	3%
	gi|604347508|gb|EYU45745.1|	hypothetical protein MIMGU_mgv1a015037mg [Erythranthe guttata]	77 bits(188)	2,52E-14	54%	4%
	gi|661887361|emb|CDP09141.1|	unnamed protein product [Coffea canephora]	83 bits(204)	1,20E-16	55%	0%
	gi|590588452|ref|XP_007016203.1|	Maternal effect embryo arrest 59 [Theobroma cacao]	79 bits(193)	5,16E-15	60%	2%
	gi|255558834|ref|XP_002520440.1|	conserved hypothetical protein [Ricinus communis]	82 bits(202)	2,97E-16	58%	2%
	gi|567864700|ref|XP_006424999.1|	hypothetical protein CICLE_v10029307mg [Citrus clementina]	78 bits(190)	1,04E-14	55%	0%
	gi|460389514|ref|XP_004240397.1|	PREDICTED: uncharacterized protein LOC101264428 [Solanum lycopersicum]	102 bits(253)	1,36E-23	76%	1%
	gi|351734542|ref|NP_001237416.1|	uncharacterized protein LOC100306349 [Glycine max]	82 bits(201)	4,16E-16	58%	3%
	gi|567864702|ref|XP_006425000.1|	hypothetical protein CICLE_v10029307mg [Citrus clementina]	78 bits(190)	1,43E-14	55%	0%
Contig31	gi|4757570|gb|AAD29084.1|AF082181_1	cysteine proteinase precursor [Solanum melongena]	181 bits(457)	3,00E-51	91%	0%
	gi|5051468|emb|CAB44983.1|	putative preprocysteine proteinase [Nicotiana tabacum]	176 bits(446)	9,61E-50	89%	0%
	gi|52546912|gb|AAU81589.1|	cysteine proteinase [Petunia x hybrida]	180 bits(456)	2,35E-52	91%	0%
	gi|19195|emb|CAA78403.1|	pre-pro-cysteine proteinase [Solanum lycopersicum]	179 bits(454)	8,28E-51	90%	0%
	gi|19851|emb|CAA78365.1|	tobacco pre-pro-cysteine proteinase [Nicotiana tabacum]	176 bits(446)	1,11E-49	89%	0%
	gi|565350070|ref|XP_006341997.1|	PREDICTED: cysteine proteinase 15A-like [Solanum tuberosum]	183 bits(462)	6,51E-52	92%	0%
	gi|171854651|dbj|BAG16515.1|	putative cysteine proteinase [Capsicum chinense]	178 bits(450)	3,11E-50	90%	1%

	gi|19849|emb|CAA78361.1|	tobacco pre-pro-cysteine proteinase [Nicotiana tabacum]	176 bits(446)	1,19E-49	89%	0%
	gi|460385244|ref|XP_004238314.1|	PREDICTED: cysteine proteinase 15A [Solanum lycopersicum]	181 bits(459)	1,28E-51	91%	0%
	gi|28192375|gb|AAK07731.1|	CPR2-like cysteine proteinase [Nicotiana tabacum]	177 bits(447)	8,92E-50	89%	0%
Contig32	gi|565374005|ref|XP_006353555.1|	PREDICTED: uncharacterized protein LOC102596339 [Solanum tuberosum]	82 bits(201)	5,97E-44	80%	3%
	gi|413968468|gb|AFW90571.1|	ultraviolet-B-repressible protein [Solanum tuberosum]	74 bits(180)	1,03E-40	74%	3%
	gi|255546007|ref|XP_002514063.1|	conserved hypothetical protein [Ricinus communis]	54 bits(127)	1,88E-29	61%	1%
	gi|460412595|ref|XP_004251683.1|	PREDICTED: uncharacterized protein LOC101247889 [Solanum lycopersicum]	81 bits(199)	1,60E-43	77%	3%
	gi|460412597|ref|XP_004251684.1|	PREDICTED: uncharacterized protein LOC101248173 [Solanum lycopersicum]	69 bits(168)	8,12E-40	73%	4%
	gi|460412599|ref|XP_004251685.1|	PREDICTED: uncharacterized protein LOC101248456 [Solanum lycopersicum]	78 bits(190)	8,08E-42	76%	3%
	gi|460387290|ref|XP_004239313.1|	PREDICTED: uncharacterized protein LOC101259747 [Solanum lycopersicum]	60 bits(144)	2,75E-32	69%	1%
	gi|565374001|ref|XP_006353553.1|	PREDICTED: uncharacterized protein LOC102595674 [Solanum tuberosum]	86 bits(210)	1,29E-44	82%	3%
	gi|565374003|ref|XP_006353554.1|	PREDICTED: uncharacterized protein LOC102596015 [Solanum tuberosum]	75 bits(184)	3,33E-41	76%	3%
	gi|45356861|gb|AAS58469.1|	ultraviolet-B-repressible protein [Gossypium hirsutum]	51 bits(120)	7,26E-30	57%	2%
Contig33	gi|108802671|ref|YP_636329.1|	cytochrome b6 (chloroplast) [Eucalyptus globulus subsp. globulus]	351 bits(899)	7,98E-120	99%	0%
	gi|28261747|ref|NP_783261.1|	cytochrome b6 [Atropa belladonna]	352 bits(902)	2,51E-120	99%	0%
	gi|14017601|ref|NP_114287.1|	cytochrome b6 [Triticum aestivum]	351 bits(899)	6,77E-120	99%	0%
	gi|38605706|sp|P06247.2|CYB6_TOBAC	RecName: Full=Cytochrome b6 (chloroplast) [Nicotiana tabacum]	353 bits(904)	1,52E-120	100%	0%
	gi|139389294|ref|YP_001123060.1|	cytochrome B6 [Aethionema grandiflorum]	352 bits(902)	2,89E-120	99%	0%
	gi|225544153|ref|YP_002720142.1|	petB [Jatropha curcas]	351 bits(899)	6,92E-120	99%	0%
	gi|164597830|ref|NP_084723.2|	cytochrome b6 [Oenothera elata subsp. hookeri]	352 bits(903)	1,75E-120	99%	0%
	gi|575771037|ref|YP_009000363.1|	petB protein (chloroplast) [Arabis alpina]	352 bits(903)	3,43E-120	94%	3%
	gi|11465988|ref|NP_054530.1|	cytochrome b6 [Nicotiana tabacum]	352 bits(903)	1,93E-120	100%	0%
	gi|11466819|ref|NP_039415.1|	cytochrome b6 [Oryza sativa Japonica Group]	352 bits(901)	4,24E-120	99%	0%
Contig34	gi|568872594|ref|XP_006489452.1|	PREDICTED: serine/threonine-protein phosphatase 5-like isoform X2 [Citrus sinensis]	70 bits(169)	6,30E-44	86%	0%
	gi|224099829|ref|XP_002311636.1|	hypothetical protein POPTR_0008s15630g [Populus trichocarpa]	71 bits(172)	4,93E-43	79%	0%
	gi|147769544|emb|CAN61400.1|	hypothetical protein VITISV_011488 [Vitis vinifera]	69 bits(167)	2,39E-44	84%	0%
	gi|641855684|gb|KDO74464.1|	hypothetical protein CISIN_1g0209142mg, partial [Citrus sinensis]	70 bits(169)	7,38E-44	86%	0%
	gi|657402143|gb|KEH41070.1|	RNA polymerase II-associated-like protein [Medicago truncatula]	70 bits(170)	2,97E-42	84%	0%
	gi|255552073|ref|XP_002517081.1|	heat shock protein 70 (HSP70)-interacting protein, putative [Ricinus communis]	68 bits(165)	2,96E-44	86%	0%
	gi|567853810|ref|XP_006420025.1|	hypothetical protein CICLE_v10005444mg [Citrus clementina]	69 bits(168)	1,21E-43	86%	0%
	gi|527199415|gb|EPS67206.1|	hypothetical protein M569_07567, partial [Genlisea aurea]	69 bits(168)	5,72E-42	91%	0%
	gi|224111122|ref|XP_002315755.1|	tetratricopeptide repeat-containing family protein [Populus trichocarpa]	72 bits(175)	4,15E-44	81%	0%
	gi|502123055|ref|XP_004497984.1|	PREDICTED: serine/threonine-protein phosphatase 5-like [Cicer arietinum]	70 bits(169)	4,73E-43	86%	0%
Contig35	gi|460380425|ref|XP_004235957.1|	PREDICTED: uncharacterized protein LOC101251458 isoform 1 [Solanum lycopersicum]	76 bits(185)	3,88E-13	57%	0%
	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	4,98E-11	100%	0%
	gi|460380427|ref|XP_004235958.1|	PREDICTED: uncharacterized protein LOC101251458 isoform 2 [Solanum lycopersicum]	76 bits(185)	3,61E-13	57%	0%
Contig36	gi|565345680|ref|XP_006339919.1|	PREDICTED: ferredoxin-1, chloroplastic-like [Solanum tuberosum]	242 bits(616)	5,81E-78	81%	2%
	gi|78192120|gb|ABB30150.1|	chloroplast Tsip1-interacting ferredoxin [Nicotiana tabacum]	229 bits(583)	7,43E-73	76%	2%
	gi|14041724|emb|CAC38395.1|	ferredoxin I [Solanum tuberosum]	242 bits(616)	6,06E-78	81%	2%
	gi|58045197|gb|AAW64931.1|	chloroplast ferredoxin I [Nicotiana tabacum]	228 bits(580)	1,74E-72	77%	2%
	gi|565403919|ref|XP_006367399.1|	PREDICTED: ferredoxin-1, chloroplastic-like [Solanum tuberosum]	245 bits(624)	4,70E-79	82%	2%
	gi|350537877|ref|NP_001234059.1|	ferredoxin-1, chloroplastic [Solanum lycopersicum]	240 bits(610)	5,83E-77	80%	2%
	gi|34921349|sp|Q9ZTS2.1|FER_CAPAN	RecName: Full=Ferredoxin, chloroplastic; AltName: Full=PFLP; Flags: Precursor	226 bits(575)	1,15E-71	76%	2%
	gi|460407208|ref|XP_004249046.1|	PREDICTED: ferredoxin-1, chloroplastic-like [Solanum lycopersicum]	244 bits(621)	5,48E-78	79%	2%
	gi|45357074|gb|AAS58496.1|	chloroplast ferredoxin I [Nicotiana tabacum]	230 bits(584)	5,14E-73	77%	2%
	gi|169930149|gb|ACB05671.1|	chloroplast ferredoxin [Capsicum annuum]	215 bits(545)	3,82E-67	71%	3%

Apêndice D – Resultado da busca *in silico* da funcionalidade hipotética em Singlets, da biblioteca de folhas de *Solanum lycocarpum*
Fonte de dados: Blastx/NCBI
Elaborada pelo autor

Name Sequence	**Sequence**	**Name**	**score**	**expert**	**indentities**	**gaps**
SLFLPL01A08	No Hits.					
SLFLPL01A09	No Hits.					
SLFLPL01B07	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	6,78E-11	100%	0%
SLFLPL01B11	gi|590707667|ref|XP_007048068.1|	Uncharacterized protein TCM_001206 [Theobroma cacao]	69 bits(167)	4,18E-12	49%	11%
	gi|595831139|ref|XP_007206209.1|	hypothetical protein PRUPE_ppa015169mg [Prunus persica]	66 bits(159)	5,38E-11	45%	14%
	gi|661894401|emb|CDP01400.1|	unnamed protein product [Coffea canephora]	68 bits(165)	9,04E-12	49%	8%
	gi|645219202|ref|XP_008234569.1|	PREDICTED: uncharacterized protein LOC103333497 [Prunus mume]	66 bits(159)	6,05E-11	45%	14%
	gi|359480702|ref|XP_003632516.1|	PREDICTED: uncharacterized protein LOC100854604 [Vitis vinifera]	67 bits(163)	2,13E-11	47%	10%
	gi|565378165|ref|XP_006355532.1|	PREDICTED: uncharacterized protein LOC102596678 [Solanum tuberosum]	104 bits(258)	3,32E-25	65%	6%
	gi|224096243|ref|XP_002310589.1|	hypothetical protein POPTR_0007s06150g [Populus trichocarpa]	67 bits(161)	3,10E-11	49%	10%
SLFLPL01C12	gi|629099069|gb|KCW64834.1|	hypothetical protein EUGRSUZ_G02403 [Eucalyptus grandis]	76 bits(185)	5,78E-14	39%	0%
	gi|587854901|gb|EXB44926.1|	hypothetical protein L484_026514 [Morus notabilis]	67 bits(162)	6,89E-11	35%	2%
	gi|629097980|gb|KCW63745.1|	hypothetical protein EUGRSUZ_G01398 [Eucalyptus grandis]	74 bits(180)	2,46E-13	38%	0%
	gi|460365061|ref|XP_004228424.1|	PREDICTED: uncharacterized protein LOC101261845 [Solanum lycopersicum]	188 bits(477)	1,45E-56	74%	2%
	gi|587854905|gb|EXB44930.1|	hypothetical protein L484_026518 [Morus notabilis]	70 bits(171)	2,72E-12	36%	3%
	gi|629098129|gb|KCW63894.1|	hypothetical protein EUGRSUZ_G01572 [Eucalyptus grandis]	77 bits(188)	1,81E-14	39%	0%
	gi|297738219|emb|CBI27420.3|	unnamed protein product [Vitis vinifera]	69 bits(166)	3,19E-11	46%	1%
SLFLPL01E07	gi|661883548|emb|CDP12892.1|	unnamed protein product [Coffea canephora]	92 bits(228)	1,67E-21	91%	0%
	gi|641814552|gb|KDO37892.1|	hypothetical protein CISIN_1g0424881mg, partial [Citrus sinensis]	89 bits(218)	9,91E-21	91%	0%
	gi|565390782|ref|XP_006361114.1|	PREDICTED: DNA-directed RNA polymerase II subunit 4-like [Solanum tuberosum]	96 bits(236)	1,26E-22	98%	0%
	gi|357513239|ref|XP_003626908.1|	DNA-directed RNA polymerase II subunit RPB4 [Medicago truncatula]	90 bits(222)	6,42E-21	91%	0%
	gi|351727683|ref|NP_001237937.1|	uncharacterized protein LOC100499661 [Glycine max]	90 bits(221)	1,68E-20	91%	0%
	gi|460391507|ref|XP_004241362.1|	PREDICTED: DNA-directed RNA polymerase II subunit RPB4-like [Solanum lycopersicum]	96 bits(236)	1,33E-22	98%	0%
	gi|567870775|ref|XP_006428009.1|	hypothetical protein CICLE_v10026735mg [Citrus clementina]	90 bits(222)	7,87E-21	91%	0%
	gi|357513237|ref|XP_003626907.1|	DNA-directed RNA polymerase II subunit RPB4 [Medicago truncatula]	90 bits(221)	1,70E-20	91%	0%
	gi|629088105|gb|KCW54358.1|	hypothetical protein EUGRSUZ_I00318 [Eucalyptus grandis]	93 bits(230)	8,92E-22	94%	0%
	gi|641840984|gb|KDO59899.1|	hypothetical protein CISIN_1g0325681mg, partial [Citrus sinensis]	89 bits(218)	9,27E-21	91%	0%
SLFLPL01E09	gi|661882229|emb|CDP14205.1|	unnamed protein product [Coffea canephora]	65 bits(156)	9,51E-11	48%	4%
SLFLPL01E10	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	6,66E-11	100%	0%
SLFLPL01F08	No Hits.					
SLFLPL01F12	gi|661899058|emb|CDO97052.1|	unnamed protein product [Coffea canephora]	281 bits(718)	7,85E-89	79%	1%
	gi|297741461|emb|CBI32592.3|	unnamed protein product [Vitis vinifera]	263 bits(671)	1,65E-81	77%	0%
	gi|566187546|ref|XP_002313046.2|	hypothetical protein POPTR_0009s11900g [Populus trichocarpa]	275 bits(703)	6,73E-85	76%	0%
	gi|645262732|ref|XP_008236896.1|	PREDICTED: uncharacterized protein LOC103335654 isoform X1 [Prunus mume]	265 bits(677)	3,96E-81	75%	0%
	gi|565399114|ref|XP_006365103.1|	PREDICTED: uncharacterized protein LOC102586135 [Solanum tuberosum]	346 bits(887)	5,98E-112	93%	0%
	gi|255536843|ref|XP_002509488.1|	conserved hypothetical protein [Ricinus communis]	267 bits(681)	7,25E-82	77%	0%
	gi|359475176|ref|XP_003631610.1|	PREDICTED: uncharacterized protein LOC100852464 [Vitis vinifera]	262 bits(669)	9,38E-80	77%	0%
	gi|460370116|ref|XP_004230900.1|	PREDICTED: uncharacterized protein LOC101250346 [Solanum lycopersicum]	334 bits(856)	3,30E-107	90%	0%
	gi|604333448|gb|EYU37799.1|	hypothetical protein MIMGU_mgv1a002705mg [Erythranthe guttata]	266 bits(679)	1,55E-81	80%	0%
	gi|567861222|ref|XP_006423265.1|	hypothetical protein CICLE_v10028120mg [Citrus clementina]	259 bits(661)	9,66E-80	65%	26%
SLFLPL01G08	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	8,55E-11	100%	0%
SLFLPL01G10	gi|330752400|emb|CBL87351.1|	hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]	69 bits(166)	8,21E-12	97%	0%
	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	6,20E-11	100%	0%
SLFLPL01H12	gi|340002457|gb|AEK26371.1|	chloroplast photosystem II subunit [Sedum alfredii]	72 bits(175)	2,98E-12	71%	0%
	gi|84620804|gb|ABC59516.1|	chloroplast photosystem II 22 kDa component [Nicotiana benthamiana]	72 bits(176)	2,73E-12	64%	2%
	gi|475587298|gb|EMT20518.1|	Photosystem II 22 kDa protein, chloroplastic [Aegilops tauschii]	200 bits(507)	1,93E-60	85%	1%
	gi|449465453|ref|XP_004150442.1|	PREDICTED: photosystem II 22 kDa protein, chloroplastic-like [Cucumis sativus]	75 bits(184)	2,10E-13	55%	4%
	gi|669030590|emb|CDM85166.1|	unnamed protein product [Triticum aestivum]	72 bits(175)	3,59E-12	71%	0%
	gi|116778734|gb|ABK20973.1|	unknown [Picea sitchensis]	77 bits(187)	1,03E-13	50%	13%
	gi|659133395|ref|XP_008466710.1|	PREDICTED: photosystem II 22 kDa protein, chloroplastic [Cucumis melo]	74 bits(181)	5,78E-13	54%	4%
	gi|643723197|gb|KDP32802.1|	hypothetical protein JCGZ_12094 [Jatropha curcas]	72 bits(175)	3,16E-12	71%	0%

	gi|84620802|gb|ABC59515.1|	chloroplast photosystem II 22 kDa component [Nicotiana benthamiana]	73 bits(178)	1,33E-12	64%	2%
	gi|18203444|sp|Q9SMB4.1|PSBS_TOBAC	RecName: Full=Photosystem II 22 kDa protein, chloroplastic; AltName: Full=CP22; Flags: Precursor [Nicotiana tabacum]	72 bits(176)	2,70E-12	64%	2%
SLFLPL02A04	No Hits.					
SLFLPL02A05	No Hits.					
SLFLPL02A11	gi|255549422|ref|XP_002515764.1|	ATPase inhibitor, putative [Ricinus communis]	82 bits(202)	8,89E-18	57%	8%
	gi|670361368|ref|XP_008647717.1|	PREDICTED: uncharacterized protein LOC100502427 isoform X1 [Zea mays]	75 bits(184)	3,94E-15	52%	6%
	gi|565391559|ref|XP_006361489.1|	PREDICTED: rho GTPase-activating protein gacHH-like [Solanum tuberosum]	146 bits(366)	2,44E-42	91%	0%
	gi|661896732|emb|CDO99921.1|	unnamed protein product [Coffea canephora]	82 bits(201)	1,58E-17	71%	1%
	gi|388492352|gb|AFK34242.1|	unknown [Lotus japonicus]	74 bits(180)	1,53E-14	57%	5%
	gi|1096930|prf||2113194A	H ATPase inhibitor	91 bits(225)	1,94E-21	91%	0%
	gi|356536342|ref|XP_003536698.1|	PREDICTED: uncharacterized protein At2g27730, mitochondrial isoform 1 [Glycine max]	81 bits(199)	2,39E-17	58%	6%
	gi|470141411|ref|XP_004306426.1|	PREDICTED: uncharacterized protein LOC101312379 isoform 2 [Fragaria vesca subsp. vesca]	73 bits(178)	2,94E-14	53%	6%
	gi|565358106|ref|XP_006345870.1|	PREDICTED: uncharacterized protein At2g27730, mitochondrial-like [Solanum tuberosum]	92 bits(227)	2,27E-21	71%	5%
	gi|225464420|ref|XP_002269381.1|	PREDICTED: uncharacterized protein At2g27730, mitochondrial [Vitis vinifera]	77 bits(188)	1,22E-15	67%	3%
SLFLPL02B10	No Hits.					
SLFLPL02B11	No Hits.					
SLFLPL02C01	No Hits.					
SLFLPL02C10	No Hits.					
SLFLPL02C11	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	4,97E-11	100%	0%
SLFLPL02D01	No Hits.					
SLFLPL02D02	gi|356541215|ref|XP_003539076.1|	PREDICTED: bax inhibitor 1 [Glycine max]	189 bits(479)	1,65E-56	83%	0%
	gi|449461265|ref|XP_004148362.1|	PREDICTED: bax inhibitor 1-like isoform 2 [Cucumis sativus]	186 bits(471)	2,96E-55	82%	2%
	gi|350535435|ref|NP_001234450.1|	Bax inhibitor [Solanum lycopersicum]	215 bits(545)	2,15E-66	99%	0%
	gi|593787096|ref|XP_007156587.1|	hypothetical protein PHAVU_002G001400g [Phaseolus vulgaris]	188 bits(476)	3,62E-56	81%	0%
	gi|511637478|gb|AGN90990.1|	BAX inhibitor-1, partial [Cucumis sativus]	186 bits(471)	3,24E-55	82%	2%
	gi|502152661|ref|XP_004509031.1|	PREDICTED: bax inhibitor 1-like, partial [Cicer arietinum]	188 bits(476)	8,17E-57	82%	0%
	gi|255638175|gb|ACU19401.1|	unknown [Glycine max]	188 bits(475)	5,88E-56	82%	0%
	gi|543177293|gb|AGV54668.1|	Bax inhibitor 1 [Phaseolus vulgaris]	185 bits(468)	5,85E-55	80%	0%
	gi|358248370|ref|NP_001240126.1|	uncharacterized protein LOC100804444 [Glycine max]	190 bits(480)	1,10E-56	83%	0%
	gi|659131854|ref|XP_008465890.1|	PREDICTED: bax inhibitor 1-like [Cucumis melo]	187 bits(473)	1,50E-55	83%	2%
SLFLPL02D04	No Hits.					
SLFLPL02D10	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	4,78E-11	100%	0%
SLFLPL02E03	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	4,69E-11	100%	0%
SLFLPL02E12	gi|671775162|gb|AII99814.1|	cytoplasmic ribosomal protein S13 [Nicotiana tabacum]	304 bits(778)	4,33E-102	99%	0%
	gi|643706262|gb|KDP22394.1|	hypothetical protein JCGZ_26225 [Jatropha curcas]	302 bits(771)	4,88E-101	98%	0%
	gi|350534834|ref|NP_001234162.1|	cytoplasmic ribosomal protein S13 [Solanum lycopersicum]	304 bits(777)	5,75E-102	99%	0%
	gi|590671851|ref|XP_007038446.1|	Ribosomal protein S13A [Theobroma cacao]	301 bits(769)	9,81E-101	98%	0%
	gi|568214822|ref|NP_001275221.1|	40S ribosomal protein S13-like [Solanum tuberosum]	305 bits(781)	1,12E-102	100%	0%
	gi|604321408|gb|EYU31984.1|	hypothetical protein MIMGU_mgv1a015623mg [Erythranthe guttata]	303 bits(775)	1,13E-101	99%	0%
	gi|643712172|gb|KDP25600.1|	hypothetical protein JCGZ_20756 [Jatropha curcas]	300 bits(767)	1,93E-100	97%	0%
	gi|460388786|ref|XP_004240045.1|	PREDICTED: 40S ribosomal protein S13-like [Solanum lycopersicum]	304 bits(778)	4,14E-102	99%	0%
	gi|567858120|ref|XP_006421743.1|	hypothetical protein CICLE_v10006145mg [Citrus clementina]	302 bits(772)	2,77E-101	99%	0%
	gi|449459684|ref|XP_004147576.1|	PREDICTED: 40S ribosomal protein S13-like [Cucumis sativus]	300 bits(766)	2,10E-100	97%	0%
SLFLPL02F03	No Hits.					
SLFLPL02F04	gi|565373754|ref|XP_006353433.1|	PREDICTED: uncharacterized protein LOC102583756 isoform X2 [Solanum tuberosum]	240 bits(610)	4,58E-70	89%	4%
	gi|657955623|ref|XP_008369281.1|	PREDICTED: uncharacterized protein LOC103432852 [Malus domestica]	203 bits(514)	8,59E-57	71%	4%
	gi|587917107|gb|EXC04704.1|	UDP-sugar pyrophospharylase [Morus notabilis]	198 bits(502)	1,20E-55	69%	4%
	gi|460390596|ref|XP_004240914.1|	PREDICTED: uncharacterized protein LOC101246145 [Solanum lycopersicum]	242 bits(617)	6,02E-71	90%	4%
	gi|565373752|ref|XP_006353432.1|	PREDICTED: uncharacterized protein LOC102583756 isoform X1 [Solanum tuberosum]	239 bits(609)	6,94E-70	89%	4%
	gi|225448507|ref|XP_002273020.1|	PREDICTED: uncharacterized protein LOC100241552 [Vitis vinifera]	200 bits(508)	5,31E-56	70%	4%
	gi|661882407|emb|CDP13987.1|	unnamed protein product [Coffea canephora]	204 bits(517)	8,97E-58	73%	4%
	gi|593801058|ref|XP_007163566.1|	hypothetical protein PHAVU_001G2449001g, partial [Phaseolus vulgaris]	188 bits(475)	5,69E-56	64%	4%
	gi|694386862|ref|XP_009369204.1|	PREDICTED: uncharacterized protein LOC103958637 [Pyrus x bretschneideri]	204 bits(517)	3,49E-57	72%	4%
	gi|147794750|emb|CAN60362.1|	hypothetical protein VITISV_024684 [Vitis vinifera]	200 bits(508)	5,90E-56	70%	4%
SLFLPL02F10	gi|604318628|gb|EYU30120.1|	hypothetical protein MIMGU_mgv1a017329mg [Erythranthe guttata]	66 bits(159)	3,62E-11	52%	11%
	gi|565377172|ref|XP_006355063.1|	PREDICTED: uncharacterized protein LOC102579558 [Solanum tuberosum]	111 bits(276)	2,83E-28	85%	4%

	gi|224099549|ref|XP_002311528.1|	hypothetical protein POPTR_0008s13370g [Populus trichocarpa]	65 bits(158)	5,22E-11	59%	5%
	gi|18408896|ref|NP_564914.1|	uncharacterized protein [Arabidopsis thaliana]	67 bits(162)	1,27E-11	58%	4%
	gi|297838541|ref|XP_002887152.1|	hypothetical protein ARALYDRAFT_894553 [Arabidopsis lyrata subsp. lyrata]	66 bits(160)	2,47E-11	57%	4%
SLFLPL02G01	No Hits.					
SLFLPL02G03	gi|460415399|ref|XP_004253046.1|	PREDICTED: apyrase 2-like [Solanum lycopersicum]	93 bits(229)	6,01E-19	88%	0%
	gi|117622284|gb|ABK51386.1|	apyrase-like protein [Nicotiana tabacum]	84 bits(206)	6,65E-16	82%	0%
	gi|604341831|gb|EYU41066.1|	hypothetical protein MIMGU_mgv1a004609mg [Erythranthe guttata]	75 bits(182)	1,42E-12	61%	4%
	gi|565350999|ref|XP_006342448.1|	PREDICTED: apyrase 2-like [Solanum tuberosum]	94 bits(231)	2,87E-19	90%	0%
	gi|359478310|ref|XP_002280863.2|	PREDICTED: nucleoside-triphosphatase [Vitis vinifera]	73 bits(178)	4,20E-12	46%	7%
SLFLPL02G12	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	4,52E-11	100%	0%
SLFLPL03A01	No Hits.					
SLFLPL03A02	No Hits.					
SLFLPL03A05	No Hits.					
SLFLPL03A06	No Hits.					
SLFLPL03A08	gi|565369507|ref|XP_006351376.1|	PREDICTED: ubiquitin-associated domain-containing protein 2-like [Solanum tuberosum]	71 bits(172)	2,61E-11	100%	0%
SLFLPL03A11	gi|3043432|emb|CAA06493.1|	Ubiquitin conjugating enzyme [Cicer arietinum]	122 bits(306)	6,57E-32	98%	0%
	gi|567921502|ref|XP_006452757.1|	hypothetical protein CICLE_v10009806mg [Citrus clementina]	125 bits(312)	4,77E-32	100%	0%
	gi|661882645|emb|CDP13648.1|	unnamed protein product [Coffea canephora]	125 bits(313)	7,69E-32	100%	0%
	gi|566162504|ref|XP_006385788.1|	hypothetical protein POPTR_0003s13600g [Populus trichocarpa]	124 bits(310)	6,06E-32	98%	0%
	gi|225462031|ref|XP_002274367.1|	PREDICTED: ubiquitin-conjugating enzyme E2-17 kDa isoform 2 [Vitis vinifera]	125 bits(312)	9,90E-32	100%	0%
	gi|460414273|ref|XP_004252497.1|	PREDICTED: uncharacterized protein LOC101254461 [Solanum lycopersicum]	127 bits(318)	3,34E-32	100%	0%
	gi|40287568|gb|AAR83898.1|	ubiquitin-conjugating protein [Capsicum annuum]	124 bits(311)	6,35E-32	100%	0%
	gi|568215234|ref|NP_001275336.1|	ubiquitin-conjugating enzyme E2-17 kDa-like [Solanum tuberosum]	124 bits(311)	6,51E-32	100%	0%
	gi|567921506|ref|XP_006452759.1|	hypothetical protein CICLE_v10009806mg [Citrus clementina]	125 bits(312)	1,02E-31	100%	0%
	gi|567921504|ref|XP_006452758.1|	hypothetical protein CICLE_v10009806mg [Citrus clementina]	125 bits(313)	4,61E-32	100%	0%
SLFLPL03B02	gi|460367603|ref|XP_004229662.1|	PREDICTED: uncharacterized protein LOC101256709 [Solanum lycopersicum]	190 bits(481)	2,85E-54	94%	0%
	gi|641864627|gb|KDO83313.1|	hypothetical protein CISIN_1g017076mg [Citrus sinensis]	171 bits(433)	2,34E-47	80%	0%
	gi|629100261|gb|KCW66026.1|	hypothetical protein EUGRSUZ_G03317 [Eucalyptus grandis]	163 bits(412)	8,08E-47	79%	0%
	gi|565357134|ref|XP_006345403.1|	PREDICTED: uncharacterized protein LOC102602697 [Solanum tuberosum]	188 bits(476)	1,18E-53	93%	0%
	gi|641864628|gb|KDO83314.1|	hypothetical protein CISIN_1g017076mg [Citrus sinensis]	171 bits(433)	2,59E-47	80%	0%
	gi|645251020|ref|XP_008231487.1|	PREDICTED: uncharacterized protein LOC103330662 [Prunus mume]	170 bits(430)	8,80E-47	80%	0%
	gi|641864629|gb|KDO83315.1|	hypothetical protein CISIN_1g017076mg [Citrus sinensis]	171 bits(433)	4,76E-49	80%	0%
	gi|567892863|ref|XP_006438952.1|	hypothetical protein CICLE_v10031842mg [Citrus clementina]	171 bits(433)	2,73E-47	80%	0%
	gi|641864626|gb|KDO83312.1|	hypothetical protein CISIN_1g017076mg [Citrus sinensis]	171 bits(432)	5,08E-48	80%	0%
	gi|596001086|ref|XP_007218133.1|	hypothetical protein PRUPE_ppa007145mg [Prunus persica]	170 bits(430)	7,33E-47	80%	0%
SLFLPL03B06	gi|567165796|ref|XP_006397643.1|	hypothetical protein EUTSA_v10001683mg [Eutrema salsugineum]	84 bits(205)	6,26E-17	87%	0%
	gi|297824487|ref|XP_002880126.1|	mtACP-1 [Arabidopsis lyrata subsp. lyrata]	83 bits(204)	8,69E-17	87%	0%
	gi|15450375|gb|AAK96481.1|	At2g44620/F16B22.11 [Arabidopsis thaliana]	84 bits(205)	6,35E-17	87%	0%
	gi|565475208|ref|XP_006295245.1|	hypothetical protein CARUB_v10024332mg [Capsella rubella]	83 bits(203)	1,13E-16	87%	0%
	gi|641866731|gb|KDO85415.1|	hypothetical protein CISIN_1g0332331mg, partial [Citrus sinensis]	83 bits(204)	1,92E-17	85%	0%
	gi|674244502|gb|KFK37267.1|	hypothetical protein AALP_AA4G235200 [Arabis alpina]	84 bits(205)	6,89E-17	87%	0%
	gi|460367697|ref|XP_004229707.1|	PREDICTED: acyl carrier protein 1, mitochondrial-like [Solanum lycopersicum]	95 bits(234)	5,26E-21	100%	0%
	gi|567905986|ref|XP_006445481.1|	hypothetical protein CICLE_v10022877mg [Citrus clementina]	84 bits(206)	4,52E-17	85%	0%
	gi|15224918|ref|NP_181990.1|	acyl carrier protein 1 [Arabidopsis thaliana]	83 bits(204)	8,26E-17	87%	0%
	gi|565376283|ref|XP_006354636.1|	PREDICTED: acyl carrier protein 1, mitochondrial-like [Solanum tuberosum]	95 bits(234)	5,83E-21	100%	0%
SLFLPL03B08	gi|674242997|gb|KFK35762.1|	hypothetical protein AALP_AA4G033000 [Arabis alpina]	278 bits(709)	3,89E-90	90%	0%
	gi|565494994|ref|XP_006305136.1|	hypothetical protein CARUB_v10009510mg [Capsella rubella]	276 bits(705)	1,95E-89	89%	0%
	gi|674907050|emb|CDY26037.1|	BnaC06g05870D [Brassica napus]	277 bits(706)	8,87E-90	91%	0%
	gi|685314110|ref|XP_009147654.1|	PREDICTED: uncharacterized protein LOC103871177 [Brassica rapa]	275 bits(703)	3,39E-89	90%	0%
	gi|460397292|ref|XP_004244201.1|	PREDICTED: uncharacterized protein LOC101247444 [Solanum lycopersicum]	289 bits(739)	2,44E-94	96%	0%
	gi|567132013|ref|XP_006392859.1|	hypothetical protein EUTSA_v10011607mg [Eutrema salsugineum]	277 bits(706)	1,17E-89	91%	0%
	gi|30695366|ref|NP_564615.3|	peroxisomal membrane Mpv17/PMP22 family protein [Arabidopsis thaliana]	274 bits(699)	1,61E-88	89%	0%
	gi|565388766|ref|XP_006360143.1|	PREDICTED: uncharacterized protein LOC102590255 [Solanum tuberosum]	287 bits(733)	1,39E-93	96%	0%
	gi|674878207|emb|CDY53804.1|	BnaA06g01790D [Brassica napus]	277 bits(707)	1,31E-89	91%	0%
	gi|297847674|ref|XP_002891718.1|	hypothetical protein ARALYDRAFT_474411 [Arabidopsis lyrata subsp. lyrata]	273 bits(696)	5,01E-88	89%	0%
SLFLPL03B09	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	5,66E-11	100%	0%

SLFLPL03C01	gi|225455513|ref|XP_002265347.1|	PREDICTED: 40S ribosomal protein S20-2 isoform 1 [Vitis vinifera]	243 bits(619)	1,04E-78	98%	0%
	gi|658016709|ref|XP_008343705.1|	PREDICTED: 40S ribosomal protein S20-2 [Malus domestica]	240 bits(611)	1,67E-77	98%	0%
	gi|565361869|ref|XP_006347675.1|	PREDICTED: 40S ribosomal protein S20-2-like [Solanum tuberosum]	247 bits(629)	3,51E-80	98%	0%
	gi|565377617|ref|XP_006355268.1|	PREDICTED: 40S ribosomal protein S20-2-like [Solanum tuberosum]	243 bits(618)	1,72E-78	98%	0%
	gi|604305933|gb|EYU24990.1|	hypothetical protein MIMGU_mgv1a016427mg [Erythranthe guttata]	240 bits(611)	1,74E-77	98%	0%
	gi|460368376|ref|XP_004230043.1|	PREDICTED: 40S ribosomal protein S20-1-like [Solanum lycopersicum]	246 bits(626)	8,68E-80	98%	0%
	gi|590671815|ref|XP_007038436.1|	Ribosomal protein S10p/S20e family protein isoform 1 [Theobroma cacao]	242 bits(617)	2,60E-78	98%	0%
	gi|351725235|ref|NP_001237853.1|	uncharacterized protein LOC100499912 [Glycine max]	239 bits(609)	3,99E-77	95%	0%
	gi|460368374|ref|XP_004230042.1|	PREDICTED: 40S ribosomal protein S20-1-like [Solanum lycopersicum]	245 bits(625)	1,45E-79	97%	0%
	gi|587932429|gb|EXC19483.1|	40S ribosomal protein S20-2 [Morus notabilis]	240 bits(612)	1,43E-77	98%	0%
SLFLPL03C05	gi|565390445|ref|XP_006360948.1|	PREDICTED: light-regulated protein-like [Solanum tuberosum]	178 bits(449)	2,51E-52	68%	14%
	gi|224057830|ref|XP_002299345.1|	gene GA family protein [Populus trichocarpa]	118 bits(295)	1,62E-29	52%	18%
	gi|694408210|ref|XP_009378810.1|	PREDICTED: light-regulated protein-like [Pyrus x bretschneideri]	117 bits(291)	7,71E-29	58%	11%
	gi|460404800|ref|XP_004247868.1|	PREDICTED: light-regulated protein-like [Solanum lycopersicum]	164 bits(414)	3,87E-47	66%	18%
	gi|567855337|ref|XP_006420788.1|	hypothetical protein CICLE_v10006190mg [Citrus clementina]	119 bits(296)	1,66E-29	51%	15%
	gi|590691514|ref|XP_007043804.1|	Light-regulated protein precursor, putative isoform 1 [Theobroma cacao]	128 bits(321)	3,85E-33	56%	17%
	gi|255543196|ref|XP_002512661.1|	Light-regulated protein precursor, putative [Ricinus communis]	117 bits(292)	4,87E-29	51%	13%
	gi|257831441|gb|ACV71021.1|	UPA22 [Capsicum annuum]	181 bits(458)	1,52E-53	66%	13%
	gi|225425246|ref|XP_002269300.1|	PREDICTED: light-regulated protein [Vitis vinifera]	122 bits(306)	5,54E-31	50%	21%
	gi|118489528|gb|ABK96566.1|	unknown [Populus trichocarpa x Populus deltoides]	117 bits(291)	7,15E-29	51%	18%
SLFLPL03C07	No Hits.					
SLFLPL03C10	gi|694330284|ref|XP_009355851.1|	PREDICTED: farnesylcysteine lyase [Pyrus x bretschneideri]	278 bits(711)	3,85E-87	69%	1%
	gi|359480755|ref|XP_002275222.2|	PREDICTED: farnesylcysteine lyase-like [Vitis vinifera]	287 bits(733)	1,57E-90	70%	0%
	gi|643718123|gb|KDP29468.1|	hypothetical protein JCGZ_19297 [Jatropha curcas]	278 bits(710)	4,14E-87	68%	0%
	gi|587866990|gb|EXB56421.1|	Farnesylcysteine lyase [Morus notabilis]	284 bits(726)	1,56E-89	72%	0%
	gi|460414737|ref|XP_004252720.1|	PREDICTED: farnesylcysteine lyase-like [Solanum lycopersicum]	367 bits(941)	7,84E-122	90%	0%
	gi|567879119|ref|XP_006432118.1|	hypothetical protein CICLE_v10000962mg [Citrus clementina]	282 bits(719)	1,32E-88	68%	0%
	gi|645242447|ref|XP_008227553.1|	PREDICTED: farnesylcysteine lyase [Prunus mume]	278 bits(710)	7,03E-87	68%	1%
	gi|565401887|ref|XP_006366424.1|	PREDICTED: farnesylcysteine lyase-like [Solanum tuberosum]	359 bits(920)	1,27E-118	89%	0%
	gi|641838558|gb|KDO57499.1|	hypothetical protein CISIN_1g043512mg [Citrus sinensis]	282 bits(719)	1,34E-88	68%	0%
	gi|661887988|emb|CDP08400.1|	unnamed protein product [Coffea canephora]	277 bits(707)	1,10E-86	66%	1%
SLFLPL03D01	No Hits.					
SLFLPL03D04	gi|106879609|emb|CAJ38388.1|	actin-depolymerizing factor [Plantago major]	129 bits(322)	7,75E-34	92%	0%
	gi|643738216|gb|KDP44204.1|	hypothetical protein JCGZ_05671 [Jatropha curcas]	127 bits(319)	1,69E-33	92%	0%
	gi|460401918|ref|XP_004246462.1|	PREDICTED: actin-depolymerizing factor 1-like [Solanum lycopersicum]	133 bits(334)	1,49E-35	98%	0%
	gi|317134431|gb|ADV02778.1|	actin depolymerizing factor 1 [Ipomoea batatas]	129 bits(322)	9,59E-34	92%	0%
	gi|590589598|ref|XP_007016496.1|	Actin depolymerizing factor 4 [Theobroma cacao]	128 bits(320)	1,78E-33	92%	0%
	gi|170773914|gb|ACB32233.1|	actin-depolymerizing factor 1 [Solanum chacoense]	132 bits(332)	2,80E-35	97%	0%
	gi|661887233|emb|CDP09013.1|	unnamed protein product [Coffea canephora]	128 bits(320)	1,41E-33	92%	0%
	gi|255584766|ref|XP_002533101.1|	actin depolymerizing factor, putative [Ricinus communis]	127 bits(319)	2,11E-33	91%	0%
	gi|565348103|ref|XP_006341057.1|	PREDICTED: actin-depolymerizing factor 1-like [Solanum tuberosum]	131 bits(329)	9,06E-35	95%	0%
SLFLPL03D04	gi|661889921|emb|CDP06641.1|	unnamed protein product [Coffea canephora]	129 bits(322)	1,44E-33	94%	0%
SLFLPL03E06	gi|629102651|gb|KCW68120.1|	hypothetical protein EUGRSUZ_F01794 [Eucalyptus grandis]	66 bits(159)	9,93E-11	94%	0%
	gi|661888827|emb|CDP07270.1|	unnamed protein product [Coffea canephora]	67 bits(161)	4,74E-11	97%	0%
SLFLPL03E12	gi|567901860|ref|XP_006443418.1|	hypothetical protein CICLE_v10019090mg [Citrus clementina]	252 bits(641)	7,79E-76	97%	0%
	gi|629081303|gb|KCW47748.1|	hypothetical protein EUGRSUZ_K01498 [Eucalyptus grandis]	249 bits(635)	4,27E-75	96%	0%
	gi|641836080|gb|KDO55049.1|	hypothetical protein CISIN_1g005214mg [Citrus sinensis]	252 bits(643)	1,18E-77	97%	0%
	gi|568850838|ref|XP_006479104.1|	PREDICTED: uncharacterized protein LOC102619111 isoform X1 [Citrus sinensis]	251 bits(640)	8,96E-76	97%	0%
	gi|604336151|gb|EYU39997.1|	hypothetical protein MIMGU_mgv1a002328mg [Erythranthe guttata]	248 bits(633)	6,81E-75	96%	0%
	gi|565369484|ref|XP_006351365.1|	PREDICTED: uncharacterized protein LOC102603072 [Solanum tuberosum]	256 bits(652)	2,00E-77	99%	0%
	gi|661882099|emb|CDP14324.1|	unnamed protein product [Coffea canephora]	250 bits(637)	2,94E-75	97%	0%
	gi|593797798|ref|XP_007161937.1|	hypothetical protein PHAVU_001G110300g [Phaseolus vulgaris]	247 bits(630)	2,96E-74	95%	0%
	gi|460407731|ref|XP_004249304.1|	PREDICTED: uncharacterized protein LOC101268442 [Solanum lycopersicum]	256 bits(652)	2,00E-77	99%	0%
	gi|643732610|gb|KDP39706.1|	hypothetical protein JCGZ_02726 [Jatropha curcas]	250 bits(636)	3,60E-75	96%	0%
SLFLPL03F04	No Hits.					
SLFLPL03F06	gi|565372146|ref|XP_006352658.1|	PREDICTED: uncharacterized protein LOC102587508 isoform X1 [Solanum tuberosum]	309 bits(790)	2,07E-103	89%	8%

	gi|672171788|ref|XP_008805971.1|	PREDICTED: uncharacterized protein LOC103718781 [Phoenix dactylifera]	160 bits(403)	5,47E-45	50%	34%
	gi|567201933|ref|XP_006407837.1|	hypothetical protein EUTSA_v10021454mg [Eutrema salsugineum]	153 bits(385)	2,13E-42	57%	5%
	gi|460393668|ref|XP_004242431.1|	PREDICTED: uncharacterized protein LOC101255803 isoform 1 [Solanum lycopersicum]	295 bits(753)	7,72E-98	87%	8%
	gi|297829292|ref|XP_002882528.1|	hypothetical protein ARALYDRAFT_478063 [Arabidopsis lyrata subsp. lyrata]	160 bits(403)	6,28E-45	56%	20%
	gi|694438733|ref|XP_009346313.1|	PREDICTED: uncharacterized protein LOC103938040 [Pyrus x bretschneideri]	152 bits(382)	4,95E-42	70%	3%
	gi|657976949|ref|XP_008380376.1|	PREDICTED: uncharacterized protein LOC103443337 [Malus domestica]	161 bits(407)	9,97E-46	60%	3%
	gi|672171786|ref|XP_008805970.1|	PREDICTED: uncharacterized protein LOC103718780 [Phoenix dactylifera]	158 bits(398)	3,03E-44	50%	34%
	gi|255572626|ref|XP_002527246.1|	conserved hypothetical protein [Ricinus communis]	161 bits(405)	2,44E-45	54%	22%
	gi|565481440|ref|XP_006298360.1|	hypothetical protein CARUB_v10014430mg, partial [Capsella rubella]	157 bits(395)	1,70E-43	55%	18%
SLFLPL03F09	gi|312231980|gb|ADQ53451.1|	plastid thioredoxin F precursor [Nicotiana tabacum]	107 bits(266)	5,88E-27	91%	0%
	gi|586752159|ref|XP_006852197.1|	hypothetical protein AMTR_s00049p00119540 [Amborella trichopoda]	104 bits(258)	9,77E-26	88%	0%
	gi|643714216|gb|KDP26881.1|	hypothetical protein JCGZ_18039 [Jatropha curcas]	105 bits(261)	3,65E-26	89%	0%
	gi|672128493|ref|XP_008787736.1|	PREDICTED: thioredoxin F, chloroplastic-like [Phoenix dactylifera]	103 bits(255)	3,09E-25	86%	0%
	gi|460387979|ref|XP_004239649.1|	PREDICTED: thioredoxin F1, chloroplastic-like [Solanum lycopersicum]	114 bits(283)	1,97E-29	98%	0%
	gi|661891962|emb|CDP04188.1|	unnamed protein product [Coffea canephora]	105 bits(260)	3,84E-26	88%	0%
	gi|388498704|gb|AFK37418.1|	unknown [Lotus japonicus]	102 bits(254)	3,31E-25	88%	0%
	gi|565357915|ref|XP_006345775.1|	PREDICTED: thioredoxin F1, chloroplastic-like [Solanum tuberosum]	111 bits(276)	6,47E-28	98%	0%
	gi|255547546|ref|XP_002514830.1|	thioredoxin f-type, putative [Ricinus communis]	104 bits(259)	8,10E-26	86%	0%
	gi|470132602|ref|XP_004302168.1|	PREDICTED: thioredoxin F2, chloroplastic-like [Fragaria vesca subsp. vesca]	102 bits(254)	3,90E-25	82%	0%
SLFLPL03G02	gi|661892239|emb|CDP04465.1|	unnamed protein product [Coffea canephora]	296 bits(757)	5,18E-98	84%	0%
	gi|566192978|ref|XP_002317121.2|	hypothetical protein POPTR_0011s00810g [Populus trichocarpa]	287 bits(732)	9,15E-95	80%	0%
	gi|460381892|ref|XP_004236675.1|	PREDICTED: dehydrogenase/reductase SDR family member 4-like isoform 1 [Solanum lycopersicum]	310 bits(792)	2,81E-103	92%	0%
	gi|587851389|gb|EXB41538.1|	Dehydrogenase/reductase SDR family member 4 [Morus notabilis]	292 bits(747)	1,77E-96	81%	0%
	gi|595865114|ref|XP_007211893.1|	hypothetical protein PRUPE_ppa010299mg [Prunus persica]	288 bits(735)	1,12E-94	79%	0%
	gi|565371577|ref|XP_006352379.1|	PREDICTED: tropinone reductase-like 3-like [Solanum tuberosum]	301 bits(769)	7,91E-100	83%	0%
	gi|470114279|ref|XP_004293343.1|	PREDICTED: dehydrogenase/reductase SDR family member 4-like [Fragaria vesca subsp. vesca]	292 bits(745)	3,58E-96	81%	0%
	gi|224113857|ref|XP_002316593.1|	hypothetical protein POPTR_0011s00810g [Populus trichocarpa]	287 bits(733)	2,22E-94	80%	0%
	gi|359496979|ref|XP_002264497.2|	PREDICTED: dehydrogenase/reductase SDR family member 4 [Vitis vinifera]	290 bits(742)	1,65E-95	81%	0%
	gi|645236446|ref|XP_008224741.1|	PREDICTED: tropinone reductase-like 3 [Prunus mume]	286 bits(730)	7,67E-94	79%	0%
SLFLPL03G06	gi|350535643|ref|NP_001234461.1|	dehydration-induced protein ERD15 [Solanum lycopersicum]	204 bits(517)	3,04E-63	92%	0%
	gi|565383620|ref|XP_006358032.1|	PREDICTED: protein EARLY RESPONSIVE TO DEHYDRATION 15-like [Solanum tuberosum]	156 bits(392)	2,01E-44	72%	11%
	gi|604298665|gb|EYU18667.1|	hypothetical protein MIMGU_mgv1a015406mg [Erythranthe guttata]	100 bits(248)	4,44E-23	57%	11%
	gi|565369322|ref|XP_006351285.1|	PREDICTED: protein EARLY RESPONSIVE TO DEHYDRATION 15-like [Solanum tuberosum]	200 bits(508)	5,65E-62	91%	0%
	gi|460381664|ref|XP_004236564.1|	PREDICTED: protein EARLY RESPONSIVE TO DEHYDRATION 15-like [Solanum lycopersicum]	153 bits(384)	3,85E-43	72%	11%
	gi|661882224|emb|CDP14200.1|	unnamed protein product [Coffea canephora]	93 bits(230)	2,32E-20	50%	9%
	gi|418729862|gb|AFX66978.1|	dehydration-induced protein ERD15 [Solanum tuberosum]	198 bits(503)	3,17E-61	89%	0%
	gi|82734828|gb|ABB89735.1|	ERD15 [Capsicum annuum]	145 bits(364)	3,74E-40	68%	11%
	gi|294440434|gb|ADE74634.1|	early responsive to dehydration 1 protein [Nicotiana tabacum]	177 bits(447)	1,07E-52	77%	7%
	gi|567773326|gb|AHC94919.1|	early responsive to dehydration protein 15 [Ipomoea batatas]	110 bits(273)	1,36E-26	52%	15%
SLFLPL03G09	gi|565368491|ref|XP_006350878.1|	PREDICTED: probable serine/threonine-protein kinase WNK4-like [Solanum tuberosum]	82 bits(200)	1,33E-15	88%	0%
	gi|460393779|ref|XP_004242486.1|	PREDICTED: probable serine/threonine-protein kinase WNK4-like isoform 2 [Solanum lycopersicum]	82 bits(201)	8,70E-16	84%	0%
	gi|460393777|ref|XP_004242485.1|	PREDICTED: probable serine/threonine-protein kinase WNK4-like isoform 1 [Solanum lycopersicum]	82 bits(201)	8,78E-16	84%	0%
SLFLPL03G10	gi|568841936|ref|XP_006474910.1|	PREDICTED: zinc transporter 2-like [Citrus sinensis]	131 bits(328)	3,20E-74	67%	3%
	gi|225461878|ref|XP_002265400.1|	PREDICTED: zinc transporter 11-like [Vitis vinifera]	117 bits(293)	1,10E-70	76%	1%
	gi|350538565|ref|NP_001234349.1|	zinc transporter-like precursor [Solanum lycopersicum]	179 bits(454)	1,01E-91	87%	1%
	gi|359494259|ref|XP_003634744.1|	PREDICTED: zinc transporter 2-like isoform 2 [Vitis vinifera]	125 bits(312)	1,18E-73	68%	1%
	gi|225461884|ref|XP_002265697.1|	PREDICTED: zinc transporter 11-like [Vitis vinifera]	114 bits(283)	1,65E-70	74%	1%
	gi|565358678|ref|XP_006346153.1|	PREDICTED: zinc transporter 2-like [Solanum tuberosum]	170 bits(429)	8,84E-89	87%	3%
	gi|225461882|ref|XP_002265634.1|	PREDICTED: zinc transporter 2-like isoform 1 [Vitis vinifera]	120 bits(300)	2,65E-72	73%	2%
	gi|296089899|emb|CBI39718.3|	unnamed protein product [Vitis vinifera]	113 bits(281)	2,09E-70	72%	2%
	gi|567921124|ref|XP_006452568.1|	hypothetical protein CICLE_v10010292mg [Citrus clementina]	131 bits(329)	7,94E-75	67%	3%
	gi|661882725|emb|CDP13728.1|	unnamed protein product [Coffea canephora]	118 bits(295)	1,69E-71	56%	11%
SLFLPL03G11	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	7,69E-11	100%	0%
SLFLPL03H03	gi|683502|emb|CAA57528.1|	protein phosphatase 2A 65 kDa regulatory subunit [Arabidopsis thaliana]	70 bits(171)	8,49E-11	28%	0%
	gi|460386518|ref|XP_004238945.1|	PREDICTED: serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform-like [Solanum lycopersicum]	74 bits(181)	3,60E-12	29%	0%
	gi|604318466|gb|EYU29958.1|	hypothetical protein MIMGU_mgv1a005777mg [Erythranthe guttata]	75 bits(183)	1,73E-12	29%	0%

	gi|297818092|ref|XP_002876929.1|	hypothetical protein ARALYDRAFT_904748 [Arabidopsis lyrata subsp. lyrata]	74 bits(181)	4,56E-12	29%	0%
	gi|565393797|ref|XP_006362557.1|	PREDICTED: serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform-like [Solanum tuberosum]	75 bits(182)	3,28E-12	29%	0%
	gi|661896018|emb|CDP00596.1|	unnamed protein product [Coffea canephora]	75 bits(183)	2,53E-12	29%	0%
	gi|15230896|ref|NP_189208.1|	protein phosphatase 2A subunit A2 [Arabidopsis thaliana]	74 bits(181)	4,60E-12	29%	0%
	gi|1568511|emb|CAA66487.1|	protein phosphatase 2A [Nicotiana tabacum]	75 bits(183)	2,49E-12	29%	0%
	gi|596286016|ref|XP_007225550.1|	hypothetical protein PRUPE_ppa003299m2g [Prunus persica]	71 bits(172)	4,93E-11	28%	0%
	gi|425872890|gb|AFY06655.1|	protein phosphatase 2A regulatory subunit, partial [Carica papaya]	77 bits(187)	3,28E-13	30%	0%
SLFLPL03H07	gi|595864657|ref|XP_007211811.1|	hypothetical protein PRUPE_ppa009987mg [Prunus persica]	242 bits(616)	6,78E-77	84%	5%
	gi|671775148|gb|AII99807.1|	chlorophyll a-b binding protein 13, chloroplastic-like protein [Nicotiana tabacum]	264 bits(673)	1,72E-85	91%	1%
	gi|566154166|ref|XP_006370338.1|	LIGHT-HARVESTING CHLOROPHYLL BINDING protein 3 [Populus trichocarpa]	242 bits(615)	1,01E-76	85%	2%
	gi|460397262|ref|XP_004244187.1|	PREDICTED: chlorophyll a-b binding protein 13, chloroplastic-like [Solanum lycopersicum]	253 bits(644)	3,96E-81	90%	1%
	gi|661890355|emb|CDP05852.1|	unnamed protein product [Coffea canephora]	240 bits(612)	2,49E-76	84%	1%
	gi|565366629|ref|XP_006349989.1|	PREDICTED: chlorophyll a-b binding protein 13, chloroplastic-like [Solanum tuberosum]	267 bits(681)	1,16E-86	93%	1%
	gi|20671|emb|CAA49149.1|	chlorophyll a/b-binding protein [Pisum sativum]	246 bits(626)	2,17E-78	84%	1%
	gi|56809383|gb|AAW31513.1|	light-harvesting chlorophyll-a/b binding protein Lhcb3 [Pisum sativum]	243 bits(619)	2,26E-77	85%	3%
	gi|460412906|ref|XP_004251837.1|	PREDICTED: chlorophyll a-b binding protein 13, chloroplastic-like [Solanum lycopersicum]	265 bits(675)	9,17E-86	91%	1%
	gi|225461315|ref|XP_002284493.1|	PREDICTED: chlorophyll a-b binding protein 13, chloroplastic-like [Vitis vinifera]	245 bits(624)	5,15E-78	85%	3%
SLFLPL04A04	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	4,97E-11	100%	0%
SLFLPL04A07	gi|565402980|ref|XP_006366946.1|	PREDICTED: uncharacterized protein LOC102588894 [Solanum tuberosum]	248 bits(631)	5,06E-77	93%	0%
	gi|527196043|gb|EPS65057.1|	hypothetical protein M569_09721, partial [Genlisea aurea]	200 bits(507)	5,43E-60	72%	0%
	gi|255582658|ref|XP_002532108.1|	conserved hypothetical protein [Ricinus communis]	200 bits(506)	1,58E-58	72%	0%
	gi|460402500|ref|XP_004246750.1|	PREDICTED: uncharacterized protein LOC101248326 [Solanum lycopersicum]	243 bits(618)	5,38E-75	92%	0%
	gi|604313345|gb|EYU26676.1|	hypothetical protein MIMGU_mgv1a006839mg [Erythranthe guttata]	203 bits(515)	1,15E-59	73%	0%
	gi|661889744|emb|CDP06464.1|	unnamed protein product [Coffea canephora]	198 bits(503)	5,13E-58	71%	0%
	gi|460407256|ref|XP_004249070.1|	PREDICTED: uncharacterized protein LOC101247477 [Solanum lycopersicum]	219 bits(556)	5,60E-66	79%	0%
	gi|672131146|ref|XP_008789128.1|	PREDICTED: protein trichome birefringence-like 3 [Phoenix dactylifera]	201 bits(509)	6,41E-59	72%	0%
	gi|565365682|ref|XP_006349533.1|	PREDICTED: uncharacterized protein LOC102582870 [Solanum tuberosum]	218 bits(553)	2,20E-65	78%	0%
	gi|643710221|gb|KDP24428.1|	hypothetical protein JCGZ_24992 [Jatropha curcas]	199 bits(504)	6,92E-59	73%	0%
SLFLPL04A08	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	8,55E-11	100%	0%
SLFLPL04A10	gi|460374988|ref|XP_004233290.1|	PREDICTED: uncharacterized protein LOC101246891 [Solanum lycopersicum]	124 bits(309)	3,12E-34	90%	0%
	gi|672158381|ref|XP_008798930.1|	PREDICTED: uncharacterized protein LOC103713698 [Phoenix dactylifera]	87 bits(215)	4,05E-20	66%	0%
	gi|224060267|ref|XP_002300114.1|	hypothetical protein POPTR_0001s33640g [Populus trichocarpa]	85 bits(208)	4,56E-19	66%	0%
	gi|629089569|gb|KCW55822.1|	hypothetical protein EUGRSUZ_I01639 [Eucalyptus grandis]	92 bits(227)	6,37E-22	74%	0%
	gi|356571543|ref|XP_003553936.1|	PREDICTED: uncharacterized protein LOC100794064 [Glycine max]	87 bits(214)	4,76E-20	60%	0%
	gi|565343153|ref|XP_006338704.1|	PREDICTED: uncharacterized protein LOC102579145 [Solanum tuberosum]	91 bits(224)	2,03E-21	72%	0%
	gi|460371900|ref|XP_004231772.1|	PREDICTED: uncharacterized protein LOC101266377 [Solanum lycopersicum]	87 bits(213)	7,55E-20	74%	0%
	gi|565398963|ref|XP_006365033.1|	PREDICTED: uncharacterized protein LOC102587365 [Solanum tuberosum]	124 bits(310)	1,96E-34	91%	0%
	gi|356561821|ref|XP_003549176.1|	PREDICTED: uncharacterized protein LOC100820286 [Glycine max]	88 bits(216)	2,97E-20	60%	0%
	gi|590647459|ref|XP_007031907.1|	Uncharacterized protein TCM_017236 [Theobroma cacao]	87 bits(214)	2,55E-19	68%	0%
SLFLPL04B03	gi|350537547|ref|NP_001234042.1|	photosystem II 10 kDa polypeptide, chloroplastic [Solanum lycopersicum]	238 bits(607)	3,33E-77	89%	4%
	gi|661882615|emb|CDP13618.1|	unnamed protein product [Coffea canephora]	226 bits(574)	4,37E-72	83%	4%
	gi|3914472|sp|Q40519.1|PSBR_TOBAC	RecName: Full=Photosystem II 10 kDa polypeptide, chloroplastic; Short=PII10; Flags: Precursor [Nicotiana tabacum]	246 bits(626)	5,32E-80	90%	0%
	gi|645239765|ref|XP_008226285.1|	PREDICTED: photosystem II 10 kDa polypeptide, chloroplastic [Prunus mume]	231 bits(588)	3,08E-74	82%	3%
	gi|595876424|ref|XP_007212214.1|	hypothetical protein PRUPE_ppa013107mg [Prunus persica]	225 bits(573)	6,39E-72	81%	3%
	gi|568214281|ref|NP_001275173.1|	photosystem II 10 kDa polypeptide, chloroplastic [Solanum tuberosum]	243 bits(620)	4,31E-79	91%	4%
	gi|1418984|emb|CAA99757.1|	photosystem II 10 kD polypeptide [Solanum lycopersicum]	230 bits(586)	4,38E-74	89%	1%
	gi|83776786|gb|ABC46708.1|	chloroplast photosystem II 10 kDa protein [Arachis hypogaea]	224 bits(569)	1,62E-71	84%	0%
	gi|21491|emb|CAA27989.1|	unnamed protein product [Solanum tuberosum]	240 bits(611)	1,05E-77	90%	4%
	gi|588295538|gb|AHK23268.1|	chloroplast photosystem II subunit R [Gossypium hirsutum]	228 bits(579)	6,50E-73	84%	5%
SLFLPL04B05	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	4,87E-11	100%	0%
SLFLPL04B07	No Hits.					
SLFLPL04C05	No Hits.					
SLFLPL04C06	gi|571031205|ref|YP_008992101.1|	ie1 [Choristoneura murinana alphabaculovirus]	79 bits(194)	4,34E-14	56%	8%
	gi|37651338|ref|NP_932749.1|	immediate early protein 1 [Choristoneura fumiferana DEF multiple nucleopolyhedrovirus]	285 bits(729)	3,83E-90	91%	8%
	gi|15320786|ref|NP_203298.1|	IE1 [Epiphyas postvittana nucleopolyhedrovirus]	127 bits(318)	4,21E-31	66%	9%
	gi|529153323|ref|YP_008378363.1|	IE-1 [Choristoneura rosaceana alphabaculovirus]	76 bits(186)	5,06E-13	49%	12%

	gi|16506803|gb|AAL23956.1|AF426175_1	viral transactivator IE1 [Hyphantria cunea nucleopolyhedrovirus]	80 bits(195)	3,42E-14	45%	7%
	gi|9630083|ref|NP_046301.1|	immediate early gene 1 [Orgyia pseudotsugata multiple nucleopolyhedrovirus]	73 bits(178)	6,37E-12	50%	12%
	gi|116326211|ref|YP_803537.1|	immediate early protein 1 [Anticarsia gemmatalis nucleopolyhedrovirus]	325 bits(831)	4,11E-105	100%	0%
	gi|86355530|ref|YP_473198.1|	IE1 [Hyphantria cunea nucleopolyhedrovirus]	80 bits(195)	3,52E-14	45%	7%
	gi|22535901|gb|AAN01112.1|AF368905_1	immediate early 1 protein [Anticarsia gemmatalis nucleopolyhedrovirus]	323 bits(826)	1,81E-104	99%	0%
	gi|30387372|ref|NP_848451.1|	immediate early gene 1 [Choristoneura fumiferana multiple nucleopolyhedrovirus]	70 bits(171)	4,15E-11	52%	7%
SLFLPL04C08	No Hits.					
SLFLPL04C10	gi|565392770|ref|XP_006362064.1|	PREDICTED: uncharacterized protein At2g23090-like [Solanum tuberosum]	151 bits(379)	1,14E-43	94%	0%
	gi|449448256|ref|XP_004141882.1|	PREDICTED: uncharacterized protein At2g23090-like [Cucumis sativus]	147 bits(370)	2,33E-42	91%	1%
	gi|460384812|ref|XP_004238102.1|	PREDICTED: uncharacterized protein At2g23090-like [Solanum lycopersicum]	154 bits(388)	4,63E-45	95%	0%
	gi|449448254|ref|XP_004141881.1|	PREDICTED: uncharacterized protein At2g23090-like [Cucumis sativus]	149 bits(374)	6,71E-43	92%	1%
	gi|643734971|gb|KDP41641.1|	hypothetical protein JCGZ_16048 [Jatropha curcas]	147 bits(370)	2,67E-42	87%	0%
	gi|659079627|ref|XP_008440357.1|	PREDICTED: uncharacterized protein At2g23090 [Cucumis melo]	151 bits(380)	6,98E-44	94%	1%
	gi|595798954|ref|XP_007201472.1|	hypothetical protein PRUPE_ppa014259mg [Prunus persica]	148 bits(372)	1,21E-42	90%	0%
	gi|194466179|gb|ACF74320.1|	unknown [Arachis hypogaea]	147 bits(370)	2,67E-42	89%	0%
	gi|586686652|ref|XP_006841988.1|	hypothetical protein AMTR_s00144p00063280 [Amborella trichopoda]	151 bits(379)	1,05E-43	92%	0%
	gi|225458800|ref|XP_002285206.1|	PREDICTED: uncharacterized protein At2g23090 [Vitis vinifera]	147 bits(370)	2,26E-42	91%	1%
	gi|565376142|ref|XP_006354571.1|	PREDICTED: glutathione transferase GST 23-like isoform X2 [Solanum tuberosum]	337 bits(862)	5,13E-114	87%	0%
	gi|225436164|ref|XP_002264054.1|	PREDICTED: glutathione transferase GST 23 [Vitis vinifera]	253 bits(646)	2,99E-81	64%	2%
SLFLPL04C12	gi|359495384|ref|XP_002265322.2|	PREDICTED: probable glutathione S-transferase-like [Vitis vinifera]	243 bits(620)	3,73E-77	63%	7%
	gi|565376148|ref|XP_006354574.1|	PREDICTED: glutathione transferase GST 23-like [Solanum tuberosum]	328 bits(840)	1,17E-110	84%	0%
	gi|147857860|emb|CAN78656.1|	hypothetical protein VITISV_006850 [Vitis vinifera]	249 bits(635)	1,46E-79	63%	2%
	gi|460367324|ref|XP_004229524.1|	PREDICTED: glutathione transferase GST 23-like [Solanum lycopersicum]	326 bits(835)	6,66E-110	84%	0%
	gi|604313653|gb|EYU26814.1|	hypothetical protein MIMGU_mgv1a013348mg [Erythranthe guttata]	247 bits(630)	6,92E-79	62%	2%
	gi|460367326|ref|XP_004229525.1|	PREDICTED: glutathione transferase GST 23-like [Solanum lycopersicum]	339 bits(868)	6,05E-115	87%	0%
	gi|565376140|ref|XP_006354570.1|	PREDICTED: glutathione transferase GST 23-like isoform X1 [Solanum tuberosum]	322 bits(823)	4,21E-108	84%	1%
	gi|225436273|ref|XP_002264117.1|	PREDICTED: probable glutathione S-transferase [Vitis vinifera]	243 bits(619)	3,68E-77	62%	3%
SLFLPL04D08	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	4,97E-11	100%	0%
SLFLPL04E10	gi|567903508|ref|XP_006444242.1|	hypothetical protein CICLE_v10023018mg [Citrus clementina]	92 bits(226)	4,19E-20	80%	0%
	gi|225436777|ref|XP_002268050.1|	PREDICTED: glutaredoxin-C13 [Vitis vinifera]	90 bits(222)	1,54E-19	79%	0%
	gi|502112444|ref|XP_004494333.1|	PREDICTED: monothiol glutaredoxin-S11-like [Cicer arietinum]	91 bits(224)	6,85E-20	79%	0%
	gi|378464973|gb|AFC01204.1|	glutaredoxin family protein [Ammopiptanthus mongolicus]	88 bits(216)	9,56E-19	76%	0%
	gi|568214312|ref|NP_001275008.1|	glutaredoxin [Solanum tuberosum]	109 bits(270)	1,57E-26	93%	0%
	gi|590718382|ref|XP_007050806.1|	Glutaredoxin [Theobroma cacao]	90 bits(222)	1,31E-19	81%	0%
	gi|566260248|ref|XP_006389677.1|	glutaredoxin family protein [Populus trichocarpa]	88 bits(216)	9,56E-19	77%	0%
	gi|460389771|ref|XP_004240522.1|	PREDICTED: glutaredoxin-C13-like [Solanum lycopersicum]	105 bits(260)	3,94E-25	89%	0%
	gi|661892381|emb|CDP03539.1|	unnamed protein product [Coffea canephora]	90 bits(222)	1,48E-19	82%	0%
	gi|255559312|ref|XP_002520676.1|	glutaredoxin, grx, putative [Ricinus communis]	87 bits(215)	1,45E-18	64%	2%
SLFLPL04E11	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	4,98E-11	100%	0%
SLFLPL04F11	gi|659111487|ref|XP_008455762.1|	PREDICTED: 50S ribosomal protein 5, chloroplastic [Cucumis melo]	114 bits(285)	1,04E-28	52%	6%
	gi|604330696|gb|EYU35679.1|	hypothetical protein MIMGU_mgv1a015792mg [Erythranthe guttata]	99 bits(246)	4,65E-23	64%	3%
	gi|357509165|ref|XP_003624871.1|	50S ribosomal protein [Medicago truncatula]	96 bits(238)	5,81E-22	42%	9%
	gi|565344275|ref|XP_006339242.1|	PREDICTED: 50S ribosomal protein 5, chloroplastic-like [Solanum tuberosum]	228 bits(581)	3,12E-73	87%	3%
	gi|565398401|ref|XP_006364763.1|	PREDICTED: 50S ribosomal protein 5 alpha, chloroplastic-like isoform X1 [Solanum tuberosum]	105 bits(261)	2,30E-25	61%	4%
	gi|657967706|ref|XP_008375544.1|	PREDICTED: 50S ribosomal protein 5, chloroplastic-like [Malus domestica]	94 bits(231)	3,48E-21	60%	4%
	gi|460407798|ref|XP_004249337.1|	PREDICTED: 50S ribosomal protein 5, chloroplastic-like [Solanum lycopersicum]	179 bits(452)	9,14E-54	83%	3%
	gi|565398403|ref|XP_006364764.1|	PREDICTED: 50S ribosomal protein 5 alpha, chloroplastic-like isoform X2 [Solanum tuberosum]	103 bits(255)	1,11E-24	65%	4%
	gi|449453131|ref|XP_004144312.1|	PREDICTED: 50S ribosomal protein 5, chloroplastic-like [Cucumis sativus]	116 bits(288)	4,10E-29	52%	6%
	gi|565398405|ref|XP_006364765.1|	PREDICTED: 50S ribosomal protein 5 alpha, chloroplastic-like isoform X3 [Solanum tuberosum]	101 bits(250)	5,15E-24	68%	4%
SLFLPL04G03	gi|460402331|ref|XP_004246666.1|	PREDICTED: fasciclin-like arabinogalactan protein 11-like [Solanum lycopersicum]	272 bits(694)	1,72E-88	83%	5%
	gi|47717925|gb|AAT37954.1|	fasciclin-like AGP 11 [Populus tremula x Populus alba]	176 bits(444)	6,53E-51	59%	4%
	gi|565343936|ref|XP_006339076.1|	PREDICTED: fasciclin-like arabinogalactan protein 12-like [Solanum tuberosum]	194 bits(491)	1,15E-57	81%	0%
	gi|147841991|emb|CAN60933.1|	hypothetical protein VITISV_022591 [Vitis vinifera]	173 bits(437)	4,06E-50	58%	0%
	gi|565392256|ref|XP_006361822.1|	PREDICTED: fasciclin-like arabinogalactan protein 12-like [Solanum tuberosum]	192 bits(487)	3,19E-57	81%	0%
	gi|460402333|ref|XP_004246667.1|	PREDICTED: fasciclin-like arabinogalactan protein 11-like [Solanum lycopersicum]	190 bits(480)	3,23E-56	79%	0%
	gi|567872429|ref|XP_006428804.1|	hypothetical protein CICLE_v10012588mg [Citrus clementina]	171 bits(432)	3,97E-49	56%	8%

	gi|565392236|ref|XP_006361812.1|	PREDICTED: fasciclin-like arabinogalactan protein 12-like [Solanum tuberosum]	273 bits(698)	3,49E-89	86%	5%
	gi|672131077|ref|XP_008789092.1|	PREDICTED: fasciclin-like arabinogalactan protein 12 [Phoenix dactylifera]	179 bits(454)	1,86E-52	58%	6%
	gi|460391320|ref|XP_004241271.1|	PREDICTED: fasciclin-like arabinogalactan protein 11-like [Solanum lycopersicum]	171 bits(432)	4,75E-49	52%	7%
SLFLPL04G06	No Hits.					
SLFLPL04G07	gi|227343507|gb|ACP27606.1|	methyltransferase [Dimocarpus longan]	78 bits(191)	6,35E-15	75%	3%
	gi|641838633|gb|KDO57573.1|	hypothetical protein CISIN_1g007128mg [Citrus sinensis]	77 bits(187)	2,08E-13	67%	3%
	gi|460404924|ref|XP_004247928.1|	PREDICTED: probable methyltransferase PMT8-like [Solanum lycopersicum]	104 bits(258)	1,42E-22	98%	0%
	gi|356501308|ref|XP_003519467.1|	PREDICTED: probable methyltransferase PMT3-like [Glycine max]	78 bits(190)	9,39E-14	67%	2%
	gi|571569382|ref|XP_006606384.1|	PREDICTED: probable methyltransferase PMT8-like isoform X1 [Glycine max]	77 bits(187)	2,34E-13	73%	1%
	gi|565375955|ref|XP_006354480.1|	PREDICTED: probable methyltransferase PMT3-like [Solanum tuberosum]	101 bits(250)	8,49E-22	98%	0%
	gi|567854263|ref|XP_006420251.1|	hypothetical protein CICLE_v10004560mg [Citrus clementina]	77 bits(188)	1,64E-13	67%	3%
	gi|596127153|ref|XP_007222001.1|	hypothetical protein PRUPE_ppa002881mg [Prunus persica]	76 bits(186)	2,88E-13	69%	2%
	gi|661897532|emb|CDO99244.1|	unnamed protein product [Coffea canephora]	82 bits(200)	3,78E-15	76%	2%
	gi|568873155|ref|XP_006489716.1|	PREDICTED: probable methyltransferase PMT8-like [Citrus sinensis]	77 bits(188)	1,82E-13	67%	3%
SLFLPL04G08	gi|302141992|emb|CBI19195.3|	unnamed protein product [Vitis vinifera]	193 bits(489)	1,48E-58	90%	1%
	gi|568837106|ref|XP_006472571.1|	PREDICTED: 14-3-3-like protein-like [Citrus sinensis]	195 bits(495)	4,56E-58	96%	1%
	gi|15778152|dbj|BAB68526.1|	14-3-3 protein [Nicotiana tabacum]	202 bits(512)	9,73E-61	99%	0%
	gi|3912948|sp|O49995.1|1433B_TOBAC	RecName: Full=14-3-3-like protein B	201 bits(511)	1,11E-60	99%	0%
	gi|255545792|ref|XP_002513956.1|	14-3-3 protein, putative [Ricinus communis]	195 bits(494)	3,87E-58	89%	2%
	gi|460414338|ref|XP_004252529.1|	PREDICTED: 14-3-3 protein 2-like [Solanum lycopersicum]	200 bits(506)	6,66E-60	98%	0%
	gi|643734743|gb|KDP41413.1|	hypothetical protein JCGZ_15820 [Jatropha curcas]	195 bits(495)	3,91E-58	90%	1%
	gi|42491254|dbj|BAD10939.1|	14-3-3 protein [Nicotiana tabacum]	196 bits(498)	1,31E-58	93%	1%
	gi|661895293|emb|CDP01098.1|	unnamed protein product [Coffea canephora]	191 bits(483)	4,36E-58	89%	1%
	gi|568214539|ref|NP_001275217.1|	14-3-3 protein 2-like [Solanum tuberosum]	203 bits(515)	3,04E-61	99%	0%
SLFLPL04H05	gi|118485365|gb|ABK94540.1|	unknown [Populus trichocarpa]	115 bits(287)	9,32E-30	73%	0%
	gi|242093376|ref|XP_002437178.1|	hypothetical protein SORBIDRAFT_10g022410 [Sorghum bicolor]	111 bits(276)	3,23E-28	72%	0%
	gi|460412564|ref|XP_004251668.1|	PREDICTED: transmembrane protein 258-like [Solanum lycopersicum]	149 bits(375)	7,13E-43	96%	0%
	gi|115468596|ref|NP_001057897.1|	Os06g0567000 [Oryza sativa Japonica Group]	114 bits(283)	3,97E-29	74%	0%
	gi|357124075|ref|XP_003563732.1|	PREDICTED: UPF0197 transmembrane protein Y57E12AM.1-like [Brachypodium distachyon]	109 bits(271)	2,19E-27	70%	0%
	gi|565373956|ref|XP_006353532.1|	PREDICTED: transmembrane protein 258-like [Solanum tuberosum]	148 bits(373)	1,24E-42	96%	0%
	gi|326528217|dbj|BAJ93290.1|	predicted protein [Hordeum vulgare subsp. vulgare]	113 bits(282)	4,86E-29	71%	0%
	gi|514766698|ref|XP_004966060.1|	PREDICTED: transmembrane protein 258 homolog [Setaria italica]	108 bits(268)	5,16E-27	68%	0%
	gi|593783235|ref|XP_007154658.1|	hypothetical protein PHAVU_003G136800g [Phaseolus vulgaris]	120 bits(300)	1,13E-31	81%	0%
	gi|473907595|gb|EMS49445.1|	hypothetical protein TRIUR3_24651 [Triticum urartu]	112 bits(279)	1,26E-28	70%	0%
SLFLPL04G11	gi|565381833|ref|XP_006357265.1|	PREDICTED: alpha-amylase 3, chloroplastic-like [Solanum tuberosum]	101 bits(251)	3,16E-21	78%	0%
	gi|356526892|ref|XP_003532050.1|	PREDICTED: alpha-amylase 3, chloroplastic-like [Glycine max]	93 bits(230)	2,35E-18	69%	0%
	gi|60652321|gb|AAX33233.1|	plastid alpha-amylase [Actinidia chinensis]	91 bits(225)	7,73E-18	69%	0%
	gi|645229859|ref|XP_008221657.1|	PREDICTED: alpha-amylase 3, chloroplastic [Prunus mume]	96 bits(237)	2,37E-19	72%	0%
	gi|587874684|gb|EXB63819.1|	Alpha-amylase isozyme 3A [Morus notabilis]	93 bits(229)	3,07E-18	71%	0%
	gi|380504960|gb|AFD62767.1|	putative alpha-amylase, partial [Citrus sinensis]	87 bits(215)	6,20E-19	62%	0%
	gi|596126220|ref|XP_007221942.1|	hypothetical protein PRUPE_ppa001575mg [Prunus persica]	92 bits(227)	4,53E-18	69%	0%
	gi|460386165|ref|XP_004238770.1|	PREDICTED: alpha-amylase 3, chloroplastic-like [Solanum lycopersicum]	103 bits(255)	8,92E-22	78%	0%
	gi|11139274|gb|AAG31655.1|	PRLI-interacting factor E [Arabidopsis thaliana]	87 bits(214)	2,35E-18	64%	0%
	gi|398363555|gb|AFO84072.1|	alpha-amylase [Actinidia chinensis]	92 bits(226)	7,10E-18	69%	0%

Apêndice E – Resultado da busca *in silico* da funcionalidade hipotética em Contigs, da biblioteca de calos de *Solanum lycocarpum*
Fonte de dados: Blastx/NCBI
Elaborada pelo autor

Name Sequence	**Sequence**	**Name**	**score**	**expert**	**indentities**	**gaps**
Contig0	gi|1545805|dbj|BAA10929.1|	cytochrome P450 like_TBP [Nicotiana tabacum]	209 bits(531)	1,52E-59	74%	10%
	gi|195610700|gb|ACG27180.1|	hypothetical protein [Zea mays]	169 bits(426)	7,20E-49	88%	0%
	gi|357488215|ref|XP_003614395.1|	hypothetical protein MTR_5g051140 [Medicago truncatula]	162 bits(409)	8,80E-41	73%	27%
	gi|253760055|ref|XP_002488965.1|	hypothetical protein SORBIDRAFT_1138s002030 [Sorghum bicolor]	178 bits(450)	2,15E-52	91%	0%
	gi|242070907|ref|XP_002450730.1|	hypothetical protein SORBIDRAFT_05g016465 [Sorghum bicolor]	151 bits(381)	4,95E-42	81%	0%
	gi|357488191|ref|XP_003614383.1|	hypothetical protein MTR_5g051000 [Medicago truncatula]	163 bits(410)	9,19E-41	73%	27%
	gi|7489812|pir||T02955	probable cytochrome P450 monooxygenase - maize (fragment)	182 bits(460)	1,20E-51	76%	7%
	gi|357488197|ref|XP_003614386.1|	hypothetical protein MTR_5g051030 [Medicago truncatula]	162 bits(408)	2,75E-41	73%	27%
	gi|303291416|ref|XP_003064993.1|	predicted protein, partial [Micromonas pusilla CCMP1545]	172 bits(434)	2,88E-49	93%	0%
	gi|358348842|ref|XP_003638451.1|	hypothetical protein MTR_132s0010, partial [Medicago truncatula]	163 bits(410)	6,87E-41	73%	27%
Contig1	gi|565393152|ref|XP_006362246.1|	PREDICTED: 40S ribosomal protein S28-like [Solanum tuberosum]	125 bits(312)	1,47E-32	94%	0%
	gi|657998039|ref|XP_008391409.1|	PREDICTED: 40S ribosomal protein S28 [Malus domestica]	122 bits(304)	2,68E-31	92%	0%
	gi|595808439|ref|XP_007202760.1|	hypothetical protein PRUPE_ppa013411mg [Prunus persica]	126 bits(315)	3,44E-32	78%	2%
	gi|587916105|gb|EXC03823.1|	40S ribosomal protein S28 [Morus notabilis]	124 bits(311)	2,74E-31	91%	0%
	gi|460371422|ref|XP_004231536.1|	PREDICTED: 40S ribosomal protein S28-like isoform 1 [Solanum lycopersicum]	131 bits(327)	1,46E-34	91%	0%
	gi|40287500|gb|AAR83864.1|	28 kDa small subunit ribosomal protein [Capsicum annuum]	122 bits(305)	1,76E-31	92%	0%
	gi|661891636|emb|CDP04901.1|	unnamed protein product [Coffea canephora]	122 bits(306)	4,51E-31	91%	0%
	gi|460371424|ref|XP_004231537.1|	PREDICTED: 40S ribosomal protein S28-like isoform 2 [Solanum lycopersicum]	126 bits(314)	7,60E-33	95%	0%
	gi|587864162|gb|EXB53855.1|	40S ribosomal protein S28 [Morus notabilis]	122 bits(306)	2,41E-31	91%	0%
	gi|587951197|gb|EXC37044.1|	40S ribosomal protein S28 [Morus notabilis]	120 bits(300)	9,61E-31	91%	0%
Contig2	gi|27475620|emb|CAD59767.1|	putative reverse transcriptase [Cicer arietinum]	68 bits(164)	2,70E-11	94%	0%
	gi|152963813|gb|ABS50234.1|	Ran binding protein [Nicotiana benthamiana]	80 bits(197)	2,08E-14	77%	1%
	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	80 bits(195)	1,54E-13	97%	0%
	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	76 bits(186)	2,58E-14	100%	0%
	gi|27475622|emb|CAD59768.1|	putative reverse transcriptase [Cicer arietinum]	74 bits(180)	1,76E-13	100%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	76 bits(186)	2,67E-14	100%	0%
	gi|330752561|emb|CBL87507.1|	hypothetical protein S18_873_0002 [uncultured Flavobacteriia bacterium]	69 bits(168)	2,52E-11	100%	0%
	gi|330752400|emb|CBL87351.1|	hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]	77 bits(187)	5,32E-14	97%	0%
	gi|565354316|ref|XP_006344059.1|	PREDICTED: ran-binding protein 1 homolog a-like [Solanum tuberosum]	72 bits(174)	2,63E-11	75%	5%
Contig3	gi|357488191|ref|XP_003614383.1|	hypothetical protein MTR_5g051000 [Medicago truncatula]	225 bits(572)	5,02E-60	76%	27%
	gi|657370996|gb|KEH17027.1|	senescence-associated protein [Medicago truncatula]	211 bits(537)	5,46E-58	83%	3%
	gi|303291416|ref|XP_003064993.1|	predicted protein, partial [Micromonas pusilla CCMP1545]	260 bits(664)	2,32E-81	95%	0%
	gi|357488193|ref|XP_003614384.1|	hypothetical protein MTR_5g051010 [Medicago truncatula]	221 bits(561)	3,96E-59	75%	27%
	gi|357488189|ref|XP_003614382.1|	hypothetical protein MTR_5g050970 [Medicago truncatula]	215 bits(547)	1,70E-57	74%	27%
	gi|357488197|ref|XP_003614386.1|	hypothetical protein MTR_5g051030 [Medicago truncatula]	223 bits(568)	6,75E-61	76%	27%
	gi|657370959|gb|KEH16993.1|	senescence-associated protein [Medicago truncatula]	214 bits(544)	8,64E-59	84%	3%
	gi|657370960|gb|KEH16994.1|	senescence-associated protein [Medicago truncatula]	214 bits(544)	1,97E-57	84%	3%
	gi|357488215|ref|XP_003614395.1|	hypothetical protein MTR_5g051140 [Medicago truncatula]	224 bits(569)	3,76E-60	76%	27%
	gi|657370989|gb|KEH17020.1|	senescence-associated protein [Medicago truncatula]	213 bits(542)	3,50E-58	84%	3%
Contig4	gi|460407862|ref|XP_004249368.1|	PREDICTED: NADH--cytochrome b5 reductase 1-like [Solanum lycopersicum]	178 bits(450)	7,30E-51	87%	0%
	gi|661878630|emb|CDP17645.1|	unnamed protein product [Coffea canephora]	167 bits(422)	1,22E-46	82%	0%
	gi|674894358|emb|CDY38457.1|	BnaA10g17010D [Brassica napus]	170 bits(430)	7,14E-48	82%	0%
	gi|356571798|ref|XP_003554059.1|	PREDICTED: NADH--cytochrome b5 reductase 1 [Glycine max]	167 bits(421)	1,65E-46	81%	0%
	gi|645270645|ref|XP_008240549.1|	PREDICTED: NADH--cytochrome b5 reductase 1 [Prunus mume]	166 bits(420)	2,65E-46	80%	0%
	gi|685376186|ref|XP_009121057.1|	PREDICTED: NADH--cytochrome b5 reductase 1 [Brassica rapa]	170 bits(430)	7,69E-48	83%	0%
	gi|502107376|ref|XP_004493245.1|	PREDICTED: NADH--cytochrome b5 reductase 1-like [Cicer arietinum]	166 bits(420)	2,08E-46	79%	0%
	gi|565344200|ref|XP_006339205.1|	PREDICTED: NADH--cytochrome b5 reductase 1-like isoform X1 [Solanum tuberosum]	181 bits(459)	3,62E-52	89%	0%
	gi|674916208|emb|CDY16891.1|	BnaC09g40180D [Brassica napus]	178 bits(450)	1,00E-47	88%	0%
	gi|674233237|gb|KFK26002.1|	hypothetical protein AALP_AA8G190100 [Arabis alpina]	166 bits(420)	2,56E-46	80%	0%
Contig5	gi|60459403|gb|AAX20047.1|	metallothionein-like protein type 2 [Capsicum annuum]	84 bits(206)	1,69E-17	83%	0%
	gi|193085066|gb|ACF10398.1|	type 2 metallothionein [Solanum nigrum]	81 bits(198)	2,36E-16	81%	0%

	gi|565390980|ref|XP_006361209.1|	PREDICTED: metallothionein-like protein type 2-like [Solanum tuberosum]	88 bits(217)	5,20E-19	76%	0%
	gi|350537709|ref|NP_001234050.1|	metallothionein-like protein type 2 [Solanum lycopersicum]	87 bits(213)	2,43E-18	74%	0%
	gi|565368268|ref|XP_006350769.1|	PREDICTED: metallothionein-like protein [Solanum tuberosum]	83 bits(203)	4,80E-17	87%	3%
	gi|58578264|emb|CAI48068.1|	metallotionein-like protein [Capsicum chinense]	85 bits(209)	6,54E-18	84%	0%
	gi|151301842|gb|ABR92329.1|	putative metallothionin 2a [Salvia miltiorrhiza]	82 bits(200)	1,25E-16	60%	6%
	gi|661895087|emb|CDP00892.1|	unnamed protein product [Coffea canephora]	85 bits(208)	8,90E-18	62%	2%
	gi|565390974|ref|XP_006361207.1|	PREDICTED: metallothionein-like protein type 2-like [Solanum tuberosum]	81 bits(198)	2,17E-16	75%	0%
	gi|193085064|gb|ACF10397.1|	type 2 metallothionein [Solanum nigrum]	88 bits(217)	4,57E-19	83%	0%
Contig6	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	92 bits(228)	1,90E-18	98%	0%
	gi|586616619|gb|AHJ78613.1|	4-coumarate:coenzyme A ligase [Solanum tuberosum]	87 bits(214)	6,31E-16	91%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	103 bits(255)	2,48E-24	100%	0%
	gi|9652070|gb|AAF91388.1|AF263243_1	SocE [Myxococcus xanthus]	90 bits(222)	4,90E-17	54%	0%
	gi|398965|sp|P31685.1|4CL2_SOLTU	RecName: Full=4-coumarate--CoA ligase 2; Short=4CL 2; AltName: Full=4-coumaroyl-CoA synthase 2 [Solanum tuberosum]	87 bits(214)	6,36E-16	91%	0%
	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	92 bits(226)	3,16E-20	100%	0%
	gi|460380249|ref|XP_004235870.1|	PREDICTED: 4-coumarate--CoA ligase 1-like [Solanum lycopersicum]	87 bits(214)	5,81E-16	91%	0%
	gi|586616617|gb|AHJ78612.1|	4-coumarate:coenzyme A ligase [Solanum tuberosum]	87 bits(214)	6,48E-16	91%	0%
	gi|487912019|ref|WP_001985485.1|	SocE [Bacillus cereus]	91 bits(225)	7,01E-20	100%	0%
	gi|5163399|gb|AAD40664.1|AF150686_1	4-coumarate:coenzyme A ligase [Solanum tuberosum]	87 bits(214)	6,31E-16	91%	0%
Contig7	gi|565396035|ref|XP_006363639.1|	PREDICTED: uncharacterized protein LOC102603354 [Solanum tuberosum]	104 bits(259)	5,17E-85	98%	0%
	gi|357488199|ref|XP_003614387.1|	RRNA intron-encoded homing endonuclease [Medicago truncatula]	25 bits(54)	5,82E-17	82%	0%
	gi|357488225|ref|XP_003614400.1|	Cytochrome P450 likeTBP [Medicago truncatula]	47 bits(111)	9,72E-61	74%	0%
	gi|657370961|gb|KEH16995.1|	hypothetical protein MTR_0055s0130 [Medicago truncatula]	93 bits(230)	9,08E-77	87%	0%
	gi|502153899|ref|XP_004509500.1|	PREDICTED: uncharacterized protein LOC101508810 [Cicer arietinum]	92 bits(228)	2,62E-75	87%	0%
	gi|357488195|ref|XP_003614385.1|	RRNA intron-encoded homing endonuclease [Medicago truncatula]	93 bits(229)	1,27E-76	87%	0%
	gi|694380941|ref|XP_009366572.1|	PREDICTED: uncharacterized protein LOC103956333 [Pyrus x bretschneideri]	114 bits(283)	5,65E-24	33%	70%
	gi|587923547|gb|EXC10888.1|	hypothetical protein L484_002552 [Morus notabilis]	268 bits(685)	2,85E-85	78%	34%
	gi|357488203|ref|XP_003614389.1|	RRNA intron-encoded homing endonuclease [Medicago truncatula]	92 bits(228)	2,23E-76	87%	0%
	gi|357488185|ref|XP_003614380.1|	Cytochrome P450 likeTBP [Medicago truncatula]	56 bits(133)	5,67E-61	84%	0%
Contig8	gi|27475622|emb|CAD59768.1|	putative reverse transcriptase [Cicer arietinum]	74 bits(179)	4,72E-14	100%	0%
	gi|565401584|ref|XP_006366277.1|	PREDICTED: 4-coumarate--CoA ligase 2-like [Solanum tuberosum]	78 bits(191)	2,88E-13	92%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	35 bits(80)	1,26E-15	94%	0%
	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	78 bits(190)	1,26E-13	97%	0%
	gi|82581146|emb|CAJ43714.1|	4-coumaryl-CoA ligase [Plantago major]	73 bits(178)	4,38E-13	85%	0%
	gi|330752400|emb|CBL87351.1|	hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]	77 bits(187)	1,50E-14	97%	0%
	gi|1237183|dbj|BAA07828.1|	4-coumarate:coenzyme A ligase [Nicotiana tabacum]	79 bits(193)	1,43E-13	92%	0%
	gi|270211024|gb|ACZ64784.1|	4-coumarate:CoA ligase [Galega orientalis]	76 bits(185)	1,32E-12	82%	0%
	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	75 bits(182)	2,98E-14	97%	0%
	gi|12229632|sp|O24146.1|4CL2_TOBAC	RecName: Full=4-coumarate--CoA ligase 2; Short=4CL 2; AltName: Full=4-coumaroyl-CoA synthase 2 [Nicotiana tabacum]	78 bits(191)	2,46E-13	90%	0%
Contig9	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	36 bits(81)	7,32E-11	93%	0%
Contig10	gi|13359451|dbj|BAB33421.1|	putative senescence-associated protein [Pisum sativum]	89 bits(219)	3,12E-18	88%	0%
	gi|357488193|ref|XP_003614384.1|	hypothetical protein MTR_5g051010 [Medicago truncatula]	78 bits(191)	1,53E-13	41%	21%
	gi|657370954|gb|KEH16988.1|	senescence-associated protein, putative [Medicago truncatula]	76 bits(186)	6,07E-13	41%	21%
	gi|449506608|ref|XP_004162796.1|	PREDICTED: uncharacterized protein LOC101232191 [Cucumis sativus]	82 bits(202)	6,14E-16	48%	4%
	gi|358348842|ref|XP_003638451.1|	hypothetical protein MTR_132s0010, partial [Medicago truncatula]	78 bits(190)	2,70E-13	41%	21%
	gi|357488211|ref|XP_003614393.1|	hypothetical protein MTR_5g051120 [Medicago truncatula]	74 bits(179)	1,93E-12	47%	21%
	gi|357488189|ref|XP_003614382.1|	hypothetical protein MTR_5g050970 [Medicago truncatula]	81 bits(199)	1,45E-14	41%	21%
	gi|357488209|ref|XP_003614392.1|	hypothetical protein MTR_5g051110 [Medicago truncatula]	73 bits(178)	3,20E-12	40%	21%
	gi|357488195|ref|XP_003614385.1|	RRNA intron-encoded homing endonuclease [Medicago truncatula]	81 bits(198)	2,50E-14	95%	0%
Contig11	gi|77416933|gb|ABA81862.1|	unknown [Solanum tuberosum]	283 bits(723)	6,24E-93	91%	0%
	gi|565369464|ref|XP_006351355.1|	PREDICTED: 60S ribosomal protein L21-2-like [Solanum tuberosum]	275 bits(701)	1,33E-89	88%	0%
	gi|661886250|emb|CDP10172.1|	unnamed protein product [Coffea canephora]	257 bits(655)	1,18E-82	81%	0%
	gi|76161012|gb|ABA40469.1|	60S ribosomal protein L21-like protein [Solanum tuberosum]	283 bits(722)	1,02E-92	91%	0%
	gi|567874673|ref|XP_006429926.1|	hypothetical protein CICLE_v10012788mg [Citrus clementina]	260 bits(662)	4,83E-83	76%	0%
	gi|565393071|ref|XP_006362207.1|	PREDICTED: 60S ribosomal protein L21-2-like [Solanum tuberosum]	282 bits(721)	1,43E-92	91%	0%
	gi|388521615|gb|AFK48869.1|	unknown [Medicago truncatula]	258 bits(657)	7,29E-83	83%	0%
	gi|460407492|ref|XP_004249186.1|	PREDICTED: 60S ribosomal protein L21-2-like [Solanum lycopersicum]	286 bits(730)	6,44E-94	92%	0%

	gi|460407711|ref|XP_004249294.1|	PREDICTED: 60S ribosomal protein L21-2-like [Solanum lycopersicum]	278 bits(709)	8,39E-91	89%	0%
	gi|255580702|ref|XP_002531173.1|	60S ribosomal protein L21, putative [Ricinus communis]	257 bits(656)	1,02E-82	83%	0%
Contig12	gi|571207123|emb|CDK78388.1|	Transcriptional repressor of the lac operon [Klebsiella pneumoniae IS22]	79 bits(194)	6,51E-15	88%	0%
	gi|27475620|emb|CAD59767.1|	putative reverse transcriptase [Cicer arietinum]	69 bits(166)	5,61E-12	94%	0%
	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	90 bits(221)	1,80E-19	98%	0%
	gi|330752400|emb|CBL87351.1|	hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]	78 bits(190)	9,54E-15	97%	0%
	gi|386242568|gb|EII84303.1|	LacI transcriptional repressor [Escherichia coli 3003]	74 bits(179)	8,98E-12	81%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	89 bits(220)	2,17E-19	98%	0%
	gi|27475622|emb|CAD59768.1|	putative reverse transcriptase [Cicer arietinum]	74 bits(181)	3,91E-14	100%	0%
	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	92 bits(228)	2,00E-18	95%	0%
	gi|330752561|emb|CBL87507.1|	hypothetical protein S18_873_0002 [uncultured Flavobacteriia bacterium]	70 bits(171)	3,81E-12	100%	0%
Contig13	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	92 bits(228)	2,00E-18	95%	0%
	gi|330752561|emb|CBL87507.1|	hypothetical protein S18_873_0002 [uncultured Flavobacteriia bacterium]	70 bits(171)	3,81E-12	100%	0%
	gi|571207123|emb|CDK78388.1|	Transcriptional repressor of the lac operon [Klebsiella pneumoniae IS22]	79 bits(194)	6,51E-15	88%	0%
	gi|27475620|emb|CAD59767.1|	putative reverse transcriptase [Cicer arietinum]	69 bits(166)	5,61E-12	94%	0%
	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	90 bits(221)	1,80E-19	98%	0%
	gi|330752400|emb|CBL87351.1|	hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]	78 bits(190)	9,54E-15	97%	0%
	gi|386242568|gb|EII84303.1|	LacI transcriptional repressor [Escherichia coli 3003]	74 bits(179)	8,98E-12	81%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	89 bits(220)	2,17E-19	98%	0%
	gi|27475622|emb|CAD59768.1|	putative reverse transcriptase [Cicer arietinum]	74 bits(181)	3,91E-14	100%	0%
Contig14	No Hits.					
Contig15	gi|6009909|dbj|BAA85117.1|	histone H2A-like protein [Solanum melongena]	145 bits(365)	4,77E-39	100%	0%
	gi|672114329|ref|XP_008776490.1|	PREDICTED: histone H2A [Phoenix dactylifera]	134 bits(335)	1,65E-34	95%	1%
	gi|629124485|gb|KCW88910.1|	hypothetical protein EUGRSUZ_A01241 [Eucalyptus grandis]	132 bits(332)	4,54E-34	93%	1%
	gi|460411856|ref|XP_004251320.1|	PREDICTED: histone H2A-like [Solanum lycopersicum]	143 bits(360)	3,76E-38	97%	0%
	gi|604315708|gb|EYU28273.1|	hypothetical protein MIMGU_mgv1a015602mg [Erythranthe guttata]	133 bits(334)	3,01E-34	88%	4%
	gi|587948817|gb|EXC35050.1|	putative histone H2A.4 [Morus notabilis]	132 bits(332)	4,54E-34	93%	1%
	gi|358248452|ref|NP_001239884.1|	uncharacterized protein LOC100784431 [Glycine max]	136 bits(340)	3,17E-35	93%	0%
	gi|359478989|ref|XP_003632202.1|	PREDICTED: probable histone H2A.4 isoform 2 [Vitis vinifera]	134 bits(335)	3,02E-34	92%	1%
	gi|330318556|gb|AEC10950.1|	histone H2A [Camellia sinensis]	135 bits(339)	4,29E-35	93%	2%
	gi|629083196|gb|KCW49641.1|	hypothetical protein EUGRSUZ_K03160 [Eucalyptus grandis]	133 bits(333)	3,31E-34	93%	1%
Contig16	gi|27475620|emb|CAD59767.1|	putative reverse transcriptase [Cicer arietinum]	68 bits(164)	1,01E-11	94%	0%
	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	92 bits(228)	2,11E-18	98%	0%
	gi|330752400|emb|CBL87351.1|	hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]	76 bits(185)	5,08E-14	100%	0%
	gi|386242568|gb|EII84303.1|	LacI transcriptional repressor [Escherichia coli 3003]	77 bits(187)	9,11E-13	88%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	103 bits(255)	2,78E-24	100%	0%
	gi|27475622|emb|CAD59768.1|	putative reverse transcriptase [Cicer arietinum]	74 bits(180)	6,70E-14	100%	0%
	gi|330752561|emb|CBL87507.1|	hypothetical protein S18_873_0002 [uncultured Flavobacteriia bacterium]	69 bits(168)	1,01E-11	100%	0%
	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	92 bits(226)	3,42E-20	100%	0%
	gi|571207123|emb|CDK78388.1|	Transcriptional repressor of the lac operon [Klebsiella pneumoniae IS22]	75 bits(184)	1,55E-13	88%	3%
Contig17	gi|460408248|ref|XP_004249558.1|	PREDICTED: phenylalanine ammonia-lyase-like [Solanum lycopersicum]	29 bits(64)	6,20E-17	100%	0%
	gi|330752400|emb|CBL87351.1|	hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]	78 bits(191)	6,64E-15	97%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	99 bits(245)	6,56E-23	100%	0%
	gi|110559308|gb|ABG75910.1|	phenylalanine ammonia-lyase 1 [Nicotiana attenuata]	26 bits(56)	2,54E-16	85%	0%
	gi|460377708|ref|XP_004234632.1|	PREDICTED: phenylalanine ammonia-lyase-like [Solanum lycopersicum]	28 bits(61)	7,91E-15	92%	0%
	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	93 bits(230)	1,11E-20	100%	0%
	gi|1171997|sp|P45733.1|PAL3_TOBAC	RecName: Full=Phenylalanine ammonia-lyase [Nicotiana tabacum]	26 bits(56)	2,78E-16	85%	0%
	gi|129594|sp|P25872.1|PAL1_TOBAC	RecName: Full=Phenylalanine ammonia-lyase [Nicotiana tabacum]	83 bits(204)	1,44E-14	70%	1%
	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	94 bits(233)	5,02E-19	98%	0%
	gi|3123241|sp|P35513.2|PAL2_TOBAC	RecName: Full=Phenylalanine ammonia-lyase [Nicotiana tabacum]	87 bits(213)	1,22E-15	90%	0%
Contig18	gi|357488213|ref|XP_003614394.1|	hypothetical protein MTR_5g051130 [Medicago truncatula]	87 bits(213)	1,80E-44	90%	0%
	gi|657370961|gb|KEH16995.1|	hypothetical protein MTR_0055s0130 [Medicago truncatula]	51 bits(121)	2,55E-48	69%	1%
	gi|359496372|ref|XP_003635221.1|	PREDICTED: uncharacterized protein LOC100854821 [Vitis vinifera]	168 bits(424)	9,79E-48	94%	0%
	gi|565396035|ref|XP_006363639.1|	PREDICTED: uncharacterized protein LOC102603354 [Solanum tuberosum]	84 bits(206)	3,65E-15	43%	37%
	gi|686983426|gb|AIQ78384.1|	rRNA intron-encoded homing endonuclease, partial [Cenchrus americanus]	168 bits(425)	2,83E-48	97%	0%
	gi|357488191|ref|XP_003614383.1|	hypothetical protein MTR_5g051000 [Medicago truncatula]	94 bits(231)	1,58E-17	78%	2%

	gi|357488203|ref|XP_003614389.1|	RRNA intron-encoded homing endonuclease [Medicago truncatula]	50 bits(119)	2,91E-48	77%	0%
	gi|587923547|gb|EXC10888.1|	hypothetical protein L484_002552 [Morus notabilis]	213 bits(540)	3,94E-64	75%	34%
	gi|357488207|ref|XP_003614391.1|	Tar1p [Medicago truncatula]	57 bits(136)	7,64E-50	100%	0%
	gi|502153899|ref|XP_004509500.1|	PREDICTED: uncharacterized protein LOC101508810 [Cicer arietinum]	50 bits(118)	3,57E-48	77%	0%
Contig19	No Hits.					
Contig20	No Hits.					
Contig21	No Hits.					
Contig22	gi|357488199|ref|XP_003614387.1|	RRNA intron-encoded homing endonuclease [Medicago truncatula]	97 bits(239)	4,87E-19	64%	19%
	gi|545700705|ref|XP_005702705.1|	hypothetical protein Gasu_61700 [Galdieria sulphuraria]	82 bits(202)	1,36E-16	67%	1%
	gi|502174732|ref|XP_004515588.1|	PREDICTED: uncharacterized protein LOC101511867 [Cicer arietinum]	75 bits(182)	1,62E-13	88%	0%
	gi|357488207|ref|XP_003614391.1|	Tar1p [Medicago truncatula]	94 bits(233)	1,17E-18	64%	19%
	gi|545699775|ref|XP_005702341.1|	hypothetical protein Gasu_65200 [Galdieria sulphuraria]	82 bits(201)	2,09E-16	67%	1%
	gi|574143403|dbj|BAO41194.1|	hypothetical protein KLMA_50540 [Kluyveromyces marxianus DMKU3-1042]	74 bits(180)	1,89E-13	62%	1%
	gi|357488213|ref|XP_003614394.1|	hypothetical protein MTR_5g051130 [Medicago truncatula]	95 bits(235)	1,66E-18	64%	19%
	gi|545700148|ref|XP_005702479.1|	hypothetical protein Gasu_nc0100 [Galdieria sulphuraria]	82 bits(202)	2,71E-16	67%	1%
	gi|357488191|ref|XP_003614383.1|	hypothetical protein MTR_5g051000 [Medicago truncatula]	94 bits(232)	3,78E-18	64%	19%
	gi|545712678|ref|XP_005708643.1|	hypothetical protein Gasu_05410 [Galdieria sulphuraria]	81 bits(198)	1,27E-15	65%	1%
Contig23	gi|270064310|gb|ACZ60133.1|	abscisic stress ripening [Musa balbisiana]	87 bits(213)	1,66E-17	78%	0%
	gi|269852824|gb|ACZ50739.1|	abscisic stress ripening [Musa acuminata AAA Group]	86 bits(210)	3,73E-17	78%	1%
	gi|270064287|gb|ACZ60122.1|	abscisic stress ripening [Musa ABB Group]	87 bits(213)	1,72E-17	78%	0%
	gi|269852844|gb|ACZ50749.1|	abscisic stress ripening [Musa ABB Group]	86 bits(210)	4,59E-17	78%	1%
	gi|321156020|emb|CBY05747.1|	ASR2 protein [Solanum chilense]	96 bits(236)	3,98E-21	96%	0%
	gi|270064283|gb|ACZ60120.1|	abscisic stress ripening [Musa itinerans var. itinerans]	87 bits(213)	1,72E-17	78%	0%
	gi|269852834|gb|ACZ50744.1|	abscisic stress ripening [Musa balbisiana]	86 bits(210)	4,68E-17	78%	1%
	gi|269852848|gb|ACZ50751.1|	abscisic stress ripening [Musa acuminata AAA Group]	87 bits(215)	7,54E-18	80%	1%
	gi|270064289|gb|ACZ60123.1|	abscisic stress ripening [Musa ABB Group]	86 bits(211)	2,46E-17	76%	0%
	gi|270064308|gb|ACZ60132.1|	abscisic stress ripening [Musa AAB Group]	85 bits(209)	5,00E-17	76%	0%
Contig24	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	103 bits(255)	3,98E-24	100%	0%
	gi|502150863|ref|XP_004508161.1|	PREDICTED: 60S ribosomal protein L29-1-like isoform X1 [Cicer arietinum]	92 bits(227)	4,44E-20	88%	0%
	gi|590661718|ref|XP_007035751.1|	Ribosomal L29e protein family [Theobroma cacao]	91 bits(223)	1,52E-19	85%	0%
	gi|460388442|ref|XP_004239876.1|	PREDICTED: 60S ribosomal protein L29-2-like [Solanum lycopersicum]	94 bits(233)	6,32E-21	92%	0%
	gi|356521797|ref|XP_003529537.1|	PREDICTED: 60S ribosomal protein L29-1-like [Glycine max]	92 bits(227)	4,57E-20	88%	0%
	gi|502127329|ref|XP_004499658.1|	PREDICTED: 60S ribosomal protein L29-1-like isoform X1 [Cicer arietinum]	90 bits(222)	2,08E-19	85%	0%
	gi|388509690|gb|AFK42911.1|	unknown [Medicago truncatula]	92 bits(226)	5,31E-20	88%	0%
	gi|593331109|ref|XP_007138981.1|	hypothetical protein PHAVU_009G254800g [Phaseolus vulgaris]	92 bits(227)	3,75E-20	88%	0%
	gi|657390953|gb|AES91950.2|	60S ribosomal protein L29-1 [Medicago truncatula]	95 bits(234)	9,87E-20	86%	0%
	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	92 bits(226)	4,33E-20	100%	0%
Contig25	gi|487912019|ref|WP_001985485.1|	SocE [Bacillus cereus]	91 bits(225)	3,35E-19	100%	0%
	gi|576095869|gb|AHH11877.1|	hypothetical protein BCO_0900155 [Borrelia coriaceae Co53]	77 bits(189)	2,48E-14	98%	0%
	gi|9652070|gb|AAF91388.1|AF263243_1	SocE [Myxococcus xanthus]	96 bits(236)	5,48E-18	50%	1%
	gi|553657069|gb|ESD75150.1|	hypothetical protein HMPREF1610_00242 [Escherichia coli 908555]	75 bits(184)	1,61E-13	80%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	103 bits(255)	1,13E-23	100%	0%
	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	92 bits(228)	1,52E-17	98%	0%
	gi|330752400|emb|CBL87351.1|	hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]	77 bits(187)	1,63E-13	97%	0%
	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	92 bits(226)	1,49E-19	100%	0%
	gi|674267870|emb|CDI96482.1|	hypothetical protein EmuJ_000005500 [Echinococcus multilocularis]	47 bits(110)	1,83E-14	95%	0%
	gi|571207123|emb|CDK78388.1|	Transcriptional repressor of the lac operon [Klebsiella pneumoniae IS22]	77 bits(187)	3,53E-13	88%	3%
Contig26	gi|1545805|dbj|BAA10929.1|	cytochrome P450 like_TBP [Nicotiana tabacum]	176 bits(445)	4,66E-47	75%	2%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	103 bits(255)	3,78E-24	100%	0%
	gi|357488197|ref|XP_003614386.1|	hypothetical protein MTR_5g051030 [Medicago truncatula]	101 bits(251)	2,97E-20	64%	27%
	gi|253760055|ref|XP_002488965.1|	hypothetical protein SORBIDRAFT_1138s002030 [Sorghum bicolor]	146 bits(366)	1,14E-39	91%	0%
	gi|147835464|emb|CAN61119.1|	hypothetical protein VITISV_022570 [Vitis vinifera]	104 bits(257)	3,04E-23	81%	0%
	gi|357488191|ref|XP_003614383.1|	hypothetical protein MTR_5g051000 [Medicago truncatula]	102 bits(252)	3,09E-20	64%	27%
	gi|7489812|pir||T02955	probable cytochrome P450 monooxygenase - maize (fragment)	146 bits(368)	4,54E-38	63%	8%
	gi|565396033|ref|XP_006363638.1|	PREDICTED: uncharacterized protein LOC102601005 [Solanum tuberosum]	103 bits(255)	2,04E-22	94%	0%
	gi|195610700|gb|ACG27180.1|	hypothetical protein [Zea mays]	136 bits(342)	3,86E-36	87%	0%

	gi|358348842|ref|XP_003638451.1|	hypothetical protein MTR_132s0010, partial [Medicago truncatula]	102 bits(254)	2,11E-20	64%	27%
Contig27	gi|357488207|ref|XP_003614391.1|	Tar1p [Medicago truncatula]	153 bits(384)	2,81E-37	79%	19%
	gi|357488191|ref|XP_003614383.1|	hypothetical protein MTR_5g051000 [Medicago truncatula]	153 bits(384)	5,10E-36	79%	19%
	gi|403333060|gb|EJY65597.1|	hypothetical protein OXYTRI_14248 [Oxytricha trifallax]	46 bits(107)	6,42E-37	63%	0%
	gi|669214567|emb|CDW61368.1|	hypothetical protein TTRE_0000982701, partial [Trichuris trichiura]	136 bits(340)	1,43E-32	55%	27%
	gi|678336953|emb|CDW75723.1|	UNKNOWN [Stylonychia lemnae]	44 bits(101)	7,21E-44	54%	1%
	gi|403334965|gb|EJY66653.1|	hypothetical protein OXYTRI_13058 [Oxytricha trifallax]	46 bits(107)	7,27E-37	63%	0%
	gi|574143403|dbj|BAO41194.1|	hypothetical protein KLMA_50540 [Kluyveromyces marxianus DMKU3-1042]	127 bits(318)	1,19E-31	72%	1%
	gi|357488199|ref|XP_003614387.1|	RRNA intron-encoded homing endonuclease [Medicago truncatula]	45 bits(106)	2,04E-24	72%	0%
	gi|357488213|ref|XP_003614394.1|	hypothetical protein MTR_5g051130 [Medicago truncatula]	153 bits(384)	3,65E-36	77%	19%
	gi|656185041|emb|CDR95662.1|	hypothetical protein, conserved [Babesia bigemina]	119 bits(298)	1,87E-28	63%	14%
Contig28	gi|357488207|ref|XP_003614391.1|	Tar1p [Medicago truncatula]	140 bits(352)	6,63E-35	78%	19%
	gi|242009491|ref|XP_002425519.1|	conserved hypothetical protein [Pediculus humanus corporis]	118 bits(294)	1,82E-29	63%	6%
	gi|545699775|ref|XP_005702341.1|	hypothetical protein Gasu_65200 [Galdieria sulphuraria]	106 bits(264)	2,47E-25	74%	1%
	gi|357488199|ref|XP_003614387.1|	RRNA intron-encoded homing endonuclease [Medicago truncatula]	96 bits(237)	1,06E-18	88%	0%
	gi|574143403|dbj|BAO41194.1|	hypothetical protein KLMA_50540 [Kluyveromyces marxianus DMKU3-1042]	114 bits(284)	4,18E-28	69%	3%
	gi|545700148|ref|XP_005702479.1|	hypothetical protein Gasu_nc0100 [Galdieria sulphuraria]	107 bits(266)	2,52E-25	74%	1%
	gi|357488213|ref|XP_003614394.1|	hypothetical protein MTR_5g051130 [Medicago truncatula]	140 bits(351)	1,02E-33	76%	19%
	gi|675375456|gb|KFM68358.1|	hypothetical protein X975_16721, partial [Stegodyphus mimosarum]	111 bits(275)	8,08E-27	58%	1%
	gi|357488191|ref|XP_003614383.1|	hypothetical protein MTR_5g051000 [Medicago truncatula]	140 bits(352)	1,18E-33	78%	19%
	gi|545700705|ref|XP_005702705.1|	hypothetical protein Gasu_61700 [Galdieria sulphuraria]	106 bits(264)	2,39E-25	74%	1%
Contig29	gi|357488199|ref|XP_003614387.1|	RRNA intron-encoded homing endonuclease [Medicago truncatula]	42 bits(97)	6,99E-11	100%	0%
	gi|296473176|tpg|DAA15291.1|	TPA: hypothetical protein BOS_23236 [Bos taurus]	106 bits(263)	2,02E-23	53%	3%
	gi|648151311|gb|KDR65241.1|	hypothetical protein GALMADRAFT_232962 [Galerina marginata CBS 339.88]	90 bits(222)	7,07E-19	71%	0%
	gi|357488213|ref|XP_003614394.1|	hypothetical protein MTR_5g051130 [Medicago truncatula]	67 bits(163)	4,86E-29	85%	0%
	gi|242009491|ref|XP_002425519.1|	conserved hypothetical protein [Pediculus humanus corporis]	49 bits(114)	7,37E-20	92%	0%
	gi|628331617|ref|XP_007738810.1|	hypothetical protein A1O3_10530 [Capronia epimyces CBS 606.96]	90 bits(221)	1,10E-18	68%	0%
	gi|357488191|ref|XP_003614383.1|	hypothetical protein MTR_5g051000 [Medicago truncatula]	67 bits(162)	5,17E-29	100%	0%
	gi|358348842|ref|XP_003638451.1|	hypothetical protein MTR_132s0010, partial [Medicago truncatula]	100 bits(248)	2,14E-19	65%	25%
	gi|357488207|ref|XP_003614391.1|	Tar1p [Medicago truncatula]	67 bits(163)	5,85E-29	85%	0%
	gi|646383642|gb|KDQ49123.1|	hypothetical protein JAAARDRAFT_63854 [Jaapia argillacea MUCL 33604]	91 bits(223)	5,60E-19	74%	0%
Contig30	gi|487912019|ref|WP_001985485.1|	SocE [Bacillus cereus]	91 bits(225)	2,23E-19	100%	0%
	gi|576095869|gb|AHH11877.1|	hypothetical protein BCO_0900155 [Borrelia coriaceae Co53]	77 bits(189)	1,86E-14	98%	0%
	gi|9652070|gb|AAF91388.1|AF263243_1	SocE [Myxococcus xanthus]	96 bits(237)	3,00E-18	50%	4%
	gi|553657069|gb|ESD75150.1|	hypothetical protein HMPREF1610_00242 [Escherichia coli 908555]	75 bits(184)	1,24E-13	80%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	103 bits(255)	8,80E-24	100%	0%
	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	92 bits(228)	1,06E-17	98%	0%
	gi|330752400|emb|CBL87351.1|	hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]	77 bits(187)	1,25E-13	97%	0%
	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	92 bits(226)	1,01E-19	100%	0%
	gi|674267870|emb|CDI96482.1|	hypothetical protein EmuJ_000005500 [Echinococcus multilocularis]	47 bits(110)	1,65E-14	95%	0%
	gi|571207123|emb|CDK78388.1|	Transcriptional repressor of the lac operon [Klebsiella pneumoniae IS22]	77 bits(187)	2,66E-13	88%	3%
Contig31	gi|643708491|gb|KDP23407.1|	hypothetical protein JCGZ_23240 [Jatropha curcas]	27 bits(59)	7,33E-54	60%	0%
	gi|449454034|ref|XP_004144761.1|	PREDICTED: LOW QUALITY PROTEIN: zinc finger matrin-type protein 2-like [Cucumis sativus]	27 bits(59)	8,56E-51	65%	0%
	gi|566198757|ref|XP_006375726.1|	hypothetical protein POPTR_0013s01160g [Populus trichocarpa]	97 bits(240)	7,33E-49	72%	2%
	gi|590644599|ref|XP_007031126.1|	C2H2 and C2HC zinc fingers superfamily protein isoform 1 [Theobroma cacao]	27 bits(58)	2,85E-53	65%	0%
	gi|566198755|ref|XP_002319487.2|	hypothetical protein POPTR_0013s01160g [Populus trichocarpa]	25 bits(54)	2,42E-50	75%	0%
	gi|326509317|dbj|BAJ91575.1|	predicted protein [Hordeum vulgare subsp. vulgare]	26 bits(55)	1,30E-48	83%	0%
	gi|449490847|ref|XP_004158724.1|	PREDICTED: zinc finger matrin-type protein 2-like [Cucumis sativus]	27 bits(59)	2,33E-52	65%	0%
	gi|674245219|gb|KFK37984.1|	hypothetical protein AALP_AA3G055200 [Arabis alpina]	104 bits(257)	1,70E-49	73%	0%
	gi|659070162|ref|XP_008453709.1|	PREDICTED: zinc finger matrin-type protein 2 [Cucumis melo]	27 bits(59)	4,92E-52	65%	0%
	gi|604341133|gb|EYU40518.1|	hypothetical protein MIMGU_mgv1a013989mg [Erythranthe guttata]	104 bits(259)	2,60E-49	74%	1%

Apêndice F – Resultado da busca *in silico* da funcionalidade hipotética em Singlets, da biblioteca de calos de *Solanum lycocarpum*
Fonte de dados: Blastx/NCBI
Elaborada pelo autor

Name Sequence	**Sequence**	**Name**	**score**	**expert**	**indentities**	**gaps**
SLCAPL01A04	gi|565377487|ref|XP_006355210.1|	PREDICTED: 40S ribosomal protein S6-like [Solanum tuberosum]	168 bits(425)	1,30E-48	87%	1%
	gi|629101100|gb|KCW66569.1|	hypothetical protein EUGRSUZ_F00368 [Eucalyptus grandis]	163 bits(410)	7,34E-46	85%	1%
	gi|3413170|emb|CAA09042.1|	40S ribosomal protein S6 [Cicer arietinum]	159 bits(401)	5,91E-45	83%	1%
	gi|460397815|ref|XP_004244462.1|	PREDICTED: 40S ribosomal protein S6-like [Solanum lycopersicum]	168 bits(424)	6,31E-48	87%	1%
	gi|255569734|ref|XP_002525831.1|	40S ribosomal protein S6, putative [Ricinus communis]	161 bits(405)	1,14E-45	83%	1%
	gi|604319824|gb|EYU30988.1|	hypothetical protein MIMGU_mgv1a012493mg [Erythranthe guttata]	160 bits(403)	8,28E-45	83%	1%
	gi|568215148|ref|NP_001275029.1|	40S ribosomal protein S6-like [Solanum tuberosum]	168 bits(424)	6,44E-48	87%	1%
	gi|643734740|gb|KDP41410.1|	hypothetical protein JCGZ_15817 [Jatropha curcas]	161 bits(407)	2,19E-45	84%	1%
	gi|460401129|ref|XP_004246081.1|	PREDICTED: 40S ribosomal protein S6-like [Solanum lycopersicum]	168 bits(423)	8,79E-48	87%	1%
	gi|225468188|ref|XP_002273865.1|	PREDICTED: 40S ribosomal protein S6 isoform 1 [Vitis vinifera]	161 bits(407)	2,57E-45	83%	1%
SLCAPL01A06	gi|565400629|ref|XP_006365824.1|	PREDICTED: omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 2-like, partial [Solanum tuberosum]	149 bits(374)	3,43E-40	81%	4%
	gi|460415029|ref|XP_004252863.1|	PREDICTED: omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 2-like isoform 2 [Solanum lycopersicum]	146 bits(368)	3,35E-38	80%	3%
	gi|565400583|ref|XP_006365801.1|	PREDICTED: omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 2-like [Solanum tuberosum]	149 bits(374)	9,51E-39	81%	4%
	gi|584200039|gb|AHI85708.1|	stress-induced protein 3, partial [Capsicum annuum]	143 bits(359)	9,76E-38	77%	3%
	gi|565401335|ref|XP_006366157.1|	PREDICTED: omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 2-like [Solanum tuberosum]	163 bits(412)	2,41E-44	91%	0%
	gi|565400589|ref|XP_006365804.1|	PREDICTED: omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 2-like [Solanum tuberosum]	148 bits(372)	1,39E-38	80%	4%
	gi|565400577|ref|XP_006365798.1|	PREDICTED: omega-6 fatty acid desaturase, endoplasmic reticulum-like [Solanum tuberosum]	146 bits(366)	1,04E-37	78%	3%
	gi|350536351|ref|NP_001234242.1|	lipid desaturase-like protein [Solanum lycopersicum]	160 bits(403)	2,04E-43	88%	0%
	gi|565359743|ref|XP_006346654.1|	PREDICTED: omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 1-like [Solanum tuberosum]	148 bits(371)	2,66E-38	80%	3%
	gi|460415033|ref|XP_004252865.1|	PREDICTED: omega-6 fatty acid desaturase, endoplasmic reticulum-like isoform 2 [Solanum lycopersicum]	145 bits(365)	1,39E-37	78%	3%
SLCAPL01A08	gi|171190268|gb|ACB42440.1|	aquaporin PIP2;3 [Gossypium hirsutum]	125 bits(313)	5,59E-31	89%	0%
	gi|568214816|ref|NP_001275065.1|	major intrinsic protein 2 [Solanum tuberosum]	136 bits(341)	4,79E-35	97%	0%
	gi|350539001|ref|NP_001234625.1|	aquaporin [Solanum lycopersicum]	129 bits(323)	2,07E-32	91%	0%
	gi|300793596|tpg|DAA33864.1|	TPA_inf: aquaporin PIP2;4 [Gossypium hirsutum]	124 bits(311)	7,96E-31	89%	0%
	gi|460411471|ref|XP_004251134.1|	PREDICTED: aquaporin PIP2-4-like [Solanum lycopersicum]	136 bits(341)	4,94E-35	97%	0%
	gi|560891740|dbj|BAO18629.1|	plasmamembrane intrinsic protein 2;6 [Solanum lycopersicum]	127 bits(318)	1,14E-31	92%	0%
	gi|5327263|emb|CAB46351.1|	major intrinsic protein 2 [Solanum tuberosum]	136 bits(341)	5,79E-35	97%	0%
	gi|104391599|gb|ABB13430.2|	plasma membrane intrinsic protein [Olea europaea]	127 bits(317)	1,44E-31	89%	0%
	gi|565382472|ref|XP_006357563.1|	PREDICTED: probable aquaporin PIP2-1-like [Solanum tuberosum]	130 bits(326)	7,49E-33	91%	0%
	gi|641849218|gb|KDO68093.1|	hypothetical protein CISIN_1g023370mg [Citrus sinensis]	124 bits(309)	5,30E-31	88%	0%
SLCAPL01B01	No Hits.					
SLCAPL01B06	gi|514822425|ref|XP_004985877.1|	PREDICTED: ADP,ATP carrier protein 2, mitochondrial-like [Setaria italica]	64 bits(155)	1,23E-26	81%	0%
	gi|15231937|ref|NP_187470.1|	ADP,ATP carrier protein 1 [Arabidopsis thaliana]	64 bits(153)	2,33E-26	83%	0%
	gi|596000973|ref|XP_007218125.1|	hypothetical protein PRUPE_ppa007062mg [Prunus persica]	63 bits(152)	4,17E-26	83%	0%
	gi|242042393|ref|XP_002468591.1|	hypothetical protein SORBIDRAFT_01g048660 [Sorghum bicolor]	64 bits(155)	1,28E-26	81%	0%
	gi|502165914|ref|XP_004513729.1|	PREDICTED: ADP,ATP carrier protein 1, mitochondrial-like [Cicer arietinum]	63 bits(152)	2,48E-26	83%	0%
	gi|573943726|ref|XP_006654224.1|	PREDICTED: ADP,ATP carrier protein, mitochondrial-like [Oryza brachyantha]	64 bits(155)	1,49E-26	81%	0%
	gi|672119343|ref|XP_008782907.1|	PREDICTED: ADP,ATP carrier protein 1, mitochondrial-like [Phoenix dactylifera]	62 bits(150)	3,78E-26	83%	0%
	gi|226504250|ref|NP_001150672.1|	LOC100284305 [Zea mays]	64 bits(155)	1,16E-26	81%	0%
	gi|566211344|ref|XP_006372724.1|	ADP/ATP CARRIER 3 family protein [Populus trichocarpa]	64 bits(155)	1,76E-26	81%	0%
	gi|255582238|ref|XP_002531911.1|	ADP,ATP carrier protein, putative [Ricinus communis]	64 bits(153)	3,81E-26	83%	0%
SLCAPL01B08	No Hits.					
SLCAPL01B09	gi|587900943|gb|EXB89231.1|	putative isoaspartyl peptidase/L-asparaginase 2 [Morus notabilis]	170 bits(429)	2,78E-48	83%	0%
	gi|502132833|ref|XP_004501550.1|	PREDICTED: probable isoaspartyl peptidase/L-asparaginase 2-like [Cicer arietinum]	174 bits(441)	4,29E-50	85%	0%
	gi|502125672|ref|XP_004499019.1|	PREDICTED: probable isoaspartyl peptidase/L-asparaginase 2-like [Cicer arietinum]	170 bits(429)	2,81E-48	83%	0%
	gi|604331461|gb|EYU36319.1|	hypothetical protein MIMGU_mgv1a014365mg [Erythranthe guttata]	168 bits(423)	7,34E-49	82%	0%
	gi|645226935|ref|XP_008220275.1|	PREDICTED: probable isoaspartyl peptidase/L-asparaginase 2 [Prunus mume]	170 bits(430)	2,52E-48	84%	0%
	gi|565376716|ref|XP_006354842.1|	PREDICTED: probable isoaspartyl peptidase/L-asparaginase 2-like [Solanum tuberosum]	185 bits(468)	4,42E-54	90%	0%
	gi|357465627|ref|XP_003603098.1|	L-asparaginase [Medicago truncatula]	170 bits(430)	1,84E-48	83%	0%
	gi|685311181|ref|XP_009146165.1|	PREDICTED: probable isoaspartyl peptidase/L-asparaginase 2 [Brassica rapa]	170 bits(429)	2,59E-48	82%	0%
	gi|460384861|ref|XP_004238125.1|	PREDICTED: probable isoaspartyl peptidase/L-asparaginase 2-like [Solanum lycopersicum]	184 bits(465)	1,40E-53	89%	0%

	gi|596146967|ref|XP_007222672.1|	hypothetical protein PRUPE_ppa008583mg [Prunus persica]	170 bits(430)	2,29E-48	84%	0%
SLCAPL01B12	gi|565390710|ref|XP_006361078.1|	PREDICTED: 60S ribosomal protein L10a-1-like [Solanum tuberosum]	200 bits(507)	2,17E-60	92%	0%
	gi|460411305|ref|XP_004251053.1|	PREDICTED: 60S ribosomal protein L10a-1-like isoform 1 [Solanum lycopersicum]	198 bits(501)	1,90E-59	92%	0%
	gi|460365121|ref|XP_004228453.1|	PREDICTED: 60S ribosomal protein L10a-1-like [Solanum lycopersicum]	199 bits(505)	4,24E-60	92%	0%
	gi|357160171|ref|XP_003578680.1|	PREDICTED: 60S ribosomal protein L10a-3-like [Brachypodium distachyon]	196 bits(497)	8,16E-59	85%	0%
	gi|629084478|gb|KCW50835.1|	hypothetical protein EUGRSUZ_J00492 [Eucalyptus grandis]	205 bits(521)	8,15E-62	81%	1%
	gi|641839146|gb|KDO58080.1|	hypothetical protein CISIN_1g027063mg [Citrus sinensis]	199 bits(505)	6,32E-60	87%	2%
	gi|326492474|dbj|BAK02020.1|	predicted protein [Hordeum vulgare subsp. vulgare]	196 bits(497)	8,34E-59	85%	0%
	gi|460391427|ref|XP_004241322.1|	PREDICTED: 60S ribosomal protein L10a-1-like [Solanum lycopersicum]	200 bits(508)	1,91E-60	92%	0%
	gi|565394503|ref|XP_006362897.1|	PREDICTED: 60S ribosomal protein L10a-1-like isoform X1 [Solanum tuberosum]	198 bits(501)	1,76E-59	92%	0%
	gi|661881026|emb|CDP15411.1|	unnamed protein product [Coffea canephora]	194 bits(491)	1,11E-58	89%	0%
SLCAPL01C01	gi|545372048|ref|XP_005650530.1|	ribosomal protein L22 component of cytosolic 80S ribosome and 60S large subunit [Coccomyxa subellipsoidea C-169]	123 bits(307)	4,18E-31	81%	0%
	gi|460368799|ref|XP_004230252.1|	PREDICTED: 60S ribosomal protein L22-2-like [Solanum lycopersicum]	113 bits(282)	1,49E-27	96%	0%
	gi|629095856|gb|KCW61851.1|	hypothetical protein EUGRSUZ_H04540 [Eucalyptus grandis]	104 bits(258)	4,92E-24	86%	0%
	gi|168014447|ref|XP_001759763.1|	predicted protein [Physcomitrella patens]	121 bits(302)	2,28E-30	76%	0%
	gi|674908085|emb|CDY25022.1|	BnaC02g39860D [Brassica napus]	104 bits(257)	3,01E-24	75%	0%
	gi|225431737|ref|XP_002268941.1|	PREDICTED: 60S ribosomal protein L22-2 [Vitis vinifera]	104 bits(257)	6,46E-24	86%	0%
	gi|255072417|ref|XP_002499883.1|	predicted protein [Micromonas sp. RCC299]	114 bits(284)	6,60E-28	76%	0%
	gi|460403882|ref|XP_004247415.1|	PREDICTED: 60S ribosomal protein L22-2-like [Solanum lycopersicum]	104 bits(259)	3,29E-24	86%	0%
	gi|567156219|ref|XP_006418299.1|	hypothetical protein EUTSA_v10009107mg [Eutrema salsugineum]	114 bits(284)	7,60E-28	74%	0%
	gi|587864749|gb|EXB54358.1|	60S ribosomal protein L22-2 [Morus notabilis]	104 bits(258)	4,48E-24	86%	0%
SLCAPL01C04	gi|350535300|ref|NP_001234443.1|	uncharacterized protein LOC544160 precursor [Solanum lycopersicum]	86 bits(211)	3,37E-17	86%	1%
	gi|565345500|ref|XP_006339834.1|	PREDICTED: lysine-rich arabinogalactan protein 18-like isoform X2 [Solanum tuberosum]	86 bits(211)	3,85E-17	86%	1%
	gi|10945615|gb|AAG24616.1|AF298594_1	arabinogalactan protein [Nicotiana alata]	110 bits(274)	3,85E-26	87%	0%
	gi|568215055|ref|NP_001275418.1|	lysine-rich arabinogalactan protein 18-like precursor [Solanum tuberosum]	86 bits(211)	4,29E-17	86%	1%
	gi|661894122|emb|CDP02563.1|	unnamed protein product [Coffea canephora]	89 bits(218)	4,85E-18	67%	1%
SLCAPL01C05	gi|460413640|ref|XP_004252192.1|	PREDICTED: exportin-4-like [Solanum lycopersicum]	116 bits(289)	5,38E-26	95%	0%
	gi|470132449|ref|XP_004302094.1|	PREDICTED: exportin-4-like [Fragaria vesca subsp. vesca]	92 bits(226)	1,04E-17	71%	0%
	gi|565484030|ref|XP_006299655.1|	hypothetical protein CARUB_v10015843mg [Capsella rubella]	89 bits(220)	5,98E-17	67%	0%
	gi|694432857|ref|XP_009343761.1|	PREDICTED: exportin-4 [Pyrus x bretschneideri]	96 bits(236)	4,85E-19	72%	0%
	gi|595811288|ref|XP_007203214.1|	hypothetical protein PRUPE_ppa000522mg [Prunus persica]	91 bits(224)	1,64E-17	69%	0%
	gi|657958443|ref|XP_008370746.1|	PREDICTED: LOW QUALITY PROTEIN: exportin-4 [Malus domestica]	96 bits(236)	5,08E-19	72%	0%
	gi|645270626|ref|XP_008240541.1|	PREDICTED: exportin-4 [Prunus mume]	91 bits(224)	1,70E-17	69%	0%
	gi|565379191|ref|XP_006356018.1|	PREDICTED: exportin-4-like [Solanum tuberosum]	117 bits(292)	1,88E-26	97%	0%
	gi|658056569|ref|XP_008364039.1|	PREDICTED: exportin-4-like [Malus domestica]	96 bits(236)	5,18E-19	72%	0%
	gi|7547108|gb|AAF63780.1|	hypothetical protein [Arabidopsis thaliana]	90 bits(222)	3,20E-17	67%	0%
SLCAPL01C11	No Hits.					
SLCAPL01D01	gi|296085587|emb|CBI29319.3|	unnamed protein product [Vitis vinifera]	312 bits(799)	2,29E-100	69%	0%
	gi|225462386|ref|XP_002264702.1|	PREDICTED: laccase-14-like [Vitis vinifera]	309 bits(789)	3,85E-98	68%	0%
	gi|296081093|emb|CBI18287.3|	unnamed protein product [Vitis vinifera]	299 bits(765)	1,56E-97	66%	0%
	gi|296080996|emb|CBI18500.3|	unnamed protein product [Vitis vinifera]	303 bits(774)	3,25E-100	68%	0%
	gi|658016945|ref|XP_008343826.1|	PREDICTED: laccase-15-like [Malus domestica]	309 bits(789)	5,46E-98	68%	0%
	gi|359495139|ref|XP_002264394.2|	PREDICTED: laccase-14 [Vitis vinifera]	307 bits(784)	2,17E-97	67%	0%
	gi|460384303|ref|XP_004237852.1|	PREDICTED: laccase-14-like [Solanum lycopersicum]	417 bits(1070)	3,65E-140	94%	0%
	gi|359495133|ref|XP_002269593.2|	PREDICTED: laccase-14-like [Vitis vinifera]	314 bits(802)	5,79E-100	69%	0%
	gi|661895328|emb|CDP01133.1|	unnamed protein product [Coffea canephora]	330 bits(845)	1,86E-106	71%	1%
	gi|359495123|ref|XP_003634918.1|	PREDICTED: putative laccase-9-like [Vitis vinifera]	314 bits(803)	1,05E-99	69%	0%
SLCAPL01D02	gi|565392858|ref|XP_006362106.1|	PREDICTED: ATP synthase subunit epsilon, mitochondrial-like [Solanum tuberosum]	114 bits(283)	1,05E-28	93%	0%
	gi|242129052|gb|ACS83605.1|	ATP synthase epsilon subunit 1 [Gossypium hirsutum]	110 bits(273)	2,48E-27	87%	0%
	gi|460414527|ref|XP_004252620.1|	PREDICTED: ATP synthase subunit epsilon, mitochondrial-like [Solanum lycopersicum]	113 bits(282)	1,24E-28	93%	0%
	gi|543868|sp|Q06450.2|ATP5E_IPOBA	RecName: Full=ATP synthase subunit epsilon, mitochondrial; Short=ATPase subunit epsilon [Ipomoea batatas]	109 bits(272)	4,12E-27	85%	0%
	gi|565351855|ref|XP_006342867.1|	PREDICTED: ATP synthase subunit epsilon, mitochondrial-like [Solanum tuberosum]	116 bits(289)	1,37E-29	96%	0%
	gi|255552368|ref|XP_002517228.1|	ATP synthase epsilon chain, mitochondrial, putative [Ricinus communis]	112 bits(278)	5,98E-28	87%	0%
	gi|661889306|emb|CDP06893.1|	unnamed protein product [Coffea canephora]	109 bits(271)	5,26E-27	87%	0%
	gi|460392651|ref|XP_004241929.1|	PREDICTED: ATP synthase subunit epsilon, mitochondrial-like [Solanum lycopersicum]	114 bits(283)	9,72E-29	93%	0%
	gi|568878061|ref|XP_006492024.1|	PREDICTED: ATP synthase subunit epsilon, mitochondrial-like [Citrus sinensis]	111 bits(277)	6,65E-28	89%	0%

	gi|590708455|ref|XP_007048282.1|	ATP synthase epsilon chain, mitochondrial isoform 1 [Theobroma cacao]	109 bits(270)	8,20E-27	85%	0%
SLCAPL01D05	gi|460372281|ref|XP_004231959.1|	PREDICTED: cytochrome c oxidase subunit 6a, mitochondrial-like [Solanum lycopersicum]	165 bits(416)	1,31E-48	86%	0%
	gi|225438196|ref|XP_002264013.1|	PREDICTED: cytochrome c oxidase subunit 6a, mitochondrial [Vitis vinifera]	112 bits(280)	2,13E-28	59%	3%
	gi|657949346|ref|XP_008342645.1|	PREDICTED: cytochrome c oxidase subunit 6a, mitochondrial [Malus domestica]	106 bits(264)	6,00E-26	60%	3%
	gi|565382844|ref|XP_006357740.1|	PREDICTED: cytochrome c oxidase subunit 6a, mitochondrial-like [Solanum tuberosum]	161 bits(405)	5,08E-47	84%	0%
	gi|659098495|ref|XP_008450167.1|	PREDICTED: cytochrome c oxidase subunit 6a, mitochondrial [Cucumis melo]	108 bits(269)	1,18E-26	60%	3%
	gi|694401705|ref|XP_009375885.1|	PREDICTED: cytochrome c oxidase subunit 6a, mitochondrial-like [Pyrus x bretschneideri]	106 bits(264)	6,13E-26	60%	3%
	gi|255582409|ref|XP_002531993.1|	cytochrome-c oxidase, putative [Ricinus communis]	116 bits(290)	8,07E-30	64%	3%
	gi|449478071|ref|XP_004155214.1|	PREDICTED: cytochrome c oxidase subunit 6a, mitochondrial-like isoform 2 [Cucumis sativus]	107 bits(267)	2,26E-26	59%	3%
	gi|661894215|emb|CDP02656.1|	unnamed protein product [Coffea canephora]	116 bits(289)	1,20E-29	62%	3%
	gi|629088447|gb|KCW54700.1|	hypothetical protein EUGRSUZ_I00649 [Eucalyptus grandis]	107 bits(267)	2,46E-26	59%	3%
SLCAPL01D09	No Hits.					
SLCAPL01E01	gi|54292100|gb|AAT68778.2|	manganese superoxide dismutase [Camellia sinensis]	287 bits(733)	6,59E-94	84%	0%
	gi|565385810|ref|XP_006358755.1|	PREDICTED: superoxide dismutase [Mn], mitochondrial-like [Solanum tuberosum]	311 bits(796)	1,56E-103	94%	0%
	gi|3915002|sp|O49066.1|SODM_CAPAN	RecName: Full=Superoxide dismutase [Mn], mitochondrial; Flags: Precursor [Capsicum annuum]	294 bits(750)	1,91E-96	86%	0%
	gi|460390498|ref|XP_004240868.1|	PREDICTED: superoxide dismutase [Mn], mitochondrial-like [Solanum lycopersicum]	309 bits(790)	1,73E-102	93%	0%
	gi|590570449|ref|XP_007011340.1|	Superoxide dismutase [Theobroma cacao]	293 bits(749)	2,46E-96	86%	0%
	gi|37999810|sp|Q9SM64.1|SODM_PRUPE	RecName: Full=Superoxide dismutase [Mn], mitochondrial; Flags: Precursor [Prunus persica]	302 bits(772)	7,06E-100	91%	0%
	gi|629100007|gb|KCW65772.1|	hypothetical protein EUGRSUZ_G03132 [Eucalyptus grandis]	292 bits(745)	1,30E-95	86%	0%
	gi|113472840|gb|ABI35908.1|	manganese superoxide dismutase [Rheum australe]	287 bits(734)	5,26E-94	82%	0%
	gi|134672|sp|P11796.1|SODM_NICPL	RecName: Full=Superoxide dismutase [Mn], mitochondrial; Flags: Precursor [Nicotiana plumbaginifolia]	314 bits(804)	1,03E-104	94%	0%
	gi|661882335|emb|CDP13915.1|	unnamed protein product [Coffea canephora]	295 bits(754)	4,30E-97	87%	0%
SLCAPL01E02	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	7,16E-11	100%	0%
SLCAPL01E04	No Hits.					
SLCAPL01E11	gi|565399311|ref|XP_006365198.1|	PREDICTED: heterogeneous nuclear ribonucleoprotein U-like protein 2-like [Solanum tuberosum]	82 bits(200)	5,21E-15	67%	9%
	gi|460411037|ref|XP_004250921.1|	PREDICTED: uncharacterized protein LOC101243859 [Solanum lycopersicum]	94 bits(232)	2,19E-19	61%	8%
SLCAPL01F03	gi|604348652|gb|EYU46807.1|	hypothetical protein MIMGU_mgv1a016182mg [Erythranthe guttata]	145 bits(365)	9,26E-41	61%	6%
	gi|225425676|ref|XP_002275043.1|	PREDICTED: calvin cycle protein CP12-like [Vitis vinifera]	141 bits(354)	3,97E-39	59%	4%
	gi|565378803|ref|XP_006355835.1|	PREDICTED: calvin cycle protein CP12-1, chloroplastic-like [Solanum tuberosum]	184 bits(466)	5,38E-56	77%	7%
	gi|645259000|ref|XP_008235152.1|	PREDICTED: calvin cycle protein CP12-1, chloroplastic [Prunus mume]	145 bits(365)	3,22E-40	56%	8%
	gi|449469032|ref|XP_004152225.1|	PREDICTED: calvin cycle protein CP12-2, chloroplastic-like [Cucumis sativus]	138 bits(346)	6,25E-38	61%	4%
	gi|460389876|ref|XP_004240573.1|	PREDICTED: calvin cycle protein CP12-2, chloroplastic-like [Solanum lycopersicum]	180 bits(456)	1,69E-54	73%	6%
	gi|595797340|ref|XP_007201261.1|	hypothetical protein PRUPE_ppa013259mg [Prunus persica]	142 bits(356)	1,95E-39	56%	8%
	gi|658047494|ref|XP_008359430.1|	PREDICTED: calvin cycle protein CP12-1, chloroplastic-like [Malus domestica]	138 bits(345)	9,79E-38	58%	9%
	gi|1617197|emb|CAA96569.1|	CP12 [Nicotiana tabacum]	177 bits(448)	3,23E-53	78%	5%
	gi|659108610|ref|XP_008454293.1|	PREDICTED: calvin cycle protein CP12-2, chloroplastic [Cucumis melo]	142 bits(356)	2,17E-39	63%	4%
SLCAPL01F04	gi|694450210|ref|XP_009350563.1|	PREDICTED: CTL-like protein DDB_G0288717 [Pyrus x bretschneideri]	114 bits(283)	2,16E-26	65%	0%
	gi|659115679|ref|XP_008457679.1|	PREDICTED: choline transporter-like protein 3 [Cucumis melo]	112 bits(279)	7,94E-26	68%	2%
	gi|658041473|ref|XP_008356344.1|	PREDICTED: LOW QUALITY PROTEIN: CTL-like protein 2 [Malus domestica]	114 bits(283)	2,27E-26	67%	0%
	gi|657950697|ref|XP_008349254.1|	PREDICTED: choline transporter-like protein 2 [Malus domestica]	112 bits(279)	8,90E-26	64%	0%
	gi|565387805|ref|XP_006359678.1|	PREDICTED: choline transporter-like protein 3-like [Solanum tuberosum]	141 bits(353)	4,55E-36	83%	0%
	gi|658021872|ref|XP_008346341.1|	PREDICTED: LOW QUALITY PROTEIN: CTL-like protein 2 [Malus domestica]	114 bits(283)	2,34E-26	67%	0%
	gi|595796468|ref|XP_007201153.1|	hypothetical protein PRUPE_ppa004408mg [Prunus persica]	111 bits(277)	9,75E-26	66%	0%
	gi|460370373|ref|XP_004231027.1|	PREDICTED: choline transporter-like protein 3-like isoform 1 [Solanum lycopersicum]	140 bits(351)	6,54E-36	82%	0%
	gi|604333588|gb|EYU37939.1|	hypothetical protein MIMGU_mgv1a003796mg [Erythranthe guttata]	113 bits(282)	3,84E-26	66%	1%
	gi|460370375|ref|XP_004231028.1|	PREDICTED: choline transporter-like protein 3-like isoform 2 [Solanum lycopersicum]	141 bits(355)	1,21E-36	82%	0%
SLCAPL01F07	gi|565370258|ref|XP_006351741.1|	PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP12-like [Solanum tuberosum]	223 bits(566)	9,22E-71	96%	0%
	gi|255563242|ref|XP_002522624.1|	immunophilin, putative [Ricinus communis]	199 bits(505)	1,38E-61	85%	0%
	gi|242066594|ref|XP_002454586.1|	hypothetical protein SORBIDRAFT_04g033900 [Sorghum bicolor]	197 bits(499)	9,21E-61	83%	0%
	gi|662552189|gb|AIE54297.1|	CONSTANS interacting protein 3 [Nicotiana tabacum]	213 bits(541)	5,77E-67	89%	0%
	gi|502077284|ref|XP_004485605.1|	PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP12-like [Cicer arietinum]	199 bits(504)	2,17E-61	84%	0%
	gi|629090701|gb|KCW56954.1|	hypothetical protein EUGRSUZ_I02629 [Eucalyptus grandis]	204 bits(517)	1,79E-63	86%	0%
	gi|73919361|sp|O04287.1|FKB12_VICFA	RecName: Full=Peptidyl-prolyl cis-trans isomerase FKBP12; Short=PPIase FKBP12; AltName: Full=12 kDa FK506-binding protein; Short=12 kDa FKBP; AltName: Full=FK506-binding protein 12; Short=VfFKBP12; AltName: Full=FKBP-12; AltName: Full=Immunophilin FKBP12; AltName: Full=Rotamase [Vicia faba]	198 bits(503)	2,98E-61	86%	0%
	gi|350538313|ref|NP_001233825.1|	CONSTANS interacting protein 3 [Solanum lycopersicum]	225 bits(572)	9,19E-72	97%	0%

	gi|357445945|ref|XP_003593250.1|	Peptidyl-prolyl isomerase FKBP12 [Medicago truncatula]	201 bits(509)	3,71E-62	83%	0%
	gi|565435138|ref|XP_006281193.1|	hypothetical protein CARUB_v10027228mg, partial [Capsella rubella]	200 bits(506)	8,01E-61	70%	2%
SLCAPL01F10	No Hits.					
SLCAPL01F11	No Hits.					
SLCAPL01G05	No Hits.					
SLCAPL01G07	No Hits.					
SLCAPL01G10	No Hits.					
SLCAPL01G11	No Hits.					
SLCAPL01H07	gi|226235458|dbj|BAH47641.1|	progesterone 5beta reductase-B [Nicotiana tabacum]	87 bits(214)	3,48E-17	91%	0%
	gi|374085801|gb|AEY82379.1|	putative progesterone 5-beta-reductase [Withania somnifera]	84 bits(205)	6,15E-16	89%	0%
	gi|428675604|gb|AFZ41795.1|	putative progesterone 5-beta-reductase [Duboisia hopwoodii]	81 bits(199)	3,38E-15	86%	0%
	gi|371491777|gb|AEX31544.1|	putative steroid 5beta-reductase [Solanum tuberosum]	86 bits(211)	7,72E-17	89%	0%
	gi|300433187|gb|ADK13080.1|	putative progesterone 5-beta-reductase [Nierembergia aristata]	83 bits(204)	7,90E-16	54%	3%
	gi|565374849|ref|XP_006353962.1|	PREDICTED: 3-oxo-Delta(4,5)-steroid 5-beta-reductase-like [Solanum tuberosum]	86 bits(211)	8,13E-17	89%	0%
	gi|226235456|dbj|BAH47640.1|	progesterone 5beta reductase-A [Nicotiana tabacum]	83 bits(204)	8,84E-16	89%	0%
	gi|295834059|gb|ADG41743.1|	putative progesterone 5 beta-reductase [Nicotiana tabacum]	87 bits(214)	3,25E-17	91%	0%
	gi|295855148|gb|ADG46023.1|	progesterone 5-beta-reductase [Atropa belladonna]	86 bits(210)	1,20E-16	89%	0%
	gi|525313657|ref|NP_001266103.1|	putative steroid 5beta-reductase [Solanum lycopersicum]	82 bits(201)	1,75E-15	86%	0%
SLCAPL01H08	No Hits.					
SLCAPL02A04	gi|77417031|gb|ABA81908.1|	probable 26S proteasome regulatory subunit [Larix laricina]	107 bits(265)	2,17E-25	94%	0%
	gi|674929870|emb|CDY03414.1|	BnaC01g16680D [Brassica napus]	112 bits(279)	2,58E-25	74%	1%
	gi|117607065|gb|ABK42076.1|	26S proteasome subunit RPN7 [Capsicum annuum]	112 bits(279)	2,22E-25	74%	1%
	gi|685346418|ref|XP_009109236.1|	PREDICTED: 26S proteasome non-ATPase regulatory subunit 6 homolog [Brassica rapa]	112 bits(278)	2,71E-25	74%	1%
	gi|657972809|ref|XP_008378194.1|	PREDICTED: 26S proteasome non-ATPase regulatory subunit 6 homolog [Malus domestica]	112 bits(280)	1,08E-26	98%	0%
	gi|685260134|ref|XP_009138580.1|	PREDICTED: 26S proteasome non-ATPase regulatory subunit 6 homolog [Brassica rapa]	112 bits(279)	2,41E-25	74%	1%
	gi|674908314|emb|CDY24849.1|	BnaA08g14610D [Brassica napus]	112 bits(278)	2,71E-25	74%	1%
	gi|77417033|gb|ABA81909.1|	probable 26S proteasome regulatory subunit [Larix decidua]	109 bits(272)	2,30E-26	71%	1%
	gi|674924419|emb|CDY08950.1|	BnaC08g11800D [Brassica napus]	112 bits(279)	2,53E-25	74%	1%
	gi|674940552|emb|CDX92654.1|	BnaC07g39120D [Brassica napus]	112 bits(278)	2,76E-25	74%	1%
SLCAPL02A08	gi|657972809|ref|XP_008378194.1|	PREDICTED: 26S proteasome non-ATPase regulatory subunit 6 homolog [Malus domestica]	112 bits(280)	1,08E-26	98%	0%
	gi|685260134|ref|XP_009138580.1|	PREDICTED: 26S proteasome non-ATPase regulatory subunit 6 homolog [Brassica rapa]	112 bits(279)	2,41E-25	74%	1%
	gi|674908314|emb|CDY24849.1|	BnaA08g14610D [Brassica napus]	112 bits(278)	2,71E-25	74%	1%
	gi|77417033|gb|ABA81909.1|	probable 26S proteasome regulatory subunit [Larix decidua]	109 bits(272)	2,30E-26	71%	1%
	gi|674924419|emb|CDY08950.1|	BnaC08g11800D [Brassica napus]	112 bits(279)	2,53E-25	74%	1%
	gi|674940552|emb|CDX92654.1|	BnaC07g39120D [Brassica napus]	112 bits(278)	2,76E-25	74%	1%
	gi|674929870|emb|CDY03414.1|	BnaC01g16680D [Brassica napus]	112 bits(279)	2,58E-25	74%	1%
	gi|77417031|gb|ABA81908.1|	probable 26S proteasome regulatory subunit [Larix laricina]	107 bits(265)	2,17E-25	94%	0%
	gi|685346418|ref|XP_009109236.1|	PREDICTED: 26S proteasome non-ATPase regulatory subunit 6 homolog [Brassica rapa]	112 bits(278)	2,71E-25	74%	1%
	gi|117607065|gb|ABK42076.1|	26S proteasome subunit RPN7 [Capsicum annuum]	112 bits(279)	2,22E-25	74%	1%
SLCAPL02B02	No Hits.					
SLCAPL02C05	No Hits.					
SLCAPL02C10	gi|460365659|ref|XP_004228718.1|	PREDICTED: uncharacterized protein LOC101249479 isoform 1 [Solanum lycopersicum]	90 bits(222)	1,36E-46	80%	0%
	gi|460364889|ref|XP_004228342.1|	PREDICTED: 60S acidic ribosomal protein P1-1-like [Solanum lycopersicum]	121 bits(301)	9,40E-31	73%	2%
	gi|565396073|ref|XP_006363657.1|	PREDICTED: 60S acidic ribosomal protein P1-2-like [Solanum tuberosum]	119 bits(298)	3,23E-30	81%	1%
	gi|568215342|ref|NP_001275175.1|	acidic ribosomal protein P1a-like [Solanum tuberosum]	132 bits(331)	3,38E-35	96%	0%
	gi|565365391|ref|XP_006349397.1|	PREDICTED: 60S acidic ribosomal protein P1-1-like [Solanum tuberosum]	120 bits(300)	1,42E-30	80%	0%
	gi|565383328|ref|XP_006357970.1|	PREDICTED: 60S acidic ribosomal protein P1-like [Solanum tuberosum]	119 bits(297)	4,40E-30	60%	2%
	gi|566205261|ref|XP_002321361.2|	60S acidic ribosomal protein P1 [Populus trichocarpa]	127 bits(319)	2,30E-33	67%	2%
	gi|460369324|ref|XP_004230513.1|	PREDICTED: 60S acidic ribosomal protein P1-2-like isoform 2 [Solanum lycopersicum]	120 bits(300)	1,69E-30	81%	0%
	gi|460365661|ref|XP_004228719.1|	PREDICTED: uncharacterized protein LOC101249479 isoform 2 [Solanum lycopersicum]	122 bits(306)	5,11E-31	91%	0%
	gi|225426544|ref|XP_002279082.1|	PREDICTED: 60S acidic ribosomal protein P1-1 isoform 1 [Vitis vinifera]	119 bits(298)	3,13E-30	71%	1%
SLCAPL02D04	gi|225465290|ref|XP_002268875.1|	PREDICTED: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3-B [Vitis vinifera]	109 bits(270)	3,94E-26	81%	0%
	gi|586670768|ref|XP_006836931.1|	hypothetical protein AMTR_s00099p00150850 [Amborella trichopoda]	102 bits(252)	1,81E-23	83%	0%
	gi|643722685|gb|KDP32435.1|	hypothetical protein JCGZ_13360 [Jatropha curcas]	103 bits(256)	4,74E-24	84%	0%
	gi|255556661|ref|XP_002519364.1|	conserved hypothetical protein [Ricinus communis]	101 bits(250)	2,59E-23	78%	0%
	gi|460369095|ref|XP_004230399.1|	PREDICTED: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3-B-like [Solanum lycopersicum]	146 bits(367)	3,55E-40	97%	0%

	gi|566168345|ref|XP_006385098.1|	hypothetical protein POPTR_0004s23900g [Populus trichocarpa]	103 bits(255)	5,92E-24	79%	0%
	gi|18394120|ref|NP_563952.1|	NADH dehydrogenase (ubiquinone) [Arabidopsis thaliana]	100 bits(247)	8,69E-23	66%	4%
	gi|565385124|ref|XP_006358469.1|	PREDICTED: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3-B-like [Solanum tuberosum]	144 bits(363)	1,26E-39	96%	0%
	gi|567143041|ref|XP_006395778.1|	hypothetical protein EUTSA_v10005238mg [Eutrema salsugineum]	102 bits(254)	8,73E-24	65%	0%
	gi|674923865|emb|CDY09364.1|	BnaA02g26460D [Brassica napus]	99 bits(246)	1,10E-22	65%	0%
SLCAPL02D05	No Hits.					
SLCAPL02E02	No Hits.					
SLCAPL02E09	No Hits.					
SLCAPL02E10	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	91 bits(224)	4,52E-20	98%	0%
	gi|170227|gb|AAA34070.1|	endochitinase precursor (EC 3.2.1.14), partial [Nicotiana tabacum]	89 bits(218)	1,98E-17	93%	0%
	gi|116321|sp|P24091.1|CHI2_TOBAC	RecName: Full=Endochitinase B; Short=CHN-B; Flags: Precursor [Nicotiana tabacum]	89 bits(218)	2,42E-17	93%	0%
	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	91 bits(225)	3,17E-18	95%	0%
	gi|460406368|ref|XP_004248637.1|	PREDICTED: endochitinase 3-like [Solanum lycopersicum]	89 bits(218)	2,32E-17	95%	0%
	gi|55294658|emb|CAH69226.1|	putative endochitinase B [Nicotiana glauca]	88 bits(217)	3,36E-18	93%	0%
	gi|315258225|gb|ADT91691.1|	endochitinase [Nicotiana attenuata]	89 bits(218)	2,33E-17	93%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	98 bits(242)	1,08E-22	98%	0%
	gi|1705805|sp|P52403.1|CHI1_SOLTU	RecName: Full=Endochitinase 1; Flags: Precursor, partial [Solanum tuberosum]	89 bits(219)	1,68E-17	95%	0%
	gi|11558417|emb|CAC17793.1|	endochitinase [Nicotiana sylvestris]	89 bits(218)	2,40E-17	93%	0%
SLCAPL02F01	No Hits.					
SLCAPL02F04	gi|27475622|emb|CAD59768.1|	putative reverse transcriptase [Cicer arietinum]	74 bits(181)	7,06E-14	100%	0%
	gi|685305756|ref|XP_009143610.1|	PREDICTED: ubiquitin-60S ribosomal protein L40-like [Brassica rapa]	71 bits(173)	7,85E-12	100%	0%
	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	84 bits(206)	3,69E-15	80%	0%
	gi|659102438|ref|XP_008452129.1|	PREDICTED: ubiquitin-60S ribosomal protein L40-like [Cucumis melo]	71 bits(173)	5,26E-12	100%	0%
	gi|593268622|ref|XP_007136488.1|	hypothetical protein PHAVU_009G049400g [Phaseolus vulgaris]	71 bits(173)	7,85E-12	100%	0%
	gi|330752400|emb|CBL87351.1|	hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]	77 bits(189)	2,54E-14	97%	0%
	gi|659102440|ref|XP_008452130.1|	PREDICTED: ubiquitin-60S ribosomal protein L40-like [Cucumis melo]	71 bits(173)	7,14E-12	100%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	80 bits(195)	1,18E-15	85%	1%
	gi|685305760|ref|XP_009143611.1|	PREDICTED: ubiquitin-60S ribosomal protein L40-like [Brassica rapa]	71 bits(173)	7,77E-12	100%	0%
	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	79 bits(193)	2,20E-15	100%	0%
SLCAPL02F06	No Hits.					
SLCAPL02F07	gi|565359973|ref|XP_006346757.1|	PREDICTED: 15.7 kDa heat shock protein, peroxisomal-like [Solanum tuberosum]	153 bits(385)	4,76E-42	90%	0%
	gi|358248934|ref|NP_001239965.1|	uncharacterized protein LOC100802108 [Glycine max]	115 bits(286)	1,48E-27	78%	1%
	gi|255631402|gb|ACU16068.1|	unknown [Glycine max]	113 bits(281)	8,63E-27	78%	1%
	gi|595928519|ref|XP_007215130.1|	hypothetical protein PRUPE_ppa013043mg [Prunus persica]	119 bits(296)	5,01E-29	75%	3%
	gi|657982214|ref|XP_008383146.1|	PREDICTED: 15.7 kDa heat shock protein, peroxisomal-like [Malus domestica]	115 bits(286)	3,42E-27	78%	1%
	gi|593490111|ref|XP_007141919.1|	hypothetical protein PHAVU_008G237000g [Phaseolus vulgaris]	118 bits(294)	9,89E-29	65%	2%
	gi|657978862|ref|XP_008381373.1|	PREDICTED: 15.7 kDa heat shock protein, peroxisomal-like [Malus domestica]	114 bits(284)	3,44E-27	67%	1%
	gi|460381920|ref|XP_004236689.1|	PREDICTED: 15.7 kDa heat shock protein, peroxisomal-like [Solanum lycopersicum]	153 bits(386)	3,85E-42	92%	0%
	gi|351727545|ref|NP_001238444.1|	peroxisomal small heat shock protein [Glycine max]	115 bits(287)	1,09E-27	81%	1%
	gi|661894642|emb|CDP01641.1|	unnamed protein product [Coffea canephora]	113 bits(281)	7,13E-27	68%	11%
SLCAPL02G01	No Hits.					
SLCAPL02G07	No Hits.					
SLCAPL02H01	No Hits.					
SLCAPL02H02	gi|643708436|gb|KDP23352.1|	hypothetical protein JCGZ_23185 [Jatropha curcas]	54 bits(129)	9,02E-21	85%	0%
	gi|566168629|ref|XP_006382296.1|	pyrrolidone-carboxylate peptidase family protein [Populus trichocarpa]	53 bits(126)	7,71E-20	77%	0%
	gi|224124970|ref|XP_002319470.1|	pyrrolidone-carboxylate peptidase family protein [Populus trichocarpa]	53 bits(125)	1,02E-19	81%	0%
	gi|460368975|ref|XP_004230340.1|	PREDICTED: pyrrolidone-carboxylate peptidase-like isoform 2 [Solanum lycopersicum]	55 bits(130)	3,33E-20	82%	0%
	gi|118481095|gb|ABK92501.1|	unknown [Populus trichocarpa]	54 bits(127)	7,84E-20	77%	0%
	gi|604299526|gb|EYU19421.1|	hypothetical protein MIMGU_mgv1a013492mg [Erythranthe guttata]	52 bits(122)	1,51E-19	79%	0%
	gi|225450494|ref|XP_002280759.1|	PREDICTED: pyrrolidone-carboxylate peptidase isoform 1 [Vitis vinifera]	56 bits(133)	3,80E-20	80%	0%
	gi|566168627|ref|XP_006382295.1|	hypothetical protein POPTR_0005s00740g [Populus trichocarpa]	53 bits(126)	8,00E-20	77%	0%
	gi|460368973|ref|XP_004230339.1|	PREDICTED: pyrrolidone-carboxylate peptidase-like isoform 1 [Solanum lycopersicum]	54 bits(129)	4,02E-20	82%	0%
	gi|661881156|emb|CDP15214.1|	unnamed protein product [Coffea canephora]	55 bits(132)	8,04E-20	82%	0%
SLCAPL02H07	gi|575952|emb|CAA86659.1|	extensin [Solanum lycopersicum]	70 bits(170)	1,22E-13	92%	0%
	gi|565394373|ref|XP_006362833.1|	PREDICTED: extensin-3-like [Solanum tuberosum]	69 bits(167)	5,96E-12	76%	11%
SLCAPL02H08	No Hits.					

SLCAPL02H10	No Hits.					
SLCAPL02H11	gi|357492397|ref|XP_003616487.1|	Metallocarboxypeptidase inhibitor [Medicago truncatula]	77 bits(188)	7,13E-14	66%	1%
	gi|78103322|ref|YP_358636.1|	hypothetical protein PhapfoPp090 [Phalaenopsis aphrodite subsp. formosana]	82 bits(202)	1,43E-17	54%	25%
	gi|358346026|ref|XP_003637074.1|	Cell wall-associated hydrolase, partial [Medicago truncatula]	87 bits(214)	5,50E-17	56%	25%
	gi|587914130|gb|EXC01914.1|	hypothetical protein L484_018826 [Morus notabilis]	87 bits(213)	2,14E-18	71%	1%
	gi|358349383|ref|XP_003638717.1|	Cell wall-associated hydrolase [Medicago truncatula]	82 bits(200)	1,02E-15	69%	1%
	gi|357438975|ref|XP_003589764.1|	hypothetical protein MTR_1g039020 [Medicago truncatula]	80 bits(197)	4,49E-17	78%	1%
	gi|543177598|gb|AGV54820.1|	cell wall-associated hydrolase [Phaseolus vulgaris]	126 bits(314)	2,30E-31	61%	2%
	gi|657387664|gb|KEH29749.1|	signal anchor, putative [Medicago truncatula]	79 bits(194)	3,13E-15	56%	15%
	gi|145408594|ref|YP_001152218.1|	ORF82c [Pinus koraiensis]	74 bits(181)	1,46E-14	66%	1%
	gi|357467743|ref|XP_003604156.1|	Cell wall-associated hydrolase [Medicago truncatula]	95 bits(234)	1,41E-20	61%	2%
SLCAPL03A05	No Hits.					
SLCAPL03A07	gi|565403296|ref|XP_006367098.1|	PREDICTED: myb-like protein X-like isoform X1 [Solanum tuberosum]	156 bits(392)	2,49E-39	84%	0%
	gi|565403300|ref|XP_006367100.1|	PREDICTED: myb-like protein X-like isoform X3 [Solanum tuberosum]	155 bits(391)	2,52E-39	84%	0%
	gi|330752400|emb|CBL87351.1|	hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]	70 bits(171)	3,60E-12	97%	0%
	gi|460369652|ref|XP_004230671.1|	PREDICTED: uncharacterized protein LOC101258200 isoform 1 [Solanum lycopersicum]	116 bits(289)	6,54E-26	73%	3%
SLCAPL03A08	gi|48093459|gb|AAT40106.1|	putative UDP-glucose dehydrogenase 2 [Nicotiana tabacum]	91 bits(223)	1,38E-17	70%	1%
	gi|48093457|gb|AAT40105.1|	putative UDP-glucose dehydrogenase 1 [Nicotiana tabacum]	78 bits(191)	2,12E-13	59%	5%
	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	7,69E-11	100%	0%
SLCAPL03A09	gi|460373438|ref|XP_004232526.1|	PREDICTED: uncharacterized protein At4g08330, chloroplastic-like [Solanum lycopersicum]	210 bits(533)	1,19E-64	97%	0%
	gi|225431343|ref|XP_002278070.1|	PREDICTED: uncharacterized protein At4g08330, chloroplastic [Vitis vinifera]	181 bits(459)	1,83E-53	79%	0%
	gi|629086868|gb|KCW53225.1|	hypothetical protein EUGRSUZ_J02491 [Eucalyptus grandis]	179 bits(453)	1,75E-52	80%	0%
	gi|659095313|ref|XP_008448515.1|	PREDICTED: uncharacterized protein At4g08330, chloroplastic [Cucumis melo]	184 bits(466)	1,39E-54	82%	0%
	gi|449524330|ref|XP_004169176.1|	PREDICTED: LOW QUALITY PROTEIN: uncharacterized protein At4g08330, chloroplastic-like [Cucumis sativus]	180 bits(456)	4,93E-53	81%	0%
	gi|643709409|gb|KDP23950.1|	hypothetical protein JCGZ_25338 [Jatropha curcas]	184 bits(465)	1,75E-54	82%	0%
	gi|296084062|emb|CBI24450.3|	unnamed protein product [Vitis vinifera]	180 bits(456)	5,92E-53	79%	0%
	gi|565347544|ref|XP_006340785.1|	PREDICTED: uncharacterized protein At4g08330, chloroplastic-like [Solanum tuberosum]	211 bits(537)	3,21E-65	98%	0%
	gi|449456857|ref|XP_004146165.1|	PREDICTED: uncharacterized protein At4g08330, chloroplastic-like [Cucumis sativus]	183 bits(463)	3,88E-54	82%	0%
	gi|590702299|ref|XP_007046590.1|	Uncharacterized protein TCM_000130 [Theobroma cacao]	180 bits(455)	6,52E-53	80%	0%
SLCAPL03B02	gi|629124235|gb|KCW88660.1|	hypothetical protein EUGRSUZ_A01021 [Eucalyptus grandis]	225 bits(571)	1,44E-67	95%	0%
	gi|590645036|ref|XP_007031241.1|	S-adenosylmethionine synthetase 1 [Theobroma cacao]	222 bits(565)	4,18E-66	93%	0%
	gi|568815660|ref|NP_001275609.1|	S-adenosylmethionine synthase 1 [Solanum tuberosum]	228 bits(580)	2,27E-68	96%	0%
	gi|629124236|gb|KCW88661.1|	hypothetical protein EUGRSUZ_A01021 [Eucalyptus grandis]	225 bits(571)	1,56E-67	95%	0%
	gi|383081975|dbj|BAM05640.1|	S-adenosylmethionine synthase, partial [Eucalyptus globulus subsp. globulus]	216 bits(548)	6,76E-66	91%	0%
	gi|527188606|gb|EPS60608.1|	s-adenosylmethionine synthase 1, partial [Genlisea aurea]	221 bits(561)	2,31E-68	94%	0%
	gi|75290412|sp|Q6GV10.1|METK_SOLPL	RecName: Full=S-adenosylmethionine synthase; Short=AdoMet synthase; AltName: Full=Methionine adenosyltransferase; Short=MAT [Solanum palustre]	225 bits(572)	3,70E-67	95%	0%
	gi|225432155|ref|XP_002266358.1|	PREDICTED: S-adenosylmethionine synthase 2 [Vitis vinifera]	221 bits(563)	8,36E-66	94%	0%
	gi|350534978|ref|NP_001234425.1|	S-adenosylmethionine synthase 1 [Solanum lycopersicum]	226 bits(576)	9,41E-68	96%	0%
	gi|629124237|gb|KCW88662.1|	hypothetical protein EUGRSUZ_A01021 [Eucalyptus grandis]	225 bits(571)	5,67E-67	95%	0%
SLCAPL03B06	gi|460385505|ref|XP_004238444.1|	PREDICTED: probable protein phosphatase 2C 27-like [Solanum lycopersicum]	293 bits(749)	2,89E-94	99%	0%
	gi|568839713|ref|XP_006473824.1|	PREDICTED: probable protein phosphatase 2C 27-like isoform X1 [Citrus sinensis]	263 bits(671)	1,04E-82	88%	0%
	gi|590595566|ref|XP_007018092.1|	Phosphatase 2C family protein isoform 1 [Theobroma cacao]	262 bits(667)	4,01E-82	88%	0%
	gi|225457596|ref|XP_002273479.1|	PREDICTED: probable protein phosphatase 2C 27 isoform 1 [Vitis vinifera]	265 bits(676)	1,23E-83	89%	0%
	gi|567885683|ref|XP_006435400.1|	hypothetical protein CICLE_v10001476mg [Citrus clementina]	263 bits(671)	1,04E-82	88%	0%
	gi|359491854|ref|XP_002273511.2|	PREDICTED: probable protein phosphatase 2C 27 isoform 2 [Vitis vinifera]	265 bits(676)	2,18E-83	89%	0%
	gi|629102649|gb|KCW68118.1|	hypothetical protein EUGRSUZ_F01792 [Eucalyptus grandis]	262 bits(667)	1,12E-82	86%	0%
	gi|565350386|ref|XP_006342150.1|	PREDICTED: probable protein phosphatase 2C 27-like [Solanum tuberosum]	293 bits(749)	2,89E-94	99%	0%
	gi|641866474|gb|KDO85159.1|	hypothetical protein CISIN_1g016684mg [Citrus sinensis]	262 bits(668)	3,95E-83	88%	0%
	gi|629102648|gb|KCW68117.1|	hypothetical protein EUGRSUZ_F01792 [Eucalyptus grandis]	262 bits(668)	3,31E-82	86%	0%
SLCAPL03D04	gi|270064301|gb|ACZ60129.1|	abscisic stress ripening [Musa acuminata AAA Group]	96 bits(238)	8,01E-22	79%	1%
	gi|270064318|gb|ACZ60137.1|	abscisic stress ripening [Musa banksii]	96 bits(236)	1,89E-21	78%	1%
	gi|270064289|gb|ACZ60123.1|	abscisic stress ripening [Musa ABB Group]	96 bits(236)	1,89E-21	78%	1%
	gi|270064308|gb|ACZ60132.1|	abscisic stress ripening [Musa AAB Group]	97 bits(239)	6,77E-22	79%	1%
	gi|270064287|gb|ACZ60122.1|	abscisic stress ripening [Musa ABB Group]	96 bits(238)	9,17E-22	79%	1%
	gi|47575681|gb|AAT35818.1|	abscisic stress ripening protein-like protein [Musa acuminata]	96 bits(236)	1,99E-21	78%	1%

	gi|270064281|gb|ACZ60119.1|	abscisic stress ripening [Musa acuminata subsp. burmannicoides]	97 bits(239)	7,36E-22	79%	1%
	gi|270064283|gb|ACZ60120.1|	abscisic stress ripening [Musa itinerans var. itinerans]	96 bits(238)	9,17E-22	79%	1%
	gi|584481470|gb|AHJ09608.1|	abscisic stress-ripening protein ASR [Camellia sinensis]	97 bits(241)	7,86E-22	76%	0%
	gi|270064310|gb|ACZ60133.1|	abscisic stress ripening [Musa balbisiana]	96 bits(238)	9,27E-22	79%	1%
SLCAPL03D07	gi|604348507|gb|EYU46662.1|	hypothetical protein MIMGU_mgv1a016751mg [Erythranthe guttata]	64 bits(154)	6,97E-11	89%	0%
	gi|629092438|gb|KCW58433.1|	hypothetical protein EUGRSUZ_H01111 [Eucalyptus grandis]	64 bits(153)	7,90E-11	89%	0%
	gi|297824871|ref|XP_002880318.1|	hypothetical protein ARALYDRAFT_483945 [Arabidopsis lyrata subsp. lyrata]	64 bits(153)	8,15E-11	89%	0%
	gi|604313847|gb|EYU26898.1|	hypothetical protein MIMGU_mgv1a016863mg [Erythranthe guttata]	64 bits(153)	7,08E-11	89%	0%
	gi|567911637|ref|XP_006448132.1|	hypothetical protein CICLE_v10017261mg [Citrus clementina]	64 bits(153)	8,09E-11	89%	0%
	gi|629092435|gb|KCW58430.1|	hypothetical protein EUGRSUZ_H01111 [Eucalyptus grandis]	64 bits(153)	7,31E-11	89%	0%
	gi|226506222|ref|NP_001147167.1|	LOC100280773 [Zea mays]	64 bits(153)	8,10E-11	89%	0%
	gi|460403886|ref|XP_004247417.1|	PREDICTED: probable small nuclear ribonucleoprotein Sm D2-like [Solanum lycopersicum]	66 bits(160)	7,35E-12	94%	0%
	gi|567911643|ref|XP_006448135.1|	hypothetical protein CICLE_v10017261mg [Citrus clementina]	64 bits(153)	7,89E-11	89%	0%
	gi|629092437|gb|KCW58432.1|	hypothetical protein EUGRSUZ_H01111 [Eucalyptus grandis]	64 bits(153)	8,14E-11	89%	0%
SLCAPL03E02	No Hits.					
SLCAPL03E03	gi|527194116|gb|EPS63870.1|	hypothetical protein M569_10910, partial [Genlisea aurea]	130 bits(325)	1,90E-33	91%	0%
	gi|567902672|ref|XP_006443824.1|	hypothetical protein CICLE_v10021043mg [Citrus clementina]	128 bits(320)	1,28E-32	88%	0%
	gi|590715708|ref|XP_007050273.1|	Sugar isomerase domain-containing protein isoform 1 [Theobroma cacao]	131 bits(328)	2,05E-33	90%	0%
	gi|470107235|ref|XP_004289954.1|	PREDICTED: probable arabinose 5-phosphate isomerase-like [Fragaria vesca subsp. vesca]	128 bits(320)	1,52E-32	87%	0%
	gi|460379251|ref|XP_004235377.1|	PREDICTED: probable arabinose 5-phosphate isomerase-like [Solanum lycopersicum]	139 bits(350)	7,58E-37	99%	0%
	gi|629083321|gb|KCW49766.1|	hypothetical protein EUGRSUZ_K03257 [Eucalyptus grandis]	130 bits(325)	3,69E-33	90%	0%
	gi|224082832|ref|XP_002306858.1|	sugar isomerase domain-containing family protein [Populus trichocarpa]	127 bits(319)	2,04E-32	88%	0%
	gi|565397601|ref|XP_006364377.1|	PREDICTED: probable arabinose 5-phosphate isomerase-like [Solanum tuberosum]	139 bits(349)	8,80E-37	99%	0%
	gi|643713855|gb|KDP26520.1|	hypothetical protein JCGZ_17678 [Jatropha curcas]	129 bits(322)	8,88E-33	88%	0%
	gi|657379555|gb|KEH23935.1|	arabinose 5-phosphate isomerase, putative [Medicago truncatula]	127 bits(317)	4,44E-32	87%	0%
SLCAPL03E04	gi|568876322|ref|XP_006491230.1|	PREDICTED: ubiquitin-conjugating enzyme E2-17 kDa-like isoform X2 [Citrus sinensis]	54 bits(129)	8,93E-18	83%	0%
	gi|357512497|ref|XP_003626537.1|	Ubiquitin carrier protein [Medicago truncatula]	54 bits(129)	1,51E-17	96%	0%
	gi|567874071|ref|XP_006429625.1|	hypothetical protein CICLE_v10013033mg [Citrus clementina]	56 bits(133)	3,47E-17	60%	2%
	gi|672157849|ref|XP_008798646.1|	PREDICTED: SUMO-conjugating enzyme UBC9 isoform X2 [Phoenix dactylifera]	55 bits(131)	9,42E-18	80%	0%
	gi|567904810|ref|XP_006444893.1|	hypothetical protein CICLE_v10022714mg [Citrus clementina]	54 bits(127)	1,52E-17	86%	0%
	gi|413952107|gb|AFW84756.1|	putative ubiquitin-conjugating enzyme family [Zea mays]	54 bits(128)	4,90E-17	96%	0%
	gi|557729277|dbj|GAD92267.1|	ubiquitin conjugating enzyme (UbcD), putative [Byssochlamys spectabilis No. 5]	28 bits(60)	1,08E-17	71%	0%
	gi|449444332|ref|XP_004139929.1|	PREDICTED: ubiquitin-conjugating enzyme E2 28-like isoform 2 [Cucumis sativus]	54 bits(129)	1,78E-17	96%	0%
	gi|641867709|gb|KDO86393.1|	hypothetical protein CISIN_1g032055mg [Citrus sinensis]	54 bits(127)	1,30E-17	86%	0%
	gi|567858848|ref|XP_006422107.1|	hypothetical protein CICLE_v10006155mg [Citrus clementina]	54 bits(129)	1,89E-17	86%	0%
SLCAPL03E05	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	92 bits(228)	1,52E-18	98%	0%
	gi|571207123|emb|CDK78388.1|	Transcriptional repressor of the lac operon [Klebsiella pneumoniae IS22]	77 bits(187)	4,72E-14	88%	3%
	gi|487912019|ref|WP_001985485.1|	SocE [Bacillus cereus]	86 bits(210)	5,70E-18	100%	0%
	gi|27475622|emb|CAD59768.1|	putative reverse transcriptase [Cicer arietinum]	74 bits(180)	5,53E-14	100%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	103 bits(255)	1,93E-24	100%	0%
	gi|9652070|gb|AAF91388.1|AF263243_1	SocE [Myxococcus xanthus]	90 bits(221)	4,92E-17	54%	0%
	gi|386242568|gb|EII84303.1|	LacI transcriptional repressor [Escherichia coli 3003]	77 bits(188)	4,39E-13	88%	0%
	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	92 bits(226)	2,64E-20	100%	0%
	gi|330752400|emb|CBL87351.1|	hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]	77 bits(187)	2,26E-14	97%	0%
	gi|27475620|emb|CAD59767.1|	putative reverse transcriptase [Cicer arietinum]	68 bits(164)	7,59E-12	94%	0%
SLCAPL03E08	No Hits.					
SLCAPL03F01	No Hits.					
SLCAPL03F02	gi|587933046|gb|EXC20047.1|	Eukaryotic translation initiation factor 5A-4 [Morus notabilis]	319 bits(817)	1,73E-106	94%	0%
	gi|350536527|ref|NP_001234507.1|	eukaryotic translation initiation factor 5A-3 [Solanum lycopersicum]	319 bits(815)	7,48E-107	97%	0%
	gi|604316625|gb|EYU28817.1|	hypothetical protein MIMGU_mgv1a015401mg [Erythranthe guttata]	319 bits(815)	7,65E-107	97%	0%
	gi|502126980|ref|XP_004499516.1|	PREDICTED: eukaryotic translation initiation factor 5A-4-like [Cicer arietinum]	317 bits(812)	1,93E-106	96%	0%
	gi|568214501|ref|NP_001275460.1|	eukaryotic translation initiation factor 5A-4 [Solanum tuberosum]	318 bits(814)	8,53E-107	96%	0%
	gi|658048835|ref|XP_008360103.1|	PREDICTED: eukaryotic translation initiation factor 5A-2 [Malus domestica]	317 bits(811)	2,32E-106	97%	0%
	gi|532759673|gb|AGU01536.1|	eukaryotic translation initiation factor 5A [Picrorhiza kurrooa]	317 bits(811)	2,40E-106	97%	0%
	gi|593329453|ref|XP_007138153.1|	hypothetical protein PHAVU_009G184600g [Phaseolus vulgaris]	320 bits(819)	1,54E-107	97%	0%
	gi|565354712|ref|XP_006344253.1|	PREDICTED: eukaryotic translation initiation factor 5A-4-like [Solanum tuberosum]	318 bits(813)	1,25E-106	96%	0%

	gi|3024021|sp|P56336.1|IF5A4_SOLTU	RecName: Full=Eukaryotic translation initiation factor 5A-4; Short=eIF-5A-4; AltName: Full=eIF-4D [Solanum tuberosum]	319 bits(816)	4,11E-107	97%	0%
SLCAPL03F08	No Hits.					
SLCAPL03F09	gi|343526662|gb|AEM46061.1|	actin [Viscum album]	155 bits(391)	5,51E-46	82%	0%
	gi|449518875|ref|XP_004166461.1|	PREDICTED: LOW QUALITY PROTEIN: actin-101-like [Cucumis sativus]	153 bits(386)	2,94E-45	81%	0%
	gi|209981337|gb|ACJ05349.1|	actin [Camellia sinensis]	156 bits(394)	5,46E-45	82%	0%
	gi|56961766|gb|AAW31852.1|	actin [Vitis vinifera]	156 bits(392)	1,09E-45	82%	0%
	gi|209981339|gb|ACJ05350.1|	actin [Camellia sinensis]	157 bits(396)	3,12E-45	82%	0%
	gi|3860317|emb|CAA10126.1|	actin [Cicer arietinum]	153 bits(384)	5,78E-45	80%	0%
	gi|425872892|gb|AFY06656.1|	actin 2, partial [Carica papaya]	157 bits(396)	2,17E-45	82%	0%
	gi|209981335|gb|ACJ05348.1|	actin [Camellia sinensis]	157 bits(396)	3,29E-45	82%	0%
	gi|326417692|gb|ADZ73581.1|	actin 1 [Vaccaria hispanica]	156 bits(392)	2,86E-45	81%	0%
	gi|2244734|dbj|BAA21108.1|	actin [Gossypium hirsutum]	157 bits(395)	3,81E-45	82%	0%
SLCAPL03G02	gi|565386463|ref|XP_006359031.1|	PREDICTED: probable signal peptidase complex subunit 2-like [Solanum tuberosum]	102 bits(254)	1,05E-22	86%	0%
	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	92 bits(228)	1,93E-18	98%	0%
	gi|661882480|emb|CDP14060.1|	unnamed protein product [Coffea canephora]	87 bits(214)	6,79E-18	78%	0%
	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	92 bits(226)	3,20E-20	100%	0%
	gi|449533399|ref|XP_004173663.1|	PREDICTED: probable signal peptidase complex subunit 2-like, partial [Cucumis sativus]	84 bits(206)	7,13E-17	76%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	103 bits(255)	2,52E-24	100%	0%
	gi|487912019|ref|WP_001985485.1|	SocE [Bacillus cereus]	91 bits(225)	7,09E-20	100%	0%
	gi|604342116|gb|EYU41260.1|	hypothetical protein MIMGU_mgv1a014171mg [Erythranthe guttata]	86 bits(211)	9,75E-17	78%	0%
	gi|460385621|ref|XP_004238501.1|	PREDICTED: probable signal peptidase complex subunit 2-like [Solanum lycopersicum]	100 bits(247)	7,39E-23	84%	0%
	gi|9652070|gb|AAF91388.1|AF263243_1	SocE [Myxococcus xanthus]	95 bits(234)	1,13E-18	50%	1%
SLCAPL03G03	gi|460373322|ref|XP_004232469.1|	PREDICTED: V-type proton ATPase 16 kDa proteolipid subunit c2-like isoform 1 [Solanum lycopersicum]	318 bits(814)	3,05E-106	99%	0%
	gi|661888990|emb|CDP07433.1|	unnamed protein product [Coffea canephora]	317 bits(810)	1,29E-105	99%	0%
	gi|596187519|ref|XP_007223415.1|	hypothetical protein PRUPE_ppa011277mg [Prunus persica]	318 bits(813)	2,35E-105	96%	0%
	gi|255545382|ref|XP_002513751.1|	vacuolar ATP synthase proteolipid subunit 1, 2, 3, putative [Ricinus communis]	318 bits(813)	5,24E-106	98%	0%
	gi|755150|gb|AAA82977.1|	vacuolar H+-ATPase proteolipid (16 kDa) subunit [Gossypium hirsutum]	316 bits(809)	1,60E-105	99%	0%
	gi|659088047|ref|XP_008444773.1|	PREDICTED: V-type proton ATPase 16 kDa proteolipid subunit [Cucumis melo]	315 bits(807)	2,91E-105	99%	0%
	gi|224085796|ref|XP_002307699.1|	hypothetical protein POPTR_0005s25660g [Populus trichocarpa]	317 bits(811)	6,76E-106	99%	0%
	gi|224066821|ref|XP_002302232.1|	hypothetical protein POPTR_0002s08330g [Populus trichocarpa]	316 bits(809)	1,75E-105	99%	0%
	gi|2493148|sp|Q40585.1|VATL_TOBAC	RecName: Full=V-type proton ATPase 16 kDa proteolipid subunit; Short=V-ATPase 16 kDa proteolipid subunit; AltName: Full=Vacuolar proton pump 16 kDa proteolipid subunit [Nicotiana tabacum]	317 bits(811)	7,38E-106	99%	0%
	gi|30686594|ref|NP_564098.2|	VACUOLAR-TYPE H+ ATPASE C2 [Arabidopsis thaliana]	316 bits(808)	2,10E-105	99%	0%
SLCAPL03G04	No Hits.					
SLCAPL03G09	gi|77416953|gb|ABA81872.1|	ribosome-associated protein p40-like [Solanum tuberosum]	74 bits(180)	4,00E-12	43%	16%
	gi|460377064|ref|XP_004234315.1|	PREDICTED: 40S ribosomal protein SA-like [Solanum lycopersicum]	73 bits(178)	1,14E-11	43%	17%
	gi|568215246|ref|NP_001275039.1|	40S ribosomal protein SA-like [Solanum tuberosum]	79 bits(193)	8,32E-14	44%	19%
SLCAPL03G12	No Hits.					
SLCAPL03H09	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	92 bits(226)	2,21E-20	100%	0%
	gi|571207123|emb|CDK78388.1|	Transcriptional repressor of the lac operon [Klebsiella pneumoniae IS22]	75 bits(182)	1,99E-13	100%	0%
	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	92 bits(228)	1,20E-18	98%	0%
	gi|386242568|gb|EII84303.1|	LacI transcriptional repressor [Escherichia coli 3003]	76 bits(185)	8,62E-13	97%	0%
	gi|330752400|emb|CBL87351.1|	hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]	77 bits(188)	1,15E-14	97%	0%
	gi|27475620|emb|CAD59767.1|	putative reverse transcriptase [Cicer arietinum]	69 bits(166)	3,97E-12	94%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	93 bits(230)	5,22E-21	100%	0%
	gi|27475622|emb|CAD59768.1|	putative reverse transcriptase [Cicer arietinum]	74 bits(181)	3,35E-14	100%	0%
	gi|330752561|emb|CBL87507.1|	hypothetical protein S18_873_0002 [uncultured Flavobacteriia bacterium]	70 bits(169)	4,40E-12	100%	0%
SLCAPL03H11	gi|661894310|emb|CDP02751.1|	unnamed protein product [Coffea canephora]	76 bits(186)	2,90E-16	74%	0%
	gi|590652591|ref|XP_007033193.1|	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein, putative [Theobroma cacao]	74 bits(180)	3,84E-15	70%	0%
	gi|440494829|gb|AGC08429.1|	lipid transfer protein [Gossypium hirsutum]	72 bits(174)	1,64E-14	70%	0%
	gi|587933560|gb|EXC20523.1|	hypothetical protein L484_027077 [Morus notabilis]	75 bits(182)	9,58E-16	72%	0%
	gi|225452110|ref|XP_002284213.1|	PREDICTED: non-specific lipid-transfer protein 2-like [Vitis vinifera]	73 bits(178)	4,03E-15	74%	0%
	gi|225452105|ref|XP_002284190.1|	PREDICTED: probable non-specific lipid-transfer protein AKCS9-like isoform 1 [Vitis vinifera]	71 bits(172)	3,31E-14	67%	0%
	gi|357508195|ref|XP_003624386.1|	Non-specific lipid-transfer protein [Medicago truncatula]	74 bits(179)	2,69E-15	74%	0%
	gi|502106509|ref|XP_004492965.1|	PREDICTED: probable non-specific lipid-transfer protein AKCS9-like [Cicer arietinum]	73 bits(177)	6,10E-15	70%	0%
	gi|296087247|emb|CBI33621.3|	unnamed protein product [Vitis vinifera]	73 bits(178)	3,35E-15	74%	0%

	gi|566171515|ref|XP_006383409.1|	hypothetical protein POPTR_0005s15210g [Populus trichocarpa]	73 bits(177)	6,50E-15	70%	0%
SLCAPL04A02	No Hits.					
SLCAPL04A07	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	87 bits(213)	1,73E-18	98%	0%
	gi|27475622|emb|CAD59768.1|	putative reverse transcriptase [Cicer arietinum]	74 bits(180)	5,10E-14	100%	0%
	gi|330752561|emb|CBL87507.1|	hypothetical protein S18_873_0002 [uncultured Flavobacteriia bacterium]	69 bits(168)	7,00E-12	100%	0%
	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	88 bits(216)	4,53E-17	98%	0%
	gi|571207123|emb|CDK78388.1|	Transcriptional repressor of the lac operon [Klebsiella pneumoniae IS22]	75 bits(184)	1,19E-13	88%	3%
	gi|9652070|gb|AAF91388.1|AF263243_1	SocE [Myxococcus xanthus]	83 bits(203)	8,13E-15	53%	0%
	gi|386242568|gb|EII84303.1|	LacI transcriptional repressor [Escherichia coli 3003]	77 bits(187)	5,60E-13	88%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	98 bits(242)	1,17E-22	98%	0%
	gi|330752400|emb|CBL87351.1|	hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]	77 bits(187)	2,08E-14	97%	0%
	gi|27475620|emb|CAD59767.1|	putative reverse transcriptase [Cicer arietinum]	68 bits(164)	6,78E-12	94%	0%
SLCAPL04A11	gi|641836965|gb|KDO55923.1|	hypothetical protein CISIN_1g042287mg, partial [Citrus sinensis]	108 bits(269)	1,43E-25	96%	0%
	gi|115466684|ref|NP_001056941.1|	Os06g0172600 [Oryza sativa Japonica Group]	107 bits(265)	1,94E-25	96%	0%
	gi|661881573|emb|CDP14733.1|	unnamed protein product [Coffea canephora]	110 bits(273)	4,56E-26	96%	0%
	gi|218191764|gb|EEC74191.1|	hypothetical protein OsI_09334 [Oryza sativa Indica Group]	107 bits(267)	1,46E-25	96%	0%
	gi|297743124|emb|CBI35991.3|	unnamed protein product [Vitis vinifera]	108 bits(268)	2,46E-25	96%	0%
	gi|595811839|ref|XP_007203304.1|	hypothetical protein PRUPE_ppa025859mg [Prunus persica]	109 bits(270)	8,48E-26	96%	0%
	gi|297721651|ref|NP_001173188.1|	Os02g0804150 [Oryza sativa Japonica Group]	107 bits(267)	1,64E-25	96%	0%
	gi|567918728|ref|XP_006451370.1|	hypothetical protein CICLE_v10009868mg [Citrus clementina]	109 bits(270)	2,73E-25	96%	0%
	gi|449446564|ref|XP_004141041.1|	PREDICTED: 40S ribosomal protein S30-like isoform 1 [Cucumis sativus]	108 bits(268)	9,07E-26	96%	0%
	gi|222623869|gb|EEE58001.1|	hypothetical protein OsJ_08768 [Oryza sativa Japonica Group]	107 bits(266)	1,83E-25	96%	0%
SLCAPL04B04	gi|157042763|gb|ABV02033.1|	glyceraldehyde 3-phosphate dehydrogenase [Nicotiana langsdorffii x Nicotiana sanderae]	176 bits(446)	6,06E-49	96%	0%
	gi|568214513|ref|NP_001275344.1|	glyceraldehyde-3-phosphate dehydrogenase [Solanum tuberosum]	173 bits(437)	1,33E-47	97%	0%
	gi|217071216|gb|ACJ83968.1|	unknown [Medicago truncatula]	163 bits(412)	2,28E-45	87%	0%
	gi|525314339|ref|NP_001266254.1|	glyceraldehyde-3-phosphate dehydrogenase [Solanum lycopersicum]	174 bits(439)	2,38E-48	97%	0%
	gi|586720439|ref|XP_006848721.1|	hypothetical protein AMTR_s00177p00046770 [Amborella trichopoda]	163 bits(410)	2,45E-46	88%	0%
	gi|106879589|emb|CAJ38378.1|	glyceraldehyde-3-phosphate dehydrogenase [Plantago major]	166 bits(420)	1,06E-47	90%	0%
	gi|604311946|gb|EYU25940.1|	hypothetical protein MIMGU_mgv1a009608mg [Erythranthe guttata]	169 bits(426)	5,94E-46	91%	0%
	gi|120676|sp|P09094.1|G3PC_TOBAC	RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic, partial [Nicotiana tabacum]	178 bits(451)	1,01E-49	97%	0%
	gi|22094840|gb|AAM92008.1|AF527779_1	glyceraldehyde 3-phosphate dehydrogenase [Solanum tuberosum]	173 bits(437)	1,27E-47	97%	0%
	gi|4539543|emb|CAB39974.1|	glyceraldehyde-3-phosphate dehydrogenase [Nicotiana tabacum]	168 bits(424)	1,00E-45	91%	0%
SLCAPL04B08	No Hits.					
SLCAPL04B10	No Hits.					
SLCAPL04C04	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	91 bits(224)	4,25E-20	100%	0%
	gi|571207123|emb|CDK78388.1|	Transcriptional repressor of the lac operon [Klebsiella pneumoniae IS22]	76 bits(185)	9,02E-14	80%	0%
	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	92 bits(226)	2,37E-18	76%	5%
	gi|386242568|gb|EII84303.1|	LacI transcriptional repressor [Escherichia coli 3003]	78 bits(191)	1,67E-13	86%	0%
	gi|330752400|emb|CBL87351.1|	hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]	76 bits(185)	3,32E-14	97%	0%
	gi|27475620|emb|CAD59767.1|	putative reverse transcriptase [Cicer arietinum]	68 bits(164)	6,93E-12	94%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	93 bits(229)	8,61E-21	100%	0%
	gi|27475622|emb|CAD59768.1|	putative reverse transcriptase [Cicer arietinum]	74 bits(180)	4,98E-14	100%	0%
	gi|330752561|emb|CBL87507.1|	hypothetical protein S18_873_0002 [uncultured Flavobacteriia bacterium]	69 bits(167)	8,20E-12	100%	0%
SLCAPL04D01	No Hits.					
SLCAPL04D02	No Hits.					
SLCAPL04D04	No Hits.					
SLCAPL04D07	No Hits.					
SLCAPL04D10	gi|657962143|ref|XP_008372664.1|	PREDICTED: putative ferric-chelate reductase 1 [Malus domestica]	121 bits(302)	4,71E-28	65%	0%
	gi|296088826|emb|CBI38284.3|	unnamed protein product [Vitis vinifera]	121 bits(301)	7,08E-28	68%	0%
	gi|565402691|ref|XP_006366806.1|	PREDICTED: uncharacterized protein LOC102589215 [Solanum tuberosum]	168 bits(423)	3,45E-45	100%	0%
	gi|565354913|ref|XP_006344352.1|	PREDICTED: uncharacterized protein LOC102596514 [Solanum tuberosum]	121 bits(301)	5,56E-28	66%	0%
	gi|694356420|ref|XP_009358999.1|	PREDICTED: putative ferric-chelate reductase 1 [Pyrus x bretschneideri]	120 bits(299)	1,34E-27	61%	0%
	gi|460393722|ref|XP_004242458.1|	PREDICTED: uncharacterized protein LOC101263424 [Solanum lycopersicum]	161 bits(407)	7,79E-43	96%	0%
	gi|657981045|ref|XP_008382534.1|	PREDICTED: putative ferric-chelate reductase 1 [Malus domestica]	121 bits(301)	5,56E-28	62%	0%
	gi|567911171|ref|XP_006447899.1|	hypothetical protein CICLE_v10017719mg [Citrus clementina]	119 bits(298)	1,36E-28	62%	0%
	gi|147783172|emb|CAN62113.1|	hypothetical protein VITISV_036669 [Vitis vinifera]	121 bits(301)	1,99E-28	68%	0%

	gi|359495414|ref|XP_002270178.2|	PREDICTED: putative ferric-chelate reductase 1-like [Vitis vinifera]	121 bits(301)	6,30E-28	68%	0%
SLCAPL04D12	gi|567911171|ref|XP_006447899.1|	hypothetical protein CICLE_v10017719mg [Citrus clementina]	119 bits(298)	1,36E-28	62%	0%
	gi|657981045|ref|XP_008382534.1|	PREDICTED: putative ferric-chelate reductase 1 [Malus domestica]	121 bits(301)	5,56E-28	62%	0%
	gi|147783172|emb|CAN62113.1|	hypothetical protein VITISV_036669 [Vitis vinifera]	121 bits(301)	1,99E-28	68%	0%
	gi|359495414|ref|XP_002270178.2|	PREDICTED: putative ferric-chelate reductase 1-like [Vitis vinifera]	121 bits(301)	6,30E-28	68%	0%
	gi|565402691|ref|XP_006366806.1|	PREDICTED: uncharacterized protein LOC102589215 [Solanum tuberosum]	168 bits(423)	3,45E-45	100%	0%
	gi|657962143|ref|XP_008372664.1|	PREDICTED: putative ferric-chelate reductase 1 [Malus domestica]	121 bits(302)	4,71E-28	65%	0%
	gi|296088826|emb|CBI38284.3|	unnamed protein product [Vitis vinifera]	121 bits(301)	7,08E-28	68%	0%
	gi|460393722|ref|XP_004242458.1|	PREDICTED: uncharacterized protein LOC101263424 [Solanum lycopersicum]	161 bits(407)	7,79E-43	96%	0%
	gi|565354913|ref|XP_006344352.1|	PREDICTED: uncharacterized protein LOC102596514 [Solanum tuberosum]	121 bits(301)	5,56E-28	66%	0%
	gi|694356420|ref|XP_009358999.1|	PREDICTED: putative ferric-chelate reductase 1 [Pyrus x bretschneideri]	120 bits(299)	1,34E-27	61%	0%
SLCAPL04E02	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	103 bits(255)	3,39E-24	100%	0%
	gi|9652070|gb|AAF91388.1|AF263243_1	SocE [Myxococcus xanthus]	91 bits(224)	3,04E-17	54%	1%
	gi|386242568|gb|EII84303.1|	LacI transcriptional repressor [Escherichia coli 3003]	77 bits(188)	8,92E-13	88%	0%
	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	92 bits(226)	3,90E-20	100%	0%
	gi|330752400|emb|CBL87351.1|	hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]	77 bits(187)	3,03E-14	97%	0%
	gi|674267870|emb|CDI96482.1|	hypothetical protein EmuJ_000005500 [Echinococcus multilocularis]	47 bits(110)	3,10E-12	95%	0%
	gi|487912019|ref|WP_001985485.1|	SocE [Bacillus cereus]	91 bits(225)	8,60E-20	100%	0%
	gi|571207123|emb|CDK78388.1|	Transcriptional repressor of the lac operon [Klebsiella pneumoniae IS22]	77 bits(188)	5,20E-14	88%	3%
	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	92 bits(228)	2,53E-18	98%	0%
	gi|27475622|emb|CAD59768.1|	putative reverse transcriptase [Cicer arietinum]	74 bits(180)	7,78E-14	100%	0%
SLCAPL04E04	gi|487912019|ref|WP_001985485.1|	SocE [Bacillus cereus]	91 bits(225)	8,60E-20	100%	0%
	gi|571207123|emb|CDK78388.1|	Transcriptional repressor of the lac operon [Klebsiella pneumoniae IS22]	77 bits(188)	5,20E-14	88%	3%
	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	92 bits(228)	2,53E-18	98%	0%
	gi|27475622|emb|CAD59768.1|	putative reverse transcriptase [Cicer arietinum]	74 bits(180)	7,78E-14	100%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	103 bits(255)	3,39E-24	100%	0%
	gi|9652070|gb|AAF91388.1|AF263243_1	SocE [Myxococcus xanthus]	91 bits(224)	3,04E-17	54%	1%
	gi|386242568|gb|EII84303.1|	LacI transcriptional repressor [Escherichia coli 3003]	77 bits(188)	8,92E-13	88%	0%
	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	92 bits(226)	3,90E-20	100%	0%
	gi|330752400|emb|CBL87351.1|	hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]	77 bits(187)	3,03E-14	97%	0%
	gi|674267870|emb|CDI96482.1|	hypothetical protein EmuJ_000005500 [Echinococcus multilocularis]	47 bits(110)	3,10E-12	95%	0%
SLCAPL04E08	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	103 bits(255)	3,01E-24	100%	0%
	gi|460373941|ref|XP_004232770.1|	PREDICTED: suberization-associated anionic peroxidase 2-like isoform 2 [Solanum lycopersicum]	94 bits(233)	6,18E-19	94%	0%
	gi|565360830|ref|XP_006347168.1|	PREDICTED: suberization-associated anionic peroxidase [Solanum tuberosum]	93 bits(229)	1,82E-18	91%	0%
	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	92 bits(226)	3,61E-20	100%	0%
	gi|460373939|ref|XP_004232769.1|	PREDICTED: suberization-associated anionic peroxidase 2-like isoform 1 [Solanum lycopersicum]	94 bits(233)	6,96E-19	94%	0%
	gi|110825730|sp|P12437.2|PERX_SOLTU	RecName: Full=Suberization-associated anionic peroxidase; AltName: Full=POPA; Flags: Precursor [Solanum tuberosum]	93 bits(229)	1,84E-18	91%	0%
	gi|487912019|ref|WP_001985485.1|	SocE [Bacillus cereus]	91 bits(225)	7,97E-20	100%	0%
	gi|9652070|gb|AAF91388.1|AF263243_1	SocE [Myxococcus xanthus]	96 bits(236)	7,56E-19	50%	1%
	gi|460373943|ref|XP_004232771.1|	PREDICTED: suberization-associated anionic peroxidase 1-like [Solanum lycopersicum]	95 bits(234)	3,76E-19	94%	0%
	gi|169555|gb|AAA33837.1|	anionic peroxidase, partial [Solanum tuberosum]	93 bits(229)	1,75E-18	91%	0%
SLCAPL04F01	No Hits.					
SLCAPL04G01	No Hits.					
SLCAPL04G07	No Hits.					
SLCAPL04G08	No Hits.					
SLCAPL04G10	gi|385653721|emb|CBL94689.1|	eukaryotic translation initiation factor, partial [Capsicum baccatum]	334 bits(854)	1,01E-112	96%	0%
	gi|385653731|emb|CBL94694.1|	eukaryotic translation initiation factor, partial [Capsicum pubescens]	332 bits(851)	2,65E-112	95%	0%
	gi|385145188|emb|CBL81074.1|	eukaryotyc translation initiation factor 4E, partial [Capsicum baccatum]	333 bits(853)	1,20E-112	96%	0%
	gi|385653719|emb|CBL94688.1|	eukaryotic translation initiation factor, partial [Capsicum chacoense]	332 bits(851)	2,71E-112	96%	0%
	gi|67005941|gb|AAY62607.1|	eukaryotic initiation factor 4E [Capsicum annuum]	334 bits(855)	7,62E-113	96%	0%
	gi|385653713|emb|CBL94685.1|	eukaryotic translation initiation factor, partial [Capsicum annuum]	333 bits(853)	1,29E-112	96%	0%
	gi|385653741|emb|CBL94699.1|	eukaryotic translation initiation factor, partial [Capsicum pubescens]	332 bits(851)	2,80E-112	95%	0%
	gi|290490837|emb|CBJ34336.1|	translation initiation factor eIF(iso)4E [Solanum tuberosum]	334 bits(854)	9,97E-113	96%	0%
	gi|385653733|emb|CBL94695.1|	eukaryotic translation initiation factor, partial [Capsicum pubescens]	333 bits(852)	1,49E-112	96%	0%
	gi|385653729|emb|CBL94693.1|	eukaryotic translation initiation factor, partial [Capsicum frutescens]	332 bits(850)	3,64E-112	95%	0%
SLCAPL04G12	gi|503320473|ref|WP_013555134.1|	hypothetical protein [Bacillus thuringiensis]	69 bits(166)	5,16E-11	100%	0%

<table>
<tr><td>SLCAPL04H01</td><td>gi|503320473|ref|WP_013555134.1|</td><td>hypothetical protein [Bacillus thuringiensis]</td><td>69 bits(166)</td><td>5,16E-11</td><td>100%</td><td>0%</td></tr>
<tr><td>SLCAPL04H05</td><td>No Hits.</td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>SLCAPL04H11</td><td>gi|27475622|emb|CAD59768.1|</td><td>putative reverse transcriptase [Cicer arietinum]</td><td>65 bits(158)</td><td>4,32E-11</td><td>94%</td><td>0%</td></tr>
<tr><td></td><td>gi|495126628|ref|WP_007851439.1|</td><td>hypothetical protein, partial [Bacteroides dorei]</td><td>65 bits(157)</td><td>8,61E-11</td><td>94%</td><td>0%</td></tr>
<tr><td></td><td>gi|330752400|emb|CBL87351.1|</td><td>hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]</td><td>73 bits(177)</td><td>4,45E-13</td><td>92%</td><td>0%</td></tr>
<tr><td>SLCAPL05A01</td><td>No Hits.</td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>SLCAPL05A02</td><td>gi|491131127|ref|WP_004989554.1|</td><td>hypothetical protein [Streptomyces ghanaensis]</td><td>69 bits(166)</td><td>5,15E-12</td><td>82%</td><td>0%</td></tr>
<tr><td></td><td>gi|299008123|gb|ADJ00052.1|</td><td>chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]</td><td>72 bits(174)</td><td>2,47E-11</td><td>81%</td><td>0%</td></tr>
<tr><td></td><td>gi|495126628|ref|WP_007851439.1|</td><td>hypothetical protein, partial [Bacteroides dorei]</td><td>69 bits(167)</td><td>3,76E-12</td><td>82%</td><td>0%</td></tr>
<tr><td>SLCAPL05A05</td><td>No Hits.</td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>SLCAPL05B02</td><td>No Hits.</td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>SLCAPL05B03</td><td>No Hits.</td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>SLCAPL05B04</td><td>No Hits.</td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>SLCAPL05B06</td><td>gi|460378290|ref|XP_004234906.1|</td><td>PREDICTED: salicylic acid-binding protein 2-like [Solanum lycopersicum]</td><td>61 bits(147)</td><td>5,85E-22</td><td>78%</td><td>0%</td></tr>
<tr><td></td><td>gi|56967124|pdb|1XKL|A</td><td>Chain A, Crystal Structure Of Salicylic Acid-Binding Protein 2 (Sabp2) From Nicotiana Tabacum, Nesg Target Ar2241</td><td>46 bits(108)</td><td>2,75E-19</td><td>58%</td><td>0%</td></tr>
<tr><td></td><td>gi|75324631|sp|Q6RYA0.1|SABP2_TOBAC</td><td>RecName: Full=Salicylic acid-binding protein 2; Short=NtSABP2; AltName: Full=Methyl salicylate esterase [Nicotiana tabacum]</td><td>51 bits(120)</td><td>6,42E-21</td><td>64%</td><td>0%</td></tr>
<tr><td></td><td>gi|460375257|ref|XP_004233423.1|</td><td>PREDICTED: salicylic acid-binding protein 2-like isoform 2 [Solanum lycopersicum]</td><td>79 bits(193)</td><td>7,66E-15</td><td>47%</td><td>7%</td></tr>
<tr><td></td><td>gi|565388974|ref|XP_006360241.1|</td><td>PREDICTED: salicylic acid-binding protein 2-like [Solanum tuberosum]</td><td>55 bits(131)</td><td>2,02E-23</td><td>71%</td><td>0%</td></tr>
<tr><td></td><td>gi|565388978|ref|XP_006360243.1|</td><td>PREDICTED: salicylic acid-binding protein 2-like [Solanum tuberosum]</td><td>62 bits(148)</td><td>6,21E-20</td><td>78%</td><td>0%</td></tr>
<tr><td></td><td>gi|406365498|gb|AFS35576.1|</td><td>salicylic acid-binding protein 2 [Nicotiana benthamiana]</td><td>77 bits(188)</td><td>3,57E-14</td><td>81%</td><td>0%</td></tr>
<tr><td></td><td>gi|565396023|ref|XP_006363634.1|</td><td>PREDICTED: salicylic acid-binding protein 2-like [Solanum tuberosum]</td><td>60 bits(144)</td><td>6,34E-23</td><td>75%</td><td>0%</td></tr>
<tr><td></td><td>gi|61679532|pdb|1Y7H|A</td><td>Chain A, Structural And Biochemical Studies Identify Tobacco Sabp2 As A Methylsalicylate Esterase And Further Implicate It In Plant Innate Immunity, Northeast Structural Genomics Target Ar2241</td><td>46 bits(108)</td><td>2,33E-19</td><td>58%</td><td>0%</td></tr>
<tr><td></td><td>gi|565388976|ref|XP_006360242.1|</td><td>PREDICTED: salicylic acid-binding protein 2-like [Solanum tuberosum]</td><td>75 bits(184)</td><td>1,42E-13</td><td>79%</td><td>0%</td></tr>
<tr><td>SLCAPL05B09</td><td>gi|661893199|emb|CDP03008.1|</td><td>unnamed protein product [Coffea canephora]</td><td>82 bits(200)</td><td>2,17E-16</td><td>71%</td><td>1%</td></tr>
<tr><td></td><td>gi|672163347|ref|XP_008801520.1|</td><td>PREDICTED: uncharacterized membrane protein At1g06890-like isoform X1 [Phoenix dactylifera]</td><td>75 bits(184)</td><td>3,49E-14</td><td>76%</td><td>0%</td></tr>
<tr><td></td><td>gi|460394200|ref|XP_004242692.1|</td><td>PREDICTED: uncharacterized membrane protein At1g06890-like isoform 2 [Solanum lycopersicum]</td><td>87 bits(215)</td><td>1,44E-18</td><td>86%</td><td>0%</td></tr>
<tr><td></td><td>gi|527194565|gb|EPS64147.1|</td><td>hypothetical protein M569_10633, partial [Genlisea aurea]</td><td>80 bits(195)</td><td>7,21E-16</td><td>78%</td><td>0%</td></tr>
<tr><td></td><td>gi|641843073|gb|KDO61975.1|</td><td>hypothetical protein CISIN_1g016521mg [Citrus sinensis]</td><td>75 bits(184)</td><td>4,19E-14</td><td>64%</td><td>0%</td></tr>
<tr><td></td><td>gi|460394198|ref|XP_004242691.1|</td><td>PREDICTED: uncharacterized membrane protein At1g06890-like isoform 1 [Solanum lycopersicum]</td><td>87 bits(214)</td><td>2,08E-18</td><td>86%</td><td>0%</td></tr>
<tr><td></td><td>gi|565401413|ref|XP_006366196.1|</td><td>PREDICTED: uncharacterized membrane protein At1g06890-like isoform X1 [Solanum tuberosum]</td><td>85 bits(209)</td><td>9,35E-18</td><td>84%</td><td>0%</td></tr>
<tr><td></td><td>gi|294464022|gb|ADE77531.1|</td><td>unknown [Picea sitchensis]</td><td>78 bits(190)</td><td>6,85E-15</td><td>67%</td><td>0%</td></tr>
<tr><td></td><td>gi|604332788|gb|EYU37305.1|</td><td>hypothetical protein MIMGU_mgv1a008024mg [Erythranthe guttata]</td><td>84 bits(207)</td><td>2,36E-17</td><td>80%</td><td>0%</td></tr>
<tr><td></td><td>gi|672163349|ref|XP_008801521.1|</td><td>PREDICTED: uncharacterized membrane protein At1g06890-like isoform X2 [Phoenix dactylifera]</td><td>75 bits(184)</td><td>1,79E-14</td><td>76%</td><td>0%</td></tr>
<tr><td>SLCAPL05B10</td><td>gi|661877002|emb|CDP19077.1|</td><td>unnamed protein product [Coffea canephora]</td><td>70 bits(170)</td><td>1,34E-11</td><td>59%</td><td>0%</td></tr>
<tr><td></td><td>gi|604343907|gb|EYU42724.1|</td><td>hypothetical protein MIMGU_mgv1a009970mg [Erythranthe guttata]</td><td>68 bits(165)</td><td>8,61E-11</td><td>78%</td><td>0%</td></tr>
<tr><td></td><td>gi|225449158|ref|XP_002278274.1|</td><td>PREDICTED: Golgi to ER traffic protein 4 homolog [Vitis vinifera]</td><td>69 bits(168)</td><td>2,73E-11</td><td>76%</td><td>0%</td></tr>
<tr><td></td><td>gi|565397344|ref|XP_006364258.1|</td><td>PREDICTED: Golgi to ER traffic protein 4 homolog [Solanum tuberosum]</td><td>83 bits(204)</td><td>2,71E-16</td><td>75%</td><td>0%</td></tr>
<tr><td></td><td>gi|296086073|emb|CBI31514.3|</td><td>unnamed protein product [Vitis vinifera]</td><td>70 bits(171)</td><td>4,35E-11</td><td>76%</td><td>0%</td></tr>
<tr><td></td><td>gi|460398486|ref|XP_004244790.1|</td><td>PREDICTED: Golgi to ER traffic protein 4 homolog [Solanum lycopersicum]</td><td>82 bits(201)</td><td>8,47E-16</td><td>71%</td><td>0%</td></tr>
<tr><td></td><td>gi|566182316|ref|XP_002312037.2|</td><td>hypothetical protein POPTR_0008s04370g [Populus trichocarpa]</td><td>68 bits(165)</td><td>7,12E-11</td><td>76%</td><td>0%</td></tr>
<tr><td>SLCAPL05C02</td><td>gi|1146426|gb|AAA85122.1|</td><td>polyphenol oxidase [Solanum tuberosum]</td><td>128 bits(321)</td><td>5,07E-30</td><td>85%</td><td>0%</td></tr>
<tr><td></td><td>gi|387538851|gb|AFJ79641.1|</td><td>chloroplast polyphenol oxidase [Solanum melongena]</td><td>125 bits(312)</td><td>8,94E-29</td><td>86%</td><td>1%</td></tr>
<tr><td></td><td>gi|251851953|gb|ACT22523.1|</td><td>chloroplast polyphenol oxidase precursor [Solanum melongena]</td><td>135 bits(339)</td><td>1,96E-32</td><td>93%</td><td>0%</td></tr>
<tr><td></td><td>gi|565399694|ref|XP_006365382.1|</td><td>PREDICTED: polyphenol oxidase B, chloroplastic-like [Solanum tuberosum]</td><td>127 bits(317)</td><td>1,81E-29</td><td>84%</td><td>0%</td></tr>
<tr><td></td><td>gi|387538847|gb|AFJ79639.1|</td><td>chloroplast polyphenol oxidase [Solanum melongena]</td><td>125 bits(312)</td><td>9,20E-29</td><td>86%</td><td>1%</td></tr>
<tr><td></td><td>gi|460401029|ref|XP_004246032.1|</td><td>PREDICTED: polyphenol oxidase B, chloroplastic-like [Solanum lycopersicum]</td><td>131 bits(329)</td><td>4,08E-31</td><td>87%</td><td>0%</td></tr>
<tr><td></td><td>gi|387538853|gb|AFJ79642.1|</td><td>chloroplast polyphenol oxidase [Solanum melongena]</td><td>125 bits(313)</td><td>7,27E-29</td><td>86%</td><td>1%</td></tr>
<tr><td></td><td>gi|387538855|gb|AFJ79643.1|</td><td>chloroplast polyphenol oxidase [Solanum melongena]</td><td>125 bits(312)</td><td>9,48E-29</td><td>86%</td><td>1%</td></tr>
<tr><td></td><td>gi|295881970|gb|ADG56700.1|</td><td>chloroplast polyphenol oxidase precursor [Solanum melongena]</td><td>129 bits(323)</td><td>3,58E-30</td><td>89%</td><td>1%</td></tr>
<tr><td></td><td>gi|238836380|gb|ACR61398.1|</td><td>polyphenol oxidase [Solanum melongena]</td><td>125 bits(312)</td><td>8,26E-29</td><td>86%</td><td>1%</td></tr>
<tr><td>SLCAPL05C04</td><td>gi|460401029|ref|XP_004246032.1|</td><td>PREDICTED: polyphenol oxidase B, chloroplastic-like [Solanum lycopersicum]</td><td>131 bits(329)</td><td>4,08E-31</td><td>87%</td><td>0%</td></tr>
<tr><td></td><td>gi|387538853|gb|AFJ79642.1|</td><td>chloroplast polyphenol oxidase [Solanum melongena]</td><td>125 bits(313)</td><td>7,27E-29</td><td>86%</td><td>1%</td></tr>
<tr><td></td><td>gi|387538855|gb|AFJ79643.1|</td><td>chloroplast polyphenol oxidase [Solanum melongena]</td><td>125 bits(312)</td><td>9,48E-29</td><td>86%</td><td>1%</td></tr>
<tr><td></td><td>gi|295881970|gb|ADG56700.1|</td><td>chloroplast polyphenol oxidase precursor [Solanum melongena]</td><td>129 bits(323)</td><td>3,58E-30</td><td>89%</td><td>1%</td></tr>
</table>

<table>
<tr><td></td><td>gi|238836380|gb|ACR61398.1|</td><td>polyphenol oxidase [Solanum melongena]</td><td>125 bits(312)</td><td>8,26E-29</td><td>86%</td><td>1%</td></tr>
<tr><td></td><td>gi|1146426|gb|AAA85122.1|</td><td>polyphenol oxidase [Solanum tuberosum]</td><td>128 bits(321)</td><td>5,07E-30</td><td>85%</td><td>0%</td></tr>
<tr><td></td><td>gi|387538851|gb|AFJ79641.1|</td><td>chloroplast polyphenol oxidase [Solanum melongena]</td><td>125 bits(312)</td><td>8,94E-29</td><td>86%</td><td>1%</td></tr>
<tr><td></td><td>gi|251851953|gb|ACT22523.1|</td><td>chloroplast polyphenol oxidase precursor [Solanum melongena]</td><td>135 bits(339)</td><td>1,96E-32</td><td>93%</td><td>0%</td></tr>
<tr><td></td><td>gi|565399694|ref|XP_006365382.1|</td><td>PREDICTED: polyphenol oxidase B, chloroplastic-like [Solanum tuberosum]</td><td>127 bits(317)</td><td>1,81E-29</td><td>84%</td><td>0%</td></tr>
<tr><td></td><td>gi|387538847|gb|AFJ79639.1|</td><td>chloroplast polyphenol oxidase [Solanum melongena]</td><td>125 bits(312)</td><td>9,20E-29</td><td>86%</td><td>1%</td></tr>
<tr><td>SLCAPL05C06</td><td>No Hits.</td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>SLCAPL05C07</td><td>No Hits.</td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>SLCAPL05C10</td><td>No Hits.</td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>SLCAPL05D01</td><td>gi|350539449|ref|NP_001234138.1|</td><td>profilin [Solanum lycopersicum]</td><td>228 bits(580)</td><td>1,30E-71</td><td>80%</td><td>0%</td></tr>
<tr><td></td><td>gi|460412518|ref|XP_004251645.1|</td><td>PREDICTED: profilin-1-like [Solanum lycopersicum]</td><td>243 bits(620)</td><td>1,26E-77</td><td>89%</td><td>0%</td></tr>
<tr><td></td><td>gi|255546279|ref|XP_002514199.1|</td><td>profilin, putative [Ricinus communis]</td><td>229 bits(583)</td><td>3,62E-72</td><td>80%</td><td>0%</td></tr>
<tr><td></td><td>gi|60418864|gb|AAX19859.1|</td><td>profilin 2 [Malus domestica]</td><td>228 bits(579)</td><td>1,76E-71</td><td>80%</td><td>0%</td></tr>
<tr><td></td><td>gi|565373896|ref|XP_006353502.1|</td><td>PREDICTED: profilin-1-like [Solanum tuberosum]</td><td>242 bits(615)</td><td>5,24E-77</td><td>89%</td><td>0%</td></tr>
<tr><td></td><td>gi|658004946|ref|XP_008337609.1|</td><td>PREDICTED: profilin-2 [Malus domestica]</td><td>228 bits(581)</td><td>8,53E-72</td><td>81%</td><td>0%</td></tr>
<tr><td></td><td>gi|284520994|gb|ADB93072.1|</td><td>profilin-1 [Jatropha curcas]</td><td>233 bits(594)</td><td>9,88E-74</td><td>82%</td><td>0%</td></tr>
<tr><td></td><td>gi|164510842|emb|CAK93713.1|</td><td>profilin [Malus domestica]</td><td>228 bits(581)</td><td>9,61E-72</td><td>81%</td><td>0%</td></tr>
<tr><td></td><td>gi|60418860|gb|AAX19857.1|</td><td>profilin 2 [Malus domestica]</td><td>228 bits(580)</td><td>1,07E-71</td><td>81%</td><td>0%</td></tr>
<tr><td></td><td>gi|302325341|gb|ADL18409.1|</td><td>profilin [Gossypium hirsutum]</td><td>230 bits(586)</td><td>1,21E-72</td><td>80%</td><td>0%</td></tr>
<tr><td>SLCAPL05D04</td><td>No Hits.</td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>SLCAPL05D09</td><td>gi|460412601|ref|XP_004251686.1|</td><td>PREDICTED: mediator of RNA polymerase II transcription subunit 20a-like [Solanum lycopersicum]</td><td>86 bits(212)</td><td>1,07E-16</td><td>100%</td><td>0%</td></tr>
<tr><td></td><td>gi|641835034|gb|KDO54016.1|</td><td>hypothetical protein CISIN_1g027501mg [Citrus sinensis]</td><td>70 bits(170)</td><td>6,16E-11</td><td>76%</td><td>0%</td></tr>
<tr><td></td><td>gi|661893292|emb|CDP03101.1|</td><td>unnamed protein product [Coffea canephora]</td><td>73 bits(178)</td><td>5,09E-12</td><td>83%</td><td>0%</td></tr>
<tr><td></td><td>gi|629114755|gb|KCW79430.1|</td><td>hypothetical protein EUGRSUZ_C00825 [Eucalyptus grandis]</td><td>69 bits(166)</td><td>8,41E-11</td><td>73%</td><td>0%</td></tr>
<tr><td></td><td>gi|565367569|ref|XP_006350435.1|</td><td>PREDICTED: mediator of RNA polymerase II transcription subunit 20a-like [Solanum tuberosum]</td><td>72 bits(175)</td><td>1,32E-11</td><td>80%</td><td>0%</td></tr>
<tr><td></td><td>gi|565374013|ref|XP_006353559.1|</td><td>PREDICTED: mediator of RNA polymerase II transcription subunit 20a-like [Solanum tuberosum]</td><td>87 bits(213)</td><td>1,04E-16</td><td>100%</td><td>0%</td></tr>
<tr><td></td><td>gi|567872069|ref|XP_006428624.1|</td><td>hypothetical protein CICLE_v10012695mg [Citrus clementina]</td><td>71 bits(173)</td><td>2,57E-11</td><td>76%</td><td>0%</td></tr>
<tr><td>SLCAPL05E02</td><td>gi|415666345|dbj|BAM66423.1|</td><td>calcium-sensing receptor [Nicotiana benthamiana]</td><td>137 bits(344)</td><td>1,47E-70</td><td>84%</td><td>0%</td></tr>
<tr><td></td><td>gi|565459844|ref|XP_006287921.1|</td><td>hypothetical protein CARUB_v10001156mg [Capsella rubella]</td><td>126 bits(316)</td><td>3,14E-63</td><td>76%</td><td>0%</td></tr>
<tr><td></td><td>gi|164459314|gb|ABY57764.1|</td><td>extracellular Ca2+ sensing receptor [Nicotiana tabacum]</td><td>135 bits(338)</td><td>3,61E-70</td><td>83%</td><td>0%</td></tr>
<tr><td></td><td>gi|297812453|ref|XP_002874110.1|</td><td>hypothetical protein ARALYDRAFT_489159 [Arabidopsis lyrata subsp. lyrata]</td><td>124 bits(309)</td><td>7,90E-63</td><td>73%</td><td>0%</td></tr>
<tr><td></td><td>gi|565356427|ref|XP_006345067.1|</td><td>PREDICTED: calcium sensing receptor, chloroplastic-like [Solanum tuberosum]</td><td>143 bits(358)</td><td>1,50E-73</td><td>87%</td><td>0%</td></tr>
<tr><td></td><td>gi|567138689|ref|XP_006394572.1|</td><td>hypothetical protein EUTSA_v10004373mg [Eutrema salsugineum]</td><td>124 bits(310)</td><td>1,89E-64</td><td>73%</td><td>0%</td></tr>
<tr><td></td><td>gi|255541882|ref|XP_002512005.1|</td><td>conserved hypothetical protein [Ricinus communis]</td><td>118 bits(295)</td><td>3,85E-62</td><td>68%</td><td>0%</td></tr>
<tr><td></td><td>gi|460380709|ref|XP_004236097.1|</td><td>PREDICTED: calcium sensing receptor, chloroplastic-like [Solanum lycopersicum]</td><td>143 bits(358)</td><td>2,56E-73</td><td>87%</td><td>0%</td></tr>
<tr><td></td><td>gi|255367590|gb|ACU11587.1|</td><td>extracellular calcium sensing receptor [Liquidambar formosana]</td><td>125 bits(313)</td><td>3,07E-63</td><td>73%</td><td>0%</td></tr>
<tr><td></td><td>gi|643686895|gb|KDP20060.1|</td><td>hypothetical protein JCGZ_05829 [Jatropha curcas]</td><td>120 bits(300)</td><td>6,02E-62</td><td>71%</td><td>0%</td></tr>
<tr><td>SLCAPL05E03</td><td>No Hits.</td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>SLCAPL05E05</td><td>No Hits.</td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>SLCAPL05E10</td><td>gi|296088510|emb|CBI37501.3|</td><td>unnamed protein product [Vitis vinifera]</td><td>113 bits(282)</td><td>3,55E-27</td><td>90%</td><td>0%</td></tr>
<tr><td></td><td>gi|672110587|ref|XP_008796259.1|</td><td>PREDICTED: thioredoxin reductase NTRB-like [Phoenix dactylifera]</td><td>113 bits(282)</td><td>2,82E-25</td><td>88%</td><td>0%</td></tr>
<tr><td></td><td>gi|674906276|emb|CDY26806.1|</td><td>BnaC09g09330D [Brassica napus]</td><td>111 bits(275)</td><td>3,58E-26</td><td>90%</td><td>0%</td></tr>
<tr><td></td><td>gi|225431669|ref|XP_002263864.1|</td><td>PREDICTED: thioredoxin reductase 2-like [Vitis vinifera]</td><td>113 bits(282)</td><td>2,98E-25</td><td>90%</td><td>0%</td></tr>
<tr><td></td><td>gi|565352777|ref|XP_006343316.1|</td><td>PREDICTED: thioredoxin reductase 2-like [Solanum tuberosum]</td><td>121 bits(303)</td><td>2,53E-28</td><td>93%</td><td>0%</td></tr>
<tr><td></td><td>gi|536838|gb|AAA33376.1|</td><td>NADPH thioredoxin reductase, partial [Helianthus annuus]</td><td>109 bits(271)</td><td>9,17E-26</td><td>86%</td><td>0%</td></tr>
<tr><td></td><td>gi|694358739|ref|XP_009359641.1|</td><td>PREDICTED: thioredoxin reductase NTRB-like isoform X1 [Pyrus x bretschneideri]</td><td>112 bits(279)</td><td>6,02E-25</td><td>90%</td><td>0%</td></tr>
<tr><td></td><td>gi|460377440|ref|XP_004234501.1|</td><td>PREDICTED: thioredoxin reductase 2-like [Solanum lycopersicum]</td><td>121 bits(302)</td><td>3,54E-28</td><td>92%</td><td>0%</td></tr>
<tr><td></td><td>gi|565398541|ref|XP_006364831.1|</td><td>PREDICTED: thioredoxin reductase 2-like [Solanum tuberosum]</td><td>113 bits(282)</td><td>2,79E-25</td><td>92%</td><td>0%</td></tr>
<tr><td></td><td>gi|242066214|ref|XP_002454396.1|</td><td>hypothetical protein SORBIDRAFT_04g030050 [Sorghum bicolor]</td><td>112 bits(278)</td><td>6,45E-25</td><td>90%</td><td>0%</td></tr>
<tr><td>SLCAPL05E12</td><td>No Hits.</td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>SLCAPL05F01</td><td>No Hits.</td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>SLCAPL05F03</td><td>gi|460375740|ref|XP_004233662.1|</td><td>PREDICTED: uncharacterized protein LOC101263080 [Solanum lycopersicum]</td><td>74 bits(181)</td><td>8,73E-12</td><td>50%</td><td>10%</td></tr>
<tr><td></td><td>gi|587854390|gb|EXB44453.1|</td><td>hypothetical protein L484_013871 [Morus notabilis]</td><td>71 bits(173)</td><td>6,78E-11</td><td>47%</td><td>10%</td></tr>
<tr><td></td><td>gi|460375742|ref|XP_004233663.1|</td><td>PREDICTED: uncharacterized protein LOC101263375 [Solanum lycopersicum]</td><td>71 bits(173)</td><td>1,40E-11</td><td>49%</td><td>10%</td></tr>
<tr><td></td><td>gi|565342462|ref|XP_006338364.1|</td><td>PREDICTED: uncharacterized protein LOC102584983 [Solanum tuberosum]</td><td>70 bits(171)</td><td>7,73E-11</td><td>58%</td><td>10%</td></tr>
<tr><td></td><td>gi|565343279|ref|XP_006338765.1|</td><td>PREDICTED: uncharacterized protein LOC102598759 [Solanum tuberosum]</td><td>26 bits(55)</td><td>4,13E-13</td><td>91%</td><td>0%</td></tr>
</table>

<table>
<tr><td></td><td>gi|460372696|ref|XP_004232162.1|</td><td>PREDICTED: uncharacterized protein LOC101259999 [Solanum lycopersicum]</td><td>72 bits(176)</td><td>2,91E-11</td><td>57%</td><td>10%</td></tr>
<tr><td></td><td>gi|565343283|ref|XP_006338767.1|</td><td>PREDICTED: meiosis arrest female protein 1 homolog [Solanum tuberosum]</td><td>73 bits(177)</td><td>4,38E-12</td><td>54%</td><td>10%</td></tr>
<tr><td></td><td>gi|590720180|ref|XP_007051260.1|</td><td>Endonuclease or glycosyl hydrolase with C2H2-type zinc finger domain, putative isoform 1 [Theobroma cacao]</td><td>72 bits(174)</td><td>4,84E-11</td><td>49%</td><td>10%</td></tr>
<tr><td>SLCAPL05F04</td><td>gi|503320473|ref|WP_013555134.1|</td><td>hypothetical protein [Bacillus thuringiensis]</td><td>69 bits(166)</td><td>6,31E-11</td><td>100%</td><td>0%</td></tr>
<tr><td>SLCAPL05F05</td><td>gi|118484082|gb|ABK93926.1|</td><td>unknown [Populus trichocarpa]</td><td>160 bits(403)</td><td>9,21E-46</td><td>88%</td><td>0%</td></tr>
<tr><td></td><td>gi|224123084|ref|XP_002318991.1|</td><td>hypothetical protein POPTR_0013s01830g [Populus trichocarpa]</td><td>161 bits(406)</td><td>3,62E-46</td><td>89%</td><td>0%</td></tr>
<tr><td></td><td>gi|460384529|ref|XP_004237963.1|</td><td>PREDICTED: 40S ribosomal protein S21-like [Solanum lycopersicum]</td><td>170 bits(429)</td><td>1,05E-49</td><td>95%</td><td>0%</td></tr>
<tr><td></td><td>gi|330318594|gb|AEC10964.1|</td><td>40S ribosomal protein s21e [Camellia sinensis]</td><td>159 bits(401)</td><td>1,59E-45</td><td>87%</td><td>0%</td></tr>
<tr><td></td><td>gi|255542722|ref|XP_002512424.1|</td><td>40S ribosomal protein S21e, putative [Ricinus communis]</td><td>161 bits(405)</td><td>5,22E-46</td><td>89%</td><td>0%</td></tr>
<tr><td></td><td>gi|225450765|ref|XP_002283649.1|</td><td>PREDICTED: 40S ribosomal protein S21 isoform 1 [Vitis vinifera]</td><td>166 bits(420)</td><td>2,40E-48</td><td>93%</td><td>0%</td></tr>
<tr><td></td><td>gi|527186474|gb|EPS59430.1|</td><td>hypothetical protein M569_15378 [Genlisea aurea]</td><td>158 bits(399)</td><td>4,27E-45</td><td>87%</td><td>0%</td></tr>
<tr><td></td><td>gi|147778296|emb|CAN60816.1|</td><td>hypothetical protein VITISV_033219 [Vitis vinifera]</td><td>166 bits(419)</td><td>3,45E-48</td><td>91%</td><td>0%</td></tr>
<tr><td></td><td>gi|604304305|gb|EYU23638.1|</td><td>hypothetical protein MIMGU_mgv1a021808mg [Erythranthe guttata]</td><td>163 bits(411)</td><td>5,65E-47</td><td>90%</td><td>0%</td></tr>
<tr><td></td><td>gi|460384531|ref|XP_004237964.1|</td><td>PREDICTED: 40S ribosomal protein S21-like isoform 1 [Solanum lycopersicum]</td><td>173 bits(436)</td><td>1,12E-50</td><td>96%</td><td>0%</td></tr>
<tr><td>SLCAPL05F07</td><td>gi|460411711|ref|XP_004251249.1|</td><td>PREDICTED: calmodulin-like isoform 2 [Solanum lycopersicum]</td><td>295 bits(753)</td><td>1,53E-98</td><td>97%</td><td>0%</td></tr>
<tr><td></td><td>gi|460411709|ref|XP_004251248.1|</td><td>PREDICTED: calmodulin-like isoform 1 [Solanum lycopersicum]</td><td>295 bits(753)</td><td>4,74E-98</td><td>97%</td><td>0%</td></tr>
<tr><td></td><td>gi|674233595|gb|KFK26360.1|</td><td>hypothetical protein AALP_AA8G238300 [Arabis alpina]</td><td>292 bits(747)</td><td>1,27E-97</td><td>97%</td><td>0%</td></tr>
<tr><td></td><td>gi|685375194|ref|XP_009120715.1|</td><td>PREDICTED: LOW QUALITY PROTEIN: calmodulin [Brassica rapa]</td><td>294 bits(752)</td><td>2,81E-98</td><td>97%</td><td>0%</td></tr>
<tr><td></td><td>gi|685320364|ref|XP_009150282.1|</td><td>PREDICTED: calmodulin-like [Brassica rapa]</td><td>293 bits(749)</td><td>5,79E-98</td><td>97%</td><td>0%</td></tr>
<tr><td></td><td>gi|460407314|ref|XP_004249098.1|</td><td>PREDICTED: calmodulin-like [Solanum lycopersicum]</td><td>294 bits(751)</td><td>3,32E-98</td><td>97%</td><td>0%</td></tr>
<tr><td></td><td>gi|359479174|ref|XP_003632230.1|</td><td>PREDICTED: calmodulin-related protein isoform 4 [Vitis vinifera]</td><td>294 bits(752)</td><td>6,36E-98</td><td>97%</td><td>0%</td></tr>
<tr><td></td><td>gi|568214802|ref|NP_001275359.1|</td><td>calmodulin-5/6/7/8 [Solanum tuberosum]</td><td>295 bits(755)</td><td>8,21E-99</td><td>98%</td><td>0%</td></tr>
<tr><td></td><td>gi|566150460|ref|XP_006369409.1|</td><td>calmodulin-like protein 6a [Populus trichocarpa]</td><td>294 bits(750)</td><td>3,95E-98</td><td>97%</td><td>0%</td></tr>
<tr><td></td><td>gi|152013376|sp|A2WNH1.2|CALM3_ORYSI</td><td>RecName: Full=Calmodulin-3; Short=CaM-3 [Oryza sativa Indica Group]</td><td>292 bits(747)</td><td>1,21E-97</td><td>97%</td><td>0%</td></tr>
<tr><td>SLCAPL05F12</td><td>gi|8778823|gb|AAF79822.1|AC026875_2</td><td>T6D22.2 [Arabidopsis thaliana]</td><td>74 bits(179)</td><td>1,32E-11</td><td>46%</td><td>24%</td></tr>
<tr><td>SLCAPL05G01</td><td>No Hits.</td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>SLCAPL05G10</td><td>gi|357488211|ref|XP_003614393.1|</td><td>hypothetical protein MTR_5g051120 [Medicago truncatula]</td><td>149 bits(375)</td><td>5,79E-38</td><td>74%</td><td>20%</td></tr>
<tr><td></td><td>gi|358348842|ref|XP_003638451.1|</td><td>hypothetical protein MTR_132s0010, partial [Medicago truncatula]</td><td>149 bits(375)</td><td>4,56E-36</td><td>72%</td><td>20%</td></tr>
<tr><td></td><td>gi|357488191|ref|XP_003614383.1|</td><td>hypothetical protein MTR_5g051000 [Medicago truncatula]</td><td>134 bits(335)</td><td>7,25E-31</td><td>72%</td><td>20%</td></tr>
<tr><td></td><td>gi|357488209|ref|XP_003614392.1|</td><td>hypothetical protein MTR_5g051110 [Medicago truncatula]</td><td>125 bits(312)</td><td>3,36E-29</td><td>74%</td><td>20%</td></tr>
<tr><td></td><td>gi|357488201|ref|XP_003614388.1|</td><td>hypothetical protein MTR_5g051050, partial [Medicago truncatula]</td><td>146 bits(366)</td><td>5,66E-36</td><td>71%</td><td>20%</td></tr>
<tr><td></td><td>gi|657370954|gb|KEH16988.1|</td><td>senescence-associated protein, putative [Medicago truncatula]</td><td>151 bits(380)</td><td>1,99E-37</td><td>73%</td><td>20%</td></tr>
<tr><td></td><td>gi|357488193|ref|XP_003614384.1|</td><td>hypothetical protein MTR_5g051010 [Medicago truncatula]</td><td>148 bits(373)</td><td>6,73E-36</td><td>72%</td><td>20%</td></tr>
<tr><td></td><td>gi|13359451|dbj|BAB33421.1|</td><td>putative senescence-associated protein [Pisum sativum]</td><td>179 bits(454)</td><td>1,74E-50</td><td>92%</td><td>0%</td></tr>
<tr><td></td><td>gi|357488189|ref|XP_003614382.1|</td><td>hypothetical protein MTR_5g050970 [Medicago truncatula]</td><td>151 bits(381)</td><td>4,05E-37</td><td>73%</td><td>20%</td></tr>
<tr><td></td><td>gi|657370962|gb|KEH16996.1|</td><td>senescence-associated protein, putative, partial [Medicago truncatula]</td><td>146 bits(367)</td><td>1,34E-35</td><td>71%</td><td>20%</td></tr>
<tr><td>SLCAPL05G11</td><td>gi|657370954|gb|KEH16988.1|</td><td>senescence-associated protein, putative [Medicago truncatula]</td><td>151 bits(380)</td><td>1,99E-37</td><td>73%</td><td>20%</td></tr>
<tr><td></td><td>gi|357488193|ref|XP_003614384.1|</td><td>hypothetical protein MTR_5g051010 [Medicago truncatula]</td><td>148 bits(373)</td><td>6,73E-36</td><td>72%</td><td>20%</td></tr>
<tr><td></td><td>gi|13359451|dbj|BAB33421.1|</td><td>putative senescence-associated protein [Pisum sativum]</td><td>179 bits(454)</td><td>1,74E-50</td><td>92%</td><td>0%</td></tr>
<tr><td></td><td>gi|357488189|ref|XP_003614382.1|</td><td>hypothetical protein MTR_5g050970 [Medicago truncatula]</td><td>151 bits(381)</td><td>4,05E-37</td><td>73%</td><td>20%</td></tr>
<tr><td></td><td>gi|657370962|gb|KEH16996.1|</td><td>senescence-associated protein, putative, partial [Medicago truncatula]</td><td>146 bits(367)</td><td>1,34E-35</td><td>71%</td><td>20%</td></tr>
<tr><td></td><td>gi|357488211|ref|XP_003614393.1|</td><td>hypothetical protein MTR_5g051120 [Medicago truncatula]</td><td>149 bits(375)</td><td>5,79E-38</td><td>74%</td><td>20%</td></tr>
<tr><td></td><td>gi|358348842|ref|XP_003638451.1|</td><td>hypothetical protein MTR_132s0010, partial [Medicago truncatula]</td><td>149 bits(375)</td><td>4,56E-36</td><td>72%</td><td>20%</td></tr>
<tr><td></td><td>gi|357488191|ref|XP_003614383.1|</td><td>hypothetical protein MTR_5g051000 [Medicago truncatula]</td><td>134 bits(335)</td><td>7,25E-31</td><td>72%</td><td>20%</td></tr>
<tr><td></td><td>gi|357488209|ref|XP_003614392.1|</td><td>hypothetical protein MTR_5g051110 [Medicago truncatula]</td><td>125 bits(312)</td><td>3,36E-29</td><td>74%</td><td>20%</td></tr>
<tr><td></td><td>gi|357488201|ref|XP_003614388.1|</td><td>hypothetical protein MTR_5g051050, partial [Medicago truncatula]</td><td>146 bits(366)</td><td>5,66E-36</td><td>71%</td><td>20%</td></tr>
<tr><td>SLCAPL05H01</td><td>No Hits.</td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>SLCAPL05H02</td><td>No Hits.</td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>SLCAPL05H07</td><td>No Hits.</td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>SLCAPL05H09</td><td>gi|495126628|ref|WP_007851439.1|</td><td>hypothetical protein, partial [Bacteroides dorei]</td><td>78 bits(190)</td><td>4,57E-15</td><td>97%</td><td>0%</td></tr>
<tr><td></td><td>gi|571207123|emb|CDK78388.1|</td><td>Transcriptional repressor of the lac operon [Klebsiella pneumoniae IS22]</td><td>73 bits(178)</td><td>1,40E-12</td><td>86%</td><td>3%</td></tr>
<tr><td></td><td>gi|487912019|ref|WP_001985485.1|</td><td>SocE [Bacillus cereus]</td><td>91 bits(225)</td><td>6,91E-20</td><td>100%</td><td>0%</td></tr>
<tr><td></td><td>gi|299008123|gb|ADJ00052.1|</td><td>chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]</td><td>76 bits(186)</td><td>1,53E-12</td><td>97%</td><td>0%</td></tr>
<tr><td></td><td>gi|491131127|ref|WP_004989554.1|</td><td>hypothetical protein [Streptomyces ghanaensis]</td><td>89 bits(219)</td><td>3,88E-19</td><td>98%</td><td>0%</td></tr>
<tr><td></td><td>gi|386242568|gb|EII84303.1|</td><td>LacI transcriptional repressor [Escherichia coli 3003]</td><td>73 bits(178)</td><td>2,16E-11</td><td>85%</td><td>0%</td></tr>
</table>

Apêndice G – Resultado da busca *in silico* da funcionalidade hipotética em Contigs e Singlets, de genes de interesse isolados na biblioteca de sementes, folhas e calos de *Solanum lycocarpum*
Fonte de dados: Blastx/NCBI
Elaborada pelo autor

Contig - Sementes

Name Sequence	Sequence	Name	score	expert	indentities	gaps
Contig3	gi|565390980|ref|XP_006361209.1|	PREDICTED: metallothionein-like protein type 2-like [Solanum tuberosum]	90 bits(221)	1,09E-19	78%	0%
	gi|193085066|gb|ACF10398.1|	type 2 metallothionein [Solanum nigrum]	86 bits(211)	3,72E-18	79%	0%
	gi|565390974|ref|XP_006361207.1|	PREDICTED: metallothionein-like protein type 2-like [Solanum tuberosum]	83 bits(204)	3,67E-17	77%	0%
	gi|350537709|ref|NP_001234050.1|	metallothionein-like protein type 2 [Solanum lycopersicum]	89 bits(218)	4,57E-19	76%	0%
	gi|58578264|emb|CAI48068.1|	metallotionein-like protein [Capsicum chinense]	86 bits(210)	4,76E-18	82%	0%
	gi|565390978|ref|XP_006361208.1|	PREDICTED: metallothionein-like protein type 2-like [Solanum tuberosum]	82 bits(201)	8,82E-17	75%	0%
	gi|193085064|gb|ACF10397.1|	type 2 metallothionein [Solanum nigrum]	88 bits(216)	6,74E-19	81%	0%
	gi|151301842|gb|ABR92329.1|	putative metallothionin 2a [Salvia miltiorrhiza]	85 bits(208)	1,04E-17	62%	6%
	gi|661895087|emb|CDP00892.1|	unnamed protein product [Coffea canephora]	87 bits(214)	1,06E-18	64%	2%
	gi|60459403|gb|AAX20047.1|	metallothionein-like protein type 2 [Capsicum annuum]	84 bits(207)	1,38E-17	82%	0%
Contig6	gi|449531055|ref|XP_004172503.1|	PREDICTED: small heat shock protein, chloroplastic-like [Cucumis sativus]	152 bits(383)	8,44E-42	74%	0%
	gi|595848808|ref|XP_007209602.1|	hypothetical protein PRUPE_ppa011466mg [Prunus persica]	139 bits(348)	1,16E-36	66%	2%
	gi|224074141|ref|XP_002304270.1|	hypothetical protein POPTR_0003s07360g [Populus trichocarpa]	137 bits(344)	6,09E-36	63%	5%
	gi|565378014|ref|XP_006355458.1|	PREDICTED: small heat shock protein, chloroplastic-like [Solanum tuberosum]	170 bits(429)	1,39E-48	93%	0%
	gi|659095978|ref|XP_008448861.1|	PREDICTED: small heat shock protein, chloroplastic-like isoform X2 [Cucumis melo]	151 bits(381)	1,98E-41	74%	0%
	gi|645266293|ref|XP_008238549.1|	PREDICTED: heat shock 22 kDa protein, mitochondrial [Prunus mume]	138 bits(346)	2,51E-36	66%	2%
	gi|350539261|ref|NP_001233872.1|	mitochondrial small heat shock protein [Solanum lycopersicum]	169 bits(428)	2,14E-48	93%	0%
	gi|659095976|ref|XP_008448860.1|	PREDICTED: small heat shock protein, chloroplastic-like isoform X1 [Cucumis melo]	151 bits(381)	2,08E-41	74%	0%
	gi|299891471|gb|ADJ57588.1|	mitochondrial small heat shock protein [Capsicum annuum]	165 bits(417)	9,89E-47	87%	5%
	gi|661886590|emb|CDP09954.1|	unnamed protein product [Coffea canephora]	140 bits(352)	4,54E-37	74%	0%

Singlets - Sementes

Name Sequence	Sequence	Name	score	expert	indentities	gaps
SLSEPL04F05	gi|350535224|ref|NP_001234439.1|	heat shock cognate protein 80 [Solanum lycopersicum]	240 bits(610)	1,64E-71	98%	0%
	gi|565356086|ref|XP_006344905.1|	PREDICTED: heat shock cognate protein 80-like [Solanum tuberosum]	232 bits(591)	1,03E-68	93%	0%
	gi|449524954|ref|XP_004169486.1|	PREDICTED: heat shock cognate protein 80-like [Cucumis sativus]	213 bits(540)	2,07E-67	88%	0%
	gi|171854657|dbj|BAG16518.1|	putative Hsp90-2 [Capsicum chinense]	236 bits(602)	2,49E-70	96%	0%
	gi|350535174|ref|NP_001234436.1|	molecular chaperone Hsp90-1 [Solanum lycopersicum]	232 bits(590)	1,21E-68	93%	0%
	gi|38154485|gb|AAR12194.1|	molecular chaperone Hsp90-2 [Nicotiana benthamiana]	227 bits(578)	6,80E-67	91%	0%
	gi|315307966|gb|ADU04386.1|	heat shock protein 90-1 [Nicotiana attenuata]	236 bits(600)	4,50E-70	95%	0%
	gi|565371920|ref|XP_006352548.1|	PREDICTED: heat shock cognate protein 80-like [Solanum tuberosum]	230 bits(586)	5,46E-68	93%	0%
	gi|6934298|gb|AAF31705.1|AF221856_1	heat-shock protein 80 [Euphorbia esula]	225 bits(572)	1,38E-69	91%	0%
	gi|315307968|gb|ADU04387.1|	heat shock protein 90-2 [Nicotiana attenuata]	230 bits(584)	1,07E-67	93%	0%
SLSEPL04G10	gi|356496771|ref|XP_003517239.1|	PREDICTED: zinc finger protein MAGPIE-like [Glycine max]	122 bits(306)	3,30E-29	66%	0%
	gi|9858780|gb|AAG01127.1|AF273333_12	BAC19.12 [Solanum lycopersicum]	171 bits(431)	2,27E-46	91%	0%
	gi|643721914|gb|KDP31793.1|	hypothetical protein JCGZ_12254 [Jatropha curcas]	121 bits(303)	8,56E-29	69%	0%
	gi|460373151|ref|XP_004232386.1|	PREDICTED: uncharacterized protein LOC101252546 [Solanum lycopersicum]	171 bits(431)	2,58E-46	91%	0%
	gi|565360357|ref|XP_006346936.1|	PREDICTED: uncharacterized threonine-rich GPI-anchored glycoprotein PJ4664.02-like [Solanum tuberosum]	127 bits(318)	3,76E-30	77%	0%
	gi|156070761|gb|ABU45176.1|	unknown [Solanum melongena]	178 bits(451)	2,72E-49	98%	0%
	gi|565395015|ref|XP_006363144.1|	PREDICTED: zinc finger protein MAGPIE-like [Solanum tuberosum]	169 bits(427)	7,43E-46	90%	0%
	gi|460375430|ref|XP_004233509.1|	PREDICTED: uncharacterized protein LOC101262076 [Solanum lycopersicum]	125 bits(313)	1,24E-29	76%	0%
	gi|156070798|gb|ABU45210.1|	unknown [Solanum bulbocastanum]	171 bits(432)	1,51E-46	90%	0%
	gi|156070783|gb|ABU45196.1|	unknown [Petunia integrifolia subsp. inflata]	151 bits(381)	2,50E-39	84%	4%

Contig - Folhas

Name Sequence	Sequence	Name	score	expert	indentities	gaps
Contig26	gi|303291414|ref|XP_003064992.1|	senescence-associated protein [Micromonas pusilla CCMP1545]	105 bits(260)	2,38E-26	98%	0%
	gi|657371000|gb|KEH17031.1|	hypothetical protein MTR_0052s0170 [Medicago truncatula]	96 bits(237)	5,42E-21	96%	0%
	gi|403333060|gb|EJY65597.1|	hypothetical protein OXYTRI_14248 [Oxytricha trifallax]	92 bits(226)	3,30E-19	96%	0%
	gi|678336953|emb|CDW75723.1|	UNKNOWN [Stylonychia lemnae]	99 bits(245)	1,23E-21	96%	0%
	gi|630364069|ref|XP_007871309.1|	hypothetical protein GLOTRDRAFT_50878, partial [Gloeophyllum trabeum ATCC 11539]	86 bits(212)	4,51E-20	98%	0%
	gi|646383637|gb|KDQ49118.1|	hypothetical protein JAAARDRAFT_143849, partial [Jaapia argillacea MUCL 33604]	84 bits(207)	5,66E-19	95%	0%

	gi|357488225|ref|XP_003614400.1|	Cytochrome P450 likeTBP [Medicago truncatula]	97 bits(240)	2,56E-21	96%	0%
	gi|357488193|ref|XP_003614384.1|	hypothetical protein MTR_5g051010 [Medicago truncatula]	74 bits(181)	2,86E-13	78%	0%
	gi|170048439|ref|XP_001852902.1|	GLP_748_1200_211 [Culex quinquefasciatus]	89 bits(219)	3,32E-21	82%	0%
	gi|403334965|gb|EJY66653.1|	hypothetical protein OXYTRI_13058 [Oxytricha trifallax]	92 bits(226)	3,06E-19	96%	0%
Contig34	gi|568872594|ref|XP_006489452.1|	PREDICTED: serine/threonine-protein phosphatase 5-like isoform X2 [Citrus sinensis]	70 bits(169)	6,30E-44	86%	0%
	gi|224099829|ref|XP_002311636.1|	hypothetical protein POPTR_0008s15630g [Populus trichocarpa]	71 bits(172)	4,93E-43	79%	0%
	gi|147769544|emb|CAN61400.1|	hypothetical protein VITISV_011488 [Vitis vinifera]	69 bits(167)	2,39E-44	84%	0%
	gi|641855684|gb|KDO74464.1|	hypothetical protein CISIN_1g0209142mg, partial [Citrus sinensis]	70 bits(169)	7,38E-44	86%	0%
	gi|657402143|gb|KEH41070.1|	RNA polymerase II-associated-like protein [Medicago truncatula]	70 bits(170)	2,97E-42	84%	0%
	gi|255552073|ref|XP_002517081.1|	heat shock protein 70 (HSP70)-interacting protein, putative [Ricinus communis]	68 bits(165)	2,96E-44	86%	0%
	gi|567853810|ref|XP_006420025.1|	hypothetical protein CICLE_v10005444mg [Citrus clementina]	69 bits(168)	1,21E-43	86%	0%
	gi|527199415|gb|EPS67206.1|	hypothetical protein M569_07567, partial [Genlisea aurea]	69 bits(168)	5,72E-42	91%	0%
	gi|224111122|ref|XP_002315755.1|	tetratricopeptide repeat-containing family protein [Populus trichocarpa]	72 bits(175)	4,15E-44	81%	0%
	gi|502123055|ref|XP_004497984.1|	PREDICTED: serine/threonine-protein phosphatase 5-like [Cicer arietinum]	70 bits(169)	4,73E-43	86%	0%

Singlet - Folhas

Name Sequence	Sequence	Name	score	expert	indentities	gaps
SLFLPL03D04	gi|106879609|emb|CAJ38388.1|	actin-depolymerizing factor [Plantago major]	129 bits(322)	7,75E-34	92%	0%
	gi|643738216|gb|KDP44204.1|	hypothetical protein JCGZ_05671 [Jatropha curcas]	127 bits(319)	1,69E-33	92%	0%
	gi|460401918|ref|XP_004246462.1|	PREDICTED: actin-depolymerizing factor 1-like [Solanum lycopersicum]	133 bits(334)	1,49E-35	98%	0%
	gi|317134431|gb|ADV02778.1|	actin depolymerizing factor 1 [Ipomoea batatas]	129 bits(322)	9,59E-34	92%	0%
	gi|590589598|ref|XP_007016496.1|	Actin depolymerizing factor 4 [Theobroma cacao]	128 bits(320)	1,78E-33	92%	0%
	gi|170773914|gb|ACB32233.1|	actin-depolymerizing factor 1 [Solanum chacoense]	132 bits(332)	2,80E-35	97%	0%
	gi|661887233|emb|CDP09013.1|	unnamed protein product [Coffea canephora]	128 bits(320)	1,41E-33	92%	0%
	gi|255584766|ref|XP_002533101.1|	actin depolymerizing factor, putative [Ricinus communis]	127 bits(319)	2,11E-33	91%	0%
	gi|565348103|ref|XP_006341057.1|	PREDICTED: actin-depolymerizing factor 1-like [Solanum tuberosum]	131 bits(329)	9,06E-35	95%	0%
	gi|661889921|emb|CDP06641.1|	unnamed protein product [Coffea canephora]	129 bits(322)	1,44E-33	94%	0%

Contigs - Calos

Name Sequence	Sequence	Name	score	expert	indentities	gaps
Contig0	gi|1545805|dbj|BAA10929.1|	cytochrome P450 like_TBP [Nicotiana tabacum]	209 bits(531)	1,52E-59	74%	10%
	gi|195610700|gb|ACG27180.1|	hypothetical protein [Zea mays]	169 bits(426)	7,20E-49	88%	0%
	gi|357488215|ref|XP_003614395.1|	hypothetical protein MTR_5g051140 [Medicago truncatula]	162 bits(409)	8,80E-41	73%	27%
	gi|253760055|ref|XP_002488965.1|	hypothetical protein SORBIDRAFT_1138s002030 [Sorghum bicolor]	178 bits(450)	2,15E-52	91%	0%
	gi|242070907|ref|XP_002450730.1|	hypothetical protein SORBIDRAFT_05g016465 [Sorghum bicolor]	151 bits(381)	4,95E-42	81%	0%
	gi|357488191|ref|XP_003614383.1|	hypothetical protein MTR_5g051000 [Medicago truncatula]	163 bits(410)	9,19E-41	73%	27%
	gi|7489812|pir||T02955	probable cytochrome P450 monooxygenase - maize (fragment)	182 bits(460)	1,20E-51	76%	7%
	gi|357488197|ref|XP_003614386.1|	hypothetical protein MTR_5g051030 [Medicago truncatula]	162 bits(408)	2,75E-41	73%	27%
	gi|303291416|ref|XP_003064993.1|	predicted protein, partial [Micromonas pusilla CCMP1545]	172 bits(434)	2,88E-49	93%	0%
	gi|358348842|ref|XP_003638451.1|	hypothetical protein MTR_132s0010, partial [Medicago truncatula]	163 bits(410)	6,87E-41	73%	27%
Contig5	gi|60459403|gb|AAX20047.1|	metallothionein-like protein type 2 [Capsicum annuum]	84 bits(206)	1,69E-17	83%	0%
	gi|193085066|gb|ACF10398.1|	type 2 metallothionein [Solanum nigrum]	81 bits(198)	2,36E-16	81%	0%
	gi|565390980|ref|XP_006361209.1|	PREDICTED: metallothionein-like protein type 2-like [Solanum tuberosum]	88 bits(217)	5,20E-19	76%	0%
	gi|350537709|ref|NP_001234050.1|	metallothionein-like protein type 2 [Solanum lycopersicum]	87 bits(213)	2,43E-18	74%	0%
	gi|565368268|ref|XP_006350769.1|	PREDICTED: metallothionein-like protein [Solanum tuberosum]	83 bits(203)	4,80E-17	87%	3%
	gi|58578264|emb|CAI48068.1|	metallotionein-like protein [Capsicum chinense]	85 bits(209)	6,54E-18	84%	0%
	gi|151301842|gb|ABR92329.1|	putative metallothionin 2a [Salvia miltiorrhiza]	82 bits(200)	1,25E-16	60%	6%
	gi|661895087|emb|CDP00892.1|	unnamed protein product [Coffea canephora]	85 bits(208)	8,90E-18	62%	2%
	gi|565390974|ref|XP_006361207.1|	PREDICTED: metallothionein-like protein type 2-like [Solanum tuberosum]	81 bits(198)	2,17E-16	75%	0%
	gi|193085064|gb|ACF10397.1|	type 2 metallothionein [Solanum nigrum]	88 bits(217)	4,57E-19	83%	0%
Contig6	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	92 bits(228)	1,90E-18	98%	0%
	gi|586616619|gb|AHJ78613.1|	4-coumarate:coenzyme A ligase [Solanum tuberosum]	87 bits(214)	6,31E-16	91%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	103 bits(255)	2,48E-24	100%	0%
	gi|9652070|gb|AAF91388.1|AF263243_1	SocE [Myxococcus xanthus]	90 bits(222)	4,90E-17	54%	0%
	gi|398965|sp|P31685.1|4CL2_SOLTU	RecName: Full=4-coumarate--CoA ligase 2; Short=4CL 2; AltName: Full=4-coumaroyl-CoA synthase 2 [Solanum tuberosum]	87 bits(214)	6,36E-16	91%	0%
	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	92 bits(226)	3,16E-20	100%	0%
	gi|460380249|ref|XP_004235870.1|	PREDICTED: 4-coumarate--CoA ligase 1-like [Solanum lycopersicum]	87 bits(214)	5,81E-16	91%	0%
	gi|586616617|gb|AHJ78612.1|	4-coumarate:coenzyme A ligase [Solanum tuberosum]	87 bits(214)	6,48E-16	91%	0%

	gi|487912019|ref|WP_001985485.1|	SocE [Bacillus cereus]	91 bits(225)	7,01E-20	100%	0%
	gi|5163399|gb|AAD40664.1|AF150686_1	4-coumarate:coenzyme A ligase [Solanum tuberosum]	87 bits(214)	6,31E-16	91%	0%
Contig7	gi|565396035|ref|XP_006363639.1|	PREDICTED: uncharacterized protein LOC102603354 [Solanum tuberosum]	104 bits(259)	5,17E-85	98%	0%
	gi|357488199|ref|XP_003614387.1|	RRNA intron-encoded homing endonuclease [Medicago truncatula]	25 bits(54)	5,82E-17	82%	0%
	gi|357488225|ref|XP_003614400.1|	Cytochrome P450 likeTBP [Medicago truncatula]	47 bits(111)	9,72E-61	74%	0%
	gi|657370961|gb|KEH16995.1|	hypothetical protein MTR_0055s0130 [Medicago truncatula]	93 bits(230)	9,08E-77	87%	0%
	gi|502153899|ref|XP_004509500.1|	PREDICTED: uncharacterized protein LOC101508810 [Cicer arietinum]	92 bits(228)	2,62E-75	87%	0%
	gi|357488195|ref|XP_003614385.1|	RRNA intron-encoded homing endonuclease [Medicago truncatula]	93 bits(229)	1,27E-76	87%	0%
	gi|694380941|ref|XP_009366572.1|	PREDICTED: uncharacterized protein LOC103956333 [Pyrus x bretschneideri]	114 bits(283)	5,65E-24	33%	70%
	gi|587923547|gb|EXC10888.1|	hypothetical protein L484_002552 [Morus notabilis]	268 bits(685)	2,85E-85	78%	34%
	gi|357488203|ref|XP_003614389.1|	RRNA intron-encoded homing endonuclease [Medicago truncatula]	92 bits(228)	2,23E-76	87%	0%
	gi|357488185|ref|XP_003614380.1|	Cytochrome P450 likeTBP [Medicago truncatula]	56 bits(133)	5,67E-61	84%	0%
Contig8	gi|27475622|emb|CAD59768.1|	putative reverse transcriptase [Cicer arietinum]	74 bits(179)	4,72E-14	100%	0%
	gi|565401584|ref|XP_006366277.1|	PREDICTED: 4-coumarate--CoA ligase 2-like [Solanum tuberosum]	78 bits(191)	2,88E-13	92%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	35 bits(80)	1,26E-15	94%	0%
	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	78 bits(190)	1,26E-13	97%	0%
	gi|82581146|emb|CAJ43714.1|	4-coumaryl-CoA ligase [Plantago major]	73 bits(178)	4,38E-13	85%	0%
	gi|330752400|emb|CBL87351.1|	hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]	77 bits(187)	1,50E-14	97%	0%
	gi|1237183|dbj|BAA07828.1|	4-coumarate:coenzyme A ligase [Nicotiana tabacum]	79 bits(193)	1,43E-13	92%	0%
	gi|270211024|gb|ACZ64784.1|	4-coumarate:CoA ligase [Galega orientalis]	76 bits(185)	1,32E-12	82%	0%
	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	75 bits(182)	2,98E-14	97%	0%
	gi|12229632|sp|O24146.1|4CL2_TOBAC	RecName: Full=4-coumarate--CoA ligase 2; Short=4CL 2; AltName: Full=4-coumaroyl-CoA synthase 2 [Nicotiana tabacum]	78 bits(191)	2,46E-13	90%	0%
Contig17	gi|460408248|ref|XP_004249558.1|	PREDICTED: phenylalanine ammonia-lyase-like [Solanum lycopersicum]	29 bits(64)	6,20E-17	100%	0%
	gi|330752400|emb|CBL87351.1|	hypothetical protein S18_1082_0001 [uncultured Flavobacteriia bacterium]	78 bits(191)	6,64E-15	97%	0%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	99 bits(245)	6,56E-23	100%	0%
	gi|110559308|gb|ABG75910.1|	phenylalanine ammonia-lyase 1 [Nicotiana attenuata]	26 bits(56)	2,54E-16	85%	0%
	gi|460377708|ref|XP_004234632.1|	PREDICTED: phenylalanine ammonia-lyase-like [Solanum lycopersicum]	28 bits(61)	7,91E-15	92%	0%
	gi|495126628|ref|WP_007851439.1|	hypothetical protein, partial [Bacteroides dorei]	93 bits(230)	1,11E-20	100%	0%
	gi|1171997|sp|P45733.1|PAL3_TOBAC	RecName: Full=Phenylalanine ammonia-lyase [Nicotiana tabacum]	26 bits(56)	2,78E-16	85%	0%
	gi|129594|sp|P25872.1|PAL1_TOBAC	RecName: Full=Phenylalanine ammonia-lyase [Nicotiana tabacum]	83 bits(204)	1,44E-14	70%	1%
	gi|299008123|gb|ADJ00052.1|	chloramphenicol acetyltransferase [Promoter probe vector pEvoGlowRed]	94 bits(233)	5,02E-19	98%	0%
	gi|3123241|sp|P35513.2|PAL2_TOBAC	RecName: Full=Phenylalanine ammonia-lyase [Nicotiana tabacum]	87 bits(213)	1,22E-15	90%	0%
Contig26	gi|1545805|dbj|BAA10929.1|	cytochrome P450 like_TBP [Nicotiana tabacum]	176 bits(445)	4,66E-47	75%	2%
	gi|491131127|ref|WP_004989554.1|	hypothetical protein [Streptomyces ghanaensis]	103 bits(255)	3,78E-24	100%	0%
	gi|357488197|ref|XP_003614386.1|	hypothetical protein MTR_5g051030 [Medicago truncatula]	101 bits(251)	2,97E-20	64%	27%
	gi|253760055|ref|XP_002488965.1|	hypothetical protein SORBIDRAFT_1138s002030 [Sorghum bicolor]	146 bits(366)	1,14E-39	91%	0%
	gi|147835464|emb|CAN61119.1|	hypothetical protein VITISV_022570 [Vitis vinifera]	104 bits(257)	3,04E-23	81%	0%
	gi|357488191|ref|XP_003614383.1|	hypothetical protein MTR_5g051000 [Medicago truncatula]	102 bits(252)	3,09E-20	64%	27%
	gi|7489812|pir||T02955	probable cytochrome P450 monooxygenase - maize (fragment)	146 bits(368)	4,54E-38	63%	8%
	gi|565396033|ref|XP_006363638.1|	PREDICTED: uncharacterized protein LOC102601005 [Solanum tuberosum]	103 bits(255)	2,04E-22	94%	0%
	gi|195610700|gb|ACG27180.1|	hypothetical protein [Zea mays]	136 bits(342)	3,86E-36	87%	0%
	gi|358348842|ref|XP_003638451.1|	hypothetical protein MTR_132s0010, partial [Medicago truncatula]	102 bits(254)	2,11E-20	64%	27%
Contig31	gi|643708491|gb|KDP23407.1|	hypothetical protein JCGZ_23240 [Jatropha curcas]	27 bits(59)	7,33E-54	60%	0%
	gi|449454034|ref|XP_004144761.1|	PREDICTED: LOW QUALITY PROTEIN: zinc finger matrin-type protein 2-like [Cucumis sativus]	27 bits(59)	8,56E-51	65%	0%
	gi|566198757|ref|XP_006375726.1|	hypothetical protein POPTR_0013s01160g [Populus trichocarpa]	97 bits(240)	7,33E-49	72%	2%
	gi|590644599|ref|XP_007031126.1|	C2H2 and C2HC zinc fingers superfamily protein isoform 1 [Theobroma cacao]	27 bits(58)	2,85E-53	65%	0%
	gi|566198755|ref|XP_002319487.2|	hypothetical protein POPTR_0013s01160g [Populus trichocarpa]	25 bits(54)	2,42E-50	75%	0%
	gi|326509317|dbj|BAJ91575.1|	predicted protein [Hordeum vulgare subsp. vulgare]	26 bits(55)	1,30E-48	83%	0%
	gi|449490847|ref|XP_004158724.1|	PREDICTED: zinc finger matrin-type protein 2-like [Cucumis sativus]	27 bits(59)	2,33E-52	65%	0%
	gi|674245219|gb|KFK37984.1|	hypothetical protein AALP_AA3G055200 [Arabis alpina]	104 bits(257)	1,70E-49	73%	0%
	gi|659070162|ref|XP_008453709.1|	PREDICTED: zinc finger matrin-type protein 2 [Cucumis melo]	27 bits(59)	4,92E-52	65%	0%
	gi|604341133|gb|EYU40518.1|	hypothetical protein MIMGU_mgv1a013989mg [Erythranthe guttata]	104 bits(259)	2,60E-49	74%	1%

Singlets - Calos

Name Sequence	**Sequence**	**Name**	score	expert	**indentities**	**gaps**
SLCAPL01D01	gi|296085587|emb|CBI29319.3|	unnamed protein product [Vitis vinifera]	312 bits(799)	2,29E-100	69%	0%
	gi|225462386|ref|XP_002264702.1|	PREDICTED: laccase-14-like [Vitis vinifera]	309 bits(789)	3,85E-98	68%	0%

	gi|296081093|emb|CBI18287.3|	unnamed protein product [Vitis vinifera]	299 bits(765)	1,56E-97	66%	0%
	gi|296080996|emb|CBI18500.3|	unnamed protein product [Vitis vinifera]	303 bits(774)	3,25E-100	68%	0%
	gi|658016945|ref|XP_008343826.1|	PREDICTED: laccase-15-like [Malus domestica]	309 bits(789)	5,46E-98	68%	0%
	gi|359495139|ref|XP_002264394.2|	PREDICTED: laccase-14 [Vitis vinifera]	307 bits(784)	2,17E-97	67%	0%
	gi|460384303|ref|XP_004237852.1|	PREDICTED: laccase-14-like [Solanum lycopersicum]	417 bits(1070)	3,65E-140	94%	0%
	gi|359495133|ref|XP_002269593.2|	PREDICTED: laccase-14-like [Vitis vinifera]	314 bits(802)	5,79E-100	69%	0%
	gi|661895328|emb|CDP01133.1|	unnamed protein product [Coffea canephora]	330 bits(845)	1,86E-106	71%	1%
	gi|359495123|ref|XP_003634918.1|	PREDICTED: putative laccase-9-like [Vitis vinifera]	314 bits(803)	1,05E-99	69%	0%
SLCAPL01D05	gi|460372281|ref|XP_004231959.1|	PREDICTED: cytochrome c oxidase subunit 6a, mitochondrial-like [Solanum lycopersicum]	165 bits(416)	1,31E-48	86%	0%
	gi|225438196|ref|XP_002264013.1|	PREDICTED: cytochrome c oxidase subunit 6a, mitochondrial [Vitis vinifera]	112 bits(280)	2,13E-28	59%	3%
	gi|657949346|ref|XP_008342645.1|	PREDICTED: cytochrome c oxidase subunit 6a, mitochondrial [Malus domestica]	106 bits(264)	6,00E-26	60%	3%
	gi|565382844|ref|XP_006357740.1|	PREDICTED: cytochrome c oxidase subunit 6a, mitochondrial-like [Solanum tuberosum]	161 bits(405)	5,08E-47	84%	0%
	gi|659098495|ref|XP_008450167.1|	PREDICTED: cytochrome c oxidase subunit 6a, mitochondrial [Cucumis melo]	108 bits(269)	1,18E-26	60%	3%
	gi|694401705|ref|XP_009375885.1|	PREDICTED: cytochrome c oxidase subunit 6a, mitochondrial-like [Pyrus x bretschneideri]	106 bits(264)	6,13E-26	60%	3%
	gi|255582409|ref|XP_002531993.1|	cytochrome-c oxidase, putative [Ricinus communis]	116 bits(290)	8,07E-30	64%	3%
	gi|449478071|ref|XP_004155214.1|	PREDICTED: cytochrome c oxidase subunit 6a, mitochondrial-like isoform 2 [Cucumis sativus]	107 bits(267)	2,26E-26	59%	3%
	gi|661894215|emb|CDP02656.1|	unnamed protein product [Coffea canephora]	116 bits(289)	1,20E-29	62%	3%
	gi|629088447|gb|KCW54700.1|	hypothetical protein EUGRSUZ_I00649 [Eucalyptus grandis]	107 bits(267)	2,46E-26	59%	3%
SLCAPL01E01	gi|54292100|gb|AAT68778.2|	manganese superoxide dismutase [Camellia sinensis]	287 bits(733)	6,59E-94	84%	0%
	gi|565385810|ref|XP_006358755.1|	PREDICTED: superoxide dismutase [Mn], mitochondrial-like [Solanum tuberosum]	311 bits(796)	1,56E-103	94%	0%
	gi|3915002|sp|O49066.1|SODM_CAPAN	RecName: Full=Superoxide dismutase [Mn], mitochondrial; Flags: Precursor [Capsicum annuum]	294 bits(750)	1,91E-96	86%	0%
	gi|460390498|ref|XP_004240868.1|	PREDICTED: superoxide dismutase [Mn], mitochondrial-like [Solanum lycopersicum]	309 bits(790)	1,73E-102	93%	0%
	gi|590570449|ref|XP_007011340.1|	Superoxide dismutase [Theobroma cacao]	293 bits(749)	2,46E-96	86%	0%
	gi|37999810|sp|Q9SM64.1|SODM_PRUPE	RecName: Full=Superoxide dismutase [Mn], mitochondrial; Flags: Precursor [Prunus persica]	302 bits(772)	7,06E-100	91%	0%
	gi|629100007|gb|KCW65772.1|	hypothetical protein EUGRSUZ_G03132 [Eucalyptus grandis]	292 bits(745)	1,30E-95	86%	0%
	gi|113472840|gb|ABI35908.1|	manganese superoxide dismutase [Rheum australe]	287 bits(734)	5,26E-94	82%	0%
	gi|134672|sp|P11796.1|SODM_NICPL	RecName: Full=Superoxide dismutase [Mn], mitochondrial; Flags: Precursor [Nicotiana plumbaginifolia]	314 bits(804)	1,03E-104	94%	0%
	gi|661882335|emb|CDP13915.1|	unnamed protein product [Coffea canephora]	295 bits(754)	4,30E-97	87%	0%
SLCAPL01H07	gi|226235458|dbj|BAH47641.1|	progesterone 5beta reductase-B [Nicotiana tabacum]	87 bits(214)	3,48E-17	91%	0%
	gi|374085801|gb|AEY82379.1|	putative progesterone 5-beta-reductase [Withania somnifera]	84 bits(205)	6,15E-16	89%	0%
	gi|428675604|gb|AFZ41795.1|	putative progesterone 5-beta-reductase [Duboisia hopwoodii]	81 bits(199)	3,38E-15	86%	0%
	gi|371491777|gb|AEX31544.1|	putative steroid 5beta-reductase [Solanum tuberosum]	86 bits(211)	7,72E-17	89%	0%
	gi|300433187|gb|ADK13080.1|	putative progesterone 5-beta-reductase [Nierembergia aristata]	83 bits(204)	7,90E-16	54%	3%
	gi|565374849|ref|XP_006353962.1|	PREDICTED: 3-oxo-Delta(4,5)-steroid 5-beta-reductase-like [Solanum tuberosum]	86 bits(211)	8,13E-17	89%	0%
	gi|226235456|dbj|BAH47640.1|	progesterone 5beta reductase-A [Nicotiana tabacum]	83 bits(204)	8,84E-16	89%	0%
	gi|295834059|gb|ADG41743.1|	putative progesterone 5 beta-reductase [Nicotiana tabacum]	87 bits(214)	3,25E-17	91%	0%
	gi|295855148|gb|ADG46023.1|	progesterone 5-beta-reductase [Atropa belladonna]	86 bits(210)	1,20E-16	89%	0%
	gi|525313657|ref|NP_001266103.1|	putative steroid 5beta-reductase [Solanum lycopersicum]	82 bits(201)	1,75E-15	86%	0%
SLCAPL02F07	gi|565359973|ref|XP_006346757.1|	PREDICTED: 15.7 kDa heat shock protein, peroxisomal-like [Solanum tuberosum]	153 bits(385)	4,76E-42	90%	0%
	gi|358248934|ref|NP_001239965.1|	uncharacterized protein LOC100802108 [Glycine max]	115 bits(286)	1,48E-27	78%	1%
	gi|255631402|gb|ACU16068.1|	unknown [Glycine max]	113 bits(281)	8,63E-27	78%	1%
	gi|595928519|ref|XP_007215130.1|	hypothetical protein PRUPE_ppa013043mg [Prunus persica]	119 bits(296)	5,01E-29	75%	3%
	gi|657982214|ref|XP_008383146.1|	PREDICTED: 15.7 kDa heat shock protein, peroxisomal-like [Malus domestica]	115 bits(286)	3,42E-27	78%	1%
	gi|593490111|ref|XP_007141919.1|	hypothetical protein PHAVU_008G237000g [Phaseolus vulgaris]	118 bits(294)	9,89E-29	65%	2%
	gi|657978862|ref|XP_008381373.1|	PREDICTED: 15.7 kDa heat shock protein, peroxisomal-like [Malus domestica]	114 bits(284)	3,44E-27	67%	1%
	gi|460381920|ref|XP_004236689.1|	PREDICTED: 15.7 kDa heat shock protein, peroxisomal-like [Solanum lycopersicum]	153 bits(386)	3,85E-42	92%	0%
	gi|351727545|ref|NP_001238444.1|	peroxisomal small heat shock protein [Glycine max]	115 bits(287)	1,09E-27	81%	1%
	gi|661894642|emb|CDP01641.1|	unnamed protein product [Coffea canephora]	113 bits(281)	7,13E-27	68%	11%
SLCAPL03F09	gi|343526662|gb|AEM46061.1|	actin [Viscum album]	155 bits(391)	5,51E-46	82%	0%
	gi|449518875|ref|XP_004166461.1|	PREDICTED: LOW QUALITY PROTEIN: actin-101-like [Cucumis sativus]	153 bits(386)	2,94E-45	81%	0%
	gi|209981337|gb|ACJ05349.1|	actin [Camellia sinensis]	156 bits(394)	5,46E-45	82%	0%
	gi|56961766|gb|AAW31852.1|	actin [Vitis vinifera]	156 bits(392)	1,09E-45	82%	0%
	gi|209981339|gb|ACJ05350.1|	actin [Camellia sinensis]	157 bits(396)	3,12E-45	82%	0%
	gi|3860317|emb|CAA10126.1|	actin [Cicer arietinum]	153 bits(384)	5,78E-45	80%	0%
	gi|425872892|gb|AFY06656.1|	actin 2, partial [Carica papaya]	157 bits(396)	2,17E-45	82%	0%
	gi|209981335|gb|ACJ05348.1|	actin [Camellia sinensis]	157 bits(396)	3,29E-45	82%	0%

	gi|326417692|gb|ADZ73581.1|	actin 1 [Vaccaria hispanica]	156 bits(392)	2,86E-45	81%	0%
	gi|2244734|dbj|BAA21108.1|	actin [Gossypium hirsutum]	157 bits(395)	3,81E-45	82%	0%
SLCAPL03H11	gi|661894310|emb|CDP02751.1|	unnamed protein product [Coffea canephora]	76 bits(186)	2,90E-16	74%	0%
	gi|590652591|ref|XP_007033193.1|	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein, putative [Theobroma cacao]	74 bits(180)	3,84E-15	70%	0%
	gi|440494829|gb|AGC08429.1|	lipid transfer protein [Gossypium hirsutum]	72 bits(174)	1,64E-14	70%	0%
	gi|587933560|gb|EXC20523.1|	hypothetical protein L484_027077 [Morus notabilis]	75 bits(182)	9,58E-16	72%	0%
	gi|225452110|ref|XP_002284213.1|	PREDICTED: non-specific lipid-transfer protein 2-like [Vitis vinifera]	73 bits(178)	4,03E-15	74%	0%
	gi|225452105|ref|XP_002284190.1|	PREDICTED: probable non-specific lipid-transfer protein AKCS9-like isoform 1 [Vitis vinifera]	71 bits(172)	3,31E-14	67%	0%
	gi|357508195|ref|XP_003624386.1|	Non-specific lipid-transfer protein [Medicago truncatula]	74 bits(179)	2,69E-15	74%	0%
	gi|502106509|ref|XP_004492965.1|	PREDICTED: probable non-specific lipid-transfer protein AKCS9-like [Cicer arietinum]	73 bits(177)	6,10E-15	70%	0%
	gi|296087247|emb|CBI33621.3|	unnamed protein product [Vitis vinifera]	73 bits(178)	3,35E-15	74%	0%
	gi|566171515|ref|XP_006383409.1|	hypothetical protein POPTR_0005s15210g [Populus trichocarpa]	73 bits(177)	6,50E-15	70%	0%
SLCAPL05D01	gi|350539449|ref|NP_001234138.1|	profilin [Solanum lycopersicum]	228 bits(580)	1,30E-71	80%	0%
	gi|460412518|ref|XP_004251645.1|	PREDICTED: profilin-1-like [Solanum lycopersicum]	243 bits(620)	1,26E-77	89%	0%
	gi|255546279|ref|XP_002514199.1|	profilin, putative [Ricinus communis]	229 bits(583)	3,62E-72	80%	0%
	gi|60418864|gb|AAX19859.1|	profilin 2 [Malus domestica]	228 bits(579)	1,76E-71	80%	0%
	gi|565373896|ref|XP_006353502.1|	PREDICTED: profilin-1-like [Solanum tuberosum]	242 bits(615)	5,24E-77	89%	0%
	gi|658004946|ref|XP_008337609.1|	PREDICTED: profilin-2 [Malus domestica]	228 bits(581)	8,53E-72	81%	0%
	gi|284520994|gb|ADB93072.1|	profilin-1 [Jatropha curcas]	233 bits(594)	9,88E-74	82%	0%
	gi|164510842|emb|CAK93713.1|	profilin [Malus domestica]	228 bits(581)	9,61E-72	81%	0%
	gi|60418860|gb|AAX19857.1|	profilin 2 [Malus domestica]	228 bits(580)	1,07E-71	81%	0%
	gi|302325341|gb|ADL18409.1|	profilin [Gossypium hirsutum]	230 bits(586)	1,21E-72	80%	0%
SLCAPL05E10	gi|296088510|emb|CBI37501.3|	unnamed protein product [Vitis vinifera]	113 bits(282)	3,55E-27	90%	0%
	gi|672110587|ref|XP_008796259.1|	PREDICTED: thioredoxin reductase NTRB-like [Phoenix dactylifera]	113 bits(282)	2,82E-25	88%	0%
	gi|674906276|emb|CDY26806.1|	BnaC09g09330D [Brassica napus]	111 bits(275)	3,58E-26	90%	0%
	gi|225431669|ref|XP_002263864.1|	PREDICTED: thioredoxin reductase 2-like [Vitis vinifera]	113 bits(282)	2,98E-25	90%	0%
	gi|565352777|ref|XP_006343316.1|	PREDICTED: thioredoxin reductase 2-like [Solanum tuberosum]	121 bits(303)	2,53E-28	93%	0%
	gi|536838|gb|AAA33376.1|	NADPH thioredoxin reductase, partial [Helianthus annuus]	109 bits(271)	9,17E-26	86%	0%
	gi|694358739|ref|XP_009359641.1|	PREDICTED: thioredoxin reductase NTRB-like isoform X1 [Pyrus x bretschneideri]	112 bits(279)	6,02E-25	90%	0%
	gi|460377440|ref|XP_004234501.1|	PREDICTED: thioredoxin reductase 2-like [Solanum lycopersicum]	121 bits(302)	3,54E-28	92%	0%
	gi|565398541|ref|XP_006364831.1|	PREDICTED: thioredoxin reductase 2-like [Solanum tuberosum]	113 bits(282)	2,79E-25	92%	0%
	gi|242066214|ref|XP_002454396.1|	hypothetical protein SORBIDRAFT_04g030050 [Sorghum bicolor]	112 bits(278)	6,45E-25	90%	0%
SLCAPL05F03	gi|460375740|ref|XP_004233662.1|	PREDICTED: uncharacterized protein LOC101263080 [Solanum lycopersicum]	74 bits(181)	8,73E-12	50%	10%
	gi|587854390|gb|EXB44453.1|	hypothetical protein L484_013871 [Morus notabilis]	71 bits(173)	6,78E-11	47%	10%
	gi|460375742|ref|XP_004233663.1|	PREDICTED: uncharacterized protein LOC101263375 [Solanum lycopersicum]	71 bits(173)	1,40E-11	49%	10%
	gi|565342462|ref|XP_006338364.1|	PREDICTED: uncharacterized protein LOC102584983 [Solanum tuberosum]	70 bits(171)	7,73E-11	58%	10%
	gi|565343279|ref|XP_006338765.1|	PREDICTED: uncharacterized protein LOC102598759 [Solanum tuberosum]	26 bits(55)	4,13E-13	91%	0%
	gi|460372696|ref|XP_004232162.1|	PREDICTED: uncharacterized protein LOC101259999 [Solanum lycopersicum]	72 bits(176)	2,91E-11	57%	10%
	gi|565343283|ref|XP_006338767.1|	PREDICTED: meiosis arrest female protein 1 homolog [Solanum tuberosum]	73 bits(177)	4,38E-12	54%	10%
	gi|590720180|ref|XP_007051260.1|	Endonuclease or glycosyl hydrolase with C2H2-type zinc finger domain, putative isoform 1 [Theobroma cacao]	72 bits(174)	4,84E-11	49%	10%
SLCAPL05F07	gi|460411711|ref|XP_004251249.1|	PREDICTED: calmodulin-like isoform 2 [Solanum lycopersicum]	295 bits(753)	1,53E-98	97%	0%
	gi|460411709|ref|XP_004251248.1|	PREDICTED: calmodulin-like isoform 1 [Solanum lycopersicum]	295 bits(753)	4,74E-98	97%	0%
	gi|674233595|gb|KFK26360.1|	hypothetical protein AALP_AA8G238300 [Arabis alpina]	292 bits(747)	1,27E-97	97%	0%
	gi|685375194|ref|XP_009120715.1|	PREDICTED: LOW QUALITY PROTEIN: calmodulin [Brassica rapa]	294 bits(752)	2,81E-98	97%	0%
	gi|685320364|ref|XP_009150282.1|	PREDICTED: calmodulin-like [Brassica rapa]	293 bits(749)	5,79E-98	97%	0%
	gi|460407314|ref|XP_004249098.1|	PREDICTED: calmodulin-like [Solanum lycopersicum]	294 bits(751)	3,32E-98	97%	0%
	gi|359479174|ref|XP_003632230.1|	PREDICTED: calmodulin-related protein isoform 4 [Vitis vinifera]	294 bits(752)	6,36E-98	97%	0%
	gi|568214802|ref|NP_001275359.1|	calmodulin-5/6/7/8 [Solanum tuberosum]	295 bits(755)	8,21E-99	98%	0%
	gi|566150460|ref|XP_006369409.1|	calmodulin-like protein 6a [Populus trichocarpa]	294 bits(750)	3,95E-98	97%	0%
	gi|152013376|sp|A2WNH1.2|CALM3_ORYSI	RecName: Full=Calmodulin-3; Short=CaM-3 [Oryza sativa Indica Group]	292 bits(747)	1,21E-97	97%	0%

Apêndice H – Pesquisa por primers das 15 enzimas alvo, listadas na figura 5
Fonte de dados: Blastx/NCBI
Elaborada pelo autor

1 - cytochrome P450

Contig26 – Folha

Primer 1	Sequence (5'->3')	Template strand	Length	Start	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	SEQUÊNCIA PEQUENA, SEM							
Reverse primer	POSSIBILIDADE DE PRIMERS							
Product length								

Primer 2	Sequence (5'->3')	Template strand	Length	Start	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	SEQUÊNCIA PEQUENA, SEM							
Reverse primer	POSSIBILIDADE DE PRIMERS							
Product length								

Contig0 – Calos

Primer 1	Sequence (5'->3')	Template strand	Length	Start	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	CTGTCGGTGGACTGCTCG	Plus	18	106	60.13	66.67	3.00	2.00
Reverse primer	GACGTCGCATGCTCCCG	Minus	17	381	60.97	70.59	6.00	2.00
Product length	276							

Primer 2	Sequence (5'->3')	Template strand	Length	Start	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	GTCGGCTGTCGGTGGAC	Plus	17	101	60.10	70.59	3.00	3.00
Reverse primer	TCGCATGCTCCCGGC	Minus	15	377	59.38	73.33	6.00	2.00
Product length	277							

Contig7 – Calos

Primer 1	Sequence (5'->3')	Template strand	Length	Start	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	SEQUÊNCIA PEQUENA, SEM							
Reverse primer	POSSIBILIDADE DE PRIMERS							
Product length								

Primer 2	Sequence (5'->3')	Template strand	Length	Start	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	SEQUÊNCIA PEQUENA, SEM							
Reverse primer	POSSIBILIDADE DE PRIMERS							
Product length								

Contig26 – Calos

Primer 1	Sequence (5'->3')	Template strand	Length	Start	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	ATCCAACGCGTATGGGAGC	Plus	19	6	60.23	57.89	8.00	2.00
Reverse primer	CTCTGCGATGATACCACTGCT	Minus	21	94	59.93	52.38	4.00	3.00
Product length	89							

Primer 2	Sequence (5'->3')	Template strand	Length	Start	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	AGCAGTGGTATCATCGCAGA	Plus	20	74	58.89	50.00	4.00	2.00
Reverse primer	CTCGAGCAGTCCACCGACA	Minus	19	166	61.63	63.16	6.00	0.00
Product length	93							

2 - zinc finger

SLSEPL04G10 – Semente

Primer 1	Sequence (5'->3')	Template strand	Length	Start	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	TCTTGGATTGGGAATGGCGG	Plus	20	51	60.40	55.00	3.00	1.00
Reverse primer	AAAGATCCAGCGGAAGTCACC	Minus	21	155	60.34	52.38	4.00	1.00

Product length	105							
Primer 2	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	TGTTGGGAACTCCCTCTGTTT	Plus	21	2	59.15	47.62	6.00	0.00
Reverse primer	AATCCAGGTGCTGGACTGAC	Minus	20	95	59.67	55.00	7.00	1.00
Product length	94							

Contig31 - Calos

Primer 1	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	GATTTTGCAACGTGCTCGTGA	Plus	21	50	60.33	47.62	6.00	2.00
Reverse primer	ACACTGGAGGTCCTCTTGAC	Minus	20	126	58.66	55.00	7.00	1.00
Product length	77							
Primer 2	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	GTGCTCGTGAACGCGAAGAA	Plus	20	61	61.55	55.00	4.00	2.00
Reverse primer	TCAAGGGCTTCCTAAACACTGG	Minus	22	141	60.22	50.00	4.00	3.00
Product length	81							

SLCAPL05F03 – Calos

Primer 1	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	AGAGAACTGTCAGGGGATGC	Plus	20	21	59.09	55.00	5.00	2.00
Reverse primer	GAATCGACGAGGGAATGCCA	Minus	20	130	60.18	55.00	5.00	3.00
Product length	110							
Primer 2	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	GGCATTCCCTCGTCGATTCC	Plus	20	112	60.88	60.00	5.00	1.00
Reverse primer	ACTATACCATCGGGGGCATGA	Minus	21	185	60.48	52.38	4.00	2.00
Product length	74							

3 - laccase-14

SLCAPL01D01 – Calos

Primer 1	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	TGTGAGCTGGGGAATGGAAAT	Plus	21	24	59.64	47.62	4.00	2.00
Reverse primer	TCAACACTGGGGCATATCAGG	Minus	21	120	59.79	52.38	4.00	0.00
Product length	97							
Primer 2	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	ATGCATTGCCACTTAGAACGG	Plus	21	1	59.25	47.62	6.00	1.00
Reverse primer	TGGGAGCCCTTTCCATCTTTC	Minus	21	77	59.99	52.38	4.00	0.00
Product length	77							

4 - cytochrome c oxidase

SLCAPL01D05 – Calos

Primer 1	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	TGTGAGCTGGGGAATGGAAAT	Plus	21	24	59.64	47.62	4.00	2.00
Reverse primer	TCAACACTGGGGCATATCAGG	Minus	21	120	59.79	52.38	4.00	0.00
Product length	97							
Primer 2	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	ATGCATTGCCACTTAGAACGG	Plus	21	1	59.25	47.62	6.00	1.00
Reverse primer	TGGGAGCCCTTTCCATCTTTC	Minus	21	77	59.99	52.38	4.00	0.00

Product length	77							

5 - superoxide dismutase

SLCAPL01E01 – Calos

Primer 1	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	GTGTGGCTTGGTGTGGACAA	Plus	20	40	61.03	55.00	4.00	2.00
Reverse primer	TGTTCCCAGACGCCTATACC	Minus	20	161	58.88	55.00	4.00	0.00
Product length	122							
Primer 2	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	AATGCAGAAGGTGCTGCTTTAC	Plus	22	4	59.77	45.45	8.00	2.00
Reverse primer	GGCGCTTAAGCTCTTTGTCC	Minus	20	73	59.55	55.00	8.00	0.00
Product length	70							

6 - steroid 5beta-reductase

SLCAPL01H07 – Calos

Primer 1	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	GCAGAGTACAGGGGGAGTTT	Plus	20	86	59.02	55.00	4.00	0.00
Reverse primer	CGGAATCCCAAGAAACCGTG	Minus	20	191	59.20	55.00	5.00	1.00
Product length	106							
Primer 2	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	TCCCATATGGTCGACCTGC	Plus	19	25	58.87	57.89	8.00	2.00
Reverse primer	AAACCACCAAACTCCCCCTG	Minus	20	113	60.11	55.00	2.00	1.00
Product length	89							

7 - lipid-transfer protein

SLCAPL03H11 – Calos

Primer 1	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	GTTGCGCTAAGTTGAGAGAGC	Plus	21	8	59.61	52.38	4.00	2.00
Reverse primer	TCCACATGCGCTTGCAAATC	Minus	20	120	60.11	50.00	6.00	2.00
Product length	113							
Primer 2	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	TTGCGCTAAGTTGAGAGAGCAA	Plus	22	9	60.55	45.45	5.00	2.00
Reverse primer	AGGTTACTCCACATGCGCT	Minus	19	127	59.02	52.63	4.00	2.00
Product length	119							

8 - actin

SLFLPL03D04 – Folha

Primer 1	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	GAGAGCTTGATGGAATTCAGGT	Plus	22	35	58.12	45.45	6.00	1.00
Reverse primer	CTAGTTGGCGCGGCTCTTA	Minus	19	120	59.86	57.89	4.00	2.00
Product length	86							
Primer 2	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	TGCCAGTACAAAGGAAAGATTCA	Plus	23	9	58.28	39.13	4.00	1.00
Reverse primer	CCATTTCAGTCGGGTCGGTT	Minus	20	88	60.32	55.00	2.00	0.00

Product length	80

SLCAPL03F09 – Calos

Primer 1	Sequence (5'->3')	Template strand	Length	Start	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	GTCGCTCCCCCAGAGAGAAA	Plus	20	76	61.26	60.00	4.00	1.00
Reverse primer	TGGACAATGGATGGACCAGAC	Minus	21	200	59.72	52.38	6.00	3.00
Product length	125							

Primer 2	Sequence (5'->3')	Template strand	Length	Start	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	AAGGAAATCACTGCCTTGGCT	Plus	21	31	60.20	47.62	7.00	2.00
Reverse primer	ACTCGTCATACTCGCCCTTT	Minus	20	181	58.82	50.00	2.00	0.00
Product length	151							

9 - profilin-1-like

SLCAPL05D01 – Calos

Primer 1	Sequence (5'->3')	Template strand	Length	Start	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	TGTCGGGGCAAGAATACGTC	Plus	20	2	60.11	55.00	4.00	2.00
Reverse primer	TCGAATGACAACCCCAGCTC	Minus	20	252	60.04	55.00	4.00	2.00
Product length	251							

Primer 2	Sequence (5'->3')	Template strand	Length	Start	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	ATGGTCATTCTAGGCGGAGC	Plus	20	217	59.61	55.00	4.00	2.00
Reverse primer	CCGAGCCTCTCAACAACCAG	Minus	20	368	60.67	60.00	5.00	1.00
Product length	152							

10 - thioredoxin reductase

SLCAPL05E10 – Calos

Primer 1	Sequence (5'->3')	Template strand	Length	Start	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	GCCTTGGATGCAGAGCACTA	Plus	20	11	60.11	55.00	4.00	2.00
Reverse primer	TTCTGTCGTGGCAAGAATGC	Minus	20	97	59.13	50.00	5.00	2.00
Product length	87							

Primer 2	Sequence (5'->3')	Template strand	Length	Start	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	AGAGCGATTGATAGCATGGCA	Plus	21	60	59.93	47.62	4.00	3.00
Reverse primer	TCCAAACCTTGAGGAAATAGGG	Minus	22	224	57.68	45.45	4.00	0.00
Product length	165							

11 - calmodulin-like

SLCAPL05F07 – Calos

Primer 1	Sequence (5'->3')	Template strand	Length	Start	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	AGGAGGCTTTCAGCCTATTCG	Plus	21	41	59.86	52.38	7.00	2.00
Reverse primer	GTCCCAACGACCTCATCACA	Minus	20	124	59.68	55.00	3.00	0.00
Product length	84							

Primer 2	Sequence (5'->3')	Template strand	Length	Start	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	AAGGACGGAGATGGTTGCATT	Plus	21	64	60.00	47.62	4.00	1.00
Reverse primer	TGGAGCTCAGCTTCGGTTG	Minus	19	149	60.00	57.89	7.00	0.00
Product length	86							

12 - metallothionein-like

Contig3 – Semente

Primer 1	Sequence (5'->3')	Template	Length	Start	Tm	GC%	Self	Self 3'

		strand					complementarity	complementarity
Forward primer	AGGATGTGGGATGTACCCCG	Plus	20	63	61.05	60.00	4.00	2.00
Reverse primer	CCTCCTTCTGCTGCTTTCTCA	Minus	21	182	60.00	52.38	3.00	1.00
Product length	120							
Primer 2	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	GTCTTGCTGTGGAGGAAACTG	Plus	21	3	59.12	52.38	3.00	1.00
Reverse primer	AAGTCGGGGTACATCCCACA	Minus	20	86	60.55	55.00	4.00	2.00
Product length	84							

Contig5 – Calos

Primer 1	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	TCTTGCTGTGGAGGAAACTGT	Plus	21	4	59.51	47.62	3.00	3.00
Reverse primer	GGTAGTGGTGCTCTCCAAGTC	Minus	21	102	60.07	57.14	4.00	1.00
Product length	99							
Primer 2	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	GATGTACCCCGACTTGGAGA	Plus	20	72	58.52	55.00	4.00	1.00
Reverse primer	AGGGTCACATGTGCAGTTTG	Minus	20	222	58.68	50.00	8.00	2.00
Product length	151							

13 - heat shock protein

Contig6 – Semente

Primer 1	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	TATGCCTGGGCTCGACAAG	Plus	19	6	59.48	57.89	4.00	3.00
Reverse primer	TTCACCTTTGGAACAGCCAC	Minus	20	215	58.60	50.00	3.00	0.00
Product length	210							
Primer 2	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	GGATATGCCTGGGCTCGACA	Plus	20	3	61.76	60.00	4.00	2.00
Reverse primer	CACCTTTGGAACAGCCACTTT	Minus	21	213	59.24	47.62	3.00	1.00
Product length	211							

SLSEPL04F05 – Semente

Primer 1	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	TGAAGGCACAGGCACTTAGG	Plus	20	14	59.96	55.00	3.00	2.00
Reverse primer	GCTGAAACCCGAGGTGAGAA	Minus	20	204	59.97	55.00	4.00	0.00
Product length	191							
Primer 2	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	TCAACCCCGAGAACTCCATC	Plus	20	80	59.10	55.00	4.00	1.00
Reverse primer	CCTCAAGGCTGAAACCCGAG	Minus	20	211	60.67	60.00	4.00	2.00
Product length	132							

Contig34 – Folha

Primer 1	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	GGAACGCTACGATGATGCCT	Plus	20	111	60.25	55.00	3.00	2.00
Reverse primer	AGCCAGCTGTGTAAGTGTCC	Minus	20	213	59.96	55.00	6.00	0.00
Product length	103							
Primer 2	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	TTGCTGATGCCGAAATGACG	Plus	20	29	59.55	50.00	2.00	2.00
Reverse	TTCCGAACTCTGCGGATTGT	Minus	20	177	59.68	50.00	5.00	2.00

primer								
Product length	149							

SLCAPL02F07 – Calos

Primer 1	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	TCACATTAATTGCGTTGCGCT	Plus	21	15	59.80	42.86	6.00	2.00
Reverse primer	TCATTAATGCAGCTGGCACG	Minus	20	85	59.27	50.00	8.00	2.00
Product length	71							
Primer 2	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	CAGTCGGGAAACCTGTCGT	Plus	19	50	59.63	57.89	3.00	0.00
Reverse primer	GAAGAGCGCCCAATACGCAA	Minus	20	132	61.37	55.00	4.00	0.00
Product length	83							

14 - 4-coumarate

Contig6 – Calos

Primer 1	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	CTCCCATATGGTCGACCTGC	Plus	20	24	59.97	60.00	8.00	2.00
Reverse primer	GCAGCCAGTCTAGCTCTCAA	Minus	20	221	59.47	55.00	7.00	0.00
Product length	198							
Primer 2	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	AAGCAGTGGTATCAACGCAGA	Plus	21	70	60.00	47.62	4.00	2.00
Reverse primer	AGCCAGTCTAGCTCTCAAGT	Minus	20	219	57.77	50.00	7.00	1.00
Product length	150							

Contig8 – Calos

Primer 1	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	AGCAGTGGTATCAACGCAGA	Plus	20	71	59.39	50.00	4.00	2.00
Reverse primer	CCAGCAGCTAGTTTAGCTCTCA	Minus	22	218	59.83	50.00	7.00	3.00
Product length	148							
Primer 2	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	TCTCCCATATGGTCGACCTGC	Plus	21	23	61.37	57.14	8.00	2.00
Reverse primer	ATCCCTGTACTCTGCGTTGAT	Minus	21	100	58.89	47.62	4.00	2.00
Product length	78							

15 - phenylalanine amônia-lyase (PAL)

Contig17 – Calos

Primer 1	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	CACCAGGTGAAGAATGTGACAA	Plus	22	8	58.79	45.45	7.00	3.00
Reverse primer	GTGGAGCACCATTCCATTCCT	Minus	21	106	60.34	52.38	6.00	0.00
Product length	99							
Primer 2	**Sequence (5'->3')**	**Template strand**	**Length**	**Start**	**Tm**	**GC%**	**Self complementarity**	**Self 3' complementarity**
Forward primer	TACAGCAATGTGCAATGGAGA	Plus	21	36	57.93	42.86	4.00	3.00
Reverse primer	AACAGATTGGAAGTGGAGCAC	Minus	21	118	58.49	47.62	3.00	3.00
Product length	83							