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DESCRIPTION

FIELD OF THE INVENTION

[0001] Disclosed herein are recombinant DNA useful for providing enhanced traits totransgenic plants, seeds, pollen, plant cells and plant nuclei of such transgenic plants, methods of making and using such recombinant DNA, plants, seeds, pollen, plant cells and plant nuclei.

SUMMARY OF THE INVENTION

[0002] This invention provides a recombinant DNA construct comprising a polynucleotide encoding the cognate amino acid sequences of SEQ ID NO: 1018. The recombinant DNA is useful for providing enhanced traits when stably integrated into the chromosomes and expressed in the nuclei of transgenic plants cells. In some aspects the recombinant DNA encodes a protein; in other aspects the recombinant DNA is transcribed to RNA that suppresses the expression of a native gene.

[0003] Such recombinant DNA in a plant cell nucleus of this invention is provided in as a construct comprising a promoter that is functional in plant cells and that is operably linked to DNA that encodes a protein or to DNA that results in gene suppression, In the invention the recombinant DNA is characterized by its cognate amino acid sequence that has at least 90% identity over the full length of SEQ ID NO: 1018, wherein transgenic plants having said recombinant DNA in their nuclei have an enhanced heat tolerance as compared to control plants that do not have said recombinant DNA in their nuclei.

[0004] This invention also provides transgenic plant cell nuclei comprising the recombinant DNA of the invention, transgenic plant cells comprising such nuclei, transgenic plants comprising a plurality of such transgenic plant cells, and transgenic seeds and transgenic pollen of such plants. Such transgenic plants are selected from a population of transgenic plants regenerated from plant cells transformed with recombinant DNA by screening transgenic plants for an enhanced trait as compared to control plants. The enhanced trait is one or more of enhanced water use efficiency, enhanced cold tolerance, increased yield, enhanced nitrogen use efficiency, enhanced heat tolerance, enhanced shade tolerance, enhanced high salinity tolerance, enhanced seed protein and enhanced seed oil. Such recombinant DNA in a plant cell nuclus of this invention is provided in as a construct comprising a promoter that is functional in plant cells and that is operably linked to DNA that encodes a protein or to DNA that results in gene suppression.

[0005] In another aspect of the invention the plant cell nuclei, cells, plants, seeds, and pollen further comprise DNA expressing a protein that provides tolerance from exposure to an herbicide applied at levels that are lethal to a wild type plant cell.

[0006] This invention also provides methods for manufacturing non-natural, transgenic seed that can be used to produce a crop of transgenic plants with an enhanced trait resulting from expression of stably-integrated, recombinant DNA in the nucleus of the plant cells. More specifically the method comprises (a) screening a population of plants for an enhanced trait and recombinant DNA, where individual plants in the population can exhibit the trait at a level less than, essentially the same as or greater than the level that the trait is exhibited incontrol plants which do not express the recombinant DNA; (b) selecting from the population one or more plants that exhibit the trait at a level greater than the level that said trait is exhibited in control plants and (c) collecting seed from a selected plant. Such method further comprises steps (a) verifying that the recombinant DNA is stably integrated in said selected plants; and (b) analyzing tissue of a selected plant to determine the production of a protein having the function of a protein of SEQ LD NO:1018. In one aspect of the invention the plants in the population further comprise DNA expressing a protein that provides tolerance to exposure to an herbicide applied at levels that are lethal to wild type plant cells and where the selecting is effected by treating the population with the herbicide, e.g. a glyphosate, dicamba, or glufosinate compound. In another aspect of the invention the plants are selected by identifying plants with the enhanced trait. The methods are especially useful for manufacturing corn, soybean, cotton, canola, alfalfa, wheat or rice seed selected as having one of the enhanced traits described above,

BRIEF DESCRIPTION OF THE DRAWINGS

[0007]

Figures 1, 2 and 3 illustrate plasmid maps.

Figure 4 illustrates a consensus amino acid sequence of SEQ ID NO: 768 and its homologs.

DETAILED DESCRIPTION OF THE INVENTION

[0008] In the attached sequence listing:

SEQ ID NO: 1-759 are nucleotide sequences of the protein coding strand of DNA " used in the recombinant DNA for imparting an enhanced trait in plant cells;

SEQ LD NO: 760-1518 are amino acid sequences of the cognate protein of the nucleotide sequences of SEQ ID NO:1-759;

SEQ ID NO: 1519- 67778 are amino acid sequences of homologous proteins;

SEQ ID NO:67779 is a nucleotide sequence of a plasmid base vector useful for corn transformation; and

SEQ ID NO:67780 is a DNA sequence of a plasmid base vector useful for soybean transformation.

SEQ ID NO:67781 is a DNA sequence of a plasmid base vector useful for cotton transformation.

SEQ ID NO: 67782-67894 are consensus sequences.

[0009] **T**able 1 lists the protein SEQ ID NOs and their corresponding consensus SEQ ID NOs.
Table 1.

Gene ID	SEQ ID NO	Consensus SEQ ID NO	Gene ID	SEQ ID NO	Consensus NO SEQ ID
CGPG1083	767	67782	CGPG6934	1239	67838
CGPG1088	768	67783	CGPG7056	1249	67839
CGPG1092	769	67784	CGPG7071	1250	67840
CGPG1108	770	67785	CGPG7243	1270	67841
CGPG1140	772	67786	CGPG7258	1271	67842
CGPG1143	773	67787	CGPG7324	1277	67843
CGPG1170	775	67788	CGPG7338	1279	67844
CGPG1192	778	67789	CGPG7352	1282	67845
CGPG1311	786	67790	CGPG7362	1285	67846
CGPG1391	792	67791	CGPG7430	1295	67847
CGPG1633	809	67792	CGPG7438	1296	67848
CGPG1715	814	67793	CGPG7450	1299	67849
CGPG1895	822	67794	CGPG7452	1300	67850
CGPG2035	836	67795	CGPG7480	1302	67851
CGPG2068	840	67796	CGPG7510	1308	67852
CGPG2118	844	67797	CGPG7517	1310	67853
CGPG2191	848	67798	CGPG7523	1311	67854
CGPG2313	855	67799	CGPG7532	1314	67855
CGPG2426	864	67800	CGPG7548	1316	67856
CGPG2437	866	67801	CGPG7599	1320	67857
CGPG2452	867	67802	CGPG7616	1324	67858
CGPG2855	882	67803	CGPG7793	1333	67859
CGPG3004	887	67804	CGPG7816	1338	67860
CGPG3084	892	67805	CGPG7826	1339	67861
CGPG3269	905	67806	CGPG7861	1340	67862
CGPG3270	906	67807	CGPG8054	1362	67863

Gene ID	SEQ ID NO	Consensus SEQ ID NO	Gene ID	SEQ ID NO	Consensus NO SEQ ID
CGPG3410	913	67808	CGPG8059	1363	67864
CGPG3605	922	67809	CGPG8084	1367	67865
CGPG3612	923	67810	CGPG8093	1368	67866
CGPG3616	924	67811	CGPG8097	1371	67867
CGPG3631	925	67812	CGPG8112	1372	67868
CGPG375	933	67813	CGPG8120	1373	67869
CGPG3931	940	67814	CGPG8157	1376	67870
CGPG3975	944	67815	CGPG8158	1377	67871
CGPG4346	974	67816	CGPG8212	1382	67872
CGPG4383	977	67817	CGPG8375	1403	67873
CGPG4437	983	67818	CGPG8383	1405	67874
CGPG4660	995	67819	CGPG8544	1422	67875
CGPG4772	1007	67820	CGPG8546	1423	67876
CGPG5196	1043	67821	CGPG8549	1424	67877
CGPG5212	1046	67822	CGPG8588	1429	67878
CGPG5304	1057	67823	CGPG8597	1430	67879
CGPG5510	1072	67824	CGPG8629	1433	67880
CGPG5732	1100	67825	CGPG8636	1437	67881
CGPG5889	1116	67826	CGPG8646	1440	67882
CGPG5925	1121	67828	CGPG8716	1446	67884
CGPG5926	1122	67829	CGPG8754	1447	67885
CGPG6049	1135	67830	CGPG9001	1471	67886
CGPG6120	1142	67831	CGPG9069	1476	67887
CGPG6201	1151	67832	CGPG9097	1480	67888
CGPG6311	1169	67833	CGPG9106	1481	67889
CGPG6353	1176	67834	CGPG9143	1487	67890
CGPG6636	1214	67835	CGPG9188	1498	67891
CGPG691	1235	67836	CGPG9248	1505	67892
CGPG6930	1238	67837	CGPG9285	1509	67893
/	/	/	CGPG9315	1513	67894

[0010] The nuclei of this invention are identified by screening transgenic plants for one or more traits including enhanced drought stress tolerance, enhanced heat stress tolerance, enhanced cold stress tolerance, enhanced high salinity stress tolerance, enhanced low nitrogen availability stress tolerance, enhanced shade stress tolerance, enhanced plant growth and development at the stages of seed imbibition through early vegetative phase, and enhanced plant growth and development at the stages of leaf development, flower production and seed maturity.

[0011] As used herein a "plant cell" means a plant cell that is transformed with stably-integrated, non-natural, recombinant DNA, e.g. by *Agrobacterium*-mediated transformation or by bombardment using microparticles coated with recombinant DNA or other means. A plant cell of this invention can be an originally-transformed plant cell that exists as a microorganism or as a progeny plant cell that is regenerated into differentiated tissue, e.g. into a transgenic plant with stably-integrated, non-natural recombinant DNA, or seed or pollen derived from a progeny transgenic plant.

[0012] As used herein a "transgenic plant" means a plant whose genome has been altered by the stable integration of recombinant DNA. A transgenic plant includes a plant regenerated from an originally-transformed plant cell and progeny transgenic plants from later generations or crosses of a transformed plant.

[0013] As used herein "recombinant DNA" means DNA which has been a genetically engineered and constructed outside of a cell including DNA containing naturally occurring DNA or cDNA or synthetic DNA.

[0014] As used herein a "homolog" means a protein in a group of proteins that perform the same biological function, e.g. proteins that belong to the same Pfam protein family and that provide a common enhanced trait in transgenic plants of this invention. Homologs are expressed by homologous genes. Homologous genes include naturally occurring alleles and artificially-created variants. Degeneracy of the genetic code provides the possibility to substitute at least one base of the protein encoding sequence of a gene with a different base without causing the amino acid sequence of the polypeptide produced from the gene to be changed. Hence, a polynucleotide useful in the present invention may have any base sequence that has been changed from SEQ ID NO;1 through SEQ ID NO: 803 through substitution in accordance with degeneracy of the genetic code. Homologs are proteins that, when optimally aligned, have at least 60% identity, more preferably about 70% or higher, more preferably at least 80% and even more preferably at least 90% identity over the full length of a protein identified as being associated with imparting an enhanced trait when expressed in plant cells. Homologs include proteins with an amino acid sequence that has at least 90% identity to a consensus amino acid sequence of proteins and homologs disclosed herein.

[0015] Homologs are identified by comparison of amino acid sequence, e.g. manually or by use of a computer-based tool using known homology-based search algorithms such as those commonly known and referred to as BLAST, FASTA, and Smith-Waterman. A local sequence alignment program, e.g. BLAST, can be used to search a database of sequences to find similar sequences, and the summary Expectation value (E-value) used to measure the sequence base similarity. As a protein hit with the best E-value for a particular organism may not necessarily be an ortholog or the only ortholog, a reciprocal query is used in the present invention to filter hit sequences with significant E-values for ortholog identification. The reciprocal query entails search of the significant hits against a database of amino acid sequences from the base organism that are similar to the sequence of the query protein. A hit can be identified as an ortholog, when the reciprocal query's best hit is the query protein itself or a protein encoded by a duplicated gene after speciation. A further aspect of the homologs encoded by DNA useful in the transgenic plants of the invention are those proteins that differ from a disclosed protein as the result of deletion or insertion of one or more amino acids in a native sequence.

[0016] As used herein, "percent identity" means the extent to which two optimally aligned DNA or protein segments are invariant throughout a window of alignment of components, for example nucleotide sequence or amino acid sequence. An "identity fraction" for aligned segments of a test sequence and a reference sequence is the number of identical components that are shared by sequences of the two aligned segments divided by the total number of sequence components in the reference segment over a window of alignment which is the smaller of the full test sequence or the full reference sequence. "Percent identity" ("% identity") is the identity fraction times 100. Such optimal alignment is understood to be deemed as local alignment of DNA sequences. For protein alignment, a local alignment of protein sequences should allow introduction of gaps to achieve optimal alignment. Percent identity is calculated over the aligned length not including the gaps introduced by the alignment per se.

[0017] As used herein "promoter" means regulatory DNA for initializing transcription. A "plant promoter" is a promoter capable of initiating transcription in plant cells whether or not its origin is a plant cell, e.g. is it well known that *Agrobacterium* promoters are functional in plant cells. Thus, plant promoters include promoter DNA obtained from plants, plant viruses and bacteria such as *Agrobacterium* and *Bradyrhizobium* bacteria. Examples of promoters under developmental control include promoters that preferentially initiate transcription in certain tissues, such as leaves, roots, or seeds. Such promoters are referred to as "tissue preferred". Promoters that initiate transcription only in certain tissues are referred to as "tissue specific". A "cell type" specific promoter primarily drives expression in certain cell types in one or more organs, for example, vascular cells in roots or leaves. An "inducible" or "repressible" promoter is a promoter which is under environmental control. Examples of environmental conditions that may effect transcription by inducible promoters include anaerobic conditions, or certain chemicals, or the presence of light. Tissue specific, tissue preferred, cell type specific, and inducible promoters constitute the class of "non-constitutive" promoters. A "constitutive" promoter is a promoter which is active under most conditions.

[0018] As used herein "operably linked" means the association of two or more DNA fragments in a DNA construct so that the function of one, e.g. protein-encoding DNA, is controlled by the other, e.g. a promoter.

[0019] As used herein "expressed" means produced, e.g. a protein is expressed in a plant cell when its cognate DNA is transcribed to mRNA that is translated to the protein.

[0020] As used herein "suppressed" means decreased, e.g. a protein is suppressed in a plant cell when there is a decrease in the amount and/or activity of the protein in the plant cell. The presence or activity of the protein can be decreased by any amount up to and including a total loss of protein expression and/or activity.

[0021] As used herein a "control plant" means a plant that does not contain the recombinant DNA that expressed a protein that imparts an enhanced trait. A control plant is to identify and select a transgenic plant that has an enhance trait. A suitable control plant can be a non-transgenic plant of the parental line used to generate a transgenic plant, i.e. devoid of recombinant

DNA. A suitable control plant may in some cases be a progeny of a hemizygous transgenic plant line that is does not contain the recombinant DNA, known as a negative segregant.

[0022] As used herein an "enhanced trait" means a characteristic of a transgenic plant that is enhanced heat tolerance.

[0023] *"Arabidopsis"* means plants of *Arabidopsis thaliana*.

[0024] "Pfam" database is a large collection of multiple sequence alignments and hidden Markov models covering many common protein families, e.g. Pfam version 19.0 (December 2005) contains alignments and models for 8183 protein families and is based on the Swissprot 47.0 and SP-TrEMBL 30.0 protein sequence databases. See S.R. Eddy, "Profile Hidden Markov Models", Bioinfonnatics 14:755-763, 1998. The Pfam database is currently maintained and updated by the Pfam Consortium. The alignments represent some height, pod number, pod position on the plant, number of internodes, incidence of pod shatter, grain size, efficiency of nodulation and nitrogen fixation, efficiency of nutrient assimilation, resistance to biotic and abiotic stress, carbon assimilation, plant architecture, resistance to lodging, percent seed germination, seedling vigor, and juvenile traits. Yield can also be affected by efficiency of germination (including germination in stressed conditions), growth rate (including growth rate in stressed conditions), ear number, seed number per ear, seed size, composition of seed (starch, oil, protein) and characteristics of seed fill.

[0025] Increased yield of a transgenic plant of the present invention can be measured in a number of ways, including test weight, seed number per plant, seed weight, seed number per unit area (i.e. seeds, or weight of seeds, per acre), bushels per acre, tonnes per acre, tons per acre, kilo per hectare. For example, maize yield may be measured as production of shelled corn kernels per unit of production area, for example in bushels per acre or metric tons per hectare, often reported on a moisture adjusted basis, for example at 15.5 percent moisture. Increased yield may result from improved utilization of key biochemical compounds, such as nitrogen, phosphorous and carbohydrate, or from improved responses to environmental stresses, such as cold, heat, drought, salt, and attack by pests or pathogens. Recombinant DNA used in this invention can also be used to provide plants having improved growth and development, and ultimately increased yield, as the result of modified expression of plant growth regulators or modification of cell cycle or photosynthesis pathways. Also of interest is the generation of transgenic plants that demonstrate enhanced yield with respect to a seed component that may or may not correspond to an increase in overall plant yield. Such properties include enhancements in seed oil, seed molecules such as tocopherol, protein and starch, or oil particular oil components as may be manifest by an alterations in the ratios of seed components.

[0026] *"Arabidopsis"* means plants of *Arabidopsis thaliana*.

[0027] "Pfam" database is a large collection of multiple sequence alignments and hidden Markov models covering many common protein families, e.g. Pfam version 19.0 (December 2005) contains alignments and models for 8183 protein families and is based on the Swissprot 47.0 and SP-TrEMBL 30.0 protein sequence databases. See S.R. Eddy, "Profile Hidden Markov Models", Bioinformatics 14:755-763, 1998. The Pfam database is currently maintained and updated by the Pfam Consortium. The alignments represent some evolutionary conserved structure that has implications for the protein's function. Profile hidden Markov models (profile HMMs) built from the protein family alignments are useful for automatically recognizing that a new protein belongs to an existing protein family even if the homology by alignment appears to be low,

[0028] A "Pfam domain module" is a representation of Pfam domains in a protein, in order from N terminus to C terminus. In a Pfam domain module individual Pfam domains are separated by double colons "::". The order and copy number of the Pfam domains from N to C terminus are attributes of a Pfam domain module. Although the copy number of repetitive domains is important, varying copy number often enables a similar function. Thus, a Pfam domain module with multiple copies of a domain should define an equivalent Pfam domain module with variance in the number of multiple copies. A Pfam domain module is not specific for distance between adjacent domains, but contemplates natural distances and variations in distance that provide equivalent function. The Pfam database contains both narrowly- and broadly-defined domains, leading to identification of overlapping domains on some proteins. A Pfam domain module is characterized by non-overlapping domains. Where there is overlap, the domain having a function that is more closely associated with the function of the protein (based on the E value of the Pfam match) is selected.

[0029] Once one DNA is identified as encoding a protein which imparts an enhanced trait when expressed in transgenic plants, other DNA encoding proteins with the same Pfam domain module are identified by querying the amino acid sequence of protein encoded by candidate DNA against the Hidden Markov Models which characterizes the Pfam domains using HMMER software which is publicly available from the Pfam Consortium. Candidate proteins meeting the same Pfam domain module are in the protein family and have cognate DNA that is useful in constructing recombinant DNA for the use in the plant cells of this invention. Hidden Markov Model databases for use with HMMER software in identifying DNA expressing protein with a common Pfam domain module for recombinant DNA in the plant cells of this invention are also publicly available from the Pfam

Consortium.

[0030] Version 19.0 of the HMMER software and Pfam databases were used to identify known domains in the proteins corresponding to amino acid sequence of SEQ ID NO: 760 through SEQ ID NO:1518. All DNA encoding proteins that have scores higher than the gathering cutoff disclosed in Table 19 by Pfam analysis disclosed herein can be used in recombinant DNA of the plant cells of this invention, e.g. for selecting transgenic plants having enhanced agronomic traits. The relevant Pfam modules for use in this invention, as more specifically disclosed below, are Saccharop_dh, Isoamylase_N::Alpha-amylase, RRM_1, Pribosyltran, Skp1_POZ::Skp1, PTR2, PSI_PsaH, OTU, Aldedh, p450, AP2, CBS, TPT, zf-UBR, zf-C3HC4, ADH_N::ADH_zinc_N, Pre-SET::SET, OstA, Myb_DNA-binding, Cpn60_TCP1, SKI, Cyt-b5::FA_desaturase, Pkinase, KTI12, SNARE, NLE::WD40::WD40::WD40: :WD40, zf-C3HC4, Complex1_30kDa::Complex1_49kDa, iPGM_N::Metalloenzyme, adh_short, IQ::IQ, Glutaredoxin, LRRNT_2::LRR_1::LRR_1::Pkinase, Pkinase, Pribosyltran, DUF623, AWPM-19, Glucokinase, Pkinase_Tyr, Ribosomal_S8, F-box::Sell::Sell::zf-MYND, DUF313, WRKY, Aa_trans, Aminotran_1_2, Cystatin, PFK, PGAM, F-box, Ras, WD40::WD40::WD40::WD40, C2, Gal-bind_lectin::Galactosyl_T, Pyr_redox_2::Pyr_redox_dim, Ank::Ank::Pkinase_Tyr, Aminotran_1_2, AMP-binding, Aminotran_3, PEARLI-4, RRM_1, LRRNT_2::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::Pkinase, SNARE_assoc, FKBP_C, ELFV_dehydrog_N::ELFV_dehydrog, Sugar_tr, SPT2, DUF23, Dehydrin, Prefoldin, WD40::WD40::WD40::WD40::WD40::WD40::WD40, IQ::IQ, zf-Tim10_DDP, PPR::PPR::PPR::PPR::PPR::PPR::PPR, F-box::FBA_3, SH3_1, RNA_pol_A14, GAF::HisKA, Pkinase::efhand::efhand, Y_phosphatase2, 60KD_IMP, ADH_zinc_N, Glutaminase, p450, p450, Transket_pyr::Transketolase_C, B3_4::B5, Zip, DUF791::MFS_1, AA_permease, Pkinase, SAC3_GANP, DUF862, Pkinase, CS, TFIIS, Ribosomal_L19, Sugar_tr, NIF, SRF-TF::K-box, MSP, PGAM, Ahal_N::AHSA1, p450, F-box::FBA_1, Amino_oxidase, Tryp_alpha_amyl, Sugar_tr, zf-CW::MBD, Cytochrom_C, Tryp_alpha_amyl, Tcp11, Cys_Met_Meta_PP, UQ_con, zf-CCHC, Pyr_redox_2, efhand::efhand::efhand, Maf, MATH::BTB, LRRNT_2::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::L RR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::Pkinas e, Glyco_hydro_17, IQ, V-SNARE, Pkinase, Thioredoxin, AA_permease, Metallothio_PEC, HLH, p450, Pyr_redox_2::efhand, PP2C, GILT, F-box::Kelch_1::Kelch_1, AlaDh_PNT_N::AlaDh_PNT_C::Saccharop_dh_N::Saccharop_dh, WD40::WD40, Molybdop_Fe4S4::Molybdopterin::Molydop_binding, Aldedh, efhand, ETC_C1_NDUFA4, PGI, Transthyretin, GRP, SpoIIE, Dirigent, NUDIX, p450, Actin, Uricase::Uricase, Xan_ur_permease, NTP_transferase::Hexapep::Hexapep, zf-C3HC4, PPDK_N::PEP-utilizers::PEP-utilizers_C, Ribosomal_L37, Globin, Peptidase_M22, NADPH_Ox::Ferric_reduct::FAD_binding_8::NAD_binding_6, Glutaminase, XG_FTase, Enolase_N::Enolase_C, F-box::FBA_1, SOR_SNZ::ThiG, ABC_tran::ABC2_membrane::PDR_assoc::ABC_tran::ABC2_membrane, HMA::HMA, GATase::GMP_synt_C, Pkinase, CN_hydrolase::NAD_synthase, Usp::Pkinase, GRAM, Pkinase, DLTF6::DUF6, Sugar_tr, Iso_dh, Timl7, Band_7, Polyketide_cyc, Cyclin_N::Cyclin_C, DUF26::DUF26::Pkinase, PPR::PPR::PPR::PPR::PPR::PPR::PPR::PPR, Amidohydro_2, 20G-FeII_Oxy, PfkB, GILT, DUF246, Response_reg, TB2_DP1_HVA22, PP2C, ArfGap, TFIIF_alpha, ABC1, Methyltransf_12, Aldedh, TB2_DP1_HVA22, DUF6::TPT, Gp_dh_N::Gp_dh_C, efhand, SRF-TF, IQ::IQ, Lectin_legB::Pkinase, Self-incomp_S1, Hin1, Aminotran_1_2, Copine, ADH_N::ADH_zinc_N, Sugar_tr, DLTF860, Pkinase, Sugar_tr, Nol1_Nop2_Fmu, zf-MYND::UCH, Aldedh, F-box::Kelch_1::Kelch_1, TOM20_plant, Sugar_tr, DHDPS, CPDase, Aldedh, Invertase_neut, Metallophos, PBP, Reticulon, Histone, DUF260, Phi_1, p450, Lectin_legB::Pkinase, Abhydrolase_1, AMP-binding, DAGK_cat, Pkinase::NAF, IQ::IQ, DnaJ::DnaJ_CXXCXGXG::DnaJ_C, RRM_1, RRM_1, Citrate_synt, Glutaminase, DUF6::DUF6, PRA-CH::PRA-PH, Aldedh, adh_short, Pkinase, Cyclin_N::Cyclin_C, CCT, AP2, Cullin, Lung_7-TM_R, DUF1677, Rib_5-P_isom_A, TPK_catalytic::TPK_B1_binding, Sugar_tr, DUF926, AstE_AspA, Cyt-b5, HEAT::Arm::HEAT::Arm, Arf, SRF-TF, Aldedh, Glyco_transf_8, F-box::LRR_2::FBD, p450, DUF833, IQ::IQ, Aldedh, PI3_PI4_kinase, p450, RNA_pol_I_A49, Abhydrolase_1, TFIIS_C, HMG-CoA_red, HEAT::HEAT::HEAT::HEAT::HEAT::HEAT::HEAT::HEAT::HEAT::HEAT::HEAT::HEA T, MMR_HSR1, Ank::Ank::Ank, CorA, DUF827, Cyclin, Glyco_transf_8, DUF623, zf-C3HC4, AA_permease, RRM_1::zf-CCHC, Ras, DEAD::Helicase_C::DSHCT, PAS_2::GAF::Phytochrome::HisKA::HATPase_c, Tetraspannin, NIR_SIR_ferr::NIR_SrR::NIR_SIR_ferr::NIR_SIR, ELFV_dehydrog_N::ELFV_dehydrog, F-box::Kelch_1::Kelch_1, Aldedh, RRM_1::RRM_1, RRM_1, PPR::PPR::PPR::PPR::PPR::PPR, DUF617, HD::RelA_SpoT, Diphthamide_syn, Gp_dh_N::Gp_dh_C, ThiC, CRAL_TRIO_N::CRAL_TRIO, FTHFS, MIP, Fibrillarin, Pkinase, Pkinase, GTP_EFTU::GTP_EFTU_D2::EFG_C, PPR::PPR::PPR::PPR::PPR::PPR, PTR2, FAD_binding_4, ScpA_ScpB, NDUF_B7, TPT, DEAD::Helicase_C, DnaJ, TPT, cobW, HIT, DHquinase_1::Shikimate-dh-N::Shikimate-DH, IQ::IQ, Aldedh, DUF231, PGI, zf-C3HC4, CorA, Transketolase_N::Transket_pyr::Transketolase_C, Dehydrin, RRM_1, Sterol_desat, eIF2A, ArfGap::C2, NTP_transferase, DAO, Sugar_tr, DUF21::CBS, Pkinase::NAF, Sulfotransfer_1, p450, PGM_PMM_I::PGM_PMM_II::PGM_PMM_III::PGM_PMM_IV, CPSase_L_chain::CPSase_L_D2::CPSase_L_D3::CPSase_L_chain::CPSase_L_D2::MGS, Pro_CA, DUF617, Voltage_CLC::CBS, F-box, Histone, 14-3-3, UBX, polyprenyl_synt, Rho_GDI, TPR_2, Aldedh, LRR_1::LRR_1::LRR_1::Pkinase, DUF239, Pkinase, Glycolytic, adh_short, DUF1001, PTR2, ATP_synt_H, p450, Mito_carr::Mito_carr::Mito_carr, Gar1, Gln-synt_N::Gln-synt_C, PseudoU_synth_1::PseudoU_synth_1, DUF1635, Pkinase, Pro_dh, DUF506, Acyltransferase, DJ-1_PfpI::DJ-1_PfpI, PAP2, IQ, Isy1, Glutaredoxin, Molybdop_Fe4S4::Molybdopterin::Molydop_binding::Fer2_BFD, DUF778, Cyclin_N, zf-C3HC4, DUF300, DUF1639,

Peptidase_C26, P21-Arc, Mo25, Pkinase, Ras, DUF788, iPGM_N::Metalloenzyme, adh_short, Pyr_redox, Gln-synt_N::Gln-synt_C, FA_desaturase, zf-MYND::UCH, Skp1_POZ::Skp1, Cornichon, IGPD, Orn_Arg_deC_N::Orn_DAP_Arg_deC, DUF260, Gln-synt_N::Gln-synt_C, RRM_1, 2OG-FeII_Oxy, SNARE, RRM_1, DUF212, F-box, Phytochelatin::DUF1984, SRF-TF, TIM, MSF1, Ribonuc_L-PSP, p450, Transaldolase, Snf7, p450, FA_desaturase, F-box, efhand_like::PI-PLC-X::PI-PLC-Y::C2, Trehalose_PPase, Aminotran_4, Thioredoxin, Chitin_bind_1 ::Barwin, TLD, GATase_2::Asn_synthase, Pkinase, Pyridoxal_deC, Biotin_lipoyl::E3_binding::2-oxoacid_dh, H_PPase, DUF914, WD40::WD40::WD40, SIR2, Pkinase::efhand::efhand::efhand::efhand, LSM, PetM, DUF23, DUF862, tRNA-synt_1g, Radical_SAM, LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::Pkinase,DUF1644, Mov34, NOI, DUF6::TPT, Transket_pyr::Transketolase_C, F-box::LRR_2, zf-C3HC4, Phosphoesterase, SET, adh_short, Exo_endo_phos, Pkinase, Stig1, TFIIS_M::SPOC, Gln-synt_N::Gln-synt_C, B56, Aminotran_1_2, Aldose_epim, DUF1645, iPGM_N::Metalloenzyme, LRRNT_2::LRR_1 ::LRR_1 ::LRR_1::LRR_1 ::LRR_1::Pkinase, DUF538, Not3::NOT2_3_5, YjeF_N::Carb_kinase, DUF538, F-box, Cyclin_N::Cyclin_C, Aldedh, F-box, Pyr_redox_2, ELFV_dehydrog_N::ELFV_dehydrog, BCNT, Mago-bind, RRM_1, DUF783, Aminotran_3, ADH_N::ADH_zinc_N, Pkinase_Tyr, Ribosomal_S8, Pkinase, LRR_1, UDPGT, Peptidase_C54, mTERF, Skp1_POZ::Skp1, WD40::WD40::WD40::WD40, MtN3_slv::MtN3_slv, LRRNT_2::LRR_1::LRR_l::LRR_1::LRR_1::Pkinase, Aminotran_1_2, adh_short, PP2C, Senescence, Response_reg, DEAD::Helicase_C, Pkinase, zf-LSD1::zf-LSD1::zf-LSD1, PB1::Pkinase_Tyr, BTB::NPH3, PBD, Exo_endo_phos, Fer4::Fer4, WD40::WD40::WD40::WD40::PWP2, LysM, NTP_transferase, Tim17, Aa_trans, Ras, IPK, F-box::LRR_2, FBPase, PP2C, Aldedh, Ank::Ank::Ank::Pkinase, Brix, PTR2, 20G-FeII_Oxy, MCM, NTP_transferase::Hexapep::Hexapep::Hexapep::Hexapep, SapB_1::SapB_2::SapB_1::SapB_2, Aldedh, DUF581, AAA, Cyclin_N, ARM_1, IQ::IQ, Pkinase, ubiquitin::UBA::XPC-binding::UBA, Pkinase, TIM, Abhydrolase_1, CBS, Pkinase, Pyr_redox_2::Pyr_redox_dim, NicO, CCT, zf-PARP::zf-PARP::PADR1::BRCT::WGR::PARP_reg::PARP, Spermine_synth, NDK, E1_dh, LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1, MATH::MATH, Cyclin_N::Cyclin_C, ADH_N::ADH_zinc_N, RRM_1, DUF393, LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_ 1::LRR_1::LRR_1, AAA, zf-C3HC4::YDG_SRA, RWD, GHMP_kinases_N::GHMP_kinases_C, DZC, Glutaredoxin, DEAD::Helicase_C, Sterol_desat, DUF212, Pkinase, DREPP, PTR2, MGDG_synth::Glyco_tran_28_C, ACT::ACT, OTU, Pkinase, Glyco_hydro_1, Nuc_sug_transp, WD40::WD40::WD40::WD40::WD40::WD40::WD40::WD40::WD40::WD40::Utp13, Nramp, MFS_1, Metallophos, DUF1005, CTP_transf_1, RNA_pol_A_bac, DUF383::DUF384, DUF676, SAC3_GANP, ADH_N::ADH_zinc_N, PLAT::Lipoxygenase, SIS::CBS, Pkinase, Bystin, Response_reg, Phi_1, MFS_1, Pkinase, Pkinase, Gln-synt_N::Gln-synt_C, NUDIX, NIR_SLR_ferr::NIR_SIR::NIR_SIR_ferr::NIR_SIR, UFD1, DUF581, p450, WD40::WD40::WD40::WD40, p450, Gp_dh_N::Gp_dh_C, Abhydrolase_3, TP_methylase, Pkinase, LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1, GATase::GMP_synt_C, PfkB, RRM_1, malic::Malic_M, DUF525, FBPase, DUF59, Pro_isomerase, Arm::Arm, Pkinase_Tyr, Pkinase::NAF, BNR::BNR::BNR, DUF1350, CAF1, TMEM14, MATH, DUF1000, PC_rep::PC_rep::PC_rep::PC_rep::PC_rep::PC_rep, Pkinase, FHA::PP2C, Pkinase, Di19, WD40::WD40, 20G-FeII_Oxy, Pkinase, adh_short, Aldedh, DUF793, DUF1749, AAA, PGK, Aminotran_3, Str_synth, eIF-1a, Hydrolase, Sugar_tr, DUF640, PCI, Sina, PBP, AOX, OPT, Pkinase_Tyr, Rib_5-P_isom_A, DUF740, PP2C, Pkinase, and Cyclin_N::Cyclin_C.

Recombinant DNA constructs

[0031] The invention uses recombinant DNA for imparting one or more enhanced traits to transgenic plant when incorporated into the nucleus of the plant cells. DNA constructs comprising one or more polynucleotides disclosed herein are assembled using methods well known to persons of ordinary skill in the art and typically comprise a promoter operably linked to DNA, the expression of which provides the enhanced agronomic trait. Other construct components may include additional regulatory elements, such as 5' leasders and introns for enhancing transcription, 3' untranslated regions (such as polyadenylation signals and sites), DNA for transit or signal peptides.

[0032] Numerous promoters that are active in plant cells have been described in the literature. These include promoters present in plant genomes as well as promoters from other sources, including nopaline synthase (NOS) promoter and octopine synthase (OCS) promoters carried on tumor-inducing plasmids of *Agrobacterium tumefaciens* and the CaMV35S promoters from the cauliflower mosaic virus as disclosed in US Patents No. 5,164,316 and 5,322,938. Useful promoters derived from plant genes are found in U.S. Patent 5,641,876, which discloses a rice actin promoter, U.S. Patent No. 7,151,204, which discloses a maize chloroplast aldolase promoter and a maize aldolase (FDA) promoter, and U.S. Patent Application Publication 2003/0131377 A1, which discloses a maize nicotianamine synthase promoter, all of which are incorporated herein by reference. These and numerous other promoters that function in plant cells are known to those skilled in the art and available for use in recombinant polynucleotides of the present invention to provide for expression of desired genes in transgenic plant cells.

[0033] In other aspects of the invention, preferential expression in plant green tissues is desired. Promoters of interest for such uses include those from genes such as Arabidopsis thaliana ribulose-1,5-bisphosphate carboxylase (Rubisco) small subunit

(Fischhoff et al. (1992) Plant Mol Biol, 20:81-93), aldolase and pyruvate orthophosphate dikinase (PPDK) (Taniguchi et al. (2000) Plant Cell Physiol, 41(1):42-48).

[0034] Furthermore, the promoters may be altered to contain multiple "enhancer sequences" to assist in elevating gene expression. Such enhancers are known in the art. By including an enhancer sequence with such constructs, the expression of the selected protein may be enhanced. These enhancers often are found 5' to the start of transcription in a promoter that functions in eukaryotic cells, but can often be inserted upstream (5') or downstream (3') to the coding sequence. In some instances, these 5' enhancing elements are introns. Particularly useful as enhancers are the 5' introns of the rice actin 1 (see US Patent 5,641,876) and rice actin 2 genes, the maize alcohol dehydrogenase gene intron, the maize heat shock protein 70 gene intron (U.S. Patent 5,593,874) and the maize shrunken 1 gene.

[0035] In other aspects of the invention, sufficient expression in plant seed tissues is desired to affect improvements in seed composition. Exemplary promoters for use for seed composition modification include promoters from seed genes such as napin (U.S. 5,420,034), maize L3 oleosin (U.S. 6,433,252), zein Z27 (Russell et al. (1997) Transgenic Res. 6(2): 157-166), globulin 1 (Belanger et al (1991) Genetics 129:863-872), glutelin 1 (Russell (1997) *supra*), and peroxiredoxin antioxidant (Perl) (Stacy et al. (1996) Plant Mol Biol. 31(6):1205-1216).

[0036] Recombinant DNA constructs prepared in accordance with the invention will also generally include a 3' element that typically contains a polyadenylation signal and site. Well-known 3' elements include those from *Agrobacterium tumefaciens* genes such as *nos 3', tml 3', tmr 3', tms 3', ocs 3', tr7 3',* for example disclosed in U.S. 6,090,627, incorporated herein by reference; 3' elements from plant genes such as wheat (*Triticum aesevitum*) heat shock protein 17 (*Hsp17 3'*), a wheat ubiquitin gene, a wheat fructose-1,6-biphosphatase gene, a rice glutelin gene, a rice lactate dehydrogenase gene and a rice beta-tubulin gene, all of which are disclosed in U.S. published patent application 2002/0192813 A1, incorporated herein by reference; and the pea (*Pisum sativum*) ribulose biphosphate carboxylase gene (*rbs* 3'), and 3' elements from the genes within the host plant.

[0037] Constructs and vectors may also include a transit peptide for targeting of a gene to a plant organelle, particularly to a chloroplast, leucoplast or other plastid organelle. For descriptions of the use of chloroplast transit peptides see U.S. Patent 5, 188,642 and U.S. Patent No. 5,728,925, incorporated herein by reference. For description of the transit peptide region of an Arabidopsis EPSPS gene useful in the present invention, see Klee, H.J. et al (MGG (1987) 210:437-442).

[0038] Gene suppression includes any of the well-known methods for suppressing transcription of a gene or the accumulation of the mRNA corresponding to that gene thereby preventing translation of the transcript into protein. Posttranscriptional gene suppression is mediated by transcription of RNA that forms double-stranded RNA (dsRNA) having homology to a gene targeted for suppression. Suppression can also be achieved by insertion mutations created by transposable elements may also prevent gene function. For example, in many dicot plants, transformation with the T-DNA of *Agrobacterium* may be readily achieved and large numbers of transformants can be rapidly obtained. Also, some species have lines with active transposable elements that can efficiently be used for the generation of large numbers of insertion mutations, while some other species lack such options. Mutant plants produced by *Agrobacterium* or transposon mutagenesis and having altered expression of a polypeptide of interest can be identified using the polynucleotides of the present invention. For example, a large population of mutated plants may be screened with polynucleotides encoding the polypeptide of interest to detect mutated plants having an insertion in the gene encoding the polypeptide of interest.

[0039] Transgenic plants comprising or derived from plant cells of this invention transformed with recombinant DNA can be further enhanced with stacked traits, e.g. a crop plant having an enhanced trait resulting from expression of DNA disclosed herein in combination with herbicide and/or pest resistance traits. For example, genes of the current invention can be stacked with other traits of agronomic interest, such as a trait providing herbicide resistance, or insect resistance, such as using a gene from *Bacillus thuringensis* to provide resistance against lepidopteran, coliopteran, homopteran, hemiopteran, and other insects. Herbicides for which transgenic plant tolerance has been demonstrated and the method of the present invention can be applied include, but are not limited to, glyphosate, dicamba, glufosinate, sulfonylurea, bromoxynil and norflurazon herbicides. Polynucleotide molecules encoding proteins involved in herbicide tolerance are well-known in the art and include, but are not limited to, a polynucleotide molecule encoding 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) disclosed in U.S. Patent 5,094,945; 5,627,061; 5,633,435 and 6,040,497 for imparting glyphosate tolerance; polynucleotide molecules encoding a glyphosate oxidoreductase (GOX) disclosed in U.S. Patent 5,463,175 and a glyphosate-N-acetyl transferase (GAT) disclosed in U.S. Patent Application publication 2003/0083480 A1 also for imparting glyphosate tolerance; dicamba monooxygenase disclosed in U.S. Patent Application publication 2003/0135879 A1 for imparting dicamba tolerance; a polynucleotide molecule encoding bromoxynil nitrilase (*Bxn*) disclosed in U.S. Patent 4,810,648 for imparting bromoxynil tolerance; a polynucleotide molecule encoding phytoene desaturase (*crtI*) described in Misawa et al, (1993) Plant J. 4:833-840 and in Misawa et al, (1994) Plant J. 6:481-489 for norflurazon tolerance; a polynucleotide molecule encoding acetohydroxyacid

synthase (AHAS, *aka* ALS) described in Sathasiivan et al. (1990) Nucl. Acids Res. 18:2188-2193 for imparting tolerance to sulfonylurea herbicides; polynucleotide molecules known as *bar* genes disclosed in DeBlock, et al. (1987) EMBO J. 6:2513-2519 for imparting glufosinate and bialaphos tolerance; polynucleotide molecules disclosed in U.S. Patent Application Publication 2003/010609 A1 for imparting N-amino methyl phosphonic acid tolerance; polynucleotide molecules disclosed in U.S. Patent 6,107,549 for impartinig pyridine herbicide resistance; molecules and methods for imparting tolerance to multiple herbicides such as glyphosate, atrazine, ALS inhibitors, isoxoflutole and glufosinate herbicides are disclosed in U.S. Patent 6,376,754 and U.S. Patent Application Publication 2002/0112260, all of said U.S. Patents and Patent Application Publications are incorporated herein by reference. Molecules and methods for imparting insect/nematode/virus resistance are disclosed in U.S. Patents 5,250,515; 5,880,275; 6,506,599; 5,986,175 and U.S. Patent Application Publication 2003/0150017 A1, all of which are incorporated herein by reference.

[0040] Table 2 provides a list of genes that provided recombinant DNA that was expressed in a model plant and identified from screening as imparting an enhanced trait. When the stated orientation is "sense", the expression of the gene or a homolog in a crop plant provides the means to identify transgenic events that provide an enhanced trait in the crop plant. When the stated orientation is "antisense", the suppression of the native homolog in a crop plant provides the means to identify transgenic events that provide an enhanced trait in the crop plant. In some cases the expression/suppression in the model plant exhibited an enhanced trait that corresponds to an enhanced agronomic trait, e.g. cold stress tolerance, water deficit stress tolerance, low nitrogen stress tolerance and like. In other cases the expression/suppression in the model plant exhibited an enhanced trait that is a surrogate to an enhanced agronomic trait, e.g. salinity stress tolerance being a surrogate to drought tolerance or improvement in plant growth and development being a surrogate to enhanced yield. Even when expression of a transgene or suppression of a native gene imparts an enhanced trait in a model plant, not every crop plant expressing the same transgene or suppressing the same native gene will necessarily demonstrate an indicated enhanced agronomic trait. For instance, it is well known that multiple transgenic events are required to identify a transgenic plant that can exhibit an enhanced agronomic trait. However, by with routine experimentation a transgenic plant cell nuclei, cell, plant or seed of this invention can be identified by making a reasonable number of transgenic events and engaging in screening process identified in this specification and illustrated in the examples. An understanding of Table 2 is facilitated by the following description of the headings:

"NUC SEQ ID NO" refers to a SEQ ID NO. for particular DNA sequence in the Sequence Listing .

"PEP SEQ ID NO" refers to a SEQ ID NO. in the Sequence Listing for the amino acid sequence of a protein cognate to a particular DNA

"construct_id" refers to an arbitrary number used to identify a particular recombinant DNA construct comprising the particular DNA.

"Gene ID" refers to an arbitrary name used to identify the particular DNA.

"orientation" refers to the orientation of the particular DNA in a recombinant DNA construct relative to the promoter.

Table 2

NUC Seq ID	PEP Seq ID	Gene ID	Construct ID	Orientation	NUC Seq ID	PEP Seq ID	Gene ID	Construct ID	Orientation
1	760	CGPG1022	12792	ANTI-SENSE	379	1138	CGPG608	70243	SENSE
2	761	CGPG1035	13673	ANTI-SENSE	380	1139	CGPG6080	74371	SENSE
3	762	CGPG1043	12020	SENSE	381	1140	CGPG6082	74373	SENSE
4	763	CGPG105	10174	ANTI-SENSE	382	1141	CGPG6089	74615	SENSE
5	764	CGPG1060	11827	ANTI-SENSE	383	1142	CGPG6120	74620	SENSE
6	765	CGPG1069	12435	SENSE	384	1143	CGPG6128	74626	SENSE
7	766	CGPG108	12015	SENSE	385	1144	CGPG614	10622	ANTI-SENSE
8	767	CGPG1083	11836	ANTI-SENSE	386	1145	CGPG6149	74636	SENSE
9	768	CGPG1088	12141	ANTI-SENSE	387	1146	CGPG6172	74656	SENSE

NUC Seq ID	PEP Seq ID	Gene ID	Construct ID	Orientation	NUC Seq ID	PEP Seq ID	Gene ID	Construct ID	Orientation
10	769	CGPG1092	12040	SENSE	388	1147	CGPG6174	74658	SENSE
11	770	CGPG1108	12437	SENSE	389	1148	CGPG6176	74659	SENSE
12	771	CGPG1136	12156	ANTI-SENSE	390	1149	CGPG6197	74673	SENSE
13	772	CGPG1140	11853	ANTI-SENSE	391	1150	CGPG620	13518	ANTI-SENSE
14	773	CGPG1143	12224	SENSE	391	1150	CGPG620	70824	SENSE
15	774	CGPG1145	11856	ANTI-SENSE	392	1151	CGPG6201	75267	SENSE
16	775	CGPG1170	12065	SENSE	393	1152	CGPG6204	75283	SENSE
17	776	CGPG1173	12419	ANTI-SENSE	394	1153	CGPG621	13805	SENSE
18	777	CGPG1176	12208	SENSE	395	1154	CGPG6210	76221	SENSE
19	778	CGPG1192	14803	SENSE	396	1155	CGPG6211	76226	SENSE
20	779	CGPG122	10176	ANTI-SENSE	397	1156	CGPG6214	76222	SENSE
21	780	CGPG126	18011	SENSE	398	1157	CGPG6215	76611	SENSE
22	781	CGPG1262	12714	ANTI-SENSE	399	1158	CGPG6222	76228	SENSE
23	782	CGPG128	10507	ANTI-SENSE	400	1159	CGPG6229	76435	SENSE
24	783	CGPG1280	15039	SENSE	401	1160	CGPG6233	76436	SENSE
25	784	CGPG1291	12733	ANTI-SENSE	402	1161	CGPG6237	78743	SENSE
26	785	CGPG1295	13237	SENSE	403	1162	CGPG6243	75814	SENSE
27	786	CGPG1311	13504	SENSE	404	1163	CGPG6248	77016	SENSE
28	787	CGPG1315	12932	SENSE	405	1164	CGPG6252	78734	SENSE
29	788	CGPG1335	75935	SENSE	406	1165	CGPG6267	75274	SENSE
30	789	CGPG1344	73333	SENSE	407	1166	CGPG6272	76233	SENSE
31	790	CGPG1352	75993	SENSE	408	1167	CGPG6294	74674	SENSE
32	791	CGPG1364	19401	SENSE	409	1168	CGPG63	70225	SENSE
33	792	CGPG1391	12766	ANTI-SENSE	410	1169	CGPG6311	75291	SENSE
34	793	CGPG1396	76025	SENSE	411	1170	CGPG6317	75292	SENSE
35	794	CGPG1398	13708	ANTI-SENSE	412	1171	CGPG6328	78607	SENSE
36	795	CGPG1399	13305	ANTI-SENSE	413	1172	CGPG6334	78367	SENSE
37	796	CGPG1429	15806	SENSE	414	1173	CGPG6336	76528	SENSE
38	797	CGPG1430	14712	SENSE	415	1174	CGPG6349	77319	SENSE
39	798	CGPG1445	76013	SENSE	416	1175	CGPG6352	74677	SENSE
40	799	CGPG146	10192	ANTI-SENSE	417	1176	CGPG6353	78109	SENSE
41	800	CGPG1492	74775	SENSE	418	1177	CGPG6364	77725	SENSE
42	801	CGPG1528	13841	ANTI-SENSE	419	1178	CGPG6366	73437	SENSE
43	802	CGPG1530	15805	SENSE	420	1179	CGPG6375	73450	SENSE
44	803	CGPG1535	14253	ANTI-SENSE	421	1180	CGPG6388	73416	SENSE
45	804	CGPG1546	13650	ANTI-	422	1181	CGPG6391	73452	SENSE

NUC Seq ID	PEP Seq ID	Gene ID	Construct ID	Orientation	NUC Seq ID	PEP Seq ID	Gene ID	Construct ID	Orientation
				SENSE					
46	805	CGPG1567	13855	ANTI-SENSE	423	1182	CGPG6399	73453	SENSE
47	806	CGPG1568	76049	SENSE	424	1183	CGPG6407	73454	SENSE
48	807	CGPG1575	14271	ANTI-SENSE	425	1184	CGPG6418	73491	SENSE
49	808	CGPG1619	73927	SENSE	426	1185	CGPG6430	73445	SENSE
50	809	CGPG1633	13657	ANTI-SENSE	427	1186	CGPG6432	73469	SENSE
51	810	CGPG1641	13938	ANTI-SENSE	428	1187	CGPG6437	73434	SENSE
51	810	CGPG1641	14730	SENSE	429	1188	CGPG6445	73471	SENSE
52	811	CGPG1651	73948	SENSE	430	1189	CGPG6450	73436	SENSE
53	812	CGPG1656	18116	ANTI-SENSE	431	1190	CGPG6458	73525	SENSE
54	813	CGPG1668	14341	ANTI-SENSE	432	1191	CGPG6465	73514	SENSE
55	814	CGPG1715	13960	ANTI-SENSE	433	1192	CGPG6476	73551	SENSE
55	814	CGPG1715	74391	SENSE	434	1193	CGPG6505	73519	SENSE
56	815	CGPG1740	75957	SENSE	435	1194	CGPG6507	73543	SENSE
57	816	CGPG177	70240	SENSE	436	1195	CGPG6509	73567	SENSE
58	817	CGPG1785	70748	ANTI-SENSE	437	1196	CGPG6510	73579	SENSE
59	818	CGPG182	70807	SENSE	438	1197	CGPG6515	73556	SENSE
60	819	CGPG1837	73986	SENSE	439	1198	CGPG6520	73545	SENSE
61	820	CGPG1873	77005	SENSE	440	1199	CGPG6531	73511	SENSE
62	821	CGPG1891	70410	ANTI-SENSE	441	1200	CGPG6553	74138	SENSE
63	822	CGPG1895	14827	ANTI-SENSE	442	1201	CGPG6557	74186	SENSE
64	823	CGPG1899	19122	SENSE	443	1202	CGPG6563	74163	SENSE
65	824	CGPG1913	16446	SENSE	444	1203	CGPG6564	74175	SENSE
66	825	CGPG1918	15143	SENSE	445	1204	CGPG6572	74176	SENSE
67	826	CGPG1919	70401	SENSE	446	1205	CGPG6577	74141	SENSE
68	827	CGPG1922	16182	SENSE	447	1206	CGPG6588	74178	SENSE
69	828	CGPG1929	15126	SENSE	448	1207	CGPG6596	74179	SENSE
70	829	CGPG1938	15628	ANTI-SENSE	449	1208	CGPG6614	74110	SENSE
71	830	CGPG1956	78355	SENSE	450	1209	CGPG6619	74170	SENSE
72	831	CGPG1964	70560	SENSE	451	1210	CGPG6623	74123	SENSE
73	832	CGPG1973	19133	SENSE	452	1211	CGPG6626	74159	SENSE
74	833	CGPG1977	73602	SENSE	453	1212	CGPG663	10633	ANTI-SENSE
75	834	CGPG1996	71702	SENSE	454	1213	CGPG6635	74172	SENSE
76	835	CGPG2005	14909	ANTI-SENSE	455	1214	CGPG6636	74184	SENSE
77	836	CGPG2035	14927	ANTI-SENSE	456	1215	CGPG6641	74582	SENSE
78	837	CGPG2044	75945	SENSE	457	1216	CGPG6642	74584	SENSE

NUC Seq ID	PEP Seq ID	Gene ID	Construct ID	Orientation	NUC Seq ID	PEP Seq ID	Gene ID	Construct ID	Orientation
79	838	CGPG2059	16553	ANTI-SENSE	458	1217	CGPG6645	74687	SENSE
80	839	CGPG2065	75221	SENSE	459	1218	CGPG6660	74461	SENSE
81	840	CGPG2068	70746	ANTI-SENSE	460	1219	CGPG6671	74403	SENSE
82	841	CGPG2072	70403	SENSE	461	1220	CGPG6697	74430	SENSE
83	842	CGPG2074	15966	ANTI-SENSE	462	1221	CGPG6706	74443	SENSE
84	843	CGPG2116	76076	SENSE	463	1222	CGPG6723	74457	SENSE
85	844	CGPG2118	17014	SENSE	464	1223	CGPG6729	74434	SENSE
86	845	CGPG2142	16007	ANTI-SENSE	465	1224	CGPG6738	74447	SENSE
87	846	CGPG2148	16208	SENSE	466	1225	CGPG6742	74495	SENSE
88	847	CGPG2190	17310	SENSE	467	1226	CGPG6752	74513	SENSE
89	848	CGPG2191	15716	ANTI-SENSE	468	1227	CGPG6760	74514	SENSE
90	849	CGPG221	15627	SENSE	469	1228	CGPG6768	74515	SENSE
91	850	CGPG2213	15409	ANTI-SENSE	470	1229	CGPG6779	74552	SENSE
91	850	CGPG2213	17201	SENSE	471	1230	CGPG6785	74529	SENSE
92	851	CGPG2247	15903	ANTI-SENSE	472	1231	CGPG6800	74519	SENSE
93	852	CGPG228	10332	ANTI-SENSE	473	1232	CGPG686	10638	ANTI-SENSE
94	853	CGPG2301	73968	SENSE	474	1233	CGPG6898	76547	SENSE
95	854	CGPG2304	17003	SENSE	475	1234	CGPG6900	76548	SENSE
96	855	CGPG2313	73847	SENSE	476	1235	CGPG691	14703	SENSE
97	856	CGPG2348	76041	SENSE	477	1236	CGPG6920	75856	SENSE
98	857	CGPG2349	74567	SENSE	478	1237	CGPG6921	76642	SENSE
99	858	CGPG2354	15809	ANTI-SENSE	479	1238	CGPG6930	77522	SENSE
100	859	CGPG2369	70110	SENSE	480	1239	CGPG6934	77516	SENSE
101	860	CGPG2382	70123	SENSE	481	1240	CGPG6945	75864	SENSE
102	861	CGPG2392	74702	SENSE	482	1241	CGPG6946	76275	SENSE
103	862	CGPG2397	75936	SENSE	483	1242	CGPG6948	76276	SENSE
104	863	CGPG240	10462	ANTI-SENSE	484	1243	CGPG6974	75869	SENSE
105	864	CGPG2426	17402	SENSE	485	1244	CGPG6976	76558	SENSE
106	865	CGPG2433	73707	SENSE	486	1245	CGPG6996	75876	SENSE
107	866	CGPG2437	17129	ANTI-SENSE	487	1246	CGPG7002	75878	SENSE
108	867	CGPG2452	72665	SENSE	488	1247	CGPG7013	75881	SENSE
109	868	CGPG2464	18206	SENSE	489	1248	CGPG7021	77525	SENSE
110	869	CGPG2472	17151	ANTI-SENSE	490	1249	CGPG7056	76454	SENSE
111	870	CGPG2480	17813	SENSE	491	1250	CGPG7071	75895	SENSE
112	871	CGPG253	70845	SENSE	492	1251	CGPG7075	78377	SENSE
113	872	CGPG2538	16607	SENSE	493	1252	CGPG7080	75896	SENSE
114	873	CGPG2567	72675	SENSE	494	1253	CGPG7094	77527	SENSE
115	874	CGPG2571	72677	SENSE	495	1254	CGPG7095	78984	SENSE

NUC Seq ID	PEP Seq ID	Gene ID	Construct ID	Orientation	NUC Seq ID	PEP Seq ID	Gene ID	Construct ID	Orientation
116	875	CGPG258	74534	SENSE	496	1255	CGPG7104	77528	SENSE
117	876	CGPG268	74535	SENSE	497	1256	CGPG7118	76752	SENSE
118	877	CGPG274	10204	ANTI-SENSE	498	1257	CGPG7122	78106	SENSE
119	878	CGPG275	10472	SENSE	499	1258	CGPG713	11720	ANTI-SENSE
120	879	CGPG277	10431	ANTI-SENSE	500	1259	CGPG7130	78740	SENSE
121	880	CGPG2785	72906	SENSE	501	1260	CGPG7145	76157	SENSE
122	881	CGPG2832	78362	SENSE	502	1261	CGPG7166	77530	SENSE
123	882	CGPG2855	17930	SENSE	503	1262	CGPG7179	76755	SENSE
124	883	CGPG2865	18442	SENSE	504	1263	CGPG7184	76166	SENSE
125	884	CGPG2874	73207	SENSE	505	1264	CGPG7185	76756	SENSE
126	885	CGPG2914	19166	SENSE	506	1265	CGPG7192	78990	SENSE
127	886	CGPG295	10469	SENSE	507	1266	CGPG7199	78460	SENSE
128	887	CGPG3004	18415	SENSE	508	1267	CGPG72	11022	ANTI-SENSE
129	888	CGPG3009	18418	SENSE	509	1268	CGPG7231	77533	SENSE
130	889	CGPG3030	19532	SENSE	510	1269	CGPG7241	76572	SENSE
131	890	CGPG3048	18423	SENSE	511	1270	CGPG7243	76186	SENSE
132	891	CGPG3056	77909	SENSE	512	1271	CGPG7258	76190	SENSE
133	892	CGPG3084	19656	SENSE	513	1272	CGPG7265	77071	SENSE
134	893	CGPG309	10217	ANTI-SENSE	514	1273	CGPG7274	76194	SENSE
135	894	CGPG3094	18874	SENSE	515	1274	CGPG7291	78112	SENSE
136	895	CGPG3095	18875	SENSE	516	1275	CGPG7303	74802	SENSE
137	896	CGPG3137	19256	SENSE	517	1276	CGPG7315	74851	SENSE
138	897	CGPG3156	19537	SENSE	518	1277	CGPG7324	74864	SENSE
139	898	CGPG3157	74201	SENSE	519	1278	CGPG7327	74805	SENSE
140	899	CGPG3205	74233	SENSE	520	1279	CGPG7338	74842	SENSE
141	900	CGPG3236	18644	SENSE	521	1280	CGPG7347	78231	SENSE
142	901	CGPG3248	18827	SENSE	522	1281	CGPG7348	74867	SENSE
143	902	CGPG3255	18220	SENSE	523	1282	CGPG7352	74820	SENSE
144	903	CGPG3258	18830	SENSE	524	1283	CGPG7356	74868	SENSE
145	904	CGPG3261	19205	SENSE	525	1284	CGPG7359	74809	SENSE
146	905	CGPG3269	18226	SENSE	526	1285	CGPG7362	74845	SENSE
147	906	CGPG3270	18227	SENSE	527	1286	CGPG7372	74870	SENSE
148	907	CGPG3283	18239	SENSE	528	1287	CGPG7379	74859	SENSE
149	908	CGPG3302	70415	SENSE	529	1288	CGPG7398	74985	SENSE
150	909	CGPG3334	18329	SENSE	530	1289	CGPG7403	74950	SENSE
151	910	CGPG3361	72606	SENSE	531	1290	CGPG7404	74962	SENSE
152	911	CGPG337	10230	ANTI-SENSE	532	1291	CGPG7410	74939	SENSE
153	912	CGPG3400	19608	SENSE	533	1292	CGPG7417	74928	SENSE
154	913	CGPG3410	18271	SENSE	534	1293	CGPG7423	74905	SENSE
155	914	CGPG3424	18347	SENSE	535	1294	CGPG7424	74917	SENSE
156	915	CGPG3428	18403	SENSE	536	1295	CGPG7430	74989	SENSE

NUC Seq ID	PEP Seq ID	Gene ID	Construct ID	Orientation	NUC Seq ID	PEP Seq ID	Gene ID	Construct ID	Orientation
157	916	CGPG3465	74206	SENSE	537	1296	CGPG7438	74990	SENSE
158	917	CGPG347	10234	ANTI-SENSE	538	1297	CGPG7443	74955	SENSE
159	918	CGPG351	71115	SENSE	539	1298	CGPG7449	74932	SENSE
160	919	CGPG3567	18406	SENSE	540	1299	CGPG7450	74944	SENSE
161	920	CGPG3575	19619	SENSE	541	1300	CGPG7452	74968	SENSE
162	921	CGPG3579	19623	SENSE	542	1301	CGPG7459	74957	SENSE
163	922	CGPG3605	18381	SENSE	543	1302	CGPG7480	75374	SENSE
164	923	CGPG3612	18408	SENSE	544	1303	CGPG7481	75386	SENSE
165	924	CGPG3616	18720	SENSE	545	1304	CGPG7483	77807	SENSE
166	925	CGPG3631	77537	SENSE	546	1305	CGPG7497	75388	SENSE
167	926	CGPG365	70833	SENSE	547	1306	CGPG7503	75365	SENSE
168	927	CGPG3665	19328	SENSE	548	1307	CGPG7504	75377	SENSE
169	928	CGPG3684	19312	SENSE	549	1308	CGPG7510	75354	SENSE
170	929	CGPG3690	70538	SENSE	550	1309	CGPG7516	75331	SENSE
171	930	CGPG3717	70440	SENSE	551	1310	CGPG7517	75343	SENSE
172	931	CGPG372	11319	ANTI-SENSE	552	1311	CGPG7523	77809	SENSE
173	932	CGPG3724	70443	SENSE	553	1312	CGPG7524	75332	SENSE
174	933	CGPG375	72357	SENSE	554	1313	CGPG7525	75344	SENSE
175	934	CGPG3781	70466	SENSE	555	1314	CGPG7532	75333	SENSE
176	935	CGPG380	70241	SENSE	556	1315	CGPG7537	75393	SENSE
177	936	CGPG3821	70476	SENSE	557	1316	CGPG7548	75335	SENSE
178	937	CGPG3824	70477	SENSE	558	1317	CGPG7575	75462	SENSE
179	938	CGPG3901	19713	SENSE	559	1318	CGPG7577	75486	SENSE
180	939	CGPG391	12601	SENSE	560	1319	CGPG7590	75452	SENSE
181	940	CGPG3931	19747	SENSE	561	1320	CGPG7599	75465	SENSE
182	941	CGPG394	11117	ANTI-SENSE	562	1321	CGPG7601	75489	SENSE
183	942	CGPG3964	70965	SENSE	563	1322	CGPG7605	75442	SENSE
184	943	CGPG397	10366	ANTI-SENSE	564	1323	CGPG7607	75466	SENSE
184	943	CGPG397	13404	SENSE	565	1324	CGPG7616	75479	SENSE
185	944	CGPG3975	70935	SENSE	566	1325	CGPG7632	75481	SENSE
186	945	CGPG3983	77717	SENSE	567	1326	CGPG7673	78233	SENSE
187	946	CGPG3986	19966	SENSE	568	1327	CGPG7683	75539	SENSE
188	947	CGPG3991	70909	SENSE	569	1328	CGPG773	11919	ANTI-SENSE
189	948	CGPG4050	19906	SENSE	570	1329	CGPG7776	75603	SENSE
190	949	CGPG4070	70974	SENSE	571	1330	CGPG7781	75663	SENSE
191	950	CGPG4071	19802	SENSE	572	1331	CGPG7785	75616	SENSE
192	951	CGPG4099	19746	SENSE	573	1332	CGPG7787	75640	SENSE
193	952	CGPG4138	70902	SENSE	574	1333	CGPG7793	75617	SENSE
194	953	CGPG4152	19933	SENSE	575	1334	CGPG7796	75653	SENSE
195	954	CGPG4153	19927	SENSE	576	1335	CGPG7797	75665	SENSE
196	955	CGPG4164	70976	SENSE	577	1336	CGPG7801	75618	SENSE
197	956	CGPG4169	71440	SENSE	578	1337	CGPG7813	78238	SENSE

NUC Seq ID	PEP Seq ID	Gene ID	Construct ID	Orientation	NUC Seq ID	PEP Seq ID	Gene ID	Construct ID	Orientation
198	957	CGPG421	10413	ANTI-SENSE	579	1338	CGPG7816	75608	SENSE
199	958	CGPG422	11119	ANTI-SENSE	580	1339	CGPG7826	75633	SENSE
200	959	CGPG4223	78659	SENSE	581	1340	CGPG7861	75761	SENSE
201	960	CGPG4240	78665	SENSE	582	1341	CGPG7863	75785	SENSE
202	961	CGPG4242	78969	SENSE	583	1342	CGPG7868	75750	SENSE
203	962	CGPG4248	78970	SENSE	584	1343	CGPG7881	75716	SENSE
204	963	CGPG425	71250	SENSE	585	1344	CGPG7887	78129	SENSE
205	964	CGPG4265	78972	SENSE	586	1345	CGPG7899	77539	SENSE
206	965	CGPG4283	78677	SENSE	587	1346	CGPG7901	77540	SENSE
207	966	CGPG4297	70632	SENSE	588	1347	CGPG7909	77542	SENSE
208	967	CGPG43	75205	SENSE	589	1348	CGPG7911	77543	SENSE
209	968	CGPG430	10359	ANTI-SENSE	590	1349	CGPG7919	77545	SENSE
209	968	CGPG430	11408	SENSE	591	1350	CGPG7935	77550	SENSE
210	969	CGPG4305	73616	SENSE	592	1351	CGPG7940	77552	SENSE
211	970	CGPG4307	78358	SENSE	593	1352	CGPG7959	77556	SENSE
212	971	CGPG4315	71839	SENSE	594	1353	CGPG7967	77559	SENSE
213	972	CGPG4320	78417	SENSE	595	1354	CGPG7975	77957	SENSE
214	973	CGPG4344	71952	SENSE	596	1355	CGPG7996	77565	SENSE
215	974	CGPG4346	78717	SENSE	597	1356	CGPG8006	78508	SENSE
216	975	CGPG4349	75040	SENSE	598	1357	CGPG801	11748	ANTI-SENSE
217	976	CGPG4365	71843	SENSE	599	1358	CGPG8023	77920	SENSE
218	977	CGPG4383	70666	SENSE	600	1359	CGPG8025	77573	SENSE
219	978	CGPG4389	71846	SENSE	601	1360	CGPG8038	77961	SENSE
220	979	CGPG4404	71314	SENSE	602	1361	CGPG8053	77922	SENSE
221	980	CGPG4405	76410	SENSE	603	1362	CGPG8054	77337	SENSE
222	981	CGPG4419	71322	SENSE	604	1363	CGPG8059	77924	SENSE
223	982	CGPG4432	73214	SENSE	605	1364	CGPG8070	77926	SENSE
224	983	CGPG4437	71963	SENSE	606	1365	CGPG8073	77964	SENSE
225	984	CGPG4443	71326	SENSE	607	1366	CGPG8076	77346	SENSE
226	985	CGPG445	70834	SENSE	608	1367	CGPG8084	77350	SENSE
227	986	CGPG4453	73215	SENSE	609	1368	CGPG8093	77929	SENSE
228	987	CGPG4481	71334	SENSE	610	1369	CGPG8095	77586	SENSE
229	988	CGPG4490	71335	SENSE	611	1370	CGPG8096	78510	SENSE
230	989	CGPG4498	71347	SENSE	612	1371	CGPG8097	77930	SENSE
231	990	CGPG4506	71820	SENSE	613	1372	CGPG8112	77590	SENSE
232	991	CGPG4553	70764	SENSE	614	1373	CGPG8120	77592	SENSE
233	992	CGPG4583	70680	SENSE	615	1374	CGPG8129	77361	SENSE
234	993	CGPG4643	72375	SENSE	616	1375	CGPG8140	77934	SENSE
235	994	CGPG4650	72469	SENSE	617	1376	CGPG8157	77367	SENSE
236	995	CGPG4660	73951	SENSE	618	1377	CGPG8158	78121	SENSE
237	996	CGPG468	11003	ANTI-SENSE	619	1378	CGPG8165	77370	SENSE
238	997	CGPG4684	71613	SENSE	620	1379	CGPG8169	78117	SENSE

NUC Seq ID	PEP Seq ID	Gene ID	Construct ID	Orientation	NUC Seq ID	PEP Seq ID	Gene ID	Construct ID	Orientation
239	998	CGPG4689	78203	SENSE	621	1380	CGPG8203	77950	SENSE
240	999	CGPG4691	71638	SENSE	622	1381	CGPG8205	78905	SENSE
241	1000	CGPG4702	71631	SENSE	623	1382	CGPG8212	75913	SENSE
242	1001	CGPG4703	72368	SENSE	624	1383	CGPG8213	75925	SENSE
243	1002	CGPG4710	78202	SENSE	625	1384	CGPG8225	75974	SENSE
244	1003	CGPG4713	78207	SENSE	626	1385	CGPG8227	75903	SENSE
245	1004	CGPG4730	75209	SENSE	627	1386	CGPG8235	75904	SENSE
246	1005	CGPG4747	72457	SENSE	628	1387	CGPG8236	75916	SENSE
247	1006	CGPG4755	73639	SENSE	629	1388	CGPG8244	75917	SENSE
248	1007	CGPG4772	72526	SENSE	630	1389	CGPG8254	75942	SENSE
249	1008	CGPG4779	72531	SENSE	631	1390	CGPG8255	75954	SENSE
250	1009	CGPG4848	73336	SENSE	632	1391	CGPG8262	75943	SENSE
251	1010	CGPG4879	73722	SENSE	633	1392	CGPG8264	75967	SENSE
252	1011	CGPG4882	72650	SENSE	634	1393	CGPG8269	75932	SENSE
253	1012	CGPG4892	73686	SENSE	635	1394	CGPG8271	75956	SENSE
254	1013	CGPG4903	78353	SENSE	636	1395	CGPG8305	78135	SENSE
255	1014	CGPG4925	73726	SENSE	637	1396	CGPG8320	78612	SENSE
256	1015	CGPG4937	74715	SENSE	638	1397	CGPG8326	77969	SENSE
257	1016	CGPG4949	73230	SENSE	639	1398	CGPG8344	78136	SENSE
258	1017	CGPG4971	72663	SENSE	640	1399	CGPG8347	77627	SENSE
259	1018	CGPG499	70822	SENSE	641	1400	CGPG8359	78142	SENSE
260	1019	CGPG5004	72827	SENSE	642	1401	CGPG8370	77973	SENSE
261	1020	CGPG5028	78339	SENSE	643	1402	CGPG8371	78141	SENSE
262	1021	CGPG5032	73309	SENSE	644	1403	CGPG8375	78963	SENSE
263	1022	CGPG5038	78725	SENSE	645	1404	CGPG8378	78153	SENSE
264	1023	CGPG5045	74222	SENSE	646	1405	CGPG8383	78156	SENSE
265	1024	CGPG5048	78341	SENSE	647	1406	CGPG841	11807	ANTI-SENSE
266	1025	CGPG5051	78342	SENSE	648	1407	CGPG8436	78528	SENSE
267	1026	CGPG5061	78349	SENSE	649	1408	CGPG8438	78530	SENSE
268	1027	CGPG5062	73683	SENSE	650	1409	CGPG8450	78618	SENSE
269	1028	CGPG5069	73280	SENSE	651	1410	CGPG8451	78919	SENSE
270	1029	CGPG5070	73281	SENSE	652	1411	CGPG8459	77974	SENSE
271	1030	CGPG5097	73313	SENSE	653	1412	CGPG8461	77630	SENSE
272	1031	CGPG510	12772	ANTI-SENSE	654	1413	CGPG8463	78921	SENSE
273	1032	CGPG5100	73314	SENSE	655	1414	CGPG8471	78620	SENSE
274	1033	CGPG5117	73861	SENSE	656	1415	CGPG8474	77975	SENSE
275	1034	CGPG5151	73676	SENSE	657	1416	CGPG8475	78536	SENSE
276	1035	CGPG5155	74212	SENSE	658	1417	CGPG8476	78537	SENSE
277	1036	CGPG5159	74218	SENSE	659	1418	CGPG8490	78540	SENSE
278	1037	CGPG516	71218	SENSE	660	1419	CGPG8510	77993	SENSE
279	1038	CGPG5161	73731	SENSE	661	1420	CGPG8530	78924	SENSE
280	1039	CGPG5186	73251	SENSE	662	1421	CGPG8533	78009	SENSE
281	1040	CGPG519	12773	ANTI-SENSE	663	1422	CGPG8544	78014	SENSE
282	1041	CGPG5190	73254	SENSE	664	1423	CGPG8546	78015	SENSE

NUC Seq ID	PEP Seq ID	Gene ID	Construct ID	Orientation	NUC Seq ID	PEP Seq ID	Gene ID	Construct ID	Orientation
283	1042	CGPG5191	73255	SENSE	665	1424	CGPG8549	78018	SENSE
284	1043	CGPG5196	73257	SENSE	666	1425	CGPG8555	78021	SENSE
285	1044	CGPG521	11049	SENSE	667	1426	CGPG8561	78158	SENSE
286	1045	CGPG5211	74231	SENSE	668	1427	CGPG8569	78026	SENSE
287	1046	CGPG5212	73266	SENSE	669	1428	CGPG8573	78028	SENSE
288	1047	CGPG5213	75823	SENSE	670	1429	CGPG8588	78032	SENSE
289	1048	CGPG522	11353	SENSE	671	1430	CGPG8597	78388	SENSE
290	1049	CGPG5223	72025	SENSE	672	1431	CGPG8607	78044	SENSE
291	1050	CGPG5224	72037	SENSE	673	1432	CGPG8611	78047	SENSE
292	1051	CGPG5225	72049	SENSE	674	1433	CGPG8629	78055	SENSE
293	1052	CGPG5254	78213	SENSE	675	1434	CGPG8632	78057	SENSE
294	1053	CGPG5257	72007	SENSE	676	1435	CGPG8634	78059	SENSE
295	1054	CGPG5262	72067	SENSE	677	1436	CGPG8635	78553	SENSE
296	1055	CGPG5265	72008	SENSE	678	1437	CGPG8636	78163	SENSE
297	1056	CGPG5282	72022	SENSE	679	1438	CGPG8640	78060	SENSE
298	1057	CGPG5304	72096	SENSE	680	1439	CGPG8642	78062	SENSE
299	1058	CGPG532	10811	ANTI-SENSE	681	1440	CGPG8646	78065	SENSE
300	1059	CGPG5336	72138	SENSE	682	1441	CGPG8666	78590	SENSE
301	1060	CGPG5350	74261	SENSE	683	1442	CGPG8677	78177	SENSE
302	1061	CGPG5355	74264	SENSE	684	1443	CGPG8688	78952	SENSE
303	1062	CGPG5376	74271	SENSE	685	1444	CGPG8689	78559	SENSE
304	1063	CGPG5377	74272	SENSE	686	1445	CGPG8704	78169	SENSE
305	1064	CGPG5382	78442	SENSE	687	1446	CGPG8716	78178	SENSE
306	1065	CGPG5385	76709	SENSE	688	1447	CGPG8754	78932	SENSE
307	1066	CGPG539	75002	SENSE	689	1448	CGPG8769	78185	SENSE
308	1067	CGPG5437	78361	SENSE	690	1449	CGPG8774	78186	SENSE
309	1068	CGPG5450	74238	SENSE	691	1450	CGPG8778	78572	SENSE
310	1069	CGPG5473	78434	SENSE	692	1451	CGPG8784	78631	SENSE
311	1070	CGPG55	73932	SENSE	693	1452	CGPG879	12425	ANTI-SENSE
312	1071	CGPG5505	72713	SENSE	694	1453	CGPG8797	78938	SENSE
313	1072	CGPG5510	72773	SENSE	695	1454	CGPG8810	78961	SENSE
314	1073	CGPG5514	72678	SENSE	696	1455	CGPG8827	78584	SENSE
315	1074	CGPG5541	72765	SENSE	697	1456	CGPG8853	78589	SENSE
316	1075	CGPG5546	72730	SENSE	698	1457	CGPG8873	78252	SENSE
317	1076	CGPG5552	72707	SENSE	699	1458	CGPG8877	76314	SENSE
318	1077	CGPG5556	72755	SENSE	700	1459	CGPG8878	76326	SENSE
319	1078	CGPG557	10610	ANTI-SENSE	701	1460	CGPG8881	76362	SENSE
320	1079	CGPG5576	73953	SENSE	702	1461	CGPG8895	76340	SENSE
321	1080	CGPG5596	73173	SENSE	703	1462	CGPG8906	76377	SENSE
322	1081	CGPG5605	73979	SENSE	704	1463	CGPG8917	76319	SENSE
323	1082	CGPG5606	73966	SENSE	705	1464	CGPG8919	76343	SENSE
324	1083	CGPG561	12776	ANTI-SENSE	706	1465	CGPG8925	76320	SENSE
325	1084	CGPG5618	72960	SENSE	707	1466	CGPG8930	76380	SENSE

NUC Seq ID	PEP Seq ID	Gene ID	Construct ID	Orientation	NUC Seq ID	PEP Seq ID	Gene ID	Construct ID	Orientation
326	1085	CGPG5642	73021	SENSE	708	1467	CGPG8937	77831	SENSE
327	1086	CGPG5644	73163	SENSE	709	1468	CGPG8942	76334	SENSE
328	1087	CGPG5647	73187	SENSE	710	1469	CGPG8946	76382	SENSE
329	1088	CGPG5655	73188	SENSE	711	1470	CGPG8990	76838	SENSE
330	1089	CGPG5660	73153	SENSE	712	1471	CGPG9001	77841	SENSE
331	1090	CGPG5662	73983	SENSE	713	1472	CGPG9008	77838	SENSE
332	1091	CGPG568	11516	ANTI-SENSE	714	1473	CGPG9016	76865	SENSE
333	1092	CGPG5686	73179	SENSE	715	1474	CGPG9036	77834	SENSE
334	1093	CGPG5702	73009	SENSE	716	1475	CGPG9060	76823	SENSE
335	1094	CGPG5712	73109	SENSE	717	1476	CGPG9069	76836	SENSE
336	1095	CGPG5713	73121	SENSE	718	1477	CGPG908	14133	ANTI-SENSE
337	1096	CGPG5715	73157	SENSE	719	1478	CGPG9093	76927	SENSE
338	1097	CGPG5723	73158	SENSE	720	1479	CGPG9096	76963	SENSE
339	1098	CGPG5729	73088	SENSE	721	1480	CGPG9097	76975	SENSE
340	1099	CGPG5730	73135	SENSE	722	1481	CGPG9106	76988	SENSE
341	1100	CGPG5732	73005	SENSE	723	1482	CGPG9111	76953	SENSE
342	1101	CGPG5741	73171	SENSE	724	1483	CGPG9112	76965	SENSE
343	1102	CGPG5752	73042	SENSE	725	1484	CGPG9123	77161	SENSE
344	1103	CGPG5771	73067	SENSE	726	1485	CGPG9124	77852	SENSE
345	1104	CGPG5778	73148	SENSE	727	1486	CGPG9138	77151	SENSE
346	1105	CGPG5782	72933	SENSE	728	1487	CGPG9143	77116	SENSE
347	1106	CGPG5785	77723	SENSE	729	1488	CGPG9150	77105	SENSE
348	1107	CGPG5797	73048	SENSE	730	1489	CGPG9152	77129	SENSE
349	1108	CGPG580	10616	ANTI-SENSE	731	1490	CGPG9162	77154	SENSE
350	1109	CGPG5805	72923	SENSE	732	1491	CGPG9165	77190	SENSE
351	1110	CGPG5810	78501	SENSE	733	1492	CGPG9166	77107	SENSE
352	1111	CGPG5822	78371	SENSE	734	1493	CGPG9171	77167	SENSE
353	1112	CGPG5837	74332	SENSE	735	1494	CGPG9177	77144	SENSE
354	1113	CGPG5855	74738	SENSE	736	1495	CGPG9178	77156	SENSE
355	1114	CGPG5868	75225	SENSE	737	1496	CGPG9179	77168	SENSE
356	1115	CGPG587	11149	SENSE	738	1497	CGPG9181	77192	SENSE
357	1116	CGPG5889	74739	SENSE	739	1498	CGPG9188	77181	SENSE
358	1117	CGPG5893	74748	SENSE	740	1499	CGPG9189	77193	SENSE
359	1118	CGPG5909	78113	SENSE	741	1500	CGPG9201	77147	SENSE
360	1119	CGPG5914	75233	SENSE	742	1501	CGPG9222	77853	SENSE
361	1120	CGPG5921	77311	SENSE	743	1502	CGPG9234	77854	SENSE
362	1121	CGPG5925	77008	SENSE	744	1503	CGPG9237	77287	SENSE
363	1122	CGPG5926	77321	SENSE	745	1504	CGPG9244	77276	SENSE
364	1123	CGPG5930	76214	SENSE	746	1505	CGPG9248	77229	SENSE
365	1124	CGPG5945	75238	SENSE	747	1506	CGPG9249	77241	SENSE
366	1125	CGPG5958	76118	SENSE	748	1507	CGPG9251	77265	SENSE
367	1126	CGPG5977	75243	SENSE	749	1508	CGPG9280	77233	SENSE
368	1127	CGPG598	72602	SENSE	750	1509	CGPG9285	77293	SENSE
369	1128	CGPG5986	75810	SENSE	751	1510	CGPG9302	77473	SENSE

NUC Seq ID	PEP Seq ID	Gene ID	Construct ID	Orientation	NUC Seq ID	PEP Seq ID	Gene ID	Construct ID	Orientation
370	1129	CGPG5994	75094	SENSE	752	1511	CGPG931	76402	SENSE
371	1130	CGPG5996	75818	SENSE	753	1512	CGPG9313	77428	SENSE
372	1131	CGPG6021	75248	SENSE	754	1513	CGPG9315	77429	SENSE
373	1132	CGPG6027	74605	SENSE	755	1514	CGPG9327	78277	SENSE
374	1133	CGPG6035	75252	SENSE	756	1515	CGPG933	11935	ANTI-SENSE
375	1134	CGPG604	10620	ANTI-SENSE	757	1516	CGPG9334	78259	SENSE
376	1135	CGPG6049	74611	SENSE	758	1517	CGPG967	12276	ANTI-SENSE
377	1136	CGPG606	11152	SENSE	759	1518	CGPG988	12365	SENSE
378	1137	CGPG6069	76610	SENSE	/	/	/	/	/

Recombinant DNA

[0041] DNA for use in the present invention to improve traits in plants have a nucleotide sequence of SEQ ID NO:1 through SEQ ID NO:759, as well as the homologs of such DNA molecules. A subset of the DNA for gene suppression aspects of the invention includes fragments of the disclosed full polynucleotides consisting of oligonucleotides of 21 or more consecutive nucleotides. Oligonucleotides the larger molecules having a sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 759 are useful as probes and primers for detection of the polynucleotides used in the invention. Also useful in this invention are variants of the DNA. Such variants may be naturally occurring, including DNA from homologous genes from the same or a different species, or may be non-natural variants, for example DNA synthesized using chemical synthesis methods, or generated using recombinant DNA techniques. Degeneracy of the genetic code provides the possibility to substitute at least one base of the protein encoding sequence of a gene with a different base without causing the amino acid sequence of the polypeptide produced from the gene to be changed. Hence, a DNA useful in the present invention may have any base sequence that has been changed from the sequences provided herein by substitution in accordance with degeneracy of the genetic code.

[0042] Homologs of the genes providing DNA demonstrated as useful in improving traits in model plants disclosed herein will generally have significant identity with the DNA disclosed herein. DNA is substantially identical to a reference DNA if, when the sequences of the polynucleotides are optimally aligned there is about 60% nucleotide equivalence; more preferably 70%; more preferably 80% equivalence; more preferably 85% equivalence; more preferably 90%; more preferably 95%; and/or more preferably 98% or 99% equivalence over a comparison window. A comparison window is preferably at least 50-100 nucleotides, and more preferably is the entire length of the polynucleotide provided herein. Optimal alignment of sequences for aligning a comparison window may be conducted by algorithms; preferably by computerized implementations of these algorithms (for example, the Wisconsin Genetics Software Package Release 7.0-10.0, Genetics Computer Group, 575 Science Dr., Madison, WI). The reference polynucleotide may be a full-length molecule or a portion of a longer molecule. Preferentially, the window of comparison for determining polynucleotide identity of protein encoding sequences is the entire coding region.

[0043] Proteins useful for imparting enhanced traits are entire proteins or at least a sufficient portion of the entire protein to impart the relevant biological activity of the protein. Proteins useful for generation of transgenic plants having enhanced traits include the proteins with an amino acid sequence provided herein as SEQ ID NO: 760 through SEQ ID NO: 1518, as well as homologs of such proteins.

[0044] Homologs of the proteins useful in the invention are identified by comparison of the amino acid sequence of the protein to amino acid sequences of proteins from the same or different plant sources, e.g., manually or by using known homology-based search algorithms such as those commonly known and referred to as BLAST, FASTA, and Smith-Waterman. As used herein, a homolog is a protein from the same or a different organism that performs the same biological function as the polypeptide to which it is compared. An orthologous relation between two organisms is not necessarily manifest as a one-to-one correspondence between two genes, because a gene can be duplicated or deleted after organism phylogenetic separation, such as speciation. For a given protein, there may be no ortholog or more than one ortholog. Other complicating factors include alternatively spliced transcripts from the same gene, limited gene identification, redundant copies of the same gene with different sequence lengths or corrected sequence. A local sequence alignment program, e.g., BLAST, can be used

to search a database of sequences to find similar sequences, and the summary Expectation value (E-value) used to measure the sequence base similarity. As a protein hit with the best E-value for a particular organism may not necessarily be an ortholog or the only ortholog, a reciprocal BLAST search is used in the present invention to filter hit sequences with significant E-values for ortholog identification. The reciprocal BLAST entails search of the significant hits against a database of amino acid sequences from the base organism that are similar to the sequence of the query protein. A hit is a likely ortholog, when the reciprocal BLAST's best hit is the query protein itself or a protein encoded by a duplicated gene after speciation. Thus, homolog is used herein to describe proteins that are assumed to have functional similarity by inference from sequence base similarity. The relationship of homologs with amino acid sequences of SEQ ID NO: 1519 to SEQ ID NO: 67778 to the proteins with amino acid sequences of SEQ ID NO: to 760 to SEQ ID NO: 1518 are found in the listing of Table 16.

[0045] Other functional homolog proteins differ in one or more amino acids from those of a trait-improving protein disclosed herein as the result of one or more of the well-known conservative amino acid substitutions, e.g., valine is a conservative substitute for alanine and threonine is a conservative substitute for serine. Conservative substitutions for an amino acid within the native sequence can be selected from other members of a class to which the naturally occurring amino acid belongs. Representative amino acids within these various classes include, but are not limited to: (1) acidic (negatively charged) amino acids such as aspartic acid and glutamic acid; (2) basic (positively charged) amino acids such as arginine, histidine, and lysine; (3) neutral polar amino acids such as glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; and (4) neutral nonpolar (hydrophobic) amino acids such as alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine. Conserved substitutes for an amino acid within a native amino acid sequence can be selected from other members of the group to which the naturally occurring amino acid belongs. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. Naturally conservative amino acids substitution groups are: valine-leucine, valine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, aspartic acid-glutamic acid, and asparagine-glutamine. A further aspect of the invention comprises proteins that differ in one or more amino acids from those of a described protein sequence as the result of deletion or insertion of one or more amino acids in a native sequence.

[0046] Homologs of the trait-improving proteins provided herein will generally demonstrate significant sequence identity. Of particular interest are proteins having at least 50% sequence identity, more preferably at least about 70% sequence identity or higher, e.g., at least about 80% sequence identity with an amino acid sequence of SEQ ID NO:760 through SEQ ID NO: 1518. Of course useful proteins also include those with higher identity, e.g., 90% to 99% identity. Identity of protein homologs is determined by optimally aligning the amino acid sequence of a putative protein homolog with a defined amino acid sequence and by calculating the percentage of identical and conservatively substituted amino acids over the window of comparison. The window of comparison for determining identity can be the entire amino acid sequence disclosed herein, *e.g.,* the full sequence of any of SEQ ID NO: 760 through SEQ ID NO: 1518.

[0047] Genes that are homologous to each other can be grouped into families and included in multiple sequence alignments. Then a consensus sequence for each group can be derived. This analysis enables the derivation of conserved and class-(family) specific residues or motifs that are functionally important. These conserved residues and motifs can be further validated with 3D protein structure if available. The consensus sequence can be used to define the full scope of the invention, *e.g.,* to identify proteins with a homolog relationship. Thus, the present invention contemplates that protein homologs include proteins with an amino acid sequence that has at least 90% identity to such a consensus amino acid sequence sequences.

Gene stacking

[0048] The present invention also contemplates that the trait-improving recombinant DNA provided herein can be used in combination with other recombinant DNA to create plants with multiple desired traits or a further enhanced trait. The combinations generated can include multiple copies of any one or more of the recombinant DNA constructs. These stacked combinations can be created by any method, including but not limited to cross breeding of transgenic plants, or multiple genetic transformation.

Transformation Methods

[0049] Numerous methods for transforming chromosomes in a plant cell nucleus with recombinant DNA are known in the art

and are used in methods of preparing a transgenic plant cell nucleus cell, and plant. Two effective methods for such transformation are *Agrobacterium*-mediated transformation and microprojectile bombardment. Microprojectile bombardment methods are illustrated in U.S. Patents 5,015,580 (soybean); 5,550,318 (corn); 5,538,880 (corn); 5,914,451 (soybean); 6,160,208 (corn); 6,399,861 (corn); 6,153,812 (wheat) and 6,365,807 (rice) and *Agrobacterium*-mediated transformation is described in U.S. Patents 5,159,135 (cotton); 5,824,877 (soybean); 5,463,174 (canola); 5,591,616 (corn); 6,384,301 (soybean), 7,026,528 (wheat) and 6,329,571 (rice), all of which are incorporated herein by reference. Transformation of plant material is practiced in tissue culture on a nutrient media, i.e. a mixture of nutrients that will allow cells to grow *in vitro*. Recipient cell targets include, but are not limited to, meristem cells, hypocotyls, calli, immature embryos and gametic cells such as microspores, pollen, sperm and egg cells. Callus may be initiated from tissue sources including, but not limited to, immature embryos, hypocotyls, seedling apical meristems, microspores and the like. Cells containing a transgenic nucleus are grown into transgenic plants.

[0050] In addition to direct transformation of a plant material with a recombinant DNA, a transgenic plant cell nucleus can be prepared by crossing a first plant having cells with a transgenic nucleus with recombinant DNA with a second plant lacking the trangenci nucleus. For example, recombinant DNA can be introduced into a nucleus from a first plant line that is amenable to transformation to transgenic nucleus in cells that are grown into a transgenic plant which can be crossed with a second plant line to introgress the recombinant DNA into the second plant line. A transgenic plant with recombinant DNA providing an enhanced trait, e.g. enhanced yield, can be crossed with transgenic plant line having other recombinant DNA that confers another trait, for example herbicide resistance or pest resistance, to produce progeny plants having recombinant DNA that confers both traits. Typically, in such breeding for combining traits the transgenic plant donating the additional trait is a male line and the transgenic plant carrying the base traits is the female line. The progeny of this cross will segregate such that some of the plants will carry the DNA for both parental traits and some will carry DNA for one parental trait; such plants can be identified by markers associated with parental recombinant DNA, e.g. marker identification by analysis for recombinant DNA or, in the case where a selectable marker is linked to the recombinant, by application of the selecting agent such as a herbicide for use with a herbicide tolerance marker, or by selection for the enhanced trait. Progeny plants carrying DNA for both parental traits can be crossed back into the female parent line multiple times, for example usually 6 to 8 generations, to produce a progeny plant with substantially the same genotype as one original transgenic parental line but for the recombinant DNA of the other transgenic parental line

[0051] In the practice of transformation DNA is typically introduced into only a small percentage of target plant cells in any one transformation experiment. Marker genes are used to provide an efficient system for identification of those cells that are stably transformed by receiving and integrating a recombinant DNA molecule into their genomes. Preferred marker genes provide selective markers which confer resistance to a selective agent, such as an antibiotic or a herbicide. Any of the herbicides to which plants of this invention may be resistant are useful agents for selective markers. Potentially transformed cells are exposed to the selective agent. In the population of surviving cells will be those cells where, generally, the resistance-conferring gene is integrated and expressed at sufficient levels to permit cell survival. Cells may be tested further to confirm stable integration of the exogenous DNA. Commonly used selective marker genes include those conferring resistance to antibiotics such as kanamycin and paromomycin (*nptII*), hygromycin B (*aph IV*), spectinomycin (a*ad*A) and gentamycin (aac*3* and aacC4) or resistance to herbicides such as glufosinate (*bar* or *pat*), dicamba (DMO) and glyphosate (*aroA* or EPSPS). Examples of such selectable markers are illustrated in U.S. Patents 5,550,318; 5,633,435; 5,780,708 and 6,118,047, all of which are incorporated herein by reference. Selectable markers which provide an ability to visually identify transformants can also be employed, for example, a gene expressing a colored or fluorescent protein such as a luciferase or green fluorescent protein (GFP) or a gene expressing a *beta*-glucuronidase or *uid*A gene (GUS) for which various chromogenic substrates are known.

[0052] Plant cells that survive exposure to the selective agent, or plant cells that have been scored positive in a screening assay, may be cultured in regeneration media and allowed to mature into plants. Developing plantlets regenerated from transformed plant cells can be transferred to plant growth mix, and hardened off, for example, in an environmentally controlled chamber at about 85% relative humidity, 600 ppm CO_2, and 25-250 microeinsteins m^{-2} s^{-1} of light, prior to transfer to a greenhouse or growth chamber for maturation. Plants are regenerated from about 6 weeks to 10 months after a transformant is identified, depending on the initial tissue, and plant species. Plants may be pollinated using conventional plant breeding methods known to those of skill in the art and seed produced, for example self-pollination is commonly used with transgenic corn. The regenerated transformed plant or its progeny seed or plants can be tested for expression of the recombinant DNA and selected for the presence of enhanced agronomic trait.

Transgenic Plants and Seeds

[0053] Transgenic plants derived from transgenic plant cells having a transgenic nucleus of this invention are grown to generate transgenic plants having an enhanced trait as compared to a control plant and produce transgenic seed and haploid pollen of this invention. Such plants with enhanced traits are identified by selection of transformed plants or progeny seed for the enhanced trait. For efficiency a selection method is designed to evaluate multiple transgenic plants (events) comprising the recombinant DNA, for example multiple plants from 2 to 20 or more transgenic events. Transgenic plants grown from transgenic seed provided herein demonstrate improved agronomic traits that contribute to increased yield or other trait that provides increased plant value, including, for example, improved seed quality. Of particular interest are plants having enhanced water use efficiency, enhanced cold tolerance, increased yield, enhanced nitrogen use efficiency, enhanced seed protein and enhanced seed oil.

Discovery of Trait-improving Recombinant DNA

[0054] To identify nuclei with recombinant DNA that confer enhanced traits to plants, *Arabidopsis thaliana* was transformed with a candidate recombinant DNA construct and screened for an enhanced trait.

[0055] *Arabidopsis thaliana* is used a model for genetics and metabolism in plants. *Arabidopsis* has a small genome, and well-documented studies are available. It is easy to grow in large numbers and mutants defining important genetically controlled mechanisms are either available, or can readily be obtained. Various methods to introduce and express isolated homologous genes are available (see Koncz, e.g., Methods in Arabidopsis Research e.g., (1992), World Scientific, New Jersey, New Jersey, in "Preface").

[0056] A two-step screening process was employed which comprised two passes of trait characterization to ensure that the trait modification was dependent on expression of the recombinant DNA, but not due to the chromosomal location of the integration of the transgene. Twelve independent transgenic lines for each recombinant DNA construct were established and assayed for the transgene expression levels. Five transgenic lines with high transgene expression levels were used in the first pass screen to evaluate the transgene's function in T2 transgenic plants. Subsequently, three transgenic events, which had been shown to have one or more enhanced traits, were further evaluated in the second pass screen to confirm the transgene's ability to impart an enhanced trait. The following Table 3 summarizes the enhanced traits that have been confirmed as provided by a recombinant DNA construct.

[0057] In particular, Table 3 reports:

"PEP SEQ ID" which is the amino acid sequence of the protein cognate to the DNA in the recombinant DNA construct corresponding to a protein sequence of a SEQ ID NO. in the Sequence Listing.

"construct_id" is an arbitrary name for the recombinant DNA describe more particularly in Table 1.

"annotation" refers to a description of the top hit protein obtained from an amino acid sequence query of each PEP SEQ ID NO to GenBank database of the National Center for Biotechnology Information (ncbi). More particularly, "gi" is the GenBank ID number for the top BLAST hit.

" description" refers to the description of the top BLAST hit.

"e-value" provides the expectation value for the BLAST hit.

" % id" refers to the percentage of identically matched amino acid residues along the length of the portion of the sequences which is aligned by BLAST between the sequence of interest provided herein and the hit sequence in GenBank.

"traits" identify by two letter codes the confirmed enhancement in a transgenic plant provided by the recombinant DNA. The codes for enhanced traits are:

"CK" which indicates cold tolerance enhancement identified under a cold shock tolerance screen;

"CS" which indicates cold tolerance enhancement identified by a cold germination tolerance screen;

"DS" which indicates drought tolerance enhancement identified by a soil drought stress tolerance screen;

"PEG" which indicates osmotic stress tolerance enhancement identified by a PEG induced osmotic stress tolerance screen;

"HS" which indicates heat stress tolerance enhancement identified by a heat stress tolerance screen;

"SS" which indicates high salinity stress tolerance enhancement identified by a salt stress tolerance screen;

"LN" which indicates nitrogen use efficiency enhancement identified by a limited nitrogen tolerance screen;

"LL" which indicates attenuated shade avoidance response identified by a shade tolerance screen under a low light condition;

"PP" which indicates enhanced growth and development at early stages identified by an early plant growth and development screen;

"SP" which indicates enhanced growth and development at late stages identified by a late plant growth and development screen provided herein.

Table 3

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
760	12792	1.00E-107	73	ref|NP_198588.2|nucleic acid binding [Arabidopsis thaliana]	DS				
761	13673	0	94	ref|NP_850412.1|peptidase [Arabidopsis thaliana]	SS				
762	12020	6.00E-50	100	gb|AAF70854.1|AC003113_21 F24O1.1 [Arabidopsis thaliana]	SP				
763	10174	1.00E-111	90	ref|NP_567720.1|DREB1A (DEHYDRATION RESPONSE ELEMENT B1A); DNA binding / transcription factor/ transcriptional activator [Arabidopsis thaliana]	HS	PEG			
764	11827	2.00E-83	89	ref|NP-565558.1| unknown protein [Arabidopsis thaliana]	LN				
765	12435	3.00E-53	100	ref|NP_565280.1|NADH dehydrogenase (ubiquinone)/ NADH dehydrogenase [Arabidopsis thaliana]	LN				
766	12015	0	94	ref|NP_197429.1|KAPP; protein phosphatase type 2C [Arabidopsis thaliana]	LN				
767	11836	1.00E-146	97	ref|NP_566060.1|unknown protein [Arabidopsis thaliana]	LN				
768	12141	1.00E-134	94	ref|NP_192755.1|unknown protein [Arabidopsis thaliana]	LN				
769	12040	5.00E-97	91	ref|NP_567673.1|unknown protein [Arabidopsis thaliana]	DS				
770	12437	7.00E-35	85	ref|NP_190335.1|unknown protein [Arabidopsis thaliana]	LN				
771	12156	6.00E-55	100	ref|NP_179093.1|RNA binding / nucleic acid binding [Arabidopsis thaliana]	DS				
772	11853	1.00E-81	94	ref|NP_565677.1|unknown protein [Arabidopsis thaliana] gb|AAC79591.1|	SS				
773	12224	1.00E-145	82	ref|NP_565860.1|unknown protein [Arabidopsis thaliana] gb|AAC98059.1|	LL				
774	11856	1.00E-103	100	ref|NP_565273.1|hydrolase [Arabidopsis thaliana]	LN				
775	12065	9.00E-20	78	ref|NP_179185.1|unknown protein [Arabidopsis thaliana]	LN				
776	12419	1.00E-148	100	ref|NP_186847.1|oxidoreductase [Arabidopsis thaliana]	LN				
777	12208	0	100	ref|NP_565169.1|unknown protein [Arabidopsis thaliana]	LN				
778	14803	2.00E-82	79	ref|NP_187893.1|unknown protein [Arabidopsis thaliana]	HS				
779	10176	0	100	ref|NP_178313.1|ATPTR2-B (NITRATE TRANSPORTER 1); transporter [Arabidopsis thaliana]	LN				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
780	18011	1.00E-109	82	ref|NP_172517.1|ARR4 (RESPONSE REGULATOR 4); transcription regulator/ two-component response regulator [Arabidopsis thaliana]	CS				
781	12714	5.00E-53	100	ref|NP_566217.1|RNA binding / rRNA binding [Arabidopsis thaliana]	CK				
782	10507	9.00E-99	100	ref|NP_201097.1|ARR6 (RESPONSE REGULATOR 6); transcription regulator/ two-component response regulator [Arabidopsis thaliana]	LN				
783	15039	0	99	dbj|BAF02191.1 |hypothetical protein [Arabidopsis thaliana]	LN				
784	12733	1.00E-137	94	ref|NP_194298.1|unknown protein [Arabidopsis thaliana]	DS				
785	13237	1.00E-52	100	ref|NP_180192.1|unknown protein [Arabidopsis thaliana]	LN				
786	13504	1.00E-137	100	ref|NP_177643.1|unknown protein [Arabidopsis thaliana]	DS				
787	12932	1.00E-174	94	ref|NP_564618.1 |unknown protein [Arabidopsis thaliana]	SP				
788	75935	0	93	ref|NP_565242.1|protein binding [Arabidopsis thaliana]	CS				
789	73333	0	95	ref|NP_198718.1|ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	SS				
790	75993	0	93	ref|NP_171661.1|ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	LL				
791	19401	0	94	ref|NP_195275.1|ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	LN				
792	12766	5.00E-74	100	ref|NP_565233.1|unknown protein [Arabidopsis thaliana]	SS				
793	76025	0	95	ref|NP_179580.1|malic enzyme/ oxidoreductase, acting on NADH or NADPH, NAD or NADP as acceptor [Arabidopsis thaliana]	PEG				
794	13708	0	100	ref|NP_181187.1|fructose-bisphosphate aldolase [Arabidopsis thaliana]	LN				
795	13305	0	94	ref|NP_180287.1|PAP1 (PURPLE ACID PHOSPHATASE 1); hydrolase/ protein serine/threonine phosphatase [Arabidopsis thaliana]	LN				
796	15806	0	97	ref|NP_174089.1|APL2 [Arabidopsis thaliana]	SS				
797	14712	0	92	ref|NP_171617.1|PDH-E1 ALPHA (PYRUVATE DEHYDROGENASE E1 ALPHA); oxidoreductase, acting on the aldehyde or oxo group of donors, disulfide as acceptor / pyruvate dehydrogenase (acetyl-transferring) [Arabidopsis thaliana]	LN				
798	76013	0	92	ref|NP_194141.2|ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	DS				
799	10192	0	99	ref|NP_180997.1|CYP710A1; heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana]	CS	PP	SS		
800	74775	0	96	ref|NP_ 175812.1|ALDH7B4; aldehyde dehydrogenase/ oxidoreductase [Arabidopsis thaliana] r	DS				
801	13841	2.00E-	100	ref|NP_194401.1|hydrogen-transporting ATP	LN				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
		33		synthase, rotational mechanism / hydrogen-transporting ATPase, rotational mechanism [Arabidopsis thaliana]					
802	15805	0	100	ref|NP_567620.1|ZAC; ARF GTPase activator [Arabidopsis thaliana]	LN				
803	14253	1.00E-167	87	ref|NP_195499.1|unknown protein [Arabidopsis thaliana]	LN				
804	13650	1.00E-151	91	ref|NP_196069.1|phosphatidate cytidylyltransferase [Arabidopsis thaliana]	LN				
805	13855	1.00E-94	86	ref|NP_567531.1|structural constituent of ribosome [Arabidopsis thaliana]	LN				
806	76049	0	99	ref|NP_182198.2|unknown protein [Arabidopsis thaliana]	DS	HS			
807	14271	0	82	ref|NP_1 81342.1|unknown protein [Arabidopsis thaliana]	DS				
808	73927	0	100	ref|NP_189059.1|FAD binding / disulfide oxidoreductase/ glutathione-disulfide reductase/ oxidoreductase [Arabidopsis thaliana]	CS				
809	13657	6.00E-76	72	ref|NP_565661.2|HDT4 [Arabidopsis thaliana]	LN				
810	13938	2.00E-90	77	gb|AAL67123.1|AT3g06760/F3E22_10 [Arabidopsis thaliana]	SP				
810	14730	2.00E-90	77	gb|AAL67123.1|AT3g06760/F3E22_10 [Arabidopsis thaliana]	SP				
811	73948	0	97	ref|NP_176185.1|ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding [Arabidopsis thaliana]	CS				
812	18116	0	100	ref|NP_182144.1|oxidoreductase [Arabidopsis thaliana]	CS				
813	14341	0	100	ref|NP_176646.1|unknown protein [Arabidopsis thaliana]	SS				
814	13960	1.00E-179	100	ref|NP_565875.1|unknown protein [Arabidopsis thaliana]	SP				
814	74391	1.00E-179	100	ref|NP_565875.1|unknown protein [Arabidopsis thaliana]	SP				
815	75957	0	95	gb|ABK28258.1|unknown [Arabidopsis thaliana]	LL				
816	70240	0	100	ref|NP_172751.1|AN11; nucleotide binding [Arabidopsis thaliana]	CS				
817	70748	0	97	ref|NP_173077.1|ATP binding / protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	CK				
818	70807	0	93	ref|NP_188160.2|protein binding [Arabidopsis thaliana]	CS				
819	73986	0	87	ref|NP_974833.1|unknown protein [Arabidopsis thaliana]	DS				
820	77005	0	97	ref|NP_566580.1|CIPK1 (CBL-INTERACTING PROTEIN KINASE 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	CS				
821	70410	5.00E-34	86	ref|NP_850158.1|CLE5 (CLAVATA3/ESR-RELATED 5); receptor binding [Arabidopsis thaliana]	SP				
822	14827	1.00E-153	88	ref|NP_564658.2|unknown protein [Arabidopsis thaliana]	DS				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
823	19122	0	93	ref|NP_566009.1|unknown protein [Arabidopsis thaliana]	LL				
824	16446	0	94	ref|NP_566277.2|unknown protein [Arabidopsis thaliana]	SP				
825	15143	6.00E-84	100	ref|NP_194152.1|SLY1 (SLEEPY1) [Arabidopsis thaliana]	LN				
826	70401	0	93	sp|Q9SMZ3|FBX13_ARATHF-box only protein 13 emb|CAB36790.1| putative protein [Arabidopsis thaliana]	PEG				
827	16182	0	100	emb|CAB44691.1|putative protein [Arabidopsis thaliana]	DS				
828	15126	1.00E-138	95	ref|NP_198741.1|unknown protein [Arabidopsis thaliana]	CS				
829	15628	0	100	ref|NP_567421.1|unknown protein [Arabidopsis thaliana]	CS				
830	78355	0	90	gb|AAD10665.1|Hypothetical protein [Arabidopsis thaliana]	SS				
831	70560	0	100	gb|AAB81879.1|putative zinc finger protein [Arabidopsis thaliana]	CS				
832	19133	0	97	ref|NP_194117.3|protein binding / ubiquitin-protein ligase/ zinc ion binding [Arabidopsis thaliana]	DS				
833	73602	0	74	gb|AAR28013.1|mutant TFIIF-alpha [Arabidopsis thaliana]	CS				
834	71702	1.00E-169	100	pir||T49271CELL DIVISION CONTROL PROTEIN 2 HOMOLOG A - Arabidopsis thaliana	LL				
835	14909	0	98	gb|AAC39477.1|respiratory burst oxidase protein C [Arabidopsis thaliana]	CS	PP	HS	SS	PEG
836	14927	1.00E-88	65	ref|NP_568285.1|unknown protein [Arabidopsis thaliana]	LN				
837	75945	0	94	ref|NP_563899.1|NRT1.1; transporter [Arabidopsis thaliana]	SP				
838	16553	0	100	ref|NP_567083.1|nucleotide-sugar transporter/ sugar porter [Arabidopsis thaliana]	SS				
839	75221	0	87	ref|NP_195567.2|unknown protein [Arabidopsis thaliana]	CS	HS			
840	70746	5.00E-60	79	gb|AAM64668.1|unknown [Arabidopsis thaliana]	PEG				
841	70403	1.00E-137	85	gb|AAK26011.1|AF360301_1unknown protein [Arabidopsis thaliana]	PP				
842	15966	2.00E-73	71	ref|NP_568974.1|ATFP3; metal ion binding [Arabidopsis thaliana]	CK				
843	76076	4.00E-34	100	ref|NP_179357.1|unknown protein [Arabidopsis thaliana]	PP				
844	17014	2.00E-57	76	ref|NP_564008.1|unknown protein [Arabidopsis thaliana]	SS	PEG			
845	16007	0	100	ref|NP_564729.1|ZW9 [Arabidopsis thaliana]	DS				
846	16208	1.00E-06	100	gb|AAF79580.1|AC022464_38F22G5.2 [Arabidopsis thaliana]	CS				
847	17310	0	96	ref|NP_188117.1|catalytic [Arabidopsis thaliana]	HS				
848	15716	1.00E-164	96	ref|NP_563630.1|BPS1 (BYPASS 1) [Arabidopsis thaliana]	LN				
849	15627	0	89	ref|NP_565533.1|heat shock protein binding /	SS				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
				unfolded protein binding [Arabidopsis thaliana]					
850	15409	0	95	ref|NP_188010. 1|unknown protein [Arabidopsis thaliana]	CK	PEG			
850	17201	0	95	ref|NP_188010.1|unknown protein [Arabidopsis thaliana]	PEG				
851	15903	0	86	ref|NP_199280.1|unknown protein [Arabidopsis thaliana]	CK				
852	10332	0	96	ref|NP_188080.1|CYP72A8; heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana]	SP				
853	73968	0	90	ref|NP_565477.1|unknown protein [Arabidopsis thaliana]	LN				
854	17003	1.00E-171	95	ref|NP_174746.1|PHI-1 (PHOSPHATE-INDUCED 1) [Arabidopsis thaliana]	DS	SS			
855	73847	0	97	ref|NP_849912.1|ATP binding / kinase [Arabidopsis thaliana]	LN				
856	76041	0	97	ref|NP_566284.1|transferase, transferring glycosyl groups / transferase, transferring hexosyl groups [Arabidopsis thaliana]	CS	LL			
857	74567	0	75	ref|NP_566917.1|calmodulin binding [Arabidopsis thaliana] ref|NP_974405.1| calmodulin binding [Arabidopsis thaliana]	CS	LL			
858	15809	0	97	ref|NP_568150.1|unknown protein [Arabidopsis thaliana]	PP				
859	70110	0	92	ref|NP_014814.1|Lcb4p [Saccharomyces cerevisiae]	LN				
860	70123	1.00E-180	100	ref|NP_014392.1|Lst8p [Saccharomyces cerevisiae]	CK	SS			
861	74702	0	87	ref|NP_850390.1|unknown protein [Arabidopsis thaliana]	SP				
862	75936	0	95	ref|NP_187671.1|CAT7 (CATIONIC AMINO ACID TRANSPORTER 7); cationic amino acid transporter [Arabidopsis thaliana]	CS				
863	10462	1.00E-136	100	ref|NP_565895.1|catalytic/ hydrolase [Arabidopsis thaliana]	DS				
864	17402	1.00E-60	100	ref|NP_190775.1|unknown protein [Arabidopsis thaliana]	CS				
865	73707	0	94	ref|NP_564272.1|unknown protein [Arabidopsis thaliana]	CS				
866	17129	3.00E-61	100	ref|NP_564630.1|unknown protein [Arabidopsis thaliana]	LN				
867	72665	3.00E-54	89	ref|NP_564090.1|unknown protein [Arabidopsis thaliana]	LL				
868	18206	0	100	ref|NP_564983.1|transferase, transferring glycosyl groups / transferase, transferring hexosyl groups [Arabidopsis thaliana]	LN				
869	17151	1.00E-155	100	ref|NP_171882.1|ATPHB2 (PROHIBITIN 2) [Arabidopsis thaliana]	LN				
870	17813	5.00E-98	100	ref|NP_199762.1|protein binding [Arabidopsis thaliana]	SS				
871	70845	0	100	ref|NP_173920.1|RCN1 (ROOTS CURL IN NPA); protein phosphatase type 2A regulator [Arabidopsis thaliana]	CS				
872	16607	1.00E-	95	ref|NP_355455.1|hypothetical protein AGR_C_4560	SP				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
		171		[Agrobacterium tumefaciens str. C58]					
873	72675	1.00E-179	78	ref|NP_200890.1|protein binding / ubiquitin-protein ligase/ zinc ion binding [Arabidopsis thaliana]	LL	LN			
874	72677	0	86	sp|Q5EAE9|ATL5C_ARATHRING-H2 finger protein ATL5C precursor dbj|BAB09675.1| unnamed protein product [Arabidopsis thaliana]	LL				
875	74534	0	95	ref|NP_196233.1|CYC1BAT; cyclin-dependent protein kinase regulator [Arabidopsis thaliana]	PP				
876	74535	0	85	ref|NP_564978.1|NTL1; calcium ion binding / transporter [Arabidopsis thaliana]	CS				
877	10204	0	89	ref|NP_179544.1|nucleotide binding [Arabidopsis thaliana]	PP	LL			
878	10472	1.00E-157	100	ref|NP_565480.1|catalytic/ protein phosphatase type 2C [Arabidopsis thaliana]	LN				
879	10431	1.00E-118	88	ref|NP_850625.1|imidazoleglycerol-phosphate dehydratase [Arabidopsis thaliana]	LN				
880	72906	0	92	ref|NP_200387.1|DNA binding [Arabidopsis thaliana]	PP				
881	78362	0	95	ref|NP_176118.2|DNA binding / transcription factor [Arabidopsis thaliana]	CS				
882	17930	1.00E-11	60	ref|NP_173425.2|unknown protein [Arabidopsis thaliana]	SS				
883	18442	0	92	ref|NP_198690.1 |transcription factor [Arabidopsis thaliana]	SS				
884	73207	0	94	ref|NP_173148.2|dimethylallyltranstransferase [Arabidopsis thaliana]	CS				
885	19166	4.00E-99	91	emb|CAB45503.1|hypothetical protein [Arabidopsis thaliana]	DS				
886	10469	1.00E-137	95	ref|NP_ 191762.1|ROC4; peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana]	LN				
887	18415	1.00E-111	71	emb|CAB85519.1|putative protein [Arabidopsis thaliana]	CS				
888	18418	1.00E-113	100	ref|NP_200034.1|ATGB1 [Arabidopsis thaliana]	CK	SS			
889	19532	1.00E-179	100	ref|NP _190986.1|CDC2B (CDC2-LIKE GENE); kinase [Arabidopsis thaliana]	CS				
890	18423	1.00E-151	100	ref|NP_180496.1|SAG13; oxidoreductase [Arabidopsis thaliana]	LN				
891	77909	0	92	ref|NP_191785.1|catalytic/ protein phosphatase type 2C	CK	DS			
892	19656	4.00E-48	77	ref|NP_200260.1|PBP1 (PINOID-BINDING PROTEIN 1); calcium ion binding [Arabidopsis thaliana]	CS	SS			
893	10217	1.00E-135	94	ref|NP_199674.1|cyclin-dependent protein kinase [Arabidopsis thaliana]	LN				
894	18874	2.00E-81	100	ref|NP_176511.1|unknown protein [Arabidopsis thaliana]	SS				
895	18875	0	96	ref|NP_198127.1|unknown protein [Arabidopsis thaliana]	SS				
896	19256	0	96	ref|NP_568785.1|SPDS3 (SPERMIDINE SYNTHASE 3) [Arabidopsis thaliana]	DS				
897	19537	0	100	ref|NP_568931.1|ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding [Arabidopsis thaliana]	LL				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
898	74201	0	90	ref|NP_567067.1|ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding [Arabidopsis thaliana]	LN				
899	74233	0	97	ref|NP_199051.1|unknown protein [Arabidopsis thaliana]	SS				
900	18644	7.00E-62	100	ref|NP_172620.1|electron transporter/ thiol-disulfide exchange intermediate [Arabidopsis thaliana]	DS				
901	18827	0	91	ref|NP_565206.1|ubiquitin-protein ligase/ zinc ion binding [Arabidopsis thaliana]	CS				
902	18220	0	100	ref|NP_177629.1|nucleotidyltransferase [Arabidopsis thaliana]	SP				
903	18830	0	96	ref|NP_188813.1|UDP-glycosyltransferase/ transferase, transferring glycosyl groups [Arabidopsis thaliana]	PEG				
904	19205	1.00E-161	84	gb|ABF55664.2|double MYC-tagged mitogen activated protein kinase kinase 4 [synthetic construct]	LN				
905	18226	7.00E-99	92	ref|NP_197890.1|unknown protein [Arabidopsis thaliana]	CS				
906	18227	1.00E-62	73	ref|NP_564432.3|OHP2 (ONE-HELIX PROTEIN 2) [Arabidopsis thaliana]	LN				
907	18239	0	100	ref|NP_193460.1|unknown protein [Arabidopsis thaliana]	SP				
908	70415	1.00E-136	96	ref|NP_849930.1|AGL3 (AGAMOUS-LIKE 3); DNA binding / transcription factor [Arabidopsis thaliana]	CK				
909	18329	7.00E-06	70	ref|NP_178619.1 |unknown protein [Arabidopsis thaliana]	LN				
910	72606	1.00E-166	79	ref|NP_566784.1|unknown protein [Arabidopsis thaliana]	CS				
911	10230	0	96	ref|NP_172406.1|transferase, transferring glycosyl groups / transferase, transferring hexosyl groups [Arabidopsis thaliana]	LN				
912	19608	0	82	ref|NP_201045.1|calmodulin binding [Arabidopsis thaliana]	CS				
913	18271	3.00E-97	82	gb|AAA21820.1|alpha-subunit; putative	LN				
914	18347	2.00E-65	100	ref|NP_566786.1|DNA binding / transcription factor [Arabidopsis thaliana]	SP				
915	18403	0	89	ref|NP_187364.1|unknown protein [Arabidopsis thaliana]	CK				
916	74206	0	91	ref|NP_201348.1|cysteine-type endopeptidase/ ubiquitin thiolesterase [Arabidopsis thaliana]	CS				
917	10234	2.00E-60	72	ref|NP_193759.1|unknown protein [Arabidopsis thaliana]	LN				
918	71115	1.00E-167	87	ref|NP_189058.1|PMP (PUTATIVE TYPE 1 MEMBRANE PROTEIN) [Arabidopsis thaliana]	DS				
919	18406	8.00E-79	100	ref|NP_564160.1|unknown protein [Arabidopsis thaliana]	SS				
920	19619	2.00E-87	83	ref|NP_563890.1|unknown protein [Arabidopsis thaliana]	HS				
921	19623	1.00E-125	100	ref|NP_563994.1|SYP51 (SYNTAXIN OF PLANTS 51) [Arabidopsis thaliana]	DS				
922	18381	9.00E-	84	ref|NP_564601.1|unknown protein [Arabidopsis	SS				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
		96		thaliana]					
923	18408	8.00E-69	91	ref|NP_564808.1|unknown protein [Arabidopsis thaliana]	DS				
924	18720	1.00E-175	89	ref|NP_564840.1|unknown protein [Arabidopsis thaliana]	CK				
925	77537	1.00E-122	81	ref|NP_565125.1|unknown protein [Arabidopsis thaliana]	CS				
926	70833	0	90	ref|NP_566212.2|ATBPM4; protein binding [Arabidopsis thaliana]	LL				
927	19328	0	93	ref|NP_638257.1|hypothetical protein XCC2909 [Xanthomonas campestris pv. campestris str. ATCC 33913]	DS				
928	19312	0	100	ref|NP_013243.1|Proline oxidase, nuclear-encoded mitochondrial protein involved in utilization of proline as sole nitrogen source; PUT1 transcription is induced by Put3p in the presence of proline and the absence of a preferred nitrogen source [Saccharomyces cerevisiae]	SS				
929	70538	1.00E-146	93	ref|NP_199892.1|unknown protein [Arabidopsis thaliana]	SS				
930	70440	0	88	ref|NP_195953.1|cysteine-type peptidase [Arabidopsis thaliana]	CK	LN			
931	11319	0	97	ref|NP_177797.2|unknown protein [Arabidopsis thaliana]	LN				
932	70443	1.00E-151	81	ref|NP_195953.1 |unknown protein [Arabidopsis thaliana]	CS				
933	72357	1.00E-141	100	ref|NP_190300.1|ubiquitin-protein ligase/zinc ion binding [Arabidopsis thaliana]	PP				
934	70466	1.00E-172	94	ref|NP_196084.1|DNA binding / transcription factor [Arabidopsis thaliana]	LL				
935	70241	5.00E-39	100	gb|EAZ44836.1|hypothetical protein OsJ_028319 [Oryza sativa (japonica cultivar-group)]	SP				
936	70476	1.00E-153	95	ref|NP_176240.1|unknown protein [Arabidopsis thaliana]	LN				
937	70477	1.00E-150	100	ref|NP_564877.1|WRKY67; transcription factor [Arabidopsis thaliana]	SS				
938	19713	0	100	ref|NP _637886.1|oxidoreductase [Xanthomonas campestris pv. campestris str. ATCC 33913]	PP				
939	12601	3.00E-70	100	ref|NP_195713.1|DNA binding [Arabidopsis thaliana] ref|NP_001050276.1|Os03g0390600 [Oryza sativa (japonica cultivar-group)] gb|AAB36494.1| histone H3.2 [Medicago sativa]	CK				
940	19747	0	69	emb|CAB54847.1|hydroperoxide lyase [Medicago sativa]	CS				
941	11117	1.00E-174	91	ref|NP_973592.1|ATPUP2 [Arabidopsis thaliana]	LN				
942	70965	3.00E-95	46	gb|EAY82507.1|hypothetical protein OsI_036466 [Oryza sativa (indica cultivar-group)]	CS				
943	10366	1.00E-153	92	ref|NP_181358.1|unknown protein [Arabidopsis thaliana]	CK				
943	13404	1.00E-153	92	ref|NP_181358.1|unknown protein [Arabidopsis thaliana]	LN				
944	70935	0	77	gb|ABE91638.1|hypothetical protein MtrDRAFT_AC142394g9v2 [Medicago truncatula]	CS				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
945	77717	1.00E-136	69	ref|NP_565111.1|unknown protein [Arabidopsis thaliana]	CS				
946	19966	1.00E-163	80	gb|AAF27919.1|AF220203_1Ttg1-like protein [Malus x domestica]	SS				
947	70909	1.00E-116	74	ref|NP_192696.3|unknown protein [Arabidopsis thaliana]	SP				
948	19906	0	79	gb|AAD11430.1|protein phosphatase 2C homolog [Mesembryanthemum crystallinum]	CK				
949	70974	0	72	gb|ABN09819.1|Not CCR4-Not complex component, N-terminal; tRNA-binding arm [Medicago truncatula]	SP				
950	19802	0	90	gb|AAK11734.1|serine/threonine/tyrosine kinase [Arachis hypogaea]	CS				
951	19746	1.00E-127	92	sp|Q96450|1433A_SOYBN14-3-3-like protein A (SGF14A) gb|AAB09580.1|SGF14A [Glycine max]	CS				
952	70902	1.00E-135	81	gb|ABE77803.1|oxidoreductase, short chain dehydrogenase/reductase family, putative [Medicago truncatula]	PEG				
953	19933	2.00E-92	68	gb|ABE81369.1|RNA-binding region RNP-1 (RNA recognition motif) [Medicago truncatula]	SP				
954	19927	0	76	gb|ABE88827.1|Hydroxymethylglutaryl-coenzyme A reductase, putative [Medicago truncatula]	CS	SS			
955	70976	1.00E-164	79	ref|NP _194914.1|catalytic/ protein phosphatase type 2C [Arabidopsis thaliana]	PEG				
956	71440	0	60	ref|NP_196473.1|nucleotide binding [Arabidopsis thaliana]	CS				
957	10413	0	93	ref|NP_197748.1|CDPK9 (CALCIUM-DEPENDENT PROTEIN KINASE 9); ATP binding / calcium ion binding / calcium- and calmodulin-dependent protein kinase/ kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	LN				
958	11119	1.00E-172	89	ref|NP_196779.1|CPK17; ATP binding / calcium ion binding / calcium- and calmodulin-dependent protein kinase/ kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	LN				
959	78659	1.00E-164	90	ref|NP_175249.1|DNA binding / transcription factor [Arabidopsis thaliana]	LN				
960	78665	0	100	ref|NP_567343.1|ubiquitin-protein ligase [Arabidopsis thaliana]	DS				
961	78969	0	100	ref|NP_194509.1|catalytic/ protein phosphatase type 2C [Arabidopsis thaliana]	LN				
962	78970	7.00E-86	100	ref|NP_196084.1|calcium ion binding [Arabidopsis thaliana]	HS				
963	71250	1.00E-160	100	ref|NP_564808.1|ATP binding / protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase/ signal transducer [Arabidopsis thaliana]	SS	LN			
964	78972	0	94	ref|NP_176647.1|catalytic [Arabidopsis thaliana]	LN				
965	78677	2.00E-25	43	gb|AAG40050.2|AF324699_1At1g76180 [Arabidopsis thaliana]	SS				
966	70632	3.00E-85	100	ref|NP_187663.1|AHB2 [Arabidopsis thaliana]	DS				
967	75205	0	92	ref|NP_196484.1|AAP2 (AMINO ACID PERMEASE 2); amino acid permease [Arabidopsis thaliana]	SS				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
968	10359	1.00E-156	100	gb|AAR10436.1|YDA [Arabidopsis thaliana]	DS				
968	11408	1.00E-156	100	gb|AAR10436.1|YDA [Arabidopsis thaliana]	LL				
969	73616	1.00E-163	100	ref|NP_ 199265.1|ribose-5-phosphate isomerase [Arabidopsis thaliana]	LN				
970	78358	0	100	ref|NP_ 188056.1|diaminopimelate decarboxylase [Arabidopsis thaliana]	LL				
971	71839	0	96	ref|NP_200945.1|unknown protein [Arabidopsis thaliana]	LN	PEG			
972	78417	0	91	ref|NP_191221.1|unknown protein [Arabidopsis thaliana]	LN				
973	71952	1.00E-169	100	ref|NP_197477.1|binding / oxidative phosphorylation uncoupler [Arabidopsis thaliana]	LL				
974	78717	0	85	ref|NP_566301.1|unknown protein [Arabidopsis thaliana]	LN	PEG			
975	75040	0	92	ref|NP_566410.1|unknown protein [Arabidopsis thaliana]	LL				
976	71843	1.00E-134	94	ref|NP_194519.1|unknown protein [Arabidopsis thaliana]	LN				
977	70666	3.00E-79	91	ref|NP_565742.1|unknown protein [Arabidopsis thaliana]	LN				
978	71846	0	100	ref|NP-177890.1|1-aminocyclopropane-1-carboxylate synthase/ transaminase/ transferase, transferring nitrogenous groups [Arabidopsis thaliana]	SP				
979	71314	0	96	ref|NP_195953.1|CYP86C4; heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana]	SP				
980	76410	0	99	ref|NP_188081.1|CYP72A9; heme binding / iron ion binding/ monooxygenase/ oxygen binding [Arabidopsis thaliana]	LL	LN			
981	71322	0	93	ref|NP_680111.1|CYP71A21; heme binding / iron ion binding/ monooxygenase/ oxygen binding [Arabidopsis thaliana]	LN				
982	73214	0	97	ref|NP_196559.1|CYP78A7; heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana]	DS				
983	71963	0	97	ref|NP _199079.1|AOS (ALLENE OXIDE SYNTHASE); hydro-lyase/ oxygen binding [Arabidopsis thaliana]	SP	PP			
984	71326	0	83	pir||T00605probable cytochrome P450 At2g02580 [imported] - Arabidopsis thaliana	LN				
985	70834	0	95	ref|NP_175900.1|LOX1; lipoxygenase [Arabidopsis thaliana]	CS				
986	73215	0	97	gb|AAF97287.1|AC010164_9Putative cytochrome P450 [Arabidopsis thaliana]	CS				
987	71334	0	97	ref|NP_193568.2|hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana]	SP	LN			
988	71335	0	96	ref|NP_173573.1|catalytic [Arabidopsis thaliana]	LN				
989	71347	0	100	ref|NP_568479.1|TGG2 (GLUCOSIDE GLUCOHYDROLASE 2); hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana]	CK				
990	71820	3.00E-	75	emb|CAC03600.1|splicing factor SC35 [Arabidopsis	LL				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
		55		thaliana]					
991	70764	1.00E-164	94	ref|NP_172084.2|unknown protein [Arabidopsis thaliana]	LL				
992	70680	8.00E-79	100	ref|NP_567038.1|protein kinase C binding / zinc ion binding [Arabidopsis thaliana]	LL				
993	72375	0	73	gb|ABE85332.1|Protein kinase [Medicago truncatula]	SP				
994	72469	0	90	dbj|BAD95891.1|Ser/Thr protein kinase [Lotus japonicus]	CK				
995	73951	0	81	gb|AAR15466.1|WD-repeat protein [Capsella rubella]	CS				
996	11003	1.00E-118	94	ref|NP_178022.1|NADH dehydrogenase (ubiquinone)/ electron transporter/ iron ion binding [Arabidopsis thaliana]	LN				
997	71613	1.00E-110	85	ref|NP_564808.1 |AtTIP2;3; water channel [Arabidopsis thaliana]	LL				
998	78203	0	93	gb|AAF27063.1|AC008262_12F4N2.23 [Arabidopsis thaliana]	CS				
999	71638	0	90	ref|NP_174210.1|ATS9 (19S PROTEOSOME SUBUNIT 9) [Arabidopsis thaliana]	CS				
1000	71631	0	96	ref|NP_564785.1|antiporter/ glucose-6-phosphate transporter [Arabidopsis thaliana]	LL				
1001	72368	0	98	ref|NP_187640.1|organic anion transporter [Arabidopsis thaliana]	SP				
1002	78202	0	98	ref|NP_564338.1|CARB (CARBAMOYL PHOSPHATE SYNTHETASE B); ATP binding / carbamoyl-phosphate synthase/ ligase [Arabidopsis thaliana]	CK				
1003	78207	0	96	ref|NP_030560.1|unknown protein [Arabidopsis thaliana]	CS	HS			
1004	75209	0	92	ref|NP_187286.1|EMB3004; 3-dehydroquinate dehydratase/ shikimate 5-dehydrogenase [Arabidopsis thaliana]	LN				
1005	72457	7.00E-86	100	ref|NP_196084.1|ubiquitin conjugating enzyme/ ubiquitin-like activating enzyme [Arabidopsis thaliana]	CS				
1006	73639	0	98	ref|NP_564808.1|ATP binding / protein binding [Arabidopsis thaliana]	CS				
1007	72526	1.00E-55	81	ref|NP_567335.1|unknown protein [Arabidopsis thaliana]	CK				
1008	72531	0	100	ref|NP_194003.1|O-sialoglycoprotein endopeptidase [Arabidopsis thaliana]	CS				
1009	73336	1.00E-167	100	ref|NP_201090.1|catalytic [Arabidopsis thaliana]	LL				
1010	73722	0	94	ref|NP_191029.1|sugar binding [Arabidopsis thaliana]	CS				
1011	72650	1.00E-168	85	ref|NP_568218.1|unknown protein [Arabidopsis thaliana]	DS				
1012	73686	5.00E-67	100	ref|NP_189296.1|unknown protein [Arabidopsis thaliana]	CK	LL			
1013	78353	1.00E-119	86	sp|Q9SLB6|LBD17_ARATHLOB domain-containing protein 17 gb|AAD23726.1| hypothetical protein [Arabidopsis thaliana]	LL	LN			
1014	73726	0	100	ref|NP_179795.1|nucleotide binding [Arabidopsis	LN				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
				thaliana]					
1015	74715	0	97	ref|NP_197059.1|nucleotide binding [Arabidopsis thaliana]	CS				
1016	73230	0	96	ref|NP_191164.1|ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	CS				
1017	72663	2.00E-97	100	ref|NP_195953.1|ATP binding / kinase/ shikimate kinase [Arabidopsis thaliana]	LN				
1018	70822	0	94	ref|NP_198905.1|ATCLC-A (CHLORIDE CHANNEL A); anion channel/ voltage-gated chloride channel [Arabidopsis thaliana]	HS				
1019	72827	1.00E-164	95	ref|NP_173856.1|oxidoreductase [Arabidopsis thaliana]	LN				
1020	78339	0	96	ref|NP_195953.1|oxidoreductase [Arabidopsis thaliana]	LL				
1021	73309	1.00E-171	100	dbj|BAA96982.1|11-beta-hydroxysteroid dehydrogenase-like [Arabidopsis thaliana]	LL				
1022	78725	0	94	ref|NP_195953.1|kinase [Arabidopsis thaliana]	LN				
1023	74222	0	93	ref|NP _174039.1|ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	LL	LN			
1024	78341	0	93	ref|NP_564808.1|ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	LN	PEG			
1025	78342	1.00E-178	93	ref|NP_564808.1|AOX1B; alternative oxidase [Arabidopsis thaliana]	LL	LN			
1026	78349	2.00E-55	100	ref|NP_568772.3|FIB1 (FIBRILLARIN 1) [Arabidopsis thaliana]	CS				
1027	73683	7.00E-90	100	ref|NP_564105.1|ASK4; ubiquitin-protein ligase [Arabidopsis thaliana]	DS				
1028	73280	7.00E-86	94	ref|NP_565297.1|ASK16 (ARABIDOPSIS SKP1-LIKE 16); ubiquitin-protein ligase [Arabidopsis thaliana]	SP				
1029	73281	3.00E-77	96	ref|NP_565467.1|MEO (MEIDOS); ubiquitin-protein ligase [Arabidopsis thaliana]	LN				
1030	73313	0	95	ref|NP_172572.1|kinase [Arabidopsis thaliana]	CS				
1031	12772	1.00E-117	94	ref|NP_ 176435.1|Rho GDP-dissociation inhibitor [Arabidopsis thaliana]	SS				
1032	73314	0	89	ref|NP_186833.1|ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	DS				
1033	73861	0	97	ref|NP_195565.2|ATPLC1; phospholipase C [Arabidopsis thaliana]	PEG				
1034	73676	1.00E-164	100	ref|NP_201532.2|CYP81G1; heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana]	PEG				
1035	74212	0	100	ref|NP_176086.1|heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana]	LL				
1036	74218	0	98	gb|AAG60111.1|AC073178_22cytochrome P450, putative [Arabidopsis thaliana]	CK	DS			
1037	71218	0	91	ref|NP_188021.1|RSH2 (RELA-SPOT HOMOLOG); catalytic [Arabidopsis thaliana]	PP				
1038	73731	0	94	ref|NP_179782.1|CYP96A5; heme binding / iron ion binding / monooxygenase/ oxygen binding	CS				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
				[Arabidopsis thaliana]					
1039	73251	1.00E-98	100	ref|NP_186922.1|electron transporter/ thiol-disulfide exchange intermediate (Arabidopsis thaliana]	CS				
1040	12773	0	100	ref|NP_565903.1|catalytic/ hydrolase [Arabidopsis thaliana]	PEG				
1041	73254	8.00E-50	80	ref|NP_564808.1|unknown protein [Arabidopsis thaliana]	CS				
1042	73255	1.00E-169	100	ref|NP_850995.1|unknown protein [Arabidopsis thaliana]	SP				
1043	73257	6.00E-39	85	gb|AAF01528.1|AC009991_24hypothetical protein [Arabidopsis thaliana]	LN				
1044	11049	0	100	ref|NP_181474.2|catalytic/ hydrolase [Arabidopsis thaliana]	LN				
1045	74231	0	84	ref|NP_190740.1|unknown protein [Arabidopsis thaliana]	CS				
1046	73266	2.00E-89	79	ref|NP_190816.1|unknown protein [Arabidopsis thaliana]	PP				
1047	75823	1.00E-101	70	ref|NP_566967.1|unknown protein [Arabidopsis thaliana]	LL				
1048	11353	1.00 E-155	85	ref|NP_565721.1|ADS2; iron ion binding / oxidoreductase/ stearoyl-CoA 9-desaturase [Arabidopsis thaliana]	LN				
1049	72025	0	95	ref|NP _199995.1|PGM (PHOSPHOGLUCOMUTASE) [Arabidopsis thaliana]	CS				
1050	72037	0	91	ref|NP_195953.1|protein binding [Arabidopsis thaliana]	SS				
1051	72049	0	100	emb|CAA16713.1|cytochrome P450 [Arabidopsis thaliana]	SP				
1052	78213	1.00E-151	93	ref|NP_181836.1|AT-P4H-1; oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors / procollagen-proline 4-dioxygenase [Arabidopsis thaliana]	CS				
1053	72007	0	100	ref|NP_011943.1|Mitochondrially localized type 2C protein phosphatase; expression induced by growth on ethanol and by sustained osmotic stress; possible role in carbon source utilization in low oxygen environments [Saccharomyces cerevisiae]	CK				
1054	72067	1.00E-171	83	ref|NP_011043.1 |Sho1 p [Saccharomyces cerevisiae]	DS				
1055	72008	4.00E-71	100	sp|P40001|YEA8_YEASTHypothetical 14.0 kDa protein in GCN4-WBP1 Intergenic region gb|AAB64485.1| Yel008wp [Saccharomyces cerevisiae]	LL				
1056	72022	1.00E-127	72	ref|NP_564894.1|unknown protein [Arabidopsis thaliana]	CK				
1057	72096	3.00E-64	66	ref|NP_001051798.1|Os03g0831900 [Oryza sativa (japonica cultivar-group)]	CS				
1058	10811	0	96	ref|NP_175947.1|BCDH BETA1 (BRANCHED-CHAIN ALPHA-KETO ACID DECARBOXYLASE E1 BETA SUBUNIT); 3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring) [Arabidopsis thaliana]	LN				
1059	72138	4.00E-	65	ref|NP_180496.1|SAG13; oxidoreductase	CK				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
		89		[Arabidopsis thaliana]					
1060	74261	0	98	ref|NP_566923.1|branched-chain-amino-acid transaminase/ catalytic [Arabidopsis thaliana]	LL				
1061	74264	1.00E-122	100	ref|NP_196452.1|unknown protein [Arabidopsis thaliana]	CS				
1062	74271	0	93	ref|NP_195096.2|unknown protein [Arabidopsis thaliana]	CS				
1063	74272	1.00E-112	90	ref|NP_195409.1 |unknown protein [Arabidopsis thaliana]	SS				
1064	78442	0	91	ref|NP_189231.1|protein phosphatase type 2A regulator [Arabidopsis thaliana]	LL				
1065	76709	0	96	ref|NP_174119.1|carboxy-lyase [Arabidopsis thaliana]	CK				
1066	75002	0	94	ref|NP-566016.1|ATCS; citrate (SI)-synthase [Arabidopsis thaliana]	CS	PP			
1067	78361	0	82	gb|AAL09767.1|AT5g03040/F15A17_70 [Arabidopsis thaliana]	SS				
1068	74238	0	92	ref|NP_850730.1|dihydrodipicotinate synthase [Arabidopsis thaliana]	SS				
1069	78434	0	100	ref|NP_180966.1|permease [Arabidopsis thaliana]	DS				
1070	73932	0	85	ref|NP_173508.1|carbohydrate transporter/ nucleoside transporter/ sugar porter [Arabidopsis thaliana]	SS				
1071	72713	0	97	ref|NP_567914.1|LKR [Arabidopsis thaliana] ref|NP_849486.1| LKR [Arabidopsis thaliana]	SS				
1072	72773	1.00E-149	93	ref|NP_013180.1|Inhibitor of Cdc28-Clb kinase complexes that controls G1/S phase transition, preventing premature S phase and ensuring genomic integrity; phosphorylation targets Sic1p for SCF(CDC4)-dependent turnover; functional homolog of mammalian Kip1 [Saccharomyces cerevisiae]	PP				
1073	72678	0	91	ref|NP_015445.1|B-type cyclin involved in DNA replication during S phase; activates Cdc28p to promote initiation of DNA synthesis; functions in formation of mitotic spindles along with Clb3p and Clb4p; most abundant during late G1 phase [Saccharomyces cerevisiae]	PEG				
1074	72765	0	88	ref|NP-009934.1|Sat4p [Saccharomyces cerevisiae]	PP	PEG			
1075	72730	1.00E-146	92	ref|NP_012214.1|Pcl7p [Saccharomyces cerevisiae]	CS				
1076	72707	5.00E-66	90	ref|NP _011461.1|Erv14p [Saccharomyces cerevisiae]	CK				
1077	72755	1.00E-134	89	ref|NP_116710.1|Rpn12p [Saccharomyces cerevisiae]	PP	PEG			
1078	10610	1.00E-110	89	ref|NP_187123.1|PR4 (PATHOGENESIS-RELATED 4) [Arabidopsis thaliana]	LN				
1079	73953	0	92	ref|NP_850165.1|DNA binding / NAD+ ADP-ribosyltransferase [Arabidopsis thaliana]	LL				
1080	73173	1.00E-113	91	ref|NP_191263.1|ARR9 (RESPONSE REACTOR 4); transcription regulator [Arabidopsis thaliana]	HS				
1081	73979	0	96	sp|O49289|RH29_ARATHPutative DEAD-box ATP-dependent RNA helicase 29 gb|AAC00620.1|Similar ATP-dependent RNA Helicase [Arabidopsis thaliana]	SS	PEG			
1082	73966	0	94	ref|NP_194578.1|HAESA (RECEPTOR-LIKE	LN				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
				PROTEIN KINASE 5); ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana]					
1083	12776	0	100	ref|NP_178421.1|FT1 (FUCOSYLTRANSFERASE 1); fucosyltransferase/ transferase, transferring glycosyl groups [Arabidopsis thaliana]	PP				
1084	72960	0	87	ref|NP_190906.1|carbohydrate binding / kinase [Arabidopsis thaliana]	PEG				
1085	73021	0	100	ref|NP_243103.1|NADP-dependent glyceraldehyde-3-phosphate dehydrogenase [Bacillus halodurans C-125]	CS	PP	PEG		
1086	73163	0	99	ref|NP_243584.1|glutamate dehydrogenase [Bacillus halodurans C-125]	CS	SS			
1087	73187	0	93	ref|NP_244808.1|1-pyrroline-5-carboxylate dehydrogenase [Bacillus halodurans C-125]	CK				
1088	73188	1.00E-173	100	ref|NP_389366.1|gtutaminase [Bacillus subtilis subsp. subtilis str. 168]	PEG				
1089	73153	1.00E-159	92	ref|NP_415018.1|predicted glutaminase [Escherichia coli K12]	CK				
1090	73983	0	99	ref|ZP_00107721.1|COG0160: 4-aminobutyrate aminotransferase and related aminotransferases [Nostoc punctiforme PCC 73102]	CK				
1091	11516	0	98	ref|NP_564571.1|THFS (10-FORMYLTETRAHYDROFOLATE SYNTHETASE); ATP binding / formate-tetrahydrofolate ligase [Arabidopsis thaliana]	LN				
1092	73179	0	97	ref|NP_387399.1|beta alanine-pyruvate transaminase [Sinorhizobium meliloti 1021]	LL				
1093	73009	0	87	ref|NP_927600.1|glutamine synthetase [Photorhabdus luminescens subsp. laumondii TTO1]	SS				
1094	73109	4.00E-95	100	ref|NP_840275.1|adenine phosphoribosyltransferase [Nitrosomonas europaea ATCC 19718]	PEG				
1095	73121	1.00E-117	94	ref|ZP_00109456.1|COG0120: Ribose 5-phosphate isomerase [Nostoc punctiforme PCC 73102]	PEG				
1096	73157	1.00E-98	100	ref|NP_791813.1|adenine phosphoribosyltransferase [Pseudomonas syringae pv. tomato str. DC3000]	CS				
1097	73158	5.00E-71	93	ref|NP_199951.1|nucleoside diphosphate kinase [Photorhabdus luminescens subsp. laumondii TTO1]	SS				
1098	73088	0	100	ref|NP_ 013311.1|B-type cyclin involved in cell cycle progression; activates Cdc28p to promote the G2/M transition; may be involved in DNA replication and spindle assembly; accumulates during S phase and G2, then targeted for ubiquitin-mediated degradation [Saccharomyces cerevisiae]	DS				
1099	73135	0	91	ref|NP_011846.1|Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein co-localizes with clathrin-coated vesicles [Saccharomyces cerevisiae]	PP				
1100	73005	2.00E-63	90	ref|NP_014508.1|Hrt1p [Saccharomyces cerevisiae]	CS				
1101	73171	0	87	ref|NP_015262.1|Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex); may promote binding of incoming precursor proteins to the intermembrane space domain of Tom22p during translocation [Saccharomyces cerevisiae]	CK				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
1102	73042	0	88	ref|NP_014450.1|Pop2p [Saccharomyces cerevisiae]	SS				
1103	73067	0	100	ref|NP_010301.1|Probable membrane protein with three predicted transmembrane domains; homologous to Ybr042cp, similar to C. elegans F55A11.5 and maize 1-acyl-glycerol-3-phosphate acyltransferase; null exhibits no apparent phenotype [Saccharomyces cerevisiae]	CS				
1104	73148	0	100	emb|CAA56013.1|A-509 protein [Saccharomyces cerevisiae]	CS				
1105	72933	0	94	ref|NP_010632.1|Hxt3p [Saccharomyces cerevisiae]	LN				
1106	77723	0	90	ref|NP_012321.1|Hxt8p [Saccharomyces cerevisiae]	CK	CS			
1107	73048	0	93	ref|NP_010331.1|Amino acid permease involved in the uptake of cysteine, leucine, isoleucine and valine [Saccharomyces cerevisiae]	CS				
1108	10616	0	100	ref|NP_194906.1|MGD1 (MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE 1); 1,2-diacylglycerol 3-beta-galactosyltransferase [Arabidopsis thaliana]	LN				
1109	72923	0	98	ref|NP_116600.1|Agp3p [Saccharomyces cerevisiae]	SP				
1110	78501	0	100	gb|AAD32292.1|putative protein kinase [Arabidopsis thaliana]	SP				
1111	78371	0	94	gb|AAF27112.1|AC011809_21 Putative protein kinase [Arabidopsis thaliana]	LL				
1112	74332	1.00E-174	95	ref|NP_ 178581.1|ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	LL				
1113	74738	0	94	ref|NP_850311.1|ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	SS	LN			
1114	75225	0	100	ref|NP_849998.1|ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	CS				
1115	11149	1.00E-110	91	ref|NP_568067.1|FK506 binding / peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana]	DS				
1116	74739	0	87	ref|NP_564844.1|ATP binding / protein kinase [Arabidopsis thaliana]	CS				
1117	74748	1.00E-172	92	ref|NP_179308.1|ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	LL				
1118	78113	0	100	ref|NP_198610.1|oxidoreductase/zinc ion binding [Arabidopsis thaliana]	PEG				
1119	75233	0	96	ref|NP _851257.1|oxidoreductase/ zinc ion binding [Arabidopsis thaliana]	CS				
1120	77311	0	83	ref|NP_850553.1|ATP binding / nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	LN				
1121	77008	0	89	ref|NP_177460.2|ATP binding / ATP-dependent peptidase/ nucleoside-triphosphatase/ nucleotide binding / serine-type endopeptidase [Arabidopsis thaliana]	CS				
1122	77321	0	98	ref|NP_565299.1|ATP binding / ATP-dependent helicase/ DNA binding / nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	CS				
1123	76214	0	100	ref|NP _564533.1|unknown protein [Arabidopsis thaliana]	DS				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
1124	75238	0	96	ref|NP_566361.1|disulfide oxidoreductase/ oxidoreductase [Arabidopsis thaliana]	PEG				
1125	76118	0	92	ref|NP_568125.1|disulfide oxidoreductase/ oxidoreductase [Arabidopsis thaliana]	PP	HS			
1126	75243	0	91	ref|NP_567074.2|ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	CS				
1127	72602	0	91	ref|NP_178198.1|NRAMP1; manganese ion transporter/ metal ion transporter [Arabidopsis thaliana]	LN				
1128	75810	0	100	gb|ABG54332.1|double HA-tagged mitogen activated protein kinase 5 [synthetic construct]	SS				
1129	75094	0	89	ref|NP_199951.1|unknown protein [Arabidopsis thaliana]	CS				
1130	75818	1.00E-150	91	ref|NP_566411.2|unknown protein [Arabidopsis thaliana]	CS				
1131	75248	0	88	ref|NP_568685.1|RNA binding / nucleic acid binding [Arabidopsis thaliana]	LL				
1132	74605	6.00E-60	86	ref|NP_200911.1|RNA binding / nucleic acid binding [Arabidopsis thaliana]	LL				
1133	75252	0	97	ref|NP_567801.1|NADH dehydrogenase/ disulfide oxidoreductase [Arabidopsis thaliana]	LL				
1134	10620	2.00E-56	77	ref|NP_175633.1|unknown protein [Arabidopsis thaliana]	LN				
1135	74611	4.00E-57	63	ref|NP_683304.1|unknown protein [Arabidopsis thaliana]	LL	LN			
1136	11152	0	91	ref|NP _199220.1|CAD1 (CADMIUM SENSITIVE 1) [Arabidopsis thaliana]	LL				
1137	76610	0	100	ref|NP_199951.1|ATRPAC43; DNA binding / DNA-directed RNA polymerase [Arabidopsis thaliana]	CS				
1138	70243	1.00E-107	100	ref|NP_177128.1|ATHVA22C [Arabidopsis thaliana]	SS				
1139	74371	1.00E-170	100	ref|NP_199951.1|strictosidine synthase [Arabidopsis thaliana]	LN				
1140	74373	1.00E-100	93	ref|NP_ 177712.1|ATROP4 (RHO-LIKE GTP BINDING PROTEIN 4); GTP binding [Arabidopsis thaliana]	CS	SS	LN		
1141	74615	1.00E-177	87	ref|NP_565394.1|nickel ion transporter [Arabidopsis thaliana]	SS				
1142	74620	6.00E-77	100	ref|NP_188045.1|unknown protein [Arabidopsis thaliana]	LN				
1143	74626	5.00E-93	88	ref|NP_566635.1|unknown protein [Arabidopsis thaliana]	LL				
1144	10622	1.00E-147	100	ref|NP_001031481.1|UREG; metal ion binding / nickel ion binding / nucleotide binding [Arabidopsis thaliana]	LN				
1145	74636	2.00E-89	94	gb|AAO19647.1|CAXIP1 protein [Arabidopsis thaliana]	LL				
1146	74656	1.00E-107	93	ref|NP_195699.1|GTP binding [Arabidopsis thaliana]	CS				
1147	74658	1.00E-115	100	ref|NP_ 195709.1|ATGB3 (GTP-BINDING PROTEIN 3); GTP binding [Arabidopsis thaliana]	HS				
1148	74659	4.00E-	88	ref|NP_568121.1|ATRAB ALPHA; GTP binding	CS				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
		99		[Arabidopsis thaliana]					
1149	74673	0	92	gb|AAL24269.1|AT5g51550/K17N15_10 [Arabidopsis thaliana]	SS				
1150	13518	0	94	ref|NP _191100.1|ATP binding / methionine-tRNA ligase/ tRNA ligase [Arabidopsis thaliana]	DS				
1150	70824	0	94	ref|NP_191100.1|ATP binding / methionine-tRNA ligase/ tRNA ligase [Arabidopsis thaliana]	CK				
1151	75267	0	90	ref|NP_200758.1|unknown protein [Arabidopsis thaliana]	LL				
1152	75283	0	93	ref|NP_199951.1 |unknown protein [Arabidopsis thaliana]	LN				
1153	13805	0	94	ref|NP_186764.1|PTB (POLYPYRIMIDINE TRACT-BINDING); RNA binding / nucleic acid binding [Arabidopsis thaliana]	LN				
1154	76221	0	97	ref|NP_187191.2|carbohydrate transporter/ sugar porter [Arabidopsis thaliana]	SP	PP			
1155	76226	0	93	ref|NP_ 187247.1|carbohydrate transporter/ sugar porter [Arabidopsis thaliana]	DS				
1156	76222	0	95	ref|NP_188627.1|STP4 (SUGAR TRANSPORTER); carbohydrate transporter/ sugar porter [Arabidopsis thaliana]	LL				
1157	76611	0	97	ref|NP_190157.2|transporter [Arabidopsis thaliana]	LL				
1158	76228	0	92	ref|NP_ 197718.1|carbohydrate transporter/ sugar porter [Arabidopsis thaliana]	LL				
1159	76435	0	93	ref|NP_ 175449.1|carbohydrate transporter/ sugar porter [Arabidopsis thaliana]	LL				
1160	76436	0	91	ref|NP_ 178054.1|carbohydrate transporter/ sugar porter [Arabidopsis thaliana]	DS				
1161	78743	0	90	ref|NP_179438.1|carbohydrate transporter/ sugar porter [Arabidopsis thaliana]	LN				
1162	75814	0	91	ref|NP_201166.1|HEN3 (HUA ENHANCER 3); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	CS	PP			
1163	77016	0	93	ref|NP_195802.1|ATSR1 (SERINE/THREONINE PROTEIN KINASE 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	CS				
1164	78734	0	98	ref|NP_199394.1|CIPK20 (CBL-INTERACTING PROTEIN KINASE 20); kinase [Arabidopsis thaliana]	PEG				
1165	75274	0	100	ref|NP_200709.2|ATP binding / protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	CS				
1166	76233	0	89	ref|NP_197154.2|ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	SP				
1167	74674	0	100	ref|NP_191331.2|ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	PEG				
1168	70225	0	94	ref|NP_187668.1|CYP77A6; heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana]	CS				
1169	75291	0	98	ref|NP_201303.1|unknown protein [Arabidopsis thaliana] dbj|BAA97310.1| unnamed protein product	CS				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
				[Arabidopsis thaliana]					
1170	75292	0	91	gb|AAL57662.1|At1g72120/F28P5_2 [Arabidopsis thaliana]	SS				
1171	78607	0	96	gb|AAC39370.1|trehalose-6-phosphate phosphatase [Arabidopsis thaliana]	LN				
1172	78367	1.00E-172	100	rei|NP_186907.1|STE1 (STEROL 1); C-5 sterol desaturase [Arabidopsis thaliana]	CK	DS			
1173	76528	1.00E-165	93	gb|AAM64961.1|putative C-4 sterol methyl oxidase [Arabidopsis thaliana]	DS	LL			
1174	77319	0	77	ref|NP_568416.1|protein binding [Arabidopsis thaliana]	CS				
1175	74677	2.00E-73	87	gb|AAM67086.1|unknown [Arabidopsis thaliana]	SS				
1176	78109	1.00E-149	87	ref|NP_182332.1|PAC (PALE CRESS) [Arabidopsis thaliana]	CS				
1177	77725	0	100	ref|NP_391274.1|glyceraldehyde-3-phosphate dehydrogenase [Bacillus subtilis subsp. subtilis str. 168]	HS				
1178	73437	0	99	ref|YP_517842.1|glyceraldehyde 3-phosphate dehydrogenase [Desulfitobacterium hafniense Y51]	SS				
1179	73450	0	100	ref|YP_350062.1|hypothetical protein Pfl_4334 [Pseudomonas fluorescens PfO-1]	CS				
1180	73416	0	100	ref|NP_443010.1|glucose-1-phosphate adenylyltransferase [Synechocystis sp. PCC 6803]	HS				
1181	73452	0	97	ref|NP_388496.1|sorbitol dehydrogenase [Bacillus subtilis subsp. subtilis str. 168]	SS	LN			
1182	73453	0	95	ref|NP_414890.1|alcohol dehydrogenase class III/glutathione-dependent formaldehyde dehydrogenase [Escherichia coli K12]	CK				
1183	73454	0	95	ref|ZP_00110545.1|COG0837: Glucokinase [Nostoc punctiforme PCC 73102]	PP	SS			
1184	73491	0	91	ref|NP_791383.1|alcohol dehydrogenase, class III [Pseudomonas syringae pv. tomato str. DC3000]	CS				
1185	73445	1.00E-176	83	ref|ZP_00709024.1|COG0473: Isocitrate/isopropylmalate dehydrogenase [Escherichia coli B171]	SP				
1186	73469	1.00E-131	65	ref|YP_958498.1|Alcohol dehydrogenase GroES domain protein [Marinobacter aquaeolei VT8]	CS				
1187	73434	0	94	ref|NP_012342.1|Putative protein of unknown function, predicted to encode a triose phosphate transporter subfamily member based on phylogenetic analysis; similar to YOR307C/SLY41; deletion mutant has a respiratory growth defect [Saccharomyces cerevisiae]	CS				
1188	73471	0	93	ref|NP_391658.1|pyrrotine-5 carboxylate dehydrogenase [Bacillus subtilis subsp. subtilis str. 168]	CS				
1189	73436	0	91	ref|YP_355035.1|Aldehyde dehydrogenase family protein [Rhodobacter sphaeroides 2.4.1]	SP	SS			
1190	73525	0	95	ref|NP_790108.1|succinate-semialdehyde dehydrogenase [Pseudomonas syringae pv. tomato str. DC3000]	PP				
1191	73514	1.00E-174	100	ref|NP_242723.1|fructokinase [Bacillus halodurans C-125] dbj|BAB05576.1| fructokinase [Bacillus	SP				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
				halodurans C-125]					
1192	73551	1.00E-171	95	ref|YP_690914.1|6-phosphofructokinase | [Shigella flexneri 5 str. 8401]	LL				
1193	73519	0	95	ref|NP_414696.1|glutamate-1-semialdehyde aminotransferase [Escherichia coli K12]	CS				
1194	73543	0	99	ref|NP_389628.1|glutamine synthetase [Bacillus subtilis subsp. subtilis str. 168]	CS				
1195	73567	1.00E-159	92	ref|NP_415018.1 |predicted glutaminase [Escherichia coli K12]	CS	DS			
1196	73579	0	96	ref|NP_792487.1|succinate-semialdehyde dehydrogenase [Pseudomonas syringae pv. tomato str. DC3000]	PP				
1197	73556	0	97	ref|NP_790150.1|succinate-semialdehyde dehydrogenase [Pseudomonas syringae pv. tomato str. DC3000]	SP				
1198	73545	0	99	ref|NP_792858.1|aldehyde dehydrogenase family protein [Pseudomonas syringae pv. tomato str. DC3000]	PEG				
1199	73511	1.00E-161	66	ref|YP_546017.1|Phosphopyruvate hydratase [Methylobacillus flagellatus KT]	LL				
1200	74138	0	97	ref|NP_415933.1|aldehyde dehydrogenase A, NAD-linked [Escherichia coli K12]	PEG				
1201	74186	0	100	ref|NP_416275.1 |glutamate dehydrogenase [Escherichia coli K12]	CS				
1202	74163	0	95	ref|NP_391649.1|hypothetical protein BSU37690 [Bacillus subtilis subsp. subtilis str. 168]	PP				
1203	74175	0	96	ref|NP_244424.1|phosphoglyceromutase [Bacillus halodurans C-125]	LN				
1204	74176	0	99	ref|YP_517842.1|glyceraldehyde 3-phosphate dehydrogenase [Desulfitobacterium hafniense Y51]	LN				
1205	74141	0	99	ref|YP_543116.1|2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Escherichia coli UTI89]	LN				
1206	74178	0	98	ref|NP_387154.1|dihydrolipoamide dehydrogenase [Sinorhizobium meliloti 1021]	LN				
1207	74179	0	83	ref|NP_441936.1|dihydrolipoamide acetyltransferase [Synechocystis sp. PCC 6803]	CS				
1208	74110	0	92	ref|NP_ 930835.1|pyruvate dehydrogenase E1 component [Photorhabdus luminescens subsp. laumondii TTO1]	SP				
1209	74170	0	98	ref|ZP_00106110.1|COG0021: Transketolase [Nostoc punctiforme PCC 73102]	CS				
1210	74123	1.00E-174	100	ref|NP_014585.1|Gpm3p [Saccharomyces cerevisiae]	LL				
1211	74159	1.00E-71	88	ref|NP_440036.1|hypothetical protein slr0250 [Synechocystis sp. PCC 6803]	PP				
1212	10633	1.00E-150	81	ref|NP_850491.1|CA1 (CARBONIC ANHYDRASE 1); carbonate dehydratase/ zinc ion binding [Arabidopsis thaliana]	LN				
1213	74172	2.00E-62	99	ref|NP_440674.1|cytochrome c553 [Synechocystis sp. PCC 6803]	SS				
1214	74184	7.00E-47	98	ref|NP_440475.1|hypothetical protein ssr1698 [Synechocystis sp. PCC 6803]	CS	PP	SS		

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
1215	74582	1.00E-164	99	ref|NP-440558.1|aspartoacylase [Synechocystis sp. PCC 6803]	CS				
1216	74584	0	99	ref|NP-009780.1|E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily-conserved multi-protein complex found in mitochondria [Saccharomyces cerevisiae]	CS				
1217	74687	1.00E-142	99	ref|NP_385544.1|PROBABLE TRIOSEPHOSPHATE ISOMERASE PROTEIN [Sinorhizobium meliloti 1021]	LL				
1218	74461	3.00E-70	99	ref|NP_638210.1|hypothetical protein XCC2862 [Xanthomonas campestris pv. campestris str. ATCC 33913]	SS				
1219	74403	0	98	ref|NP_356568.1|glucose-1-phosphate adenylyltransferase [Agrobacterium tumefaciens str. C58]	LL				
1220	74430	1.00E-178	99	ref|NP_289016.1|transaldolase [Escherichia coli O157:H7 EDL933]	SS				
1221	74443	0	97	ref|NP_391271.1|phosphoglyceromutase [Bacillus subtilis subsp. subtilis str. 168]	LL				
1222	74457	0	100	ref|YP_350062.1| hypothetical protein Pfl_4334 [Pseudomonas fluorescens PfO-1]	LL				
1223	74434	0	99	ref|NP_790208.1|glutamine synthetase, type I [Pseudomonas syringae pv. tomato str. DC3000]	CS				
1224	74447	0	91	ref|NP_385430.1|PUTATIVE AMINOTRANSFERASE PROTEIN [Sinorhizobium meliloti 1021]	LN				
1225	74495	0	94	ref|NP_386611.1|PUTATIVE ALDEHYDE DEHYDROGENASE PROTEIN [Sinorhizobium meliloti 1021]	PEG				
1226	74513	1.00E-115	87	ref|YP_052359.1|triosephosphate isomerase [Erwinia carotovora subsp. atroseptica SCRI1043]	LL				
1227	74514	0	100	ref|NP_242374.1|asparagine synthetase [Bacillus halodurans C-125]	PEG				
1228	74515	0	98	ref|YP-350541.1|glucose-6-phosphate isomerase [Pseudomonas fluorescens PfO-1]	CS	LL			
1229	74552	0	98	ref|NP_390871.1|pullulanase [Bacillus subtilis subsp. subtilis str. 168]	PEG				
1230	74529	0	96	ref|NP_418330.1|formate dehydrogenase-O, large subunit [Escherichia coli K12]	CS				
1231	74519	0	86	ref|NP_931552.1|glucose-6-phosphate isomerase [Photorhabdus luminescens subsp. laumondii TTO1]	CS				
1232	10638	1.00E-70	58	ref|NP_189273.1|ARRZ-1A; RNA binding / nucleotide binding [Arabidopsis thaliana]	LN				
1233	76547	5.00E-89	89	ref|NP_190024.1|unknown protein [Arabidopsis thaliana]	PP				
1234	76548	0	94	ref|NP_190153.1|ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	SS				
1235	14703	1.00E-56	87	gb|ABK28584.1|unknown [Arabidopsis thaliana]	LN				
1236	75856	8.00E-18	42	ref|NP_190667.2|unknown protein [Arabidopsis thaliana]	CS				
1237	76642	0	92	ref|NP_563988.1|metal ion transporter [Arabidopsis thaliana]	LL				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
1238	77522	0	83	ref|NP_190912.1|unknown protein [Arabidopsis thaliana]	CK				
1239	77516	0	90	ref|NP_191095.1|unknown protein [Arabidopsis thaliana]	CS				
1240	75864	3.00E-63	100	ref|NP_191376.1|ATBS14A; protein transporter [Arabidopsis thaliana]	LL				
1241	76275	1.00E-157	84	ref|NP_191386.1|unknown protein [Arabidopsis thaliana]	CS				
1242	76276	0	100	ref|NP_191408.1|phosphoric ester hydrolase [Arabidopsis thaliana]	SP				
1243	75869	1.00E-85	100	ref|NP_192145.1|unknown protein [Arabidopsis thaliana]	DS				
1244	76558	2.00E-77	73	ref|NP_192181.2|unknown protein [Arabidopsis thaliana]	PP				
1245	75876	1.00E-101	100	pdb|1FSI|AChain A, Crystal Structure Of Cyclic Nucleotide Phosphodiesterase Of Appr>p From Arabidopsis Thaliana	HS				
1246	75878	2.00E-82	78	emb|CAA20466.1|putative protein [Arabidopsis thaliana]	CS				
1247	75881	7.00E-91	89	ref|NP_194766.1|protein binding / ubiquitin-protein ligase/ zinc ion binding [Arabidopsis thaliana]	LL				
1248	77525	0	95	ref|NP_195212.1|beta-fructofuranosidase [Arabidopsis thaliana]	CS				
1249	76454	1.00E-176	88	ref|NP_196814.1| unknown protein [Arabidopsis thaliana]	LL				
1250	75895	2.00E-27	78	ref|NP_197316.1|unknown protein [Arabidopsis thaliana]	LL				
1251	78377	1.00E-154	85	ref|NP_197406.1| catalytic [Arabidopsis thaliana]	HS				
1252	75896	7.00E-70	100	ref|NP_197550.1|arsenate reductase (glutaredoxin)/ electron transporter/ thiol-disulfide exchange intermediate [Arabidopsis thaliana]	CS				
1253	77527	0	85	ref|NP_850871.1|unknown protein [Arabidopsis thaliana]	CS				
1254	78984	0	100	ref|NP_198084.1|catalytic [Arabidopsis thaliana]	SS				
1255	77528	0	92	ref|NP_568564.1|unknown protein [Arabidopsis thaliana]	SS				
1256	76752	0	84	ref|NP_199429.1|unknown protein [Arabidopsis thaliana]	LL				
1257	78106	0	100	gb|ABK06440.1|flag-tagged protein kinase domain of putative mitogen-activated protein kinase kinase kinase [synthetic construct]	SS				
1258	11720	0	89	ref|NP _565622.1|RCY1; cyclin-dependent protein kinase regulator [Arabidopsis thaliana]	LN				
1259	78740	1.00E-121	75	ref|NP_200152.1|unknown protein [Arabidopsis thaliana]	PP				
1260	76157	1.00E-154	88	ref|NP_001032094.1|carrier/ steroid binding [Arabidopsis thaliana]	LN				
1261	77530	0	83	ref|NP_201241.1|heat shock protein binding / unfolded protein binding [Arabidopsis thaliana]	SP	CS			
1262	76755	0	87	gb|AAM14093.1|putative bystin [Arabidopsis thaliana]	PEG				
1263	76166	4.00E-	82	ref|NP_171940.1|RIC3 (ROP-INTERACTIVE CRIB	PEG				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
		99		MOTIF-CONTAINING PROTEIN 3) [Arabidopsis thaliana]					
1264	76756	0	90	ref|NP_ 171927.1|ERS2 (ETHYLENE RESPONSE SENSOR 2); receptor [Arabidopsis thaliana]	LN				
1265	78990	0	100	ref|NP_175364.1| oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors [Arabidopsis thaliana]	CS				
1266	78460	9.00E-97	75	ref|NP_175584.1|unknown protein [Arabidopsis thaliana]	LN				
1267	11022	0	95	ref|NP_192078.1|PPOX; protoporphyrinogen oxidase [Arabidopsis thaliana]	LN				
1268	77533	0	96	ref|NP_177399.1|ATP binding / phenylalanine-tRNA ligase [Arabidopsis thaliana]	PEG				
1269	76572	0	100	ref|NP_177988.1|gamma-glutamyl hydrolase [Arabidopsis thaliana]	PEG				
1270	76186	7.00E-48	84	ref|NP_172210.1|unknown protein [Arabidopsis thaliana]	LL				
1271	76190	7.00E-35	63	ref|NP_565499.1|unknown protein [Arabidopsis thaliana]	LL				
1272	77071	1.00E-160	96	ref|NP_565626.1|unknown protein [Arabidopsis thaliana]	SP				
1273	76194	3.00E-94	79	ref|NP_565716.1|unknown protein [Arabidopsis thaliana]	LN				
1274	78112	1.00E-83	91	ref|NP_181610.1|RNA binding / translation initiation factor [Arabidopsis thaliana]	CS				
1275	74802	0	80	gb|AAO17183.1|Orf17 [Photorhabdus luminescens]	SS				
1276	74851	1.00E-163	100	ref|NP_014366.1[Siw14p [Saccharomyces cerevisiae]	CK				
1277	74864	6.00E-61	95	ref|NP_014486.1|Hxt11p [Saccharomyces cerevisiae]	CK				
1278	74805	0	97	ref|NP_ 015359.1|Actin-related protein involved in transcriptional regulation; subunit of the chromatin remodeling Snf/Swi complex [Saccharomyces cerevisiae]	HS				
1279	74842	2.00E-61	65	ref|NP _001044880.1|Os01g0862200 [Oryza sativa (japonica cultivar-group)]	SS	PEG			
1280	78231	0	66	gb|EAY94228.1|hypothetical protein OsI-015461[Oryza sativa (indica cultivar-group)]	LL				
1281	74867	1.00E-154	65	gb|EAZ43471.1|hypothetical protein OsJ_026954 [Oryza sativa (japonica cultivar-group)]	SS				
1282	74820	1.00E-136	48	gb|EAY97430.1|hypothetical protein OsI_018663 [Oryza sativa (indica cultivar-group)]	LN				
1283	74868	1.00E-101	94	ref|NP _001046499.1|Os02g0265400 [Oryza sativa (japonica cultivar-group)]	PP				
1284	74809	1.00E-122	80	gb|EAZ13333.1|hypothetical protein OsJ_003158 [Oryza sativa (japonica cultivar-group)]	LN				
1285	74845	7.00E-43	83	ref|NP_001050930.1|Os03g0685900 [Oryza sativa (japonica cultivar-group)]	CS	PP			
1286	74870	6.00E-91	48	sp|Q5XF85|ATL4J_ARATHRING-H2 finger protein ATL4J precursor emb1CAB43903.1|putative protein [Arabidopsis thaliana]	LN				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
1287	74859	1.00E-109	55	gb|ABD32420.1|Zinc finger, RING-type [Medicago truncatula]	CS				
1288	74985	3.00E-75	94	ref|NP_001045113.1|Os01g0901800 [Oryza sativa (japonica cultivar-group)]	PEG				
1289	74950	1.00E-159	75	gb|EAZ00193.1|hypothetical protein OsI_021425 [Oryza sativa (indica cultivar-group)]	LN				
1290	74962	3.00E-89	91	gb|ABB99414.1|FT-like protein [Hordeum vulgare subsp. vulgare]	CS				
1291	74939	5.00E-42	65	ref|NP_563746.1|transcription factor [Arabidopsis thaliana]	LL				
1292	74928	1.00E-134	87	ref|NP_001044154.1|Os01g0732200 [Oryza sativa (japonica cultivar-group)]	SP	CS			
1293	74905	0	87	ref|NP_927600.1|glutamine synthetase [Photorhabdus luminescens subsp. laumondii TTO1]	SP				
1294	74917	0	99	ref|YP_346085.1|Inositol phosphatase/fructose-1,6-bisphosphatase [Pseudomonas fluorescens PfO-1]	CS				
1295	74989	4.00E-69	89	ref|NP-439999.1|hypothetical protein slr0732 [Synechocystis sp. PCC 6803]	CS				
1296	74990	1.00E-92	95	ref|NP_441647.1|hypothetical protein slr1160 [Synechocystis sp. PCC 6803]	LL				
1297	74955	1.00E-110	99	ref|NP_441787.1|hypothetical protein slr1649 [Synechocystis sp. PCC 6803]	CS	PP			
1298	74932	1.00E-123	83	ref|NP_441624.1|hypothetical protein slr1530 [Synechocystis sp. PCC 6803]	CS				
1299	74944	8.00E-76	99	ref|NP_440928.1|hypothetical protein sll0871 [Synechocystis sp. PCC 6803]	SS				
1300	74968	6.00E-76	99	ref|NP_441307.1|hypothetical protein sll1979 [Synechocystis sp. PCC 6803]	CS				
1301	74957	1.00E-161	100	ref|NP_440540.1|hypothelical protein slr1699 [Synechocystis sp. PCC 6803]	LL				
1302	75374	0	72	ref|NP_001067247.1|Os12g0610500 [Oryza sativa (japonica cultivar-group)]	CK	LN			
1303	75386	1.00E-147	74	emb|CAH67158.1|H0717B12.5 [Oryza sativa (indica cultivar-group)]	CS				
1304	77807	0	85	ref|NP_001044268.1|Os01g0752700 [Oryza sativa (japonica cultivar-group)]	SP				
1305	75388	0	76	gb|EAZ29806.1|hypothetical protein OsJ_013289 [Oryza sativa (japonica cultivar-group)]	SS				
1306	75365	1.00E-82	81	ref|NP_001057701.1|Os06g0498800 [Oryza sativa (japonica cultivar-group)]	DS	LL	LN		
1307	75377	3.00E-81	77	gb|EAZ24403.1|hypothetical protein OsJ_007886 [Oryza sativa (japonica cultivar-group)]	CK				
1308	75354	8.00E-77	82	ref|NP_001062977.1|Os09g0360400 [Oryza sativa (japonica cultivar-group)]	LL				
1309	75331	1.00E-108	84	ref|NP_001061046.1|Os08g0160000 [Oryza sativa (japonica cultivar-group)]	CS				
1310	75343	1.00E-122	59	ref|NP _001053728.1|Os04g0594500 [Oryza sativa (japonica cultivar-group)]	CS	PEG			
1311	77809	1.00E-27	75	ref|NP_001059709.1 |Os07g0498300 [Oryza sativa (japonica cultivar-group)]	LL				
1312	75332	1.00E-119	72	dbj|BAD19345.1|2 coiled coil domains of eukaryotic origin (31.3 kD)-like protein (Oryza sativa (japonica cultivar-group)]	SP				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
1313	75344	1.00E-146	81	gb|EAZ31718.1|hypothetical protein OsJ_015201 [Oryza sativa (japonica cultivar-group)]	PP				
1314	75333	2.00E-78	58	gb|EAZ32939.1|hypothetical protein OsJ_016422 [Oryza sativa (japonica cultivar-group)]	LL				
1315	75393	1.00E-136	79	gb|EAT82167.1|hypothetical protein SNOG_10773 [Phaeosphaeria nodorum SN15]	CS				
1316	75335	2.00E-63	79	ref|NP_001046956.1|Os02g0515600 [Oryza sativa (japonica cultivar-group)]	CS				
1317	75462	1.00E-85	90	dbj|BAD36027.1 |putative calcineurin B subunit [Oryza sativa (japonica cultivar-group)]	CS				
1318	75486	1.00E-139	89	ref|NP_001050137.1|Os03g0355800 [Oryza sativa (japonica cultivar-group)]	HS				
1319	75452	1.00E-61	91	ref|NP_001059781.1|Os07g0516200 [Oryza sativa (japonica cultivar-group)]	CS				
1320	75465	2.00E-82	29	ref|NP_974032.1|unknown protein [Arabidopsis thaliana]	HS				
1321	75489	1.00E-115	73	gb|ABE82748.1|CCT [Medicago truncatula]	PP	LN			
1322	75442	3.00E-51	51	emb|CAG26903.1|ALY protein [Nicotiana benthamiana]	CS				
1323	75466	1.00E-147	84	ref|NP_001052646.1|Os04g0391900 [Oryza sativa (japonica cultivar-group)]	SP	CS			
1324	75479	1.00E-118	87	ref|NP_001044439.1|Os01g0780800 [Oryza sativa (japonica cultivar-group)]	LL				
1325	75481	7.00E-35	87	gb|ABE89387.1|Zinc finger, Tim10/DDP-type [Medicago truncatula]	CS				
1326	78233	0	70	gb|ABE91310.1|F20D23.20 protein - Arabidopsis thaliana-related [Medicago truncatula]	CK	CS			
1327	75539	2.00E-51	79	ref|NP_564405.1|LOL1(LSD ONE LIKE 1) [Arabidopsis thaliana]	LL				
1328	11919	0	91	ref|NP_565195.1| AVP2 [Arabidopsis thaliana]	PP				
1329	75603	1.00E-162	64	ref|NP_001067658.1|Os11g0265200 [Oryza sativa (japonica cultivar-group)]	LN				
1330	75663	7.00E-87	70	gb|AAW57783.1|unknown protein [Oryza sativa (japonica cultivar-group)]	SS				
1331	75616	0	96	ref|NP_194004.1|ATP binding / protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	CK				
1332	75640	1.00E-153	81	ref|NP_001043765.1|Os01g0658700 [Oryza sativa (japonica cultivar-group)]	LL	LN			
1333	75617	4.00E-40	88	ref|NP_001054686.1|Os05g0154900 [Oryza sativa (japonica cultivar-group)]	SS				
1334	75653	0	92	ref|NP_568338.2|TOZ (TORMOZEMBRYO DEFECTIVE); nucleotide binding [Arabidopsis thaliana]	LN				
1335	75665	2.00E-95	77	gb|EAY76352.1|hypothetical protein OsI_004199 [Oryza sativa (indica cultivar-qroup)]	SS				
1336	75618	0	85	ref|NP_178381.2|ATP binding / protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	HS				
1337	78238	0	95	ref|NP_172998.1| nucleotide binding [Arabidopsis thaliana]	DS				
1338	75608	9.00E-	70	gb|EAZ21409.1|hypothetical protein OsJ_004892	LL				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
		72		[Oryza sativa (japonica cultivar-group)]					
1339	75633	6.00E-89	64	ref|NP_001046704.1|Os02g0326000 [Oryza sativa (japonica cultivar-group)]	HS				
1340	75761	5.00E-50	54	ref|NP_174505.1|unknown protein [Arabidopsis thaliana]	PEG				
1341	75785	1.00E-74	53	gb|AAK40310.1|putative methyl-binding domain protein MBD111 [Zea mays]	CS				
1342	75750	2.00E-47	45	ref|NP_001042916.1|Os01g0328500 [Oryza sativa (japonica cultivar-group)]	PEG				
1343	75716	0	96	ref|NP_386374.1|PUTATIVE ALDEHYDE DEHYDROGENASE PROTEIN [Sinorhizobium meliloti 1021]	DS	LN			
1344	78129	0	98	ref|NP_182096.1|unknown protein [Arabidopsis thaliana]	CK				
1345	77539	1.00E-147	88	ref|NP_187983.1|RNA binding / nucleic acid binding [Arabidopsis thaliana]	SP				
1346	77540	0	86	ref|NP_188270.1|calmodulin binding [Arabidopsis thaliana]	LN				
1347	77542	1.00E-170	92	ref|NP_172882.1|unknown protein [Arabidopsis thaliana]	SP				
1348	77543	0	83	ref|NP_189492.1|[ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	LL				
1349	77545	1.00E-141	100	ref|NP_190275.1|unknown protein [Arabidopsis thaliana]	SS				
1350	77550	1.00E-163	81	ref|NP_173191.2|calmodulin binding [Arabidopsis thaliana]	SP				
1351	77552	1.00E-104	89	emb|CAB78029.1|putative protein [Arabidopsis thaliana]	CK				
1352	77556	0	94	ref|NP_173485.1|CYCB2;3; cyclin-dependent protein kinase regulator [Arabidopsis thaliana]	PP	SS			
1353	77559	1.00E-174	78	ref|NP_196341.1 |calmodulin binding [Arabidopsis thaliana]	CS				
1354	77957	1.00E-168	97	ref|NP_196955.1|unknown protein [Arabidopsis thaliana]	CK				
1355	77565	1.00E-138	100	gb|AAO00857.1|putative protein [Arabidopsis thaliana]	DS	LN			
1356	78508	0	97	ref|NP_175058.1|ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	LL	LN			
1357	11748	1.00E-105	88	ref|NP_200037.1|MSBP1 [Arabidopsis thaliana]	LN				
1358	77920	0	89	ref|NP_177325.2|RNA binding / nucleic acid binding [Arabidopsis thaliana]	CS	DS			
1359	77573	0	81	ref|NP_177411.1|calmodulin binding [Arabidopsis thaliana]	LN				
1360	77961	0	94	gb|AAD25685.1|putative membrane transporter [Arabidopsis thaliana]	CS				
1361	77922	0	100	ref|NP_181978.1|unknown protein [Arabidopsis thaliana]	LL				
1362	77337	1.00E-121	93	ref|NP_186871.1|unknown protein [Arabidopsis thaliana]	PEG				
1363	77924	4.00E-	100	ref|NP_566521.1|unknown protein [Arabidopsis	CK				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
		44		thaliana]					
1364	77926	1.00E-136	100	ref|NP_193032.1|catalytic [Arabidopsis thaliana]	SS				
1365	77964	5.00E-91	88	ref|NP_194100.1|unknown protein [Arabidopsis thaliana]	CS				
1366	77346	4.00E-62	100	emb|CAA20568.1|putative protein [Arabidopsis thaliana]	CS				
1367	77350	1.00E-51	88	ref|NP_564175.2|unknown protein [Arabidopsis thaliana]	CS				
1368	77929	0	84	ref|NP_174029.1|unknown protein [Arabidopsis thaliana]	CS				
1369	77586	1.00E-175	100	ref|NP_200984.1|ATIPK2BETA; inositol or phosphatidylinositol kinase [Arabidopsis thaliana]	PEG				
1370	78510	0	93	ref|NP_201011.1|OXA1; protein translocase [Arabidopsis thaliana]	LN				
1371	77930	1.00E-170	92	ref|NP_201115.1|S-adenosylmethionine-dependent methyltransferase [Arabidopsis thaliana]	CS				
1372	77590	1.00E-113	84	ref|NP_172126.1|unknown protein [Arabidopsis thaliana]	SS				
1373	77592	0	97	ref|NP_172535.1| unknown protein [Arabidopsis thaliana]	PEG				
1374	77361	5.00E-99	84	ref|NP_193650.2|protein binding [Arabidopsis thaliana]	CK	SS			
1375	77934	0	91	re|NP_195066.1|unknown protein [Arabidopsis thaliana]	PEG				
1376	77367	2.00E-74	66	ref|NP_196973.1|unknown protein [Arabidopsis thaliana]	CS				
1377	78121	0	100	emb|CAC01785.1|Carboxylesterase-like protein [Arabidopsis thaliana]	LL				
1378	77370	7.00E-70	100	ref|NP_197550.1|arsenate reductase (glutaredoxin)/ electron transporter/ thiol-disulfide exchange intermediate [Arabidopsis thaliana]	CS				
1379	78117	0	96	ref|NP_851079.1|unknown protein [Arabidopsis thaliana]	CS				
1380	77950	1.00E-177	100	ref|NP_180191.1|urate oxidase [Arabidopsis thaliana]	PP				
1381	78905	1.00E-155	75	ref|NP_565809.1|unknown protein [Arabidopsis thaliana]	CK				
1382	75913	2.00E-73	80	ref|NP_001052968.1|Os04g0456700 [Oryza sativa (japonica cultivar-group)]	LL				
1383	75925	0	80	gb|EAY77273.1|hypothetical protein OsI_005120 [Oryza sativa (indica cultivar-group)]	SP				
1384	75974	0	100	ref|NP_488061.1|fructose-1,6-bisphosphatase [Nostoc sp. PCC 7120]	PP				
1385	75903	0	95	ref|NP_385577.1|PUTATIVE NITRITE REDUCTASE PROTEIN [Sinorhizobium meliloti 1021]	SS				
1386	75904	0	97	ref|NP_ 244182.1|succinate-semialdehyde dehydrogenase [Bacillus halodurans C-125] dbj|BAB07035.1|	CS	LN			
1387	75916	0	100	ref|NP_792120.1|nitrate reductase [Pseudomonas syringae pv. tomato str. DC3000]	SP	SS			
1388	75917	0	98	ref|NP_487197.1|phytochrome A, two-component sensor protein [Nostoc sp. PCC 7120]	SS				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
1389	75942	0	100	ref|NP_485391.1|ferredoxin-sulfite reductase [Nostoc sp. PCC 7120]	CS				
1390	75954	0	100	ref|NP_662565.1|pyruvate phosphate dikinase [Chlorobium tepidum TLS] gb|AAM72907.1|	CS				
1391	75943	0	99	ref|NP_442685.1|glutamate dehydrogenase (NADP+) [Synechocystis sp. PCC 6803]	CS	PEG			
1392	75967	0	96	ref|ZP_00768095.1|Aldehyde dehydrogenase [Chloroflexus aurantiacus J-10-fl]	CK	LN			
1393	75932	0	96	ref|ZP_00767023.1|Phosphoglycerate kinase [Chloroflexus aurantiacus J-10-il]	CS	HS			
1394	75956	0	99	ref|NP_ 440375.1|glutamate--ammonia ligase [Synechocystis sp. PCC 6803]	HS				
1395	78135	1.00E-170	85	ref|NP_172800.2|sulfotransferase [Arabidopsis thaliana]	LL				
1396	78612	0	75	ref|NP_188602 .1|unknown protein [Arabidopsis thaliana]	DS				
1397	77969	0	90	ref|NP_188797.1|unknown protein [Arabidopsis thaliana]	PP				
1398	78136	0	93	ref|NP_171739.1|unknown protein [Arabidopsis thaliana]	CS				
1399	77627	6.00E-69	100	ref|NP_190190.1|structural constituent of ribosome [Arabidopsis thaliana]	SS				
1400	78142	4.00E-43	58	ref|NP_192985.1|PEARLI 1 1; lipid binding [Arabidopsis thaliana]	LN				
1401	77973	1.00E-103	92	emb|CAB36513.1|putative protein [Arabidopsis thaliana]	LL				
1402	78141	0	100	ref|NP_ 564112.1|pseudouridylate synthase/ tRNA-pseudouridine synthase [Arabidopsis thaliana]	PEG				
1403	78963	1.00E-102	100	ref|NP_195300.1|unknown protein [Arabidopsis thaliana]	LN				
1404	78153	0	92	emb|CAB93721.1|hypothetical protein [Arabidopsis thaliana]	CS				
1405	78156	1.00E-160	83	ref|NP_564205.1|unknown protein [Arabidopsis thaliana]	LL				
1406	11807	0	83	ref|NP_181291.1|ASP1 (PDE1 SUPPRESSOR 1); DNA binding [Arabidopsis thaliana]	LN				
1407	78528	0	90	ref|NP_177234.1|unknown protein [Arabidopsis thaliana]	LN				
1408	78530	0	100	ref|NP_177212.2|unknown protein [Arabidopsis thaliana]	CK				
1409	78618	0	91	ref|NP_565086.1|unknown protein [Arabidopsis thaliana]	LL				
1410	78919	0	95	gb|AAG52386.1|AC011765_38unknown protein; 120049-117988 [Arabidopsis thaliana]	PP				
1411	77974	1.00E-174	86	gb|AAF68123.1|AC010793_18F20B17.8[Arabidopsis thaliana]	CK				
1412	77630	7.00E-69	100	ref|NP_ _172256.1|RPS15A (RIBOSOMAL PROTEIN S15A); structural constituent of ribosome [Arabidopsis thaliana]	PP				
1413	78921	0	95	ref|NP_565307.1|inositol or phosphatidylinositol kinase/ phosphotransferase, alcohol group as acceptor [Arabidopsis thaliana]	LN				
1414	78620	0	100	gb|AAD03575.1|unknown protein [Arabidopsis	DS				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
				thaliana]					
1415	77975	4.00E-40	100	ref|NP_179905.1|zinc ion binding [Arabidopsis thaliana]	CS				
1416	78536	0	95	ref|NP_180034.1|sarcosine oxidase [Arabidopsis thaliana]	CS				
1417	78537	1.00E-179	79	ref|NP_180187.1 |calmodulin binding [Arabidopsis thaliana]	PEG				
1418	78540	0	100	ref|NP_565908.1|amino acid binding [Arabidopsis thaliana]	SS	LL			
1419	77993	3.00E-86	100	gb|AAF02163.1|AC009853_23unknown protein [Arabidopsis thaliana]	PEG				
1420	78924	0	95	ref|NP_188597.1|catalytic/ iron ion binding [Arabidopsis thaliana]	LL				
1421	78009	5.00E-63	79	ref|NP_188798.2|unknown protein [Arabidopsis thaliana]	LL				
1422	78014	1.00E-136	88	ref|NP_189478.2|unknown protein [Arabidopsis thaliana]	CS				
1423	78015	1.00E-165	96	ref|NP_190352.1|DNA binding [Arabidopsis thaliana]	CS				
1424	78018	1.00E-132	100	ref|NP_563661.1| unknown protein [Arabidopsis thaliana]	PEG				
1425	78021	1.00E-108	93	ref|NP_173266.1| hydrolase [Arabidopsis thaliana]	CK				
1426	78158	5.00E-90	87	emb|CAA16775.1|hypothetical protein [Arabidopsis thaliana]	CK				
1427	78026	1.00E-154	93	ref|NP_564109.1|oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors [Arabidopsis thaliana]	LL				
1428	78028	1.00E-102	80	ref|NP_564130.1|unknown protein [Arabidopsis thaliana] gb|ABD19644.1|	CS				
1429	78032	5.00E-78	91	gb|ABK28138.1|unknown [Arabidopsis thaliana]	PEG				
1430	78388	2.00E-68	100	ref|NP_171877.1|unknown protein [Arabidopsis thaliana]	LL				
1431	78044	1.00E-156	94	gb|AAF99798.1|AC012463_15T2E6.19 [Arabidopsis thaliana]	LL				
1432	78047	5.00E-78	88	ref|NP_175487. 1|unknown protein [Arabidopsis thaliana]	CS				
1433	78055	1.00E-167	95	ref|NP_176410.1|unknown protein [Arabidopsis thaliana]	SS				
1434	78057	1.00E-168	100	ref|NP_ 176835.1|ubiquitin-protein ligase/ zinc ion binding [Arabidopsis thaliana]	CK				
1435	78059	1.00E-167	90	ref|NP_172124.2|iron ion binding / oxidoreductase/ stearoyl-CoA 9-desaturase [Arabidopsis thaliana]	CS				
1436	78553	3.00E-77	92	ref|NP_176998.1|unknown protein [Arabidopsis thaliana]	SS				
1437	78163	1.00E-108	80	gb|AAG52601.1|AC016447_10hypothetical protein; 95246-97368 [Arabidopsis thaliana]	LN				
1438	78060	1.00E-118	100	gb|AAD55282.1|AC008263_13ESTs gb|T04387, gb|R84022 and gb|T42239 come from this gene. [Arabidopsis thaliana]	DS	PEG			

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
1439	78062	1.00E-173	100	ref|NP_177653.1|transporter [Arabidopsis thaliana]	CS	PP			
1440	78065	1 00E-113	100	gb|AAG52095.1|AC012680_6unknown protein: 48924-49705 [Arabidopsis thaliana]	CS	LL			
1441	78590	4.00E-63	100	ref|NP_565623.1|plastoquinol-plastocyanin reductase [Arabidopsis thaliana]	LL				
1442	78177	2.00E-70	72	ref|NP_180909.2|unknown protein [Arabidopsis thaliana]	DS				
1443	78952	1.00E-107	95	ref|NP_565887.1|unknown protein [Arabidopsis thaliana]	LL				
1444	78559	1.00E-155	89	ref|NP_973636.1|unknown protein [Arabidopsis thaliana]	LN				
1445	78169	1.00E-151	100	gb|AAF01548.1|AC009325_18unknown protein [Arabidopsis thaliana]	PP				
1446	78178	1.00E-157	100	ref|NP_187462.1|unknown protein [Arabidopsis thaliana]	CS				
1447	78932	0	75	emb|CAB80914.1|hypothetical protein [Arabidopsis thaliana]	CK				
1448	78185	2.00E-87	100	ref|NP_196768.1|unknown protein [Arabidopsis thaliana]	PEG				
1449	78186	1.00E-99	92	ref|NP_199091.2|unknown protein [Arabidopsis thaliana]	CS				
1450	78572	0	96	ref|NP_171850.1|unknown protein [Arabidopsis thaliana]	LL				
1451	78631	1.00E-98	91	gb|AAD10675.1|Similar to human BC-2 protein, [Arabidopsis thaliana]	LL				
1452	12425	0	93	gb|AAD39650.1|AC007591_15Similar to gb|Z70524 PDR5-like ABC transporter from Spirodela polyrrhiza and is a member of the PF|00005 ABC transporter family. ESTs gb|N97039 and gb|T43169 come from this gene. [Arabidopsis thaliana]	LN				
1453	78938	0	95	ref|NP_175579.1|(4CL1 (4-COUMARATE:COA LIGASE 1): 4-coumarate-CoA ligase [Arabidopsis thaliana]	PP				
1454	78961	1.00E-127	84	ref|NP_564988.1|unknown protein [Arabidopsis thaliana]	LN				
1455	78584	1.00E-117	75	ref|NP_178114.1|unknown protein [Arabidopsis thaliana]	PP				
1456	78589	1.00E-106	90	ref|NP_180437.2|unknown protein [Arabidopsis thaliana]	CS				
1457	78252	0	61	ref|NP_001043638.1|Os01g0628900 [Oryza sativa (japonica cultivar-group)]	LN				
1458	76314	1.00E-134	76	gb|AAR01658.1|putative inositol polyphosphate 5-phosphatase [Oryza sativa (japonica cultivar-group)]	CK				
1459	76326	0	78	ref|NP_001048842.1|Os03g0128700 [Oryza sativa (japonica cultivar-group)]	CK				
1460	76362	1.00E-47	80	gb|AAR87161.1|hypothetical protein [Oryza sativa (japonica cultivar-group)]	PEG				
1461	76340	7.00E-64	92	ref|NP_010440.1|RNA polymerase I subunit A14 [Saccharomyces cerevisiae]	LN				
1462	76377	0	98	ref|NP_199440.1|ATP binding / DNA binding / DNA-dependent ATPase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	CK				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
1463	76319	0	93	ref|NP_850426.1|kinase [Arabidopsis thaliana]	LL	LN			
1464	76343	0	90	ref|NP_173578.2|ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	LN				
1465	76320	1.00E-109	84	ref|NP_001063406.1|Os09g0463600 [Oryza sativa (japonica cultivar-group)]	LL				
1466	76380	0	76	ref|NP_001044432.1|Os01g0779300 [Oryza sativa (japonica cultivar-group)]	LN				
1467	77831	0	80	gb|ABA91110.1|leucine-rich repeat family protein, putative, expressed [Oryza sativa (japonica cultivar-group)]	SS				
1468	76334	8.00E-21	56	ref|NP_190188.1|RNA binding / nucleic acid binding [Arabidopsis thaliana]	LN				
1469	76382	0	78	emb|CAH66974.1|H0714H04.1 [Oryza sativa (indica cultivar-group)]	LN				
1470	76838	3.00E-98	81	gb|EAY84304.1|hypothetical protein OsI_005537 [Oryza sativa (indica cultivar-group)]	LL	LN			
1471	77841	1.00E-102	85	ref|NP_001067006.1|Os12g0557400 [Oryza sativa (japonica cultivar-group)]	LL				
1472	77838	1.00E-134	86	ref|NP_001043004.1|Os01g0356500 [Oryza sativa (japonica cultivar-group)]	SS				
1473	76865	2.00E-79	91	ref|NP_001060126.1|Os07g0585800 [Oryza sativa (japonica cultivar-group)]	SP				
1474	77834	1.00E-166	89	ref|NP_001043134.1|Os01g0501800 [Oryza sativa (japonica cultivar-group)]	PEG				
1475	76823	4.00E-46	100	gb|EAY97498.1|hypothetical protein OsI_018731[Oryza sativa (indica cultivar-group)]	CS				
1476	76836	1.00E-46	65	ref|NP_001049532.1|Os03g0244000 [Oryza sativa (japonica cultivar-group)]	PP				
1477	14133	0	89	pir||G71435hypothetical protein - Arabidopsis thaliana	LN				
1478	76927	5.00E-58	74	gb|EAY75504.1|hypothetical protein OsI_003351 [Oryza sativa (indica cultivar-group)]	LL				
1479	76963	1.00 E-107	90	gb|EAY84610.1|hypothetical protein OsI_005843 [Oryza sativa (indica cultivar-group)]	LN				
1480	76975	3.00E-32	62	ref|NP_001055878.1|Os05g0486200 [Oryza sativa (japonica cultivar-group)]	SS				
1481	76988	4.00E-44	81	ref|NP_001053850.1|Os04g0612900 [Oryza sativa (japonica cultivar-group)] dbj|BAF15764.1|	DS				
1482	76953	7.00E-43	75	sp|Q07764|HVA22_HORVUProtein HVA22 gb|AAA16094.1| A22	CS				
1483	76965	3.00E-89	75	gb|EAZ28929.1|hypothetical protein OsJ_012412 [Oryza sativa (japonica cultivar-group)]	SP				
1484	77161	1.00E-123	77	emb|CAH66750.1|H0409D10.8 [Oryza sativa (indica cultivar-group)	CS				
1485	77852	0	87	ref|NP_001064303.1|Os10g0203000 [Oryza sativa (japonica cultivar-group)]	CK				
1486	77151	0	91	ref|NP_001050897.1|Os03g0679700 [Oryza sativa (japonica cultivar-group)]	SS				
1487	77116	1.00E-133	84	gb|EAY87341.1|hypothetical protein OsI_008574 [Oryza sativa (indica cultivar-group)]	SP				
1488	77105	0	81	gb|EAZ26357.1|hypothetical protein OsJ_009840 [Oryza sativa (japonica cultivar-group)]	CK	PP			

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
1489	77129	0	73	dbj|BAD19332.1|putative eukaryotic translation initiation factor 2A [Oryza sativa (japonica cultivar-group)]	CS				
1490	77154	0	98	ref|NP_001056944.1|Os06g0173100 [Oryza sativa (japonica cultivar-group)]	PEG				
1491	77190	0	100	ref|NP_417002.1|bifunctional GMP synthase/glutamine amidotransferase protein [Escherichia coli K12]	LL				
1492	77107	0	100	ref|NP_ 486886.1|bifunctional GMP synthase/glutamine amidotransferase protein [Nostoc sp. PCC 7120]	SP	CS			
1493	77167	1.00E-141	92	gb|AAZ20768.1|branchy [Setaria italica]	PP				
1494	77144	0	100	ref|NP_416789.1|NADH:ubiquinone oxidoreductase, chain C,D [Escherichia coli K12]	CK				
1495	77156	1.00E-132	100	ref|NP_443063.1|bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP pyrophosphatase protein [Synechocystis sp. PCC 6803]	CS				
1496	77168	0	83	ref|NP_001047841.1|Os02g0700600 [Oryza sativa (japonica cultivar-group)]	SP				
1497	77192	7.00E-77	84	dbj|BAD27669.1| |putative actin related protein 2/3 complex, 21 kDa subunit [Oryza sativa (japonica cultivar-group)]	PEG				
1498	77181	8.00E-29	84	ref|NP_001049737.1|Os03g0280400 [Oryza sativa (japonica cultivar-group)]	LL				
1499	77193	1.00E-111	87	ref|NP_001049175.1|Os03g0182700 [Oryza sativa (japonica cultivar-group)]	PP	PEG			
1500	77147	1.00E-124	64	emb|CAE04316.1|OSJNBb0016D16.7 [Oryza sativa (japonica cultivar-group)]	DS	LL			
1501	77853	0	91	ref|NP_418588.1| predicted carbohydrate kinase [Escherichia coli K12]	LN				
1502	77854	4.00E-68	86	ref|NP_001042156.1|Os01g0173000 [Oryza sativa (japonica cultivar-group)]	SS				
1503	77287	1.00E-46	63	ref|NP_001054446.1|Os05g0111200 [Oryza sativa (japonica cultivar-group)]	CS	LL			
1504	77276	2.00E-73	66	ref|NP_001045229.1|Os01g0921600 [Oryza sativa (japonica cultivar-group)]	LN				
1505	77229	1.00E-53	90	gb|AAL67582.1|AC018929_4unknown protein [Oryza sativa]	CS	SS			
1506	77241	1.00E-159	73	ref|NP_001045995.1|Os02g0165100 [Oryza sativa (japonica cultivar-group)]	SS				
1507	77265	1.00E-115	60	gb|EAZ04741.1|hypothetical protein OsI_025973 [Oryza sativa (indica cultivar-group)]	LN				
1508	77233	1.00E-113	96	ref|NP_001043339.1|O501g0559000 [Oryza sativa (japonica cultivar-group)]	CS				
1509	77293	1.00E-102	81	ref|NP_001056330.1|Os05g0564100 [Oryza sativa (japonica cultivar-group)]	PEG				
1510	77473	0	75	ref|NP_001067661.1|Os11g0265600 [Oryza sativa (japonica cultivar-group)]	CK				
1511	76402	0	95	ref|NP_199899.1|ATP binding / protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	CK	PEG			
1512	77428	0	86	dbj|BAC07390.1 |putative NAD synthetase [Oryza	SS				

PEP Seq ID No.	Construct ID	Annotation			Trait				
		E - value	% id	Description					
				sativa (japonica cultivar-group)]					
1513	77429	3.00E-93	73	ref|NP_001044830.1|Os01g0853000 [Oryza sativa (japonica cultivar-group)]	CS				
1514	78277	0	95	ref|NP _192815.1|ATOPT7; oligopeptide transporter [Arabidopsis thaliana]	DS				
1515	11935	0	97	ref|NP_188434.2|nucleotide binding [Arabidopsis thaliana]	SP				
1516	78259	0	93	ref|NP_190717.1|carbohydrate transporter/ nucleoside transporter/ sugar porter [Arabidopsis thaliana]	LN				
1517	12276	0	87	ref|NP_199691.1|protein binding / signal transducer [Arabidopsis thaliana]	CS				
1518	12365	3.00E-66	100	ref|NP _181620.1|FL3-27; cysteine protease inhibitor [Arabidopsis thaliana]	CK				

Trait Enhancement Screens

[0058] DS- Enhancement of drought tolerance identified by a soil drought stress tolerance screen: Drought or water deficit conditions impose mainly osmotic stress on plants. Plants are particularly vulnerable to drought during the flowering stage. The drought condition in the screening process disclosed in Example 1B started from the flowering time and was sustained to the end of harvesting. The present invention provides recombinant DNA that can improve the plant survival rate under such sustained drought condition. Exemplary recombinant DNA for conferring such drought tolerance are identified as such in Table 3. Such recombinant DNA may find particular use in generating transgenic plants that are tolerant to the drought condition imposed during flowering time and in other stages of the plant life cycle. As demonstrated from the model plant screen, in some embodiments of transgenic plants with trait-improving recombinant DNA grown under such sustained drought condition can also have increased total seed weight per plant in addition to the increased survival rate within a transgenic population, providing a higher yield potential as compared to control plants.

[0059] PEG-Enhancement of drought tolerance identified by PEG induced osmotic stress tolerance screen: Various drought levels can be artificially induced by using various concentrations of polyethylene glycol (PEG) to produce different osmotic potentials (Pilon-Smits e.g., (1995) Plant Physiol. 107:125-130). Several physiological characteristics have been reported as being reliable indications for selection of plants possessing drought tolerance. These characteristics include the rate of seed germination and seedling growth. The traits can be assayed relatively easily by measuring the growth rate of seedling in PEG solution. Thus, a PEG-induced osmotic stress tolerance screen is a useful surrogate for drought tolerance screen. As demonstrated from the model plant screen, embodiments of transgenic plants with trait-improving recombinant DNA identified in the PEG-induced osmotic stress tolerance screen can survive better drought conditions providing a higher yield potential as compared to control plants.

[0060] SS-Enhancement of drought tolerance identified by high salinity stress tolerance screen: Three different factors are responsible for salt damages: (1) osmotic effects, (2) disturbances in the mineralization process, and (3) toxic effects caused by the salt ions, *e.g.,* inactivation of enzymes. While the first factor of salt stress results in the wilting of the plants that is similar to drought effect, the ionic aspect of salt stress is clearly distinct from drought. The present invention provides genes that help plants maintain biomass, root growth, and/or plant development in high salinity conditions, which are identified as such in Table 3. Since osmotic effect is one of the major components of salt stress, which is common to the drought stress, trait-improving recombinant DNA identified in a high salinity stress tolerance screen can also provide transgenic crops with enhanced drought tolerance. As demonstrated from the model plant screen, embodiments of transgenic plants with trait-improving recombinant DNA identified in a high salinity stress tolerance screen can survive better drought conditions and/or high salinity conditions providing a higher yield potential as compared to control plants.

[0061] HS-Enhancement of drought tolerance identified by heat stress tolerance screen: Heat and drought stress often occur simultaneously, limiting plant growth. Heat stress can cause the reduction in photosynthesis rate, inhibition of leaf growth and osmotic potential in plants. Thus, genes identified by the present invention as heat stress tolerance conferring genes may also

impart enhanced drought tolerance to plants. As demonstrated from the model plant screen, embodiments of transgenic plants with trait-improving recombinant DNA identified in a heat stress tolerance screen can survive better heat stress conditions and/or drought conditions providing a higher yield potential as compared to control plants.

[0062] CK and CS-Enhancement of tolerance to cold stress: Low temperature may immediately result in mechanical constraints, changes in activities of macromolecules, and reduced osmotic potential. In the present invention, two screening conditions, *i.e.*, cold shock tolerance screen (CK) and cold germination tolerance screen (CS), were set up to look for transgenic plants that display visual growth advantage at lower temperature. In cold germination tolerance screen, the transgenic *Arabidopsis* plants were exposed to a constant temperature of 8°C from planting until day 28 post plating. The trait-improving recombinant DNA identified by such screen are particular useful for the production of transgenic plant that can germinate more robustly in a cold temperature as compared to the wild type plants. In cold shock tolerance screen, the transgenic plants were first grown under the normal growth temperature of 22°C until day 8 post plating, and subsequently were placed under 8°C until day 28 post plating. As demonstrated from the model plant screen, embodiments of transgenic plants with trait-improving recombinant DNA identified in a cold shock stress tolerance screen and/or a cold germination stress tolerance screen can survive better cold conditions providing a higher yield potential as compared to control plants.

[0063] Enhancement of tolerance to multiple stresses: Different kinds of stresses often lead to identical or similar reaction in the plants. Genes that are activated or inactivated as a reaction to stress can either act directly in a way the genetic product reduces a specific stress, or they can act indirectly by activating other specific stress genes. By manipulating the activity of such regulatory genes, *i.e.*, multiple stress tolerance genes, the plant can be enabled to react to different kinds of stresses. For examples, PEP SEQ ED NO: 892 can be used to enhance both salt stress tolerance and cold stress tolerance in plants. Of particular interest, plants transformed with PEP SEQ ID NO: 835 can resist heat stress, salt stress and cold stress. Plants transformed with PEP SEQ ID NO: 835 can also improve growth in early stage and under osmotic stress. In addition to these multiple stress tolerance genes, the stress tolerance conferring genes provided by the present invention may be used in combinations to generate transgenic plants that can resist multiple stress conditions.

[0064] PP-Enhancement of early plant growth and development: It has been known in the art that to minimize the impact of disease on crop profitability, it is important to start the season with healthy and vigorous plants. This means avoiding seed and seedling diseases, leading to increased nutrient uptake and increased yield potential. Traditionally early planting and applying fertilizer are the methods used for promoting early seedling vigor. In early development stage, plant embryos establish only the basic root-shoot axis, a cotyledon storage organ(s), and stem cell populations, called the root and shoot apical meristems, that continuously generate new organs throughout post-embryonic development. "Early growth and development" used herein encompasses the stages of seed imbibition through the early vegetative phase. The present invention provides genes that are useful to produce transgenic plants that have advantages in one or more processes including, but not limited to, germination, seedling vigor, root growth and root morphology under non-stressed conditions. The transgenic plants starting from a more robust seedling are less susceptible to the fungal and bacterial pathogens that attach germinating seeds and seedling. Furthermore, seedlings with advantage in root growth are more resistant to drought stress due to extensive and deeper root architecture. Therefore, it can be recognized by those skilled in the art that genes conferring the growth advantage in early stages to plants may also be used to generate transgenic plants that are more resistant to various stress conditions due to enhanced early plant development. The present invention provides such exemplary recombinant DNA that confer both the stress tolerance and growth advantages to plants, identified as such in Table 3, *e.g.*, PEP SEQ ID NO: 799 which can improve the plant early growth and development, and impart heat and cold tolerance to plants. As demonstrated from the model plant screen, embodiments of transgenic plants with trait-improving recombinant DNA identified in the early plant development screen can grow better under non-stress conditions and/or stress conditions providing a higher yield potential as compared to control plants.

[0065] SP-Enhancement of late plant growth and development: "Late growth and development" used herein encompasses the stages of leaf development, flower production, and seed maturity. In certain embodiments, transgenic plants produced using genes that confer growth advantages to plants provided by the present invention, identified as such in Table 3, exhibit at least one phenotypic characteristics including, but not limited to, increased rosette radius, increased rosette dry weight, seed dry weight, silique dry weight, and silique length. On one hand, the rosette radius and rosette dry weight are used as the indexes of photosynthesis capacity, and thereby plant source strength and yield potential of a plant. On the other hand, the seed dry weight, silique dry weight and silique length are used as the indexes for plant sink strength, which are considered as the direct determinants of yield. As demonstrated from the model plant screen, embodiments of transgenic plants with trait-improving recombinant DNA identified in the late development screen can grow better and/or have enhanced development during leaf development and seed maturation providing a higher yield potential as compared to control plants.

[0066] LL-Enhancement of tolerance to shade stress identified in a low light screen: The effects of light on plant development are especially prominent at the seedling stage. Under normal light conditions with unobstructed direct light, a plant seeding

develops according to a characteristic photomorphogenic pattern, in which plants have open and expanded cotyledons and short hypocotyls. Then the plant's energy is devoted to cotyledon and leaf development while longitudinal extension growth is minimized. Under low light condition where light quality and intensity are reduced by shading, obstruction or high population density, a seedling displays a shade-avoidance pattern, in which the seedling displays a reduced cotyledon expansion, and hypocotyls extension is greatly increased. As the result, a plant under low light condition increases significantly its stem length at the expanse of leaf, seed or fruit and storage organ development, thereby adversely affecting of yield. The present invention provides recombinant DNA that enable plants to have an attenuated shade avoidance response so that the source of plant can be contributed to reproductive growth efficiently, resulting higher yield as compared to the wild type plants. As demonstrated from the model plant screen, embodiments of transgenic plants with trait-improving recombinant DNA identified in a shade stress tolerance screen can have attenuated shade response under shade conditions providing a higher yield potential as compared to control plants. The transgenic plants generated by the present invention may be suitable for a higher density planting, thereby resulting increased yield per unit area.

LN-Enhancement of tolerance to low nitrogen availability stress

[0067] Nitrogen is a key factor in plant growth and crop yield. The metabolism, growth and development of plants are profoundly affected by their nitrogen supply. Restricted nitrogen supply alters shoot to root ratio, root development, activity of enzymes of primary metabolism and the rate of senescence (death) of older leaves. All field crops have a fundamental dependence on inorganic nitrogenous fertilizer. Since fertilizer is rapidly depleted from most soil types, it must be supplied to growing crops two or three times during the growing season. Enhanced nitrogen use efficiency by plants should enable crops cultivated under low nitrogen availability stress condition resulted from low fertilizer input or poor soil quality.

[0068] According to the present invention, transgenic plants generated using the recombinant nucleotides, which confer enhanced nitrogen use efficiency, identified as such in Table 3, exhibit one or more desirable traits including, but not limited to, increased seedling weight, greener leaves, increased number of rosette leaves, increased or decreased root length. One skilled in the art may recognize that the transgenic plants provided by the present invention with enhanced nitrogen use efficiency may also have altered amino acid or protein compositions, increased yield and/or better seed quality. The transgenic plants of the present invention may be productively cultivated under low nitrogen growth conditions, *i.e.,* nitrogen-poor soils and low nitrogen fertilizer inputs, which would cause the growth of wild type plants to cease or to be so diminished as to make the wild type plants practically useless. The transgenic plants also may be advantageously used to achieve earlier maturing, faster growing, and/or higher yielding crops and/or produce more nutritious foods and animal feedstocks when cultivated using nitrogen non-limiting growth conditions.

[0069] Stacked Traits: The present invention also encompasses transgenic plants with stacked engineered traits, *e.g.,* a crop having an enhanced phenotype resulting from expression of a trait-improving recombinant DNA, in combination with herbicide and/or pest resistance traits. For example, genes of the current invention can be stacked with other traits of agronomic interest, such as a trait providing herbicide resistance, for example a RoundUp Ready® trait, or insect resistance, such as using a gene from *Bacillus thuringensis* to provide resistance against lepidopteran, coliopteran, homopteran, hemiopteran, and other insects. Herbicides for which resistance is useful in a plant include glyphosate herbicides, phosphinothricin herbicides, oxynil herbicides, imidazolinone herbicides, dinitroaniline herbicides, pyridine herbicides, sulfonylurea herbicides, bialaphos herbicides, sulfonamide herbicides and gluphosinate herbicides. To illustrate that the production of transgenic plants with herbicide resistance is a capability of those of ordinary skill in the art, reference is made to U.S. patent application publications 2003/0106096A1 and 2002/0112260A1 and U.S. Patents 5,034,322; 5,776,760, 6,107,549 and 6,376,754, all of which are incorporated herein by reference. To illustrate that the production of transgenic plants with pest resistance is a capability of those of ordinary skill in the art reference is made to U.S. Patents 5,250,515 and 5,880,275 which disclose plants expressing an endotoxin of *Bacillus thuringiensis* bacteria, to U.S. Patent 6,506,599 which discloses control of invertebrates which feed on transgenic plants which express dsRNA for suppressing a target gene in the invertebrate, to U.S. Patent 5,986,175 which discloses the control of viral pests by transgenic plants which express viral replicase, and to U.S. Patent Application Publication 2003/0150017 A1 which discloses control of pests by a transgenic plant which express a dsRNA targeted to suppressing a gene in the pest, all of which are incorporated herein by reference.

[0070] Once one recombinant DNA has been identified as conferring an enhanced trait of interest in transgenic *Arabidopsis* plants, several methods are available for using the sequence of that recombinant DNA and knowledge about the protein it encodes to identify homologs of that sequence from the same plant or different plant species or other organisms, *e.g.,* bacteria and yeast. Thus, in one aspect, the invention provides methods for identifying a homologous gene with a DNA sequence homologous to any of SEQ ID NO: 1 through SEQ ID NO: 759, or a homologous protein with an amino acid sequence homologous to any of SEQ ID NO: 760 through SEQ ID NO: 1518. In another aspect, the present invention provides the protein sequences of identified homologs for a sequence listed as SEQ ID NO: 1519 through SEQ ID NO: 67778. In yet

another aspect, the present invention also includes linking or associating one or more desired traits, or gene function with a homolog sequence provided herein.

[0071] The trait-improving recombinant DNA and methods of using such trait-improving recombinant DNA for generating transgenic plants with enhanced traits provided by the present invention are not limited to any particular plant species. Indeed, the plants according to the present invention may be of any plant species, *i.e.,* may be monocotyledonous or dicotyledonous. Preferably, they will be agricultural useful plants, *i.e.,* plants cultivated by man for purposes of food production or technical, particularly industrial applications. Of particular interest in the present invention are corn and soybean plants. The recombinant DNA constructs optimized for soybean transformation and recombinant DNA constructs optimized for corn transformation are provided by the present invention. Other plants of interest in the present invention for production of transgenic plants having enhanced traits include, without limitation, cotton, canola, wheat, sunflower, sorghum, alfalfa, barley, millet, rice, tobacco, fruit and vegetable crops, and turfgrass.

[0072] In certain embodiments, the present invention contemplates to use an orthologous gene in generating the transgenic plants with similarly enhanced traits as the transgenic *Arabidopsis* counterpart. Enhanced physiological properties in transgenic plants of the present invention may be confirmed in responses to stress conditions, for example in assays using imposed stress conditions to detect enhanced responses to drought stress, nitrogen deficiency, cold growing conditions, or alternatively, under naturally present stress conditions, for example under field conditions. Biomass measures may be made on greenhouse or field grown plants and may include such measurements as plant height, stem diameter, root and shoot dry weights, and, for corn plants, ear length and diameter.

[0073] Trait data on morphological changes may be collected by visual observation during the process of plant regeneration as well as in regenerated plants transferred to soil. Such trait data includes characteristics such as normal plants, bushy plants, taller plants, thicker stalks, narrow leaves, striped leaves, knotted phenotype, chlorosis, albino, anthocyanin production, or altered tassels, ears or roots. Other enhanced traits may be identified by measurements taken under field conditions, such as days to pollen shed, days to silking, leaf extension rate, chlorophyll content, leaf temperature, stand, seedling vigor, internode length, plant height, leaf number, leaf area, tillering, brace roots, stay green, stalk lodging, root lodging, plant health, barreness/prolificacy, green snap, and pest resistance. In addition, trait characteristics of harvested grain may be confirmed, including number of kernels per row on the ear, number of rows of kernels on the ear, kernel abortion, kernel weight, kernel size, kernel density and physical grain quality. To confirm hybrid yield in transgenic corn plants expressing genes of the present invention, it may be desirable to test hybrids over multiple years at multiple locations in a geographical location where maize is conventionally grown, *e.g.,* in Iowa, Illinois or other locations in the midwestern United States, under "normal" field conditions as well as under stress conditions, *e.g.,* under drought or population density stress.
Transgenic plants can be used to provide plant parts according to the invention for regeneration or tissue culture of cells or tissues containing the constructs described herein.
Plant parts for these purposes can include leaves, stems, roots, flowers, tissues, epicotyl, meristems, hypocotyls, cotyledons, pollen, ovaries, cells and protoplasts, or any other portion of the plant which can be used to regenerate additional transgenic plants, cells, protoplasts or tissue culture. Seeds of transgenic plants are provided by this invention can be used to propagate more plants containing the trait-improving recombinant DNA constructs of this invention. These descendants are intended to be included in the scope of this invention if they contain a trait-improving recombinant DNA construct of this invention, whether or not these plants are selfed or crossed with different varieties of plants. The various aspects of the invention are illustrated by means of the following examples. Examples not falling within the scope of the claims are for illustrative purpose.

EXAMPLES

Example 1. Identification of recombinant DNA that confers enhanced trait(s) to plants

A. Plant expression constructs for *Arabidopsis* transformation

[0074] Each gene of interest was amplified from a genomic or cDNA library using primers specific to sequences upstream and downstream of the coding region. Transformation vectors were prepared to constitutively transcribe DNA in either sense orientation (for enhanced
protein expression) or anti-sense orientation (for endogenous gene suppression) under the control of an enhanced *Cauliflower Mosaic Virus* 35S promoter (U.S. patent 5,359,142) directly or indirectly (Moore, e.g., PNAS 95:376-381, 1998; Guyer, e.g., Genetics 149: 633-639, 1998; International patent application NO. PCT/EP98/07577). The transformation vectors also contain

a *bar* gene as a selectable marker for resistance to glufosinate herbicide. The transformation of *Arabidopsis* plants was carried out using the vacuum infiltration method known in the art (Bethtold, e.g., Methods Mol. Biol. 82:259-66, 1998). Seeds harvested from the plants, named as T1 seeds, were subsequently grown in a glufosinate-containing selective medium to select for plants which were actually transformed and which produced T2 transgenic seed.

B. Soil Drought tolerance screen

[0075] This example describes a soil drought tolerance screen to identify *Arabidopsis* plants transformed with recombinant DNA that wilt less rapidly and/or produce higher seed yield when grown in soil under drought conditions

[0076] T2 seeds were sown in flats filled with Metro/Mix® 200 (The Scotts® Company, USA). Humidity domes were added to each flat and flats were assigned locations and placed in climate-controlled growth chambers. Plants were grown under a temperature regime of 22°C at day and 20°C at night, with a photoperiod of 16 hours and average light intensity of 170 $\mu mol/m^2/s$. After the first true leaves appeared, humidity domes were removed. The plants were sprayed with glufosinate herbicide and put back in the growth chamber for 3 additional days. Flats were watered for 1 hour the week following the herbicide treatment. Watering was continued every seven days until the flower bud primordia became apparent, at which time plants were watered for the last time.

[0077] To identify drought tolerant plants, plants were evaluated for wilting response and seed yield. Beginning ten days after the last watering, plants were examined daily until 4 plants/line had wilted. In the next six days, plants were monitored for wilting response. Five drought scores were assigned according to the visual inspection of the phenotypes: 1 for healthy, 2 for dark green, 3 for wilting, 4 severe wilting, and 5 for dead. A score of 3 or higher was considered as wilted.

[0078] At the end of this assay, seed yield measured as seed weight per plant under the drought condition was characterized for the transgenic plants and their controls and analyzed as a quantitative response according to example 1M.

[0079] Two approaches were used for statistical analysis on the wilting response. First, the risk score was analyzed for wilting phenotype and treated as a qualitative response according to the example 1L. Alternatively, the survival analysis was carried out in which the proportions of wilted and non-wilted transgenic and control plants were compared over each of the six days under scoring and an overall log rank test was performed to compare the two survival curves using S-PLUS statistical software (S-PLUS 6, Guide to statistics, Insightful, Seattle, WA, USA). A list of recombinant DNA constructs which improve drought tolerance in transgenic plants is illustrated in Table 4.

Table 4

PEP SEQ ID NO	Construct ID	Nomination ID	Orientation	Drought score		Seed yield		Time to wilting	
				Delta mean	P-value	Delta mean	P-value	Risk score mean	P-value
968	10359	CGPG430	ANTI-SENSE	-0.103	0.104	0.134	0.469	-0.147	1.000
863	10462	CGPG240	ANTI-SENSE	0.133	0.006	-0.101	0.331	0.306	1.000
1115	11149	CGPG587	SENSE	-0.021	0.741	0.277	0.158	-0.105	0.852
769	12040	CGPG1092	SENSE	0.025	0.240	0.227	0.258	0.058	1.000
771	12156	CGPG1136	ANTI-SENSE	-0.009	0.068	0.512	0.045	0.154	0.857
784	12733	CGPG1291	ANTI-SENSE	0.165	0.034	-0.368	0.009	0.209	1.000
760	12792	CGPG1022	ANTI-SENSE	0.070	0.184	0.223	0.077	0.083	1.000
786	13504	CGPG1311	SENSE	-0.055	0.704	0.109	0.445	-0.042	1.000
1150	13518	CGPG620	ANTI-SENSE	0.176	0.023	0.026	0.891	0.160	1.000
807	14271	CGPG1575	ANTI-SENSE	0.163	0.014	-0.144	0.536	-0.186	1.000
822	14827	CGPG1895	ANTI-SENSE	0.171	0.047	0.001	0.995	0.092	1.000

PEP SEQ ID NO	Construct ID	Nomination ID	Orientation	Drought score		Seed yield		Time to wilting	
				Delta mean	P-value	Delta mean	P-value	Risk score mean	P-value
845	16007	CGPG2142	ANTI-SENSE	-0.234	0.127	0.992	0.006	-0.217	1.000
827	16182	CGPG1922	SENSE	0.034	0.424	0.171	0.298	0.127	1.000
854	17003	CGPG2304	SENSE	0.372	0.005	0.083	0.267	0.613	1.000
923	18408	CGPG3612	SENSE	-0.009	0.589	0.494	0.002	0.134	0.941
900	18644	CGPG3236	SENSE	0.016	0.758	0.072	0.432	0.049	0.920
832	19133	CGPG1973	SENSE	0.308	0.019	0.410	0.074	0.192	1.000
885	19166	CGPG2914	SENSE	0.152	0.037	0.370	0.292	0.152	1.000
896	19256	CGPG3137	SENSE	-0.121	0.142	0.168	0.056	-0.087	0.939
927	19328	CGPG3665	SENSE	0.161	0.027	-0.388	0.337	-0.011	1.000
921	19623	CGPG3579	SENSE	0.039	0.689	0.232	0.084	0.051	1.000
966	70632	CGPG4297	SENSE	0.116	0.004	-0.281	0.185	0.080	1.000
918	71115	CGPG351	SENSE	0.240	0.005	-0.793	0.088	0.257	0.936
1054	72067	CGPG5262	SENSE	0.194	0.021	-0.633	0.034	0.138	1.000
1011	72650	CGPG4882	SENSE	0.187	0.032	-1.980	0.088	0.481	1.000
1098	73088	CGPG5729	SENSE	-0.134	0.488	0.027	0.792	0.066	1.000
982	73214	CGPG4432	SENSE	1.524	0.033	/	/	0.484	1.000
1032	73314	CGPG5100	SENSE	0.117	0.018	-1.005	0.082	0.056	1.000
1195	73567	CGPG6509	SENSE	0.216	0.159	0.581	0.020	0.067	0.961
1027	73683	CGPG5062	SENSE	0.275	0.012	-0.547	0.085	0.109	0.946
819	73986	CGPG1837	SENSE	-0.280	0.122	0.214	0.010	-0.152	1.000
1036	74218	CGPG5159	SENSE	0.241	0.006	-0.057	0.670	0.140	0.785
800	74775	CGPG1492	SENSE	0.156	0.105	0.231	0.049	0.122	0.804
1306	75365	CGPG7503	SENSE	0.830	0.001	-3.139	0.047	1.008	1.000
1343	75716	CGPG7881	SENSE	-0.079	0.018	0.040	0.135	0.010	0.852
1243	75869	CGPG6974	SENSE	-0.016	0.708	0.133	0.162	-0.136	0.893
798	76013	CGPG1445	SENSE	0.414	0.021	-0.269	0.297	0.386	1.000
806	76049	CGPG1568	SENSE	0.196	0.025	-0.991	0.033	0.221	1.000
1123	76214	CGPG5930	SENSE	-0.069	0.101	0.158	0.001	-0.157	1.000
1155	76226	CGPG6211	SENSE	0.261	0.019	-1.212	0.007	0.298	1.000
1160	76436	CGPG6233	SENSE	0.412	0.017	-0.566	0.040	0.316	0.837
1173	76528	CGPG6336	SENSE	0.732	0.009	-0.069	0.624	0.898	0.833
1481	76988	CGPG9106	SENSE	0.395	0.021	-0.841	0.026	0.270	1.000
1500	77147	CGPG9201	SENSE	0.493	0.005	-1.475	0.015	0.997	0.909
1355	77565	CGPG7996	SENSE	0.778	0.049	-0.185	0.190	0.170	1.000
891	77909	CGPG3056	SENSE	-0.140	0.118	0.093	0.458	-0.220	0.813
1358	77920	CGPG8023	SENSE	-0.221	0.070	0.232	0.313	-0.159	0.947
1438	78060	CGPG8640	SENSE	0.550	0.008	-2.055	0.013	0.390	0.944
1442	78177	CGPG8677	SENSE	0.029	0.548	0.496	0.007	0.020	1.000
1337	78238	CGPG7813	SENSE	0.250	0.020	-0.915	0.029	0.110	1.000
1514	78277	CGPG9327	SENSE	0.274	0.003	-0.267	0.456	0.064	1.000
1172	78367	CGPG6334	SENSE	0.169	0.037	-0.691	0.039	0.305	0.941
1069	78434	CGPG5473	SENSE	0.327	0.018	-2.055	0.112	0.196	1.000
1396	78612	CGPG8320	SENSE	0.198	0.017	0.374	0.237	-0.020	0.953

PEP SEQ ID NO	Construct ID	Nomination ID	Orientation	Drought score		Seed yield		Time to wilting	
				Delta mean	P-value	Delta mean	P-value	Risk score mean	P-value
1414	78620	CGPG8471	SENSE	0.248	0.030	-0.127	0.108	0.016	1.000
960	78665	CGPG4240	SENSE	0.605	0.035	-2.631	0.047	0.376	1.000

If p<0.05 and delta or risk score mean >0, the transgenic plants showed statistically significant trait enhancement as compared to the reference (p value, of the delta of a quantitative response or of the risk score of a qualitative response, is the probability that the observed difference between the transgenic plants and the reference occur by chance) If p<0.2 and delta or risk score mean >0, the transgenic plants showed a trend of trait enhancement as compared to the reference.

C. Heat stress tolerance screen

[0080] Under high temperatures, *Arabidopsis* seedlings become chlorotic and root growth is inhibited. This example sets forth the heat stress tolerance screen to identify *Arabidopsis* plants transformed with the gene of interest that are more resistant to heat stress based on primarily their seedling weight and root growth under high temperature.
T2 seeds were plated on 1/2 X MS salts, 1/% phytagel, with 10 µg/ml BASTA (7 per plate with 2 control seeds; 9 seeds total per plate). Plates were placed at 4°C for 3 days to stratify seeds. Plates were then incubated at room temperature for 3 hours and then held vertically for 11 additional days at temperature of 34°C at day and 20°C at night. Photoperiod was 16 h. Average light intensity was ~140 µmol/m^2/s. After 14 days of growth, plants were scored for glufosinate resistance, root length, final growth stage, visual color, and seedling fresh weight. A photograph of the whole plate was taken on day 14.

[0081] The seedling weight and root length were analyzed as quantitative responses according to example 1M. The final grow stage at day 14 was scored as success if 50% of the plants had reached 3 rosette leaves and size of leaves are greater than 1mm (Boyes, e.g., (2001) The Plant Cell 13, 1499-1510). The growth stage data was analyzed as a qualitative response according to example 1L. A list of recombinant DNA constructs that improve heat tolerance in transgenic plants illustrated in Table 5.

Table 5

PEP SEQ ID NO	Construct ID	Nomination ID	Orientation	Root length at day 14		Growth stage at day 14		Seedling weight at day 14	
				Delta mean	P-value	Risk score mean	P-value	Delta mean	P-value
763	10174	CGPG105	ANTI-SENSE	0.263	0.011	-0.010	0.930	1.029	0.003
778	14803	CGPG1192	SENSE	0.202	0.011	1.151	0.391	0.828	0.015
835	14909	CGPG2005	ANTI-SENSE	0.394	0.050	0.093	0.553	1.084	0.044
847	17310	CGPG2190	SENSE	0.140	0.039	1.726	0.160	1.100	0.027
920	19619	CGPG3575	SENSE	0.342	0.020	1.537	0.108	1.277	0.000
1018	70822	CGPG499	SENSE	0.402	0.015	0.644	0.180	1.386	0.005
1080	73173	CGPG5596	SENSE	0.686	0.003	1.254	0.054	1.482	0.002
1180	73416	CGPG6388	SENSE	0.184	0.013	0.640	0.454	0.830	0.008
1147	74658	CGPG6174	SENSE	0.298	0.036	1.390	0.166	0.933	0.008
1278	74805	CGPG7327	SENSE	0.441	0.017	0.071	0.080	1.258	0.019
839	75221	CGPG2065	SENSE	0.345	0.049	0.686	0.402	1.294	0.005
1320	75465	CGPG7599	SENSE	0.160	0.030	0.000	0.998	1.010	0.007
1318	75486	CGPG7577	SENSE	0.361	0.024	-0.046	0.172	1.009	0.008
1336	75618	CGPG7801	SENSE	0.364	0.038	0.136	0.664	1.246	0.006
1339	75633	CGPG7826	SENSE	0.325	0.010	0.100	0.609	0.948	0.024
1245	75876	CGPG6996	SENSE	0.186	0.041	-0.162	0.005	0.834	0.032
1393	75932	CGPG8269	SENSE	0.379	0.000	0.377	0.333	0.836	0.008
1394	75956	CGPG8271	SENSE	0.265	0.047	0.751	0.248	1.071	0.011

PEP SEQ ID NO	Construct ID	Nomination ID	Orientation	Root length at day 14		Growth stage at day 14		Seedling weight at day 14	
				Delta mean	P-value	Risk score mean	P-value	Delta mean	P-value
806	76049	CGPG1568	SENSE	0.422	0.035	0.795	0.179	1.058	0.088
1125	76118	CGPG5958	SENSE	0.248	0.032	0.316	0.503	0.921	0.002
1177	77725	CGPG6364	SENSE	0.181	0.029	0.469	0.266	1.059	0.005
1003	78207	CGPG4713	SENSE	0.330	0.039	0.578	0.488	1.079	0.006
1251	78377	CGPG7075	SENSE	0.519	0.004	0.051	0.442	0.908	0.004
962	78970	CGPG4248	SENSE	0.251	0.017	1.680	0.056	1.044	0.007

If $p<0.05$ and delta or risk score mean >0, the transgenic plants showed statistically significant trait enhancement as compared to the reference. If $p<0.2$ and delta or risk score mean >0, the transgenic plants showed a trend of trait enhancement as compared to the reference.

D. Salt stress tolerance screen

[0082] This example sets forth the high salinity stress screen to identify *Arabidopsis* plants transformed with the gene of interest that are tolerant to high levels of salt based on their rate of development, root growth and chlorophyll accumulation under high salt conditions.

[0083] T2 seeds were plated on glufosinate selection plates containing 90 mM NaCl and grown under standard light and temperature conditions. All seedlings used in the experiment were grown at a temperature of 22°C at day and 20°C at night, a 16-hour photoperiod, an average light intensity of approximately 120 umol/m^2. On day 11, plants were measured for primary root length. After 3 more days of growth (day 14), plants were scored for transgenic status, primary root length, growth stage, visual color, and the seedlings were pooled for fresh weight measurement. A photograph of the whole plate was also taken on day 14.

[0084] The seedling weight and root length were analyzed as quantitative responses according to example 1M. The final growth stage at day 14 was scored as success if 50% of the plants reached 3 rosette leaves and size of leaves are greater than 1mm (Boyes, D.C., et al., (2001), The Plant Cell 13, 1499/1510). The growth stage data was analyzed as a qualitative response according to example 1L. A list of recombinant DNA constructs that improve high salinity tolerance in transgenic plants illustrated in Table 6.

Table 6

PEP SEQ ID	Construct ID	Root length at day 11		Root length at day 14		Growth stage at day 14		Seedling weight at day 14	
		Delta mean	P-value	Delta mean	P-value	Delta mean	P-value	Delta mean	P-value
799	10192	0.372	0.009	0.330	0.001	0.915	0.033	0.668	0.005
772	11853	0.141	0.208	0.082	0.241	/	/	0.319	0.025
792	12766	0.317	0.048	0.253	0.112	/	/	0.360	0.006
1031	12772	0.150	0.111	0.178	0.014	/	/	0.223	0.175
761	13673	0.101	0.216	0.174	0.009	0.134	0.521	0.534	0.002
813	14341	0.490	0.012	0.487	0.014	2.561	0.007	1.051	0.025
835	14909	0.406	0.004	0.504	0.001	1.099	0.100	0.802	0.015
849	15627	0.168	0.123	0.208	0.000	0.735	0.500	0.512	0.089
796	15806	0.180	0.003	0.122	0.025	/	/	-0.023	0.780
838	16553	0.229	0.004	0.243	0.016	0.399	0.157	0.552	0.104
854	17003	0.214	0.002	0.174	0.006	0.672	0.060	0.383	0.021
844	17014	0.080	0.200	0.182	0.080	0.912	0.283	0.468	0.022
870	17813	0.385	0.044	0.428	0.038	2.319	0.112	1.246	0.006
882	17930	0.330	0.021	0.224	0.102	0.860	0.133	0.414	0.009

PEP SEQ ID	Construct ID	Root length at day 11		Root length at day 14		Growth stage at day 14		Seedling weight at day 14	
		Delta mean	P-value	Delta mean	P-value	Delta mean	P-value	Delta mean	P-value
922	18381	0.209	0.200	0.191	0.041	0.521	0.192	0.496	0.301
919	18406	0.272	0.077	0.351	0.022	1.292	0.106	0.783	0.046
888	18418	0.203	0.070	0.186	0.014	0.031	0.823	0.086	0.365
883	18442	0.186	0.152	0.205	0.038	0.341	0.307	0.417	0.072
894	18874	0.238	0.058	0.182	0.278	0.854	0.044	0.462	0.026
895	18875	0.299	0.003	0.316	0.009	0.332	0.102	0.569	0.022
928	19312	0.309	0.066	0.293	0.008	0.549	0.025	0.475	0.024
892	19656	0.093	0.126	0.198	0.008	0.054	0.698	0.453	0.031
954	19927	0.454	0.033	0.401	0.018	0.887	0.023	0.499	0.013
946	19966	0.184	0.210	0.345	0.052	0.088	0.490	0.514	0.038
860	70123	0.175	0.019	0.119	0.026	0.367	0.171	0.335	0.026
1138	70243	0.347	0.036	0.386	0.026	0.479	0.331	0.551	0.007
937	70477	0.123	0.093	0.045	0.570	0.682	0.218	0.278	0.008
929	70538	0.455	0.003	0.356	0.006	1.166	0.321	0.598	0.005
963	71250	0.262	0.147	0.299	0.033	0.999	0.124	0.592	0.067
1050	72037	0.336	0.054	0.356	0.004	0.046	0.770	0.564	0.016
1071	72713	0.064	0.675	0.204	0.183	0.520	0.383	0.528	0.030
1093	73009	0.383	0.028	0.323	0.030	2.526	0.076	0.749	0.013
1102	73042	0.278	0.087	0.216	0.031	0.703	0.011	0.360	0.158
1097	73158	0.210	0.259	0.251	0.101	0.655	0.229	0.482	0.009
1086	73163	0.327	0.016	0.422	0.028	1.516	0.357	0.666	0.034
789	73333	0.024	0.728	0.012	0.855	0.380	0.191	0.400	0.032
1189	73436	0.340	0.106	0.315	0.016	3.045	0.086	0.697	0.055
1178	73437	0.232	0.100	0.268	0.030	0.239	0.433	0.157	0.592
1181	73452	-0.026	0.593	0.238	0.029	-0.028	/	0.345	0.274
1183	73454	-0.072	0.456	0.020	0.863	-0.307	0.041	0.337	0.026
1070	73932	0.191	0.068	0.254	0.058	2.253	0.125	0.524	0.006
1081	73979	0.323	0.014	0.241	0.207	1.728	0.066	0.957	0.000
1213	74172	0.235	0.015	0.261	0.024	0.476	0.513	0.276	0.567
1214	74184	0.183	0.139	0.193	0.049	-0.143	0.317	0.308	0.305
899	74233	/	/	/	/	/	/	0.599	0.029
1068	74238	0.129	0.171	0.147	0.030	1.234	0.173	0.492	0.047
1063	74272	0.187	0.339	0.226	0.051	1.278	0.447	0.553	0.040
1140	74373	0.058	0.684	0.102	0.644	1.245	0.465	0.734	0.049
1220	74430	0.286	0.054	0.128	0.086	2.820	0.139	0.500	0.001
1218	74461	0.324	0.001	0.197	0.025	-0.064	0.428	0.457	0.017
1141	74615	0.245	0.042	0.223	0.045	2.483	0.082	0.600	0.035
1149	74673	0.083	0.465	0.160	0.052	-0.241	0.465	0.422	0.012
1175	74677	0.319	0.032	0.317	0.000	2.140	0.155	0.724	0.003
1113	74738	-0.081	0.388	-0.050	0.733	0.471	0.274	0.310	0.018
1275	74802	0.256	0.035	0.251	0.027	1.218	0.019	0.481	0.096
1279	74842	0.091	0.269	0.196	0.001	0.858	0.085	0.410	0.055
1281	74867	0.195	0.125	0.170	0.041	-0.518	0.560	-0.101	0.439
1299	74944	/	/	/	/	/	/	0.499	0.002

PEP SEQ ID	Construct ID	Root length at day 11		Root length at day 14		Growth stage at day 14		Seedling weight at day 14	
		Delta mean	P-value	Delta mean	P-value	Delta mean	P-value	Delta mean	P-value
967	75205	0.195	0.114	0.210	0.085	0.941	0.098	0.458	0.010
1170	75292	-0.056	0.658	-0.086	0.593	1.203	0.180	0.380	0.026
1305	75388	0.263	0.028	0.305	0.006	1.879	0.037	0.655	0.027
1333	75617	0.352	0.044	0.366	0.025	0.878	0.179	0.854	0.010
1330	75663	0.151	0.148	0.147	0.044	/	/	0.251	0.102
1335	75665	0.468	0.009	0.276	0.109	0.302	0.052	0.779	0.001
1128	75810	0.238	0.058	0.230	0.002	1.794	0.286	0.599	0.006
1385	75903	0.198	0.104	0.176	0.049	/	/	0.171	0.401
1387	75916	0.318	0.041	0.360	0.049	0.819	0.245	0.677	0.015
1388	75917	0.391	0.012	0.428	0.006	0.269	0.200	0.861	0.013
1234	76548	0.237	0.051	0.266	0.014	0.385	0.336	0.680	0.049
1480	76975	0.216	0.114	0.198	0.001	-0.162	0.362	0.316	0.061
1486	77151	0.181	0.001	0.235	0.017	0.641	0.099	0.365	0.034
1505	77229	0.265	0.226	0.338	0.088	1.988	0.005	1.093	0.003
1506	77241	0.039	0.795	0.038	0.632	0.903	0.388	0.350	0.038
1374	77361	0.271	0.000	0.232	0.156	0.508	0.273	0.238	0.016
1512	77428	0.355	0.005	0.429	0.012	1.455	0.381	0.800	0.042
1255	77528	0.284	0.126	0.254	0.031	0.608	0.368	0.753	0.087
1349	77545	0.469	0.004	0.324	0.072	0.283	0.300	0.652	0.022
1352	77556	0.068	0.597	0.017	0.884	1.080	0.379	0.320	0.044
1372	77590	0.342	0.026	0.250	0.145	2.393	0.019	0.549	0.039
1399	77627	0.192	0.005	0.146	0.011	-0.147	0.734	0.275	0.025
1467	77831	0.299	0.087	0.332	0.062	3.081	0.079	0.774	0.006
1472	77838	0.301	0.041	0.296	0.005	0.121	0.423	1.151	0.258
1502	77854	0.131	0.183	0.205	0.082	0.341	0.470	0.419	0.036
1364	77926	0.232	0.030	0.219	0.049	2.642	0.061	0.321	0.089
1433	78055	0.244	0.007	0.393	0.011	1.371	0.410	0.634	0.024
1257	78106	0.276	0.017	0.327	0.003	2.062	0.024	0.900	0.001
830	78355	0.295	0.044	0.309	0.005	1.146	0.284	0.549	0.028
1067	78361	0.217	0.032	0.220	0.016	1.351	0.181	0.463	0.057
1418	78540	0.116	0.039	0.166	0.021	1.290	0.473	0.170	0.191
1436	78553	0.236	0.083	0.190	0.016	/	/	0.219	0.253
965	78677	0.126	0.074	0.217	0.005	/	/	0.205	0.068
1254	78984	0.206	0.183	0.283	0.044	/	/	0.575	0.019

If $p<0.05$ and delta or risk score mean >0, the transgenic plants showed statistically significant trait enhancement as compared to the reference. If $p<0.2$ and delta or risk score mean >0, the transgenic plants showed a trend of trait enhancement as compared to the reference.

E. Polyethylene Glycol (PEG) induced osmotic stress tolerance screen

[0085] There are numerous factors, which can influence seed germination and subsequent seedling growth, one being the availability of water. Genes, which can directly affect the success rate of germination and early seedling growth, are potentially useful agronomic traits for improving the germination and growth of crop plants under drought stress. In this assay, PEG was used to induce osmotic stress on germinating transgenic lines of *Arabidopsis thaliana* seeds in order to screen for osmotically resistant seed lines.

[0086] T2 seeds were plated on BASTA selection plates containing 3% PEG and grown under standard light and temperature conditions. Seeds were plated on each plate containing 3% PEG, 1/2 X MS salts, 1% phytagel, and 10 µg/ml glufosinate. Plates were placed at 4°C for 3 days to stratify seeds. On day 11, plants were measured for primary root length. After 3 more days of growth, *i.e.*, at day 14, plants were scored for transgenic status, primary root length, growth stage, visual color, and the seedlings were pooled for fresh weight measurement. A photograph of the whole plate was taken on day 14.

[0087] Seedling weight and root length were analyzed as quantitative responses according to example 1M. The final growth stage at day 14 was scored as success or failure based on whether the plants reached 3 rosette leaves and size of leaves are greater than 1mm. The growth stage data was analyzed as a qualitative response according to example 1L. A list of recombinant DNA constructs that improve osmotic stress tolerance in transgenic plants illustrated in Table 7.

Table 7

PEP SEQ ID	Construct ID	Root length at day 11		Root length at day 14		Growth stage at day 14		Seedling weight at day 14	
		Delta mean	P-value	Delta mean	P-value	Delta mean	P-value	Delta mean	P-value
763	10174	0.193	0.202	0.148	0.120	0.926	0.610	0.228	0.043
1040	12773	0.142	0.020	0.138	0.086	3.109	0.073	0.465	0.020
835	14909	0.167	0.038	0.057	0.383	3.041	0.087	0.411	0.014
850	15409	0.017	0.742	-0.042	0.706	1.533	0.369	0.299	0.014
844	17014	0.164	0.005	0.116	0.074	4.000	0.000	0.287	0.002
850	17201	0.305	0.041	0.290	0.023	2.929	0.112	0.122	0.441
903	18830	0.038	0.553	-0.100	0.008	1.463	0.372	0.427	0.004
826	70401	0.041	0.558	0.025	0.833	3.230	0.052	0.281	0.033
840	70746	/	/	/	/	/	/	0.462	0.003
952	70902	0.268	0.064	0.276	0.021	4.000	0.000	0.510	0.013
955	70976	0.198	0.199	0.159	0.200	/	/	0.477	0.033
971	71839	0.269	0.008	0.185	0.019	1.178	0.506	0.108	0.316
1073	72678	0.373	0.087	0.404	0.027	2.998	0.096	0.188	0.527
1077	72755	0.206	0.089	0.132	0.048	4.000	0.000	0.397	0.136
1074	72765	0.169	0.040	-0.006	0.836	4.000	0.000	0.335	0.008
1084	72960	0.111	0.065	0.197	0.050	3.068	0.081	0.243	0.110
1085	73021	0.364	0.011	0.300	0.018	4.000	0.000	0.758	0.023
1094	73109	0.261	0.045	0.202	0.004	4.000	0.000	0.344	0.027
1095	73121	0.503	0.003	0.508	0.013	4.000	0.000	0.713	0.029
1088	73188	0.298	0.109	0.539	0.048	3.140	0.067	0.860	0.029
1198	73545	0.115	0.037	0.110	0.275	4.000	0.000	0.378	0.023
1034	73676	0.169	0.005	0.130	0.118	4.000	0.000	0.405	0.008
1033	73861	0.055	0.321	0.009	0.777	0.510	0.151	0.203	0.036
1081	73979	0.274	0.063	0.249	0.202	4.000	0.000	0.325	0.017
1200	74138	0.146	0.006	0.141	0.008	2.512	0.233	0.080	0.734
1225	74495	0.091	0.636	0.294	0.028	2.352	0.290	-0.029	0.911
1227	74514	0.181	0.342	0.219	0.232	4.000	0.000	0.441	0.036
1229	74552	0.238	0.100	0.177	0.092	3.055	0.084	0.261	0.005
1167	74674	0.196	0.073	0.289	0.008	2.780	0.150	0.261	0.138
1279	74842	0.012	0.920	-0.027	0.757	4.000	0.000	0.281	0.021
1288	74985	0.401	0.014	0.421	0.036	2.179	0.139	0.756	0.041
1124	75238	0.176	0.226	0.123	0.362	4.000	0.000	0.364	0.040
1310	75343	0.216	0.078	0.465	0.025	1.251	0.464	0.420	0.005
1342	75750	0.161	0.266	0.216	0.094	4.000	0.000	0.281	0.004
1340	75761	0.437	0.006	0.385	0.024	4.000	0.000	0.473	0.023

PEP SEQ ID	Construct ID	Root length at day 11		Root length at day 14		Growth stage at day 14		Seedling weight at day 14	
		Delta mean	P-value	Delta mean	P-value	Delta mean	P-value	Delta mean	P-value
1391	75943	0.316	0.001	0.390	0.025	1.263	0.454	-0.029	0.627
793	76025	0.356	0.074	0.309	0.076	2.832	0.136	0.519	0.019
1263	76166	0.179	0.190	0.003	0.894	0.470	0.590	0.397	0.038
1460	76362	0.153	0.302	0.174	0.385	2.051	0.403	0.746	0.043
1511	76402	0.224	0.153	0.215	0.192	4.000	0.000	0.448	0.006
1269	76572	0.256	0.026	0.289	0.106	2.708	0.171	0.294	0.031
1262	76755	0.245	0.141	0.153	0.143	1.174	0.493	0.299	0.043
1490	77154	0.208	0.114	0.215	0.043	4.000	0.000	0.403	0.060
1497	77192	0.075	0.400	-0.036	0.402	4.000	0.000	0.559	0.009
1499	77193	0.256	0.116	0.207	0.141	3.235	0.052	0.498	0.041
1509	77293	0.424	0.034	0.280	0.106	2.931	0.111	0.609	0.002
1362	77337	0.182	0.077	0.109	0.098	4.000	0.000	0.571	0.032
1268	77533	0.143	0.089	0.146	0.002	1.381	0.404	0.257	0.030
1369	77586	0.227	0.020	0.160	0.138	3.298	0.042	0.723	0.014
1373	77592	/	/	/	/	/	/	0.397	0.014
1474	77834	0.180	0.025	0.211	0.009	/	/	-0.019	0.787
1375	77934	0.179	0.081	0.183	0.327	0.556	0.316	0.349	0.003
1419	77993	0.074	0.395	0.131	0.147	1.394	0.406	0.380	0.004
1424	78018	0.192	0.073	0.135	0.014	0.322	0.626	0.284	0.096
1429	78032	0.142	0.010	0.099	0.050	4.000	0.000	0.266	0.049
1438	78060	0.235	0.207	0.381	0.030	1.696	0.325	0.285	0.327
1118	78113	0.122	0.032	-0.106	0.179	2.732	0.164	0.353	0.002
1402	78141	0.119	0.497	0.152	0.349	2.567	0.215	0.202	0.033
1448	78185	0.283	0.048	0.344	0.079	4.000	0.000	0.513	0.000
1024	78341	0.148	0.031	0.270	0.010	-0.914	0.129	-0.182	0.172
1417	78537	-0.001	0.988	0.191	0.014	1.801	0.499	-0.171	0.287
974	78717	-0.022	0.692	0.106	0.037	1.170	0.497	0.284	0.042
1164	78734	0.145	0.233	0.068	0.620	4.000	0.000	0.375	0.012

If $p<0.05$ and delta or risk score mean >0, the transgenic plants showed statistically significant trait enhancement as compared to the reference.

If $p<0.2$ and delta or risk score mean >0, the transgenic plants showed a trend of trait enhancement as compared to the reference.

F. Cold shock tolerance screen

[0088] This example set forth a screen to identify *Arabidopsis* plants transformed with the genes of interest that are more tolerant to cold stress subjected during day 8 to day 28 after seed planting. During these crucial early stages, seedling growth and leaf area increase were measured to assess tolerance when *Arabidopsis* seedlings were exposed to low temperatures. Using this screen, genetic alterations can be found that enable plants to germinate and grow better than wild type plants under sudden exposure to low temperatures.

[0089] Eleven seedlings from T2 seeds of each transgenic line plus one control line were plated together on a plate containing ½ X Gamborg Salts with 0.8 Phytagel™, 1% Phytagel, and 0.3% Sucrose. Plates were then oriented horizontally and stratified for three days at 4°C. At day three, plates were removed from stratification and exposed to standard conditions (16 hr photoperiod, 22°C at day and 20°C at night) until day 8. At day eight, plates were removed from standard conditions and exposed to cold shock conditions (24 hr photoperiod, 8°C at both day and night) until the final day of the assay, *i.e.*, day 28. Rosette areas were measured at day 8 and day 28, which were analyzed as quantitative responses according to example 1M.

A list of recombinant nucleotides that improve cold shock stress tolerance in plants illustrated in Table 8.

Table 8

PEP SEQ ID	Construct ID	Orientation	Rosette area at day 8		Rosette area at day 28		Rosette area difference	
			Delta mean	P-value	Risk score mean	P-value	Delta mean	P-value
943	10366	ANTI-SENSE	0.361	0.009	0.569	0.038	0.588	0.036
1518	12365	SENSE	-0.114	0.771	0.663	0.009	0.717	0.008
939	12601	SENSE	-0.240	0.390	0.612	0.034	1.531	0.003
781	12714	ANTI-SENSE	0.818	0.064	0.896	0.025	0.901	0.016
850	15409	ANTI-SENSE	0.637	0.157	0.426	0.220	0.615	0.050
851	15903	ANTI-SENSE	-0.276	0.592	0.287	0.041	0.247	0.102
842	15966	ANTI-SENSE	0.140	0.650	0.282	0.015	0.297	0.003
915	18403	SENSE	0.366	0.197	0.729	0.007	0.785	0.004
888	18418	SENSE	-0.236	0.125	0.379	0.023	0.366	0.026
924	18720	SENSE	0.620	0.144	0.740	0.015	0.659	0.014
948	19906	SENSE	0.788	0.005	0.635	0.030	0.560	0.039
860	70123	SENSE	0.556	0.114	0.968	0.067	1.245	0.028
908	70415	SENSE	0.334	0.147	0.763	0.009	0.977	0.023
930	70440	SENSE	-0.175	0.249	0.541	0.049	0.622	0.067
817	70748	ANTI-SENSE	0.503	0.075	0.700	0.048	0.527	0.116
1150	70824	SENSE	-0.134	0.679	0.829	0.002	0.921	0.011
989	71347	SENSE	-0.346	0.381	0.401	0.003	0.412	0.014
1053	72007	SENSE	0.161	0.573	1.180	0.026	1.302	0.042
1056	72022	SENSE	0.976	0.025	1.051	0.001	1.124	0.002
1059	72138	SENSE	0.486	0.009	0.817	0.005	0.669	0.000
994	72469	SENSE	0.335	0.300	0.767	0.025	0.948	0.023
1007	72526	SENSE	0.323	0.223	0.413	0.003	0.505	0.002
1076	72707	SENSE	0.146	0.596	0.396	0.012	0.400	0.074
1089	73153	SENSE	0.728	0.031	0.290	0.044	0.311	0.047
1101	73171	SENSE	0.333	0.336	0.320	0.059	0.378	0.038
1087	73187	SENSE	0.454	0.037	0.492	0.008	0.460	0.003
1182	73453	SENSE	0.672	0.013	0.708	0.010	0.879	0.004
1012	73686	SENSE	0.704	0.040	0.906	0.000	0.888	0.000
1090	73983	SENSE	-0.071	0.867	0.431	0.004	0.286	0.037
1036	74218	SENSE	0.002	0.993	0.294	0.020	0.089	0.625
1276	74851	SENSE	0.626	0.184	0.917	0.074	1.028	0.033
1277	74864	SENSE	0.879	0.041	0.742	0.031	0.752	0.044
1302	75374	SENSE	0.278	0.273	2.374	0.016	2.950	0.013
1307	75377	SENSE	-0.307	0.316	0.085	0.166	0.212	0.009
1331	75616	SENSE	0.399	0.473	0.807	0.022	1.015	0.015
1392	75967	SENSE	0.714	0.027	1.588	0.007	1.793	0.006
1458	76314	SENSE	0.420	0.049	0.787	0.004	0.970	0.002
1459	76326	SENSE	0.232	0.383	0.894	0.018	0.930	0.034
1462	76377	SENSE	0.263	0.137	0.254	0.014	0.227	0.435
1511	76402	SENSE	-0.265	0.435	0.402	0.024	0.490	0.046
1065	76709	SENSE	-0.566	0.063	0.091	0.110	0.250	0.016
1488	77105	SENSE	0.954	0.016	0.817	0.015	0.925	0.011

PEP SEQ ID	Construct ID	Orientation	Rosette area at day 8		Rosette area at day 28		Rosette area difference	
			Delta mean	P-value	Risk score mean	P-value	Delta mean	P-value
1494	77144	SENSE	0.163	0.523	0.946	0.003	0.906	0.000
1374	77361	SENSE	0.595	0.065	1.056	0.006	1.207	0.016
1510	77473	SENSE	-0.048	0.732	0.170	0.019	0.091	0.057
1238	77522	SENSE	0.132	0.616	1.709	0.011	2.008	0.009
1351	77552	SENSE	1.221	0.028	1.687	0.004	1.900	0.004
1106	77723	SENSE	-0.342	0.151	0.100	0.051	0.141	0.037
1485	77852	SENSE	0.236	0.151	0.416	0.197	0.587	0.040
891	77909	SENSE	0.722	0.034	1.330	0.003	1.285	0.010
1363	77924	SENSE	0.547	0.057	0.480	0.017	0.576	0.016
1354	77957	SENSE	0.417	0.256	0.930	0.026	0.827	0.013
1411	77974	SENSE	0.512	0.030	1.175	0.013	1.036	0.013
1425	78021	SENSE	0.391	0.250	0.460	0.005	0.532	0.009
1434	78057	SENSE	0.086	0.766	0.534	0.007	0.588	0.013
1344	78129	SENSE	1.189	0.001	0.613	0.030	0.599	0.111
1426	78158	SENSE	1.261	0.005	0.732	0.001	1.040	0.016
1002	78202	SENSE	0.842	0.004	0.835	0.000	0.865	0.000
1326	78233	SENSE	0.162	0.477	0.771	0.013	0.822	0.007
1172	78367	SENSE	-0.153	0.668	0.522	0.047	0.514	0.068
1408	78530	SENSE	2.039	0.005	2.026	0.002	2.244	0.002
1381	78905	SENSE	0.615	0.181	0.863	0.007	0.925	0.007
1447	78932	SENSE	0.472	0.046	0.626	0.027	0.715	0.030

If p<0.05 and delta or risk score mean >0, the transgenic plants showed statistically significant trait enhancement as compared to the reference (p value, of the delta of a quantitative response or of the risk score of a qualitative response, is the probability that the observed difference between the transgenic plants and the reference occur by chance)

If p<0.2 and delta or risk score mean >0, the transgenic plants showed a trend of trait enhancement as compared to the reference.

G. Cold germination tolerance screen

[0090] This example sets forth a screen to identify *Arabidopsis* plants transformed with the genes of interests are resistant to cold stress based on their rate of development, root growth and chlorophyll accumulation under low temperature conditions.

T2 seeds were plated and all seedlings used in the experiment were grown at 8°C. Seeds were first surface disinfested using chlorine gas and then seeded on assay plates containing an aqueous solution of 1/2 X Gamborg's B/5 Basal Salt Mixture (Sigma/Aldrich Corp., St. Louis, MO, USA G/5788), 1% Phytagel™ (Sigma-Aldrich, P-8169), and 10 ug/ml glufosinate with the final pH adjusted to 5.8 using KOH. Test plates were held vertically for 28 days at a constant temperature of 8°C, a photoperiod of 16 hr, and average light intensity of approximately 100 umol/m^2/s. At 28 days post plating, root length was measured, growth stage was observed, the visual color was assessed, and a whole plate photograph was taken.

[0091] The root length at day 28 was analyzed as a quantitative response according to example 1M. The growth stage at day 7 was analyzed as a qualitative response according to example 1L. A list of recombinant DNA constructs that improve cold stress tolerance in transgenic plants illustrated in Table 9.

Table 9

PEP SEQ ID	Construct ID	Nomination ID	Orientation	Root length at day 28		Growth stage at day 28	
				Delta-mean	P-value	Delta mean	P-value
799	10192	CGPG146	ANTI-SENSE	0.461	0.094	4.000	0.000
1517	12276	CGPG967	ANTI-SENSE	0.203	0.217	4.000	0.000
835	14909	CGPG2005	ANTI-SENSE	0.311	0.005	4.000	0.000

PEP SEQ ID	Construct ID	Nomination ID	Orientation	Root length at day 28		Growth stage at day 28	
				Delta-mean	P-value	Delta mean	P-value
828	15126	CGPG1929	SENSE	0.216	0.016	4.000	0.000
829	15628	CGPG1938	ANTI-SENSE	0.132	0.205	4.000	0.000
846	16208	CGPG2148	SENSE	-0.068	0.734	4.000	0.000
864	17402	CGPG2426	SENSE	0.105	0.581	4.000	0.000
780	18011	CGPG126	SENSE	-0.248	0.184	4.000	0.000
812	18116	CGPG1656	ANTI-SENSE	-0.231	0.358	4.000	0.000
905	18226	CGPG3269	SENSE	0.196	0.313	4.000	0.000
887	18415	CGPG3004	SENSE	-0.024	0.845	4.000	0.000
901	18827	CGPG3248	SENSE	0.023	0.845	4.000	0.000
889	19532	CGPG3030	SENSE	0.332	0.044	4.000	0.000
912	19608	CGPG3400	SENSE	-0.053	0.705	4.000	0.000
892	19656	CGPG3084	SENSE	0.037	0.746	4.000	0.000
951	19746	CGPG4099	SENSE	0.328	0.209	4.000	0.000
940	19747	CGPG3931	SENSE	-0.008	0.938	4.000	0.000
950	19802	CGPG4071	SENSE	0.150	0.602	4.000	0.000
954	19927	CGPG4153	SENSE	/	/	4.000	0.000
1168	70225	CGPG63	SENSE	0.291	0.006	4.000	0.000
816	70240	CGPG177	SENSE	0.033	0.755	4.000	0.000
932	70443	CGPG3724	SENSE	-0.087	0.321	4.000	0.000
831	70560	CGPG1964	SENSE	0.401	0.128	4.000	0.000
818	70807	CGPG182	SENSE	0.200	0.055	4.000	0.000
985	70834	CGPG445	SENSE	-0.300	0.322	4.000	0.000
871	70845	CGPG253	SENSE	0.094	0.290	4.000	0.000
944	70935	CGPG3975	SENSE	-0.087	0.236	4.000	0.000
942	70965	CGPG3964	SENSE	0.318	0.030	4.000	0.000
956	71440	CGPG4169	SENSE	0.046	0.154	4.000	0.000
999	71638	CGPG4691	SENSE	0.362	0.225	4.000	0.000
1049	72025	CGPG5223	SENSE	/	/	4.000	0.000
1057	72096	CGPG5304	SENSE	/	/	4.000	0.000
1005	72457	CGPG4747	SENSE	-0.010	0.907	4.000	0.000
1008	72531	CGPG4779	SENSE	0.062	0.704	4.000	0.000
910	72606	CGPG3361	SENSE	0.133	0.315	4.000	0.000
1075	72730	CGPG5546	SENSE	0.179	0.134	4.000	0.000
1100	73005	CGPG5732	SENSE	/	/	4.000	0.000
1085	73021	CGPG5642	SENSE	0.110	0.531	4.000	0.000
1107	73048	CGPG5797	SENSE	/	/	4.000	0.000
1103	73067	CGPG5771	SENSE	-0.244	0.395	4.000	0.000
1104	73148	CGPG5778	SENSE	0.211	0.260	4.000	0.000
1096	73157	CGPG5715	SENSE	0.168	0.440	4.000	0.000
1086	73163	CGPG5644	SENSE	0.327	0.003	4.000	0.000
884	73207	CGPG2874	SENSE	-0.185	0.626	4.000	0.000
986	73215	CGPG4453	SENSE	0.433	0.010	4.000	0.000
1016	73230	CGPG4949	SENSE	0.273	0.150	4.000	0.000
1039	73251	CGPG5186	SENSE	0.061	0.636	4.000	0.000
1041	73254	CGPG5190	SENSE	0.205	0.018	4.000	0.000
1030	73313	CGPG5097	SENSE	0.638	0.006	3.090	0.077

PEP SEQ ID	Construct ID	Nomination ID	Orientation	Root length at day 28		Growth stage at day 28	
				Delta-mean	P-value	Delta mean	P-value
1187	73434	CGPG6437	SENSE	0.116	0.345	4.000	0.000
1179	73450	CGPG6375	SENSE	0.174	0.250	4.000	0.000
1186	73469	CGPG6432	SENSE	/	/	4.000	0.000
1188	73471	CGPG6445	SENSE	-0.101	0.604	4.000	0.000
1184	73491	CGPG6418	SENSE	0.061	0.230	4.000	0.000
1193	73519	CGPG6505	SENSE	0.118	0.064	4.000	0.000
1194	73543	CGPG6507	SENSE	0.219	0.385	4.000	0.000
1195	73567	CGPG6509	SENSE	0.371	0.101	4.000	0.000
833	73602	CGPG1977	SENSE	-0.037	0.762	4.000	0.000
1006	73639	CGPG4755	SENSE	0.035	0.724	4.000	0.000
865	73707	CGPG2433	SENSE	0.149	0.133	4.000	0.000
1010	73722	CGPG4879	SENSE	0.022	0.763	4.000	0.000
1038	73731	CGPG5161	SENSE	0.050	0.825	3.321	0.039
808	73927	CGPG1619	SENSE	0.083	0.050	4.000	0.000
811	73948	CGPG1651	SENSE	0.203	0.154	4.000	0.000
995	73951	CGPG4660	SENSE	0.220	0.104	4.000	0.000
1209	74170	CGPG6619	SENSE	-0.054	0.750	4.000	0.000
1207	74179	CGPG6596	SENSE	0.258	0.237	4.000	0.000
1214	74184	CGPG6636	SENSE	0.415	0.000	4.000	0.000
1201	74186	CGPG6557	SENSE	-0.426	0.017	4.000	0.000
916	74206	CGPG3465	SENSE	0.346	0.088	4.000	0.000
1045	74231	CGPG5211	SENSE	0.191	0.235	4.000	0.000
1061	74264	CGPG5355	SENSE	/	/	4.000	0.000
1062	74271	CGPG5376	SENSE	0.390	0.096	4.000	0.000
1140	74373	CGPG6082	SENSE	/	/	4.000	0.000
1223	74434	CGPG6729	SENSE	-0.073	0.551	4.000	0.000
1228	74515	CGPG6768	SENSE	0.333	0.170	4.000	0.000
1231	74519	CGPG6800	SENSE	0.245	0.075	4.000	0.000
1230	74529	CGPG6785	SENSE	0.186	0.034	4.000	0.000
876	74535	CGPG268	SENSE	0.085	0.201	4.000	0.000
857	74567	CGPG2349	SENSE	0.223	0.189	4.000	0.000
1215	74582	CGPG6641	SENSE	/	/	4.000	0.000
1216	74584	CGPG6642	SENSE	0.065	0.795	4.000	0.000
1146	74656	CGPG6172	SENSE	0.225	0.005	4.000	0.000
1148	74659	CGPG6176	SENSE	-0.112	0.271	4.000	0.000
1015	74715	CGPG4937	SENSE	0.167	0.043	4.000	0.000
1116	74739	CGPG5889	SENSE	0.154	0.356	4.000	0.000
1285	74845	CGPG7362	SENSE	0.248	0.021	4.000	0.000
1287	74859	CGPG7379	SENSE	0.331	0.115	4.000	0.000
1294	74917	CGPG7424	SENSE	0.028	0.885	4.000	0.000
1292	74928	CGPG7417	SENSE	0.227	0.263	4.000	0.000
1298	74932	CGPG7449	SENSE	0.053	0.562	4.000	0.000
1297	74955	CGPG7443	SENSE	0.232	0.010	4.000	0.000
1290	74962	CGPG7404	SENSE	0.194	0.433	4.000	0.000
1300	74968	CGPG7452	SENSE	0.184	0.204	4.000	0.000

PEP SEQ ID	Construct ID	Nomination ID	Orientation	Root length at day 28		Growth stage at day 28	
				Delta-mean	P-value	Delta mean	P-value
1295	74989	CGPG7430	SENSE	0.098	0.494	4.000	0.000
1066	75002	CGPG539	SENSE	0.529	0.001	4.000	0.000
1129	75094	CGPG5994	SENSE	0.087	0.017	4.000	0.000
839	75221	CGPG2065	SENSE	0.447	0.028	4.000	0.000
1114	75225	CGPG5868	SENSE	-0.063	0.602	4.000	0.000
1119	75233	CGPG5914	SENSE	/	/	4.000	0.000
1126	75243	CGPG5977	SENSE	0.298	0.017	4.000	0.000
1165	75274	CGPG6267	SENSE	-0.038	0.744	4.000	0.000
1169	75291	CGPG6311	SENSE	-0.095	0.371	4.000	0.000
1309	75331	CGPG7516	SENSE	-0.336	0.022	4.000	0.000
1316	75335	CGPG7548	SENSE	-0.059	0.778	4.000	0.000
1310	75343	CGPG7517	SENSE	0.098	0.652	4.000	0.000
1303	75386	CGPG7481	SENSE	0.463	0.072	4.000	0.000
1315	75393	CGPG7537	SENSE	-0.122	0.605	4.000	0.000
1322	75442	CGPG7605	SENSE	0.183	0.133	4.000	0.000
1319	75452	CGPG7590	SENSE	0.554	0.054	4.000	0.000
1317	75462	CGPG7575	SENSE	0.244	0.345	4.000	0.000
1323	75466	CGPG7607	SENSE	0.028	0.042	4.000	0.000
1325	75481	CGPG7632	SENSE	0.110	0.284	4.000	0.000
1341	75785	CGPG7863	SENSE	-0.038	0.826	4.000	0.000
1162	75814	CGPG6243	SENSE	0.008	0.952	4.000	0.000
1130	75818	CGPG5996	SENSE	0.050	0.550	4.000	0.000
1236	75856	CGPG6920	SENSE	0.118	0.579	4.000	0.000
1246	75878	CGPG7002	SENSE	0.182	0.165	4.000	0.000
1252	75896	CGPG7080	SENSE	/	/	4.000	0.000
1386	75904	CGPG8235	SENSE	0.089	0.730	4.000	0.000
1393	75932	CGPG8269	SENSE	0.567	0.067	4.000	0.000
788	75935	CGPG1335	SENSE	0.306	0.098	4.000	0.000
862	75936	CGPG2397	SENSE	0.212	0.090	4.000	0.000
1389	75942	CGPG8254	SENSE	0.038	0.373	4.000	0.000
1391	75943	CGPG8262	SENSE	0.121	0.566	4.000	0.000
1390	75954	CGPG8255	SENSE	0.215	0.436	4.000	0.000
856	76041	CGPG2348	SENSE	0.362	0.096	4.000	0.000
1241	76275	CGPG6946	SENSE	-0.079	0.533	4.000	0.000
1137	76610	CGPG6069	SENSE	0.521	0.112	4.000	0.000
1475	76823	CGPG9060	SENSE	0.068	0.707	4.000	0.000
1482	76953	CGPG9111	SENSE	-0.271	0.139	4.000	0.000
820	77005	CGPG1873	SENSE	0.235	0.102	4.000	0.000
1121	77008	CGPG5925	SENSE	0.076	0.709	4.000	0.000
1163	77016	CGPG6248	SENSE	0.121	0.325	4.000	0.000
1492	77107	CGPG9166	SENSE	0.036	0.900	4.000	0.000
1489	77129	CGPG9152	SENSE	0.198	0.069	4.000	0.000
1495	77156	CGPG9178	SENSE	0.440	0.110	4.000	0.000
1484	77161	CGPG9123	SENSE	0.265	0.223	4.000	0.000
1505	77229	CGPG9248	SENSE	-0.024	0.810	4.000	0.000
1508	77233	CGPG9280	SENSE	0.451	0.020	4.000	0.000

PEP SEQ ID	Construct ID	Nomination ID	Orientation	Root length at day 28		Growth stage at day 28	
				Delta-mean	P-value	Delta mean	P-value
1503	77287	CGPG9237	SENSE	0.249	0.157	4.000	0.000
1174	77319	CGPG6349	SENSE	-0.144	0.485	4.000	0.000
1122	77321	CGPG5926	SENSE	-0.241	0.172	4.000	0.000
1366	77346	CGPG8076	SENSE	0.001	0.993	4.000	0.000
1367	77350	CGPG8084	SENSE	-0.221	0.300	4.000	0.000
1376	77367	CGPG8157	SENSE	0.130	0.228	4.000	0.000
1378	77370	CGPG8165	SENSE	-0.114	0.477	4.000	0.000
1513	77429	CGPG9315	SENSE	0.336	0.042	4.000	0.000
1239	77516	CGPG6934	SENSE	0.452	0.002	1.413	0.409
1248	77525	CGPG7021	SENSE	0.450	0.038	4.000	0.000
1253	77527	CGPG7094	SENSE	0.300	0.045	4.000	0.000
1261	77530	CGPG7166	SENSE	-0.031	0.790	4.000	0.000
925	77537	CGPG3631	SENSE	0.167	0.539	4.000	0.000
1353	77559	CGPG7967	SENSE	-0.205	0.278	4.000	0.000
945	77717	CGPG3983	SENSE	0.147	0.350	4.000	0.000
1106	77723	CGPG5785	SENSE	-0.078	0.573	4.000	0.000
1358	77920	CGPG8023	SENSE	/	/	4.000	0.000
1368	77929	CGPG8093	SENSE	0.445	0.031	4.000	0.000
1371	77930	CGPG8097	SENSE	0.039	0.737	4.000	0.000
1360	77961	CGPG8038	SENSE	0.218	0.019	4.000	0.000
1365	77964	CGPG8073	SENSE	0.270	0.022	2.762	0.156
1415	77975	CGPG8474	SENSE	0.116	0.035	1.333	0.423
1422	78014	CGPG8544	SENSE	0.415	0.030	4.000	0.000
1423	78015	CGPG8546	SENSE	0.157	0.597	4.000	0.000
1428	78028	CGPG8573	SENSE	0.238	0.346	4.000	0.000
1432	78047	CGPG8611	SENSE	/	/	4.000	0.000
1435	78059	CGPG8634	SENSE	-0.009	0.947	4.000	0.000
1439	78062	CGPG8642	SENSE	-0.034	0.909	4.000	0.000
1440	78065	CGPG8646	SENSE	0.004	0.782	4.000	0.000
1176	78109	CGPG6353	SENSE	0.198	0.277	4.000	0.000
1274	78112	CGPG7291	SENSE	-0.173	0.212	4.000	0.000
1379	78117	CGPG8169	SENSE	0.319	0.051	4.000	0.000
1398	78136	CGPG8344	SENSE	0.410	0.030	4.000	0.000
1404	78153	CGPG8378	SENSE	0.102	0.238	4.000	0.000
1446	78178	CGPG8716	SENSE	-0.027	0.861	4.000	0.000
1449	78186	CGPG8774	SENSE	-0.002	0.993	4.000	0.000
998	78203	CGPG4689	SENSE	0.001	0.995	4.000	0.000
1003	78207	CGPG4713	SENSE	0.131	0.276	4.000	0.000
1052	78213	CGPG5254	SENSE	0.260	0.001	4.000	0.000
1326	78233	CGPG7673	SENSE	0.169	0.183	4.000	0.000
1026	78349	CGPG5061	SENSE	0.096	0.479	4.000	0.000
881	78362	CGPG2832	SENSE	/	/	4.000	0.000
1416	78536	CGPG8475	SENSE	-0.104	0.537	4.000	0.000
1456	78589	CGPG8853	SENSE	-0.154	0.060	4.000	0.000
1265	78990	CGPG7192	SENSE	/	/	4.000	0.000

If p<0.05 and delta or risk score mean >0, the transgenic plants showed statistically significant trait enhancement as compared to the reference. If p<0.2 and delta or risk score mean >0, the transgenic plants showed a trend of trait enhancement as compared to the reference.

H. shade tolerance screen

[0092] Plants undergo a characteristic morphological response in shade that includes the elongation of the petiole, a change in the leaf angle, and a reduction in chlorophyll content. While these changes may confer a competitive advantage to individuals, in a monoculture the shade avoidance response is thought to reduce the overall biomass of the population. Thus, genetic alterations that prevent the shade avoidance response may be associated with higher yields. Genes that favor growth under low light conditions may also promote yield, as inadequate light levels frequently limit yield. This protocol describes a screen to look for *Arabidopsis* plants that show an attenuated shade avoidance response and/or grow better than control plants under low light intensity. Of particular interest, we were looking for plants that didn't extend their petiole length, had an increase in seedling weight relative to the reference and had leaves that were more close to parallel with the plate surface.

[0093] T2 seeds were plated on glufosinate selection plates with ½ MS medium. Seeds were sown on 1/2 X MS salts, 1% Phytagel, 10 ug/ml BASTA. Plants were grown on vertical plates at a temperature of 22°C at day, 20°C at night and under low light (approximately 30 uE/m^2/s, far/red ratio (655/665/725/735) -0.35 using PLAQ lights with GAM color filter #680). Twenty-three days after seedlings were sown, measurements were recorded including seedling status, number of rosette leaves, status of flower bud, petiole leaf angle, petiole length, and pooled fresh weights. A digital image of the whole plate was taken on the measurement day. Seedling weight and petiole length were analyzed as quantitative responses according to example 1M. The number of rosette leaves, flowering bud formation and leaf angel were analyzed as qualitative responses according to example 1L.

[0094] A list of recombinant DNA constructs that improve shade tolerance in plants illustrated in Table 10.

Table 10

PEP SEQ ID	Construct ID	Nomination ID	Orientation	Seedling weight at day 23		Petiole length at day 23	
				Delta mean	P-value	Delta mean	P-value
877	10204	CGPG274	ANTI-SENSE	0.763	0.001	0.617	0.141
1136	11152	CGPG606	SENSE	0.658	0.006	0.784	0.002
968	11408	CGPG430	SENSE	-0.458	0.210	-0.311	0.065
773	12224	CGPG1143	SENSE	0.010	0.974	-0.378	0.055
823	19122	CGPG1899	SENSE	-0.397	0.110	-0.291	0.043
897	19537	CGPG3156	SENSE	-0.299	0.107	-0.245	0.054
934	70466	CGPG3781	SENSE	-0.531	0.071	-0.342	0.031
992	70680	CGPG4583	SENSE	0.051	0.591	-0.345	0.038
991	70764	CGPG4553	SENSE	-0.407	0.550	-0.991	0.012
926	70833	CGPG365	SENSE	-0.195	0.201	-0.247	0.084
997	71613	CGPG4684	SENSE	-0.464	0.031	-0.328	0.014
1000	71631	CGPG4702	SENSE	-0.806	0.032	-0.607	0.011
834	71702	CGPG1996	SENSE	0.385	0.053	0.293	0.032
990	71820	CGPG4506	SENSE	-0.663	0.053	-0.921	0.094
973	71952	CGPG4344	SENSE	-1.336	0.011	-0.931	0.054
1055	72008	CGPG5265	SENSE	-0.515	0.042	-0.379	0.043
867	72665	CGPG2452	SENSE	-0.229	0.236	-0.314	0.052
873	72675	CGPG2567	SENSE	-1.355	0.051	-1.051	0.024
874	72677	CGPG2571	SENSE	-1.011	0.070	-1.259	0.017
1092	73179	CGPG5686	SENSE	0.230	0.030	0.186	0.133
1021	73309	CGPG5032	SENSE	-0.347	0.026	-0.277	0.007
1009	73336	CGPG4848	SENSE	-1.640	0.045	-1.744	0.008
1199	73511	CGPG6531	SENSE	0.103	0.505	-0.210	0.016

PEP SEQ ID	Construct ID	Nomination ID	Orientation	Seedling weight at day 23		Petiole length at day 23	
				Delta mean	P-value	Delta mean	P-value
1192	73551	CGPG6476	SENSE	-0.881	0.070	-0.744	0.050
1012	73686	CGPG4892	SENSE	0.080	0.905	-1.178	0.007
1079	73953	CGPG5576	SENSE	0.381	0.054	0.325	0.098
1210	74123	CGPG6623	SENSE	-0.442	0.002	-0.424	0.048
1035	74212	CGPG5155	SENSE	-0.380	0.069	-0.262	0.026
1023	74222	CGPG5045	SENSE	-0.913	0.051	-1.766	0.051
1060	74261	CGPG5350	SENSE	-0.207	0.140	-0.532	0.022
1112	74332	CGPG5837	SENSE	-0.544	0.015	-0.630	0.019
1219	74403	CGPG6671	SENSE	-1.289	0.039	-1.057	0.038
1221	74443	CGPG6706	SENSE	-0.664	0.057	-0.968	0.015
1222	74457	CGPG6723	SENSE	-0.913	0.008	-0.993	0.066
1226	74513	CGPG6752	SENSE	-0.405	0.010	-0.356	0.042
1228	74515	CGPG6768	SENSE	-0.523	0.258	-0.227	0.070
857	74567	CGPG2349	SENSE	-0.424	0.132	-0.532	0.026
1132	74605	CGPG6027	SENSE	-0.353	0.268	-0.652	0.097
1135	74611	CGPG6049	SENSE	-0.732	0.015	-0.985	0.023
1143	74626	CGPG6128	SENSE	-0.638	0.084	-0.691	0.030
1145	74636	CGPG6149	SENSE	-0.259	0.527	-0.597	0.095
1217	74687	CGPG6645	SENSE	-0.882	0.027	-0.431	0.024
1117	74748	CGPG5893	SENSE	-0.731	0.175	-0.825	0.080
1291	74939	CGPG7410	SENSE	-0.867	0.020	-0.620	0.001
1301	74957	CGPG7459	SENSE	-1.058	0.008	-0.937	0.088
1296	74990	CGPG7438	SENSE	-1.717	0.007	-1.271	0.032
975	75040	CGPG4349	SENSE	-0.643	0.100	-0.406	0.000
1131	75248	CGPG6021	SENSE	-0.504	0.069	-0.247	0.051
1133	75252	CGPG6035	SENSE	-0.395	0.097	-0.290	0.072
1151	75267	CGPG6201	SENSE	-0.243	0.267	-0.193	0.080
1314	75333	CGPG7532	SENSE	-0.632	0.031	-0.362	0.089
1308	75354	CGPG7510	SENSE	-0.658	0.018	-1.165	0.019
1306	75365	CGPG7503	SENSE	-0.329	0.033	-0.526	0.061
1324	75479	CGPG7616	SENSE	-1.296	0.018	-1.485	0.027
1327	75539	CGPG7683	SENSE	-0.463	0.183	-1.074	0.052
1338	75608	CGPG7816	SENSE	-0.392	0.145	-0.101	0.046
1332	75640	CGPG7787	SENSE	-0.603	0.006	-0.539	0.041
1047	75823	CGPG5213	SENSE	-0.433	0.132	-0.505	0.076
1240	75864	CGPG6945	SENSE	0.596	0.008	0.045	0.730
1247	75881	CGPG7013	SENSE	-1.632	0.014	-1.898	0.000
1250	75895	CGPG7071	SENSE	-0.808	0.006	-0.543	0.084
1382	75913	CGPG8212	SENSE	-0.866	0.072	-0.779	0.030
815	75957	CGPG1740	SENSE	-0.514	0.006	-0.383	0.032
790	75993	CGPG1352	SENSE	-0.606	0.040	-0.590	0.008
856	76041	CGPG2348	SENSE	0.642	0.006	0.151	0.187
1270	76186	CGPG7243	SENSE	-0.603	0.016	-0.427	0.080
1271	76190	CGPG7258	SENSE	-0.032	0.887	-0.125	0.011
1156	76222	CGPG6214	SENSE	-0.653	0.011	-0.632	0.046

PEP SEQ ID	Construct ID	Nomination ID	Orientation	Seedling weight at day 23		Petiole length at day 23	
				Delta mean	P-value	Delta mean	P-value
1158	76228	CGPG6222	SENSE	-0.259	0.179	-0.310	0.013
1463	76319	CGPG8917	SENSE	-0.354	0.147	-0.767	0.097
1465	76320	CGPG8925	SENSE	-0.655	0.087	-1.218	0.010
980	76410	CGPG4405	SENSE	-1.709	0.008	-2.126	0.042
1159	76435	CGPG6229	SENSE	-0.308	0.051	-0.453	0.078
1249	76454	CGPG7056	SENSE	-0.603	0.016	-0.821	0.052
1173	76528	CGPG6336	SENSE	-0.086	0.245	-0.337	0.069
1157	76611	CGPG6215	SENSE	-0.624	0.077	-0.668	0.008
1237	76642	CGPG6921	SENSE	-1.027	0.010	-0.738	0.041
1256	76752	CGPG7118	SENSE	-0.345	0.286	-0.600	0.066
1470	76838	CGPG8990	SENSE	-1.442	0.073	-1.521	0.049
1478	76927	CGPG9093	SENSE	-0.384	0.161	-0.261	0.039
1500	77147	CGPG9201	SENSE	-0.975	0.035	-0.888	0.099
1498	77181	CGPG9188	SENSE	-1.360	0.000	-1.347	0.016
1491	77190	CGPG9165	SENSE	0.005	0.954	-0.239	0.021
1503	77287	CGPG9237	SENSE	-0.315	0.377	-0.602	0.097
1348	77543	CGPG7911	SENSE	-0.166	0.104	-0.676	0.072
1311	77809	CGPG7523	SENSE	-0.466	0.063	-0.144	0.035
1471	77841	CGPG9001	SENSE	-0.651	0.072	-0.316	0.022
1361	77922	CGPG8053	SENSE	-0.447	0.020	-0.270	0.050
1401	77973	CGPG8370	SENSE	-0.722	0.059	-1.092	0.036
1421	78009	CGPG8533	SENSE	-0.468	0.072	-0.268	0.034
1427	78026	CGPG8569	SENSE	-0.555	0.154	-0.467	0.085
1431	78044	CGPG8607	SENSE	-0.838	0.007	-0.803	0.013
1440	78065	CGPG8646	SENSE	-0.085	0.595	-0.517	0.096
1377	78121	CGPG8158	SENSE	0.274	0.079	0.172	0.036
1395	78135	CGPG8305	SENSE	-1.246	0.024	-1.112	0.023
1405	78156	CGPG8383	SENSE	-0.343	0.243	-1.089	0.002
1280	78231	CGPG7347	SENSE	-0.441	0.022	-0.297	0.084
1020	78339	CGPG5028	SENSE	-0.295	0.147	-0.334	0.042
1025	78342	CGPG5051	SENSE	-1.534	0.023	-1.513	0.022
1013	78353	CGPG4903	SENSE	-1.018	0.043	-1.290	0.020
970	78358	CGPG4307	SENSE	-0.531	0.022	-0.430	0.066
1111	78371	CGPG5822	SENSE	-0.743	0.091	-1.382	0.002
1430	78388	CGPG8597	SENSE	-0.200	0.409	-0.417	0.055
1064	78442	CGPG5382	SENSE	-1.106	0.000	-1.187	0.012
1356	78508	CGPG8006	SENSE	-1.184	0.009	-0.784	0.071
1418	78540	CGPG8490	SENSE	0.253	0.057	0.289	0.137
1450	78572	CGPG8778	SENSE	-0.586	0.088	-0.474	0.070
1441	78590	CGPG8666	SENSE	-0.854	0.073	-0.875	0.043
1409	78618	CGPG8450	SENSE	-0.953	0.037	-1.088	0.008
1451	78631	CGPG8784	SENSE	-1.128	0.250	-1.224	0.048
1420	78924	CGPG8530	SENSE	0.213	0.001	0.305	0.058
1443	78952	CGPG8688	SENSE	-0.264	0.282	-0.721	0.023

For "seeding weight" , if p<0.05 and delta or risk score mean >0, the transgenic plants showed statistically significant trait

enhancement as compared to the reference. If p<0.2 and delta or risk score mean >0, the transgenic plants showed a trend of trait enhancement as compared to the reference with p<0.2.
For "petiole length", if p<0.05 and delta <0, the transgenic plants showed statistically significant trait enhancement as compared to the reference. If p<0.2 and delta <0, the transgenic plants showed a trend of trait enhancement as compared to the reference.

I. early plant growth and development screen

[0095] This example sets forth a plate based phenotypic analysis platform for the rapid detection of phenotypes that are evident during the first two weeks of growth. In this screen, we were looking for genes that confer advantages in the processes of germination, seedling vigor, root growth and root morphology under non-stressed growth conditions to plants. The transgenic plants with advantages in seedling growth and development were determined by the seedling weight and root length at day14 after seed planting.

[0096] T2 seeds were plated on glufosinate selection plates and grown under standard conditions (~100 uE/m^2/s, 16 h photoperiod, 22°C at day, 20°C at night). Seeds were stratified for 3 days at 4°C. Seedlings were grown vertically (at a temperature of 22°C at day 20°C at night). Observations were taken on day 10 and day 14. Both seedling weight and root length at day 14 were analyzed as quantitative responses according to example 1M.

[0097] A list recombinant DNA constructs that improve early plant growth and development illustrated in Table 11.
Table 11

PEP SEQ ID	Construct ID	Orientation	Root length at day 10		Root length at day 14		Seedling weight at day 14	
			Delta mean	P-value	Delta mean	P-value	Delta mean	P-value
799	10192	ANTI-SENSE	0.269	0.024	0.222	0.026	0.417	0.021
877	10204	ANTI-SENSE	0.290	0.057	0.234	0.095	0.512	0.014
1328	11919	ANTI-SENSE	0.207	0.249	0.115	0.330	0.537	0.035
1083	12776	ANTI-SENSE	0.237	0.002	0.092	0.280	0.233	0.147
835	14909	ANTI-SENSE	0.151	0.053	0.074	0.582	0.398	0.001
858	15809	ANTI-SENSE	0.212	0.184	0.066	0.493	0.403	0.061
938	19713	SENSE	0.139	0.141	0.008	0.954	0.177	0.090
841	70403	SENSE	0.295	0.017	0.077	0.280	0.337	0.044
1037	71218	SENSE	0.208	0.308	0.145	0.034	0.554	0.138
983	71963	SENSE	0.151	0.099	-0.094	0.359	0.106	0.030
933	72357	SENSE	0.164	0.073	-0.033	0.571	-0.168	0.023
1077	72755	SENSE	0.339	0.014	0.218	0.047	0.307	0.281
1074	72765	SENSE	0.295	0.075	0.158	0.196	0.419	0.094
1072	72773	SENSE	0.185	0.051	0.111	0.183	0.239	0.057
880	72906	SENSE	0.224	0.086	0.074	0.246	0.150	0.027
1085	73021	SENSE	0.134	0.098	0.141	0.083	0.217	0.036
1099	73135	SENSE	0.255	0.073	0.214	0.057	0.329	0.082
1046	73266	SENSE	0.222	0.085	0.038	0.745	0.175	0.183
1183	73454	SENSE	0.276	0.046	0.201	0.131	0.277	0.234
1190	73525	SENSE	0.204	0.016	-0.109	0.216	0.245	0.265
1196	73579	SENSE	0.166	0.028	0.257	0.011	0.379	0.024
1211	74159	SENSE	0.413	0.025	0.218	0.012	0.548	0.010
1202	74163	SENSE	0.188	0.140	0.126	0.244	0.408	0.096
1214	74184	SENSE	0.153	0.068	0.042	0.555	-0.084	0.710
875	74534	SENSE	0.143	0.026	0.055	0.136	0.066	0.416
1285	74845	SENSE	0.190	0.183	0.035	0.622	0.383	0.044

PEP SEQ ID	Construct ID	Orientation	Root length at day 10		Root length at day 14		Seedling weight at day 14	
			Delta mean	P-value	Delta mean	P-value	Delta mean	P-value
1283	74868	SENSE	0.111	0.017	0.081	0.014	0.257	0.041
1297	74955	SENSE	0.345	0.006	0.256	0.002	0.464	0.011
1066	75002	SENSE	0.126	0.027	0.110	0.013	0.144	0.081
1313	75344	SENSE	0.100	0.079	0.015	0.296	0.083	0.541
1321	75489	SENSE	-0.047	0.839	0.037	0.763	0.405	0.091
1162	75814	SENSE	0.246	0.021	0.144	0.041	0.233	0.107
1384	75974	SENSE	0.133	0.034	0.103	0.037	0.214	0.109
843	76076	SENSE	0.417	0.050	0.250	0.028	0.347	0.034
1125	76118	SENSE	0.200	0.035	0.127	0.024	0.311	0.125
1154	76221	SENSE	0.188	0.086	-0.010	0.913	0.353	0.039
1233	76547	SENSE	0.198	0.038	0.080	0.307	0.105	0.183
1244	76558	SENSE	0.279	0.036	0.239	0.005	0.290	0.026
1476	76836	SENSE	0.263	0.012	0.200	0.003	0.292	0.089
1488	77105	SENSE	0.325	0.114	0.235	0.056	0.224	0.170
1493	77167	SENSE	0.186	0.004	-0.068	0.308	0.235	0.068
1499	77193	SENSE	0.312	0.027	0.275	0.007	0.444	0.005
1352	77556	SENSE	/	/	/	/	0.468	0.001
1412	77630	SENSE	0.146	0.199	0.180	0.025	0.236	0.060
1380	77950	SENSE	0.121	0.084	0.088	0.302	0.141	0.259
1397	77969	SENSE	0.461	0.009	0.375	0.008	0.503	0.001
1439	78062	SENSE	0.163	0.060	0.185	0.043	0.380	0.080
1445	78169	SENSE	0.104	0.358	0.143	0.014	0.096	0.071
1455	78584	SENSE	0.164	0.056	-0.020	0.749	-0.108	0.303
1259	78740	SENSE	/	/	/	/	0.367	0.099
1410	78919	SENSE	0.273	0.052	0.155	0.085	0.225	0.310
1453	78938	SENSE	0.187	0.107	0.113	0.010	0.309	0.303

If $p<0.05$ and delta or risk score mean >0, the transgenic plants showed statistically significant trait enhancement as compared to the reference. If $p<0.2$ and delta or risk score mean >0, the transgenic plants showed a trend of trait enhancement as compared to the reference.

J. late plant growth and development screen

[0098] This example sets forth a soil based phenotypic platform to identify genes that confer advantages in the processes of leaf development, flowering production and seed maturity to plants.

[0099] *Arabidopsis* plants were grown on a commercial potting mixture (Metro Mix 360, Scotts Co., Marysville, OH) consisting of 30-40% medium grade horticultural vermiculite, 35-55% sphagnum peat moss, 10-20% processed bark ash, 1-15% pine bark and a starter nutrient charge. Soil was supplemented with Osmocote time-release fertilizer at a rate of 30 mg/ft^3. T2 seeds were imbibed in 1% agarose solution for 3 days at 4 °C and then sown at a density of ~5 per 2 ½" pot. Thirty-two pots were ordered in a 4 by 8 grid in standard greenhouse flat. Plants were grown in environmentally controlled rooms under a 16 h day length with an average light intensity of -200 µmoles/m^2/s. Day and night temperature set points were 22 °C and 20 °C, respectively. Humidity was maintained at 65%. Plants were watered by sub-irrigation every two days on average until mid-flowering, at which point the plants were watered daily until flowering was complete.

[0100] Application of the herbicide glufosinate was performed to select T2 individuals containing the target transgene. A single application of glufosinate was applied when the first true leaves were visible. Each pot was thinned to leave a single glufosinate-resistant seedling ~3 days after the selection was applied.

[0101] The rosette radius was measured at day 25. The silique length was measured at day 40. The plant parts were harvested at day 49 for dry weight measurements if flowering production was stopped. Otherwise, the dry weights of rosette and silique were carried out at day 53. The seeds were harvested at day 58. All measurements were analyzed as quantitative responses according to example 1M.

[0102] A list of recombinant DNA constructs that improve late plant growth and development illustrated in Table 12.

Table 12

PEP SEQ ID	Construct ID	Rosette dry weight at day 53		Rosette radius at day 25		Seed net dry weight at day 62		Silique dry weight at day 53		Silique length at day 40	
		Delta mean	P-value	Delta mean	P-value	Delta mean	P-value	Delta mean	P-value	Delta mean	P-value
1515	11935	0.099	0.072	-0.093	0.030	1.235	0.027	0.041	0.679	0.039	0.247
762	12020	-0.040	0.812	-0.191	0.054	0.871	0.010	-0.060	0.746	-0.075	0.107
787	12932	0.438	0.013	/	/	-0.701	0.057	0.618	0.012	-0.013	0.692
810	14730	-0.045	0.534	0.325	0.001	0.817	0.003	0.236	0.140	0.017	0.123
824	16446	-0.152	0.214	-0.097	0.367	0.701	0.032	0.055	0.450	-0.017	0.832
902	18220	0.209	0.049	-0.182	0.052	0.295	0.259	-0.205	0.036	-0.134	0.072
907	18239	0.482	0.004	0.071	0.077	-0.245	0.113	-0.024	0.818	-0.045	0.346
953	19933	0.211	0.020	/	/	-0.755	0.005	0.257	0.154	0.045	0.214
821	70410	-0.208	0.070	/	/	0.505	0.028	-0.348	0.015	-0.081	0.421
978	71846	-0.285	0.012	/	/	0.511	0.017	0.277	0.185	-0.046	0.534
983	71963	-0.146	0.231	-0.035	0.312	0.421	0.037	0.120	0.131	0.037	0.048
1051	72049	0.351	0.153	-0.047	0.683	0.419	0.025	-0.108	0.180	0.024	0.493
1001	72368	0.282	0.013	-0.407	0.051	-0.912	0.082	-0.244	0.208	-0.096	0.017
993	72375	0.327	0.002	/	/	-0.261	0.014	0.022	0.324	0.042	0.076
1185	73445	-0.042	0.704	-0.126	0.091	1.499	0.015	-0.037	0.330	0.009	0.633
852	10332	0.108	0.156	0.101	0.449	0.799	0.038	/	/	-0.072	0.208
810	13938	0.450	0.064	0.225	0.094	0.874	0.021	0.331	0.029	0.258	0.005
814	13960	-0.042	0.697	0.191	0.010	0.387	0.033	0.657	0.005	0.098	0.005
872	16607	0.246	0.041	0.170	0.076	-1.029	0.012	-0.675	0.018	0.197	0.029
914	18347	-0.240	0.238	0.188	0.026	1.183	0.017	-0.019	0.873	0.071	0.236
935	70241	-0.146	0.264	0.116	0.068	0.851	0.012	0.245	0.007	0.023	0.640
947	70909	-0.163	0.084	-0.026	0.345	0.792	0.004	0.484	0.011	0.647	0.001
949	70974	-0.111	0.119	-0.036	0.794	1.359	0.002	/	/	-0.027	0.476
979	71314	-0.076	0.209	-0.007	0.793	0.426	0.027	/	/	0.021	0.098
987	71334	1.355	0.001	-0.002	0.971	-0.472	0.206	0.328	0.052	-0.134	0.322
1109	72923	0.331	0.002	-0.108	0.335	1.545	0.005	0.345	0.297	0.630	0.002
1042	73255	0.147	0.018	-0.001	0.972	0.581	0.005	0.829	0.002	0.080	0.016
1028	73280	-0.377	0.134	-0.042	0.512	0.824	0.014	0.324	0.202	0.003	0.976
1189	73436	0.563	0.014	0.072	0.106	0.766	0.052	0.335	0.120	-0.049	0.171
1191	73514	-0.409	0.051	-0.027	0.588	0.384	0.006	0.103	0.575	-0.032	0.335
1197	73556	0.282	0.275	0.049	0.055	0.975	0.011	0.203	0.273	-0.106	0.220
1208	74110	0.745	0.014	0.177	0.116	-0.983	0.178	1.131	0.009	-0.104	0.214
814	74391	0.299	0.002	0.036	0.095	-0.578	0.004	/	/	0.076	0.044
861	74702	-0.335	0.019	0.092	0.173	1.364	0.003	0.080	0.546	0.083	0.041
1293	74905	0.143	0.537	-0.085	0.246	1.488	0.002	0.092	0.454	-0.004	0.910
1292	74928	0.330	0.031	0.087	0.114	0.303	0.173	0.542	0.050	0.082	0.019
1312	75332	-0.145	0.035	0.222	0.027	0.919	0.021	0.149	0.476	0.012	0.694

PEP SEQ ID	Construct ID	Rosette dry weight at day 53		Rosette radius at day 25		Seed net dry weight at day 62		Silique dry weight at day 53		Silique length at day 40	
		Delta mean	P-value	Delta mean	P-value	Delta mean	P-value	Delta mean	P-value	Delta mean	P-value
1323	75466	0.137	0.237	0.264	0.009	0.479	0.039	0.539	0.010	0.062	0.171
1387	75916	0.342	0.027	0.029	0.549	-0.137	0.634	0.257	0.042	0.027	0.655
1383	75925	-0.207	0.072	0.038	0.662	1.374	0.001	-0.025	0.853	-0.009	0.727
837	75945	0.550	0.001	-0.188	0.113	0.440	0.022	0.050	0.769	-0.236	0.045
1154	76221	-0.042	0.742	0.090	0.132	0.863	0.002	0.295	0.139	0.029	0.469
1166	76233	0.115	0.162	0.110	0.160	1.062	0.008	0.196	0.005	0.065	0.343
1242	76276	0.295	0.029	0.058	0.333	0.732	0.022	0.258	0.110	-0.060	0.400
1473	76865	-0.084	0.474	-0.155	0.034	0.719	0.039	0.267	0.104	-0.005	0.968
1483	76965	0.107	0.469	-0.329	0.058	0.446	0.001	0.067	0.770	-0.174	0.320
1272	77071	-0.354	0.006	0.108	0.020	0.854	0.002	-0.200	0.125	0.012	0.647
1492	77107	0.077	0.748	-0.026	0.709	1.343	0.003	-0.451	0.256	-0.092	0.349
1487	77116	-0.064	0.634	0.048	0.066	1.289	0.003	0.006	0.935	0.004	0.475
1496	77168	-0.287	0.410	-0.105	0.148	0.389	0.018	-0.407	0.281	-0.069	0.161
1261	77530	0.535	0.050	-0.055	0.706	-1.462	0.041	/	/	-0.240	0.224
1345	77539	0.655	0.009	-0.079	0.264	0.618	0.022	/	/	0.041	0.044
1347	77542	0.161	0.003	0.035	0.273	0.708	0.010	-0.480	0.039	0.025	0.461
1350	77550	0.606	0.015	-0.187	0.043	-0.907	0.002	/	/	-0.338	0.044
1304	77807	-0.079	0.511	0.078	0.184	0.770	0.008	0.162	0.258	0.039	0.112
1110	78501	0.073	0.568	-0.202	0.040	0.292	0.006	/	/	-0.009	0.796
1185	73445										

If $p<0.05$ and delta or risk score mean >0, the transgenic plants showed statistically significant trait enhancement as compared to the reference. If $p<0.2$ and delta or risk score mean >0, the transgenic plants showed a trend of trait enhancement as compared to the reference.

K. Limited nitrogen tolerance screen

[0103] Under low nitrogen conditions, *Arabidopsis* seedlings become chlorotic and have less biomass. This example sets forth the limited nitrogen tolerance screen to identify *Arabidopsis* plants transformed with the gene of interest that are altered in their ability to accumulate biomass and/or retain chlorophyll under low nitrogen condition.

[0104] T2 seeds were plated on glufosinate selection plates containing 0.5x N-Free Hoagland's T 0.1 mM NH_4NO_3 T 0.1% sucrose T 1% phytagel media and grown under standard light and temperature conditions. At 12 days of growth, plants were scored for seedling status (*i.e.,* viable or non-viable) and root length. After 21 days of growth, plants were scored for BASTA resistance, visual color, seedling weight, number of green leaves, number of rosette leaves, root length and formation of flowering buds. A photograph of each plant was also taken at this time point.

[0105] The seedling weight and root length were analyzed as quantitative responses according to example 1M. The number green leaves, the number of rosette leaves and the flowerbud formation were analyzed as qualitative responses according to example 1L. The leaf color raw data were collected on each plant as the percentages of five color elements (Green, DarkGreen, LightGreen, RedPurple, YellowChlorotic) using a computer imaging system. A statistical logistic regression model was developed to predict an overall value based on five colors for each plant.

[0106] A list of recombinant DNA constructs that improve low nitrogen availability tolerance in plants illustrated in Table 13.

Table 13

PEP SEQ ID	Construct ID	Orientation	Root length at day 21		Leaf color at day 21		Rosette weight at day 21	
			Delta mean	P-value	Risk score mean	P-value	Delta mean	P-value
779	10176	ANTI-SENSE	-0.448	0.045	2.804	0.082	0.174	0.077
893	10217	ANTI-SENSE	-0.237	0.066	0.820	0.051	0.027	0.787
911	10230	ANTI-SENSE	/	/	3.346	0.001	-0.006	0.844
917	10234	ANTI-SENSE	-0.415	0.068	7.023	0.002	0.028	0.772
957	10413	ANTI-SENSE	-0.401	0.084	3.636	0.046	-0.026	0.767
879	10431	ANTI-SENSE	-0.476	0.022	3.731	0.010	-0.037	0.731
886	10469	SENSE	-0.570	0.002	5.909	0.004	0.019	0.652
878	10472	SENSE	-0.337	0.013	3.669	0.035	-0.089	0.173
782	10507	ANTI-SENSE	-0.494	0.011	4.504	0.014	-0.134	0.200
1078	10610	ANTI-SENSE	-0.379	0.078	0.591	0.016	-0.039	0.413
1108	10616	ANTI-SENSE	-0.462	0.013	4.827	0.058	-0.122	0.054
1134	10620	ANTI-SENSE	-0.279	0.002	2.695	0.022	-0.057	0.244
1144	10622	ANTI-SENSE	-0.567	0.021	4506	0.010	-0.160	0.252
1212	10633	ANTI-SENSE	-0.320	0.051	3.471	0.012	-0.165	0.055
1232	10638	ANTI-SENSE	-0.692	0.004	5.933	0.026	-0.089	0.346
1058	10811	ANTI-SENSE	-0.290	0.005	1.439	0.021	-0.002	0.952
996	11003	ANTI-SENSE	/	/	3.118	0.019	-0.138	0.054
1267	11022	ANTI-SENSE	-0.273	0.033	4.514	0.044	0.000	0.987
1044	11049	SENSE	-0.173	0.177	0.986	0.059	0.086	0.406
941	11117	ANTI-SENSE	-0.707	0.027	5.220	0.004	-0.112	0.488
958	11119	ANTI-SENSE	/	/	6.165	0.025	-0.012	0.899
931	11319	ANTI-SENSE	-0.334	0.293	1.469	0.062	-0.099	0.149
1048	11353	SENSE	-0.152	0.034	1.063	0.058	-0.072	0.044
1091	11516	ANTI-SENSE	-0.293	0.016	4.740	0.030	0.050	0.594
1258	11720	ANTI-SENSE	-0.553	0.007	4.801	0.007	-0.044	0.519
1357	11748	ANTI-SENSE	-0.181	0.032	1.491	0.022	0.034	0.679
1406	11807	ANTI-SENSE	-0.538	0.080	5.467	0.057	-0.001	0.985
764	11827	ANTI-SENSE	-0.510	0.005	6.450	0.001	0.080	0.391
767	11836	ANTI-SENSE	-0.154	0.001	0.513	0.099	-0.112	0.127
774	11856	ANTI-SENSE	-0.127	0.273	2.401	0.035	-0.023	0.788
766	12015	SENSE	-0.402	0.088	0.799	0.030	-0.104	0.162
775	12065	SENSE	0.264	0.121	174.221	0.424	0.193	0.012
768	12141	ANTI-SENSE	-0.343	0.001	1.939	0.010	-0.059	0.278
777	12208	SENSE	0.064	0.731	1.066	0.453	0.209	0.073
776	12419	ANTI-SENSE	-0.399	0.128	4.501	0.068	0.095	0.183
1452	12425	ANTI-SENSE	-0.894	0.160	4.996	0.056	-0.176	0.184
765	12435	SENSE	0.101	0.355	-0.040	0.909	0.135	0.066
770	12437	SENSE	/	/	1.828	0.051	-0.077	0.324
785	13237	SENSE	-0.287	0.009	4.272	0.017	0.169	0.174
795	13305	ANTI-SENSE	-0.221	0.051	0.981	0.076	-0.062	0.543
943	13404	SENSE	-0.372	0.121	3.277	0.059	0.089	0.096
804	13650	ANTI-SENSE	/	/	3.220	0.055	0.302	0.004
809	13657	ANTI-SENSE	-0.500	0.018	5.368	0.037	-0.059	0.462
794	13708	ANTI-SENSE	-0.527	0.021	4.121	0.079	0.077	0.402

PEP SEQ ID	Construct ID	Orientation	Root length at day 21		Leaf color at day 21		Rosette weight at day 21	
			Delta mean	P-value	Risk score mean	P-value	Delta mean	P-value
1153	13805	SENSE	/	/	5.349	0.049	-0.085	0.433
801	13841	ANTI-SENSE	-0.460	0.009	5.012	0.009	0.162	0.031
805	13855	ANTI-SENSE	-0.141	0.024	1.477	0.072	0.056	0.426
1477	14133	ANTI-SENSE	-0.461	0.074	3.450	0.085	0.012	0.868
803	14253	ANTI-SENSE	/	/	4.232	0.034	0.023	0.906
1235	14703	SENSE	-0.450	0.039	4.394	0.019	-0.001	0.990
797	14712	SENSE	-0.429	0.034	4.370	0.025	0.152	0.112
836	14927	ANTI-SENSE	-0.293	0.083	4.557	0.006	0.134	0.255
783	15039	SENSE	-0.491	0.102	4.688	0.003	-0.096	0.230
825	15143	SENSE	/	/	5.445	0.010	-0.028	0.831
848	15716	ANTI-SENSE	-0.473	0.018	3.843	0.014	-0.087	0.024
802	15805	SENSE	-0.347	0.073	3.195	0.001	-0.003	0.931
866	17129	ANTI-SENSE	-0.356	0.185	2.082	0.099	-0.095	0.068
869	17151	ANTI-SENSE	/	/	4.021	0.022	0.024	0.747
868	18206	SENSE	-0.160	0.337	1.069	0.052	0.643	0.014
906	18227	SENSE	-0.273	0.185	1.990	0.020	-0.045	0.201
913	18271	SENSE	-0.036	0.744	0.278	0.082	0.004	0.925
909	18329	SENSE	-0.220	0.418	5.264	0.067	0.118	0.119
890	18423	SENSE	-0.304	0.018	3.789	0.079	0.025	0.771
904	19205	SENSE	-0.313	0.084	0.702	0.004	-0.061	0.491
791	19401	SENSE	-0.032	0.850	0.086	0.874	0.161	0.096
859	70110	SENSE	-0.264	0.020	2.237	0.076	0.105	0.354
930	70440	SENSE	-0.347	0.017	1.576	0.032	0.115	0.251
936	70476	SENSE	-0.297	0.072	0.965	0.044	-0.141	0.095
977	70666	SENSE	-0.351	0.007	3.536	0.039	-0.085	0.127
963	71250	SENSE	-0.018	0.901	2.025	0.110	0.278	0.022
981	71322	SENSE	-0.046	0.431	1.676	0.080	0.026	0.628
984	71326	SENSE	-0.380	0.065	3.996	0.032	-0.047	0.399
987	71334	SENSE	-0.482	0.028	3.737	0.074	0.042	0.322
988	71335	SENSE	-0.264	0.060	3.812	0.035	0.133	0.220
971	71839	SENSE	0.052	0.538	2.437	0.013	0.140	0.150
976	71843	SENSE	-0.316	0.045	1.660	0.219	0.232	0.038
1127	72602	SENSE	0.021	0.833	0.410	0.025	0.043	0.751
1017	72663	SENSE	0.002	0.989	-0.270	0.862	0.199	0.016
873	72675	SENSE	-0.173	0.135	1.435	0.055	-0.117	0.096
1019	72827	SENSE	-0.264	0.054	1.909	0.080	0.000	0.995
1105	72933	SENSE	-0.245	0.122	3.963	0.025	0.076	0.442
1043	73257	SENSE	/	/	4.972	0.090	-0.045	0.609
1029	73281	SENSE	-0.305	0.097	4.638	0.040	-0.043	0.175
1181	73452	SENSE	0.043	0.102	0.097	0.808	0.154	0.053
969	73616	SENSE	0.307	0.023	1.292	0.012	-0.036	0.222
1014	73726	SENSE	-0.049	0.097	2.396	0.041	-0.024	0.788
855	73847	SENSE	-0.100	0.149	1.517	0.044	-0.075	0.036
1082	73966	SENSE	-0.273	0.001	2.969	0.035	-0.179	0.224

PEP SEQ ID	Construct ID	Orientation	Root length at day 21		Leaf color at day 21		Rosette weight at day 21	
			Delta mean	P-value	Risk score mean	P-value	Delta mean	P-value
853	73968	SENSE	/	/	4.339	0.056	-0.022	0.584
1205	74141	SENSE	-0.362	0.112	1.484	0.051	-0.224	0.015
1203	74175	SENSE	-0.305	0.069	3.974	0.023	-0.007	0.901
1204	74176	SENSE	0.048	0.225	1.673	0.005	-0.042	0.558
1206	74178	SENSE	-0.546	0.051	3.934	0.038	-0.117	0.062
898	74201	SENSE	-0.223	0.046	1.264	0.077	-0.200	0.018
1023	74222	SENSE	/	/	5.858	0.048	-0.076	0.268
1139	74371	SENSE	/	/	4.728	0.007	-0.117	0.322
1140	74373	SENSE	-0.027	0.715	-0.646	0.465	0.106	0.051
1224	74447	SENSE	-0.867	0.064	3.200	0.055	-0.197	0.206
1135	74611	SENSE	-0.189	0.350	2.233	0.060	-0.118	0.205
1142	74620	SENSE	-0.736	0.094	5.605	0.047	0.004	0.979
1113	74738	SENSE	0.036	0.145	-0.181	0.528	0.168	0.098
1284	74809	SENSE	-0.256	0.031	2.481	0.053	-0.021	0.606
1282	74820	SENSE	-0.173	0.032	1.129	0.036	-0.168	0.064
1286	74870	SENSE	-0.448	0.051	4.227	0.061	-0.103	0.154
1289	74950	SENSE	-0.115	0.085	1.801	0.070	-0.107	0.291
1004	75209	SENSE	-0.231	0.065	2.947	0.046	0.008	0.887
1152	75283	SENSE	-0.190	0.011	0.627	0.047	-0.038	0.323
1306	75365	SENSE	0.125	0.219	1.830	0.047	-0.056	0.569
1302	75374	SENSE	-0.326	0.031	2.123	0.080	-0.193	0.015
1321	75489	SENSE	0.208	0.053	-4.236	0.035	0.184	0.054
1329	75603	SENSE	0.035	0.604	0.552	0.179	0.124	0.009
1332	75640	SENSE	-0.353	0.018	3.264	0.026	-0.152	0.231
1334	75653	SENSE	-0.256	0.151	3.269	0.076	-0.023	0.755
1343	75716	SENSE	-0.292	0.079	2.436	0.028	-0.066	0.580
1386	75904	SENSE	0.254	0.052	-1.863	0.084	0.312	0.025
1392	75967	SENSE	/	/	1.628	0.003	-0.038	0.729
1260	76157	SENSE	/	/	2.689	0.064	0.155	0.058
1273	76194	SENSE	/	/	7.881	0.009	-0.078	0.728
1463	76319	SENSE	/	/	7.442	0.029	-0.388	0.417
1468	76334	SENSE	-0.338	0.068	1.019	0.036	-0.036	0.517
1461	76340	SENSE	-0.159	0.020	0.346	0.061	-0.026	0.682
1464	76343	SENSE	-0.042	0.710	0.257	0.390	0.111	0.081
1466	76380	SENSE	/	/	2.459	0.019	-0.130	0.254
1469	76382	SENSE	-0.693	0.013	5.109	0.008	-0.304	0.007
980	76410	SENSE	-0.203	0.007	3.337	0.004	-0.107	0.294
1264	76756	SENSE	/	/	3.459	0.034	-0.147	0.126
1470	76838	SENSE	/	/	4.610	0.021	-0.067	0.168
1479	76963	SENSE	/	/	1.779	0.046	-0.188	0.096
1507	77265	SENSE	/	/	2.573	0.025	-0.097	0.265
1504	77276	SENSE	/	/	3.580	0.010	-0.113	0.219
1120	77311	SENSE	/	/	2.744	0.032	-0.035	0.696
1346	77540	SENSE	-0.322	0.016	3.433	0.004	-0.164	0.013

PEP SEQ ID	Construct ID	Orientation	Root length at day 21		Leaf color at day 21		Rosette weight at day 21	
			Delta mean	P-value	Risk score mean	P-value	Delta mean	P-value
1355	77565	SENSE	/	/	2.221	0.006	-0.026	0.272
1359	77573	SENSE	-0.404	0.005	5.266	0.007	0.092	0.178
1501	77853	SENSE	/	/	4.686	0.004	-0.072	0.264
1400	78142	SENSE	/	/	3.787	0.059	0.010	0.566
1437	78163	SENSE	/	/	1.541	0.029	0.038	0.603
1457	78252	SENSE	/	/	5.384	0.026	-0.043	0.728
1516	78259	SENSE	/	/	3.387	0.036	0.004	0.928
1024	78341	SENSE	/	/	4.261	0.040	-0.056	0.478
1025	78342	SENSE	-0.469	0.027	7.592	0.050	-0.272	0.023
1013	78353	SENSE	/	/	7.028	0.040	0.013	0.930
972	78417	SENSE	0.041	0.366	-0.590	0.551	0.282	0.076
1266	78460	SENSE	/	/	2.353	0.087	-0.159	0.017
1356	78508	SENSE	/	/	4.369	0.001	-0.241	0.000
1370	78510	SENSE	-0.216	0.041	3.626	0.043	-0.125	0.126
1407	78528	SENSE	/	/	4.716	0.014	-0.241	0.075
1444	78559	SENSE	/	/	4.385	0.022	-0.029	0.877
1171	78607	SENSE	/	/	4.547	0.049	-0.162	0.319
959	78659	SENSE	/	/	6.713	0.013	-0.060	0.637
974	78717	SENSE	/	/	1.926	0.179	0.121	0.013
1022	78725	SENSE	-0.157	0.213	1.656	0.054	0.028	0.683
1161	78743	SENSE	/	/	2.003	0.048	0.107	0.258
1413	78921	SENSE	/	/	2.641	0.040	0.039	0.795
1454	78961	SENSE	-0.475	0.006	4.949	0.000	0.002	0.972
1403	78963	SENSE	/	/	5.358	0.057	0.042	0.725
961	78969	SENSE	/	/	2.921	0.097	0.196	0.127
964	78972	SENSE	/	/	1.621	0.050	0.009	0.814

For rosette weight, if $p<0.05$ and delta or risk score mean >0, the transgenic plants showed statistically significant trait enhancement as compared to the reference. If $p<0.2$ and delta or risk score mean >0, the transgenic plants showed a trend of trait enhancement as compared to the reference with $p<0.2$. For root length, if $p<0.05$, the transgenic plants showed statistically significant trait enhancement as compared to the reference. If $p<0.2$, the transgenic plants showed a trend of trait enhancement as compared to the reference.

L. Statistic analysis for qualitative responses

[0107] A list of responses that were analyzed as qualitative responses illustrated in Table 14.

Table 14

response	**Screen**	**categories (success vs. failure)**
Wilting response Risk Score	Soil drought tolerance screen	non-wilted vs. wilted
growth stage at day 14	heat stress tolerance screen	50% of plants reach stagge 1.03 vs. not
growth stage at day 14	salt stress tolerance screen	50% of plants reach stage 1.03 vs. not
growth stage at day 14	PEG induced osmotic stress tolerance screen	50% of plants reach stage 1.03 vs. not
growth stage at day 7	cold germination tolerance screen	50% of plants reach stage 0.5 vs. not

response	Screen	categories (success vs. failure)
number of rosette leaves at day 23	Shade tolerance screen	5 leaves appeared vs. not
Flower bud formation at day 23	Shade tolerance screen	flower buds appear vs. not
leaf angle at day 23	Shade tolerance screen	>60 degree vs. <60 degree
number of green leaves at day 21	limited nitrogen tolerance screen	6 or 7 leaves appeared vs. not
number of rosette leaves at day 21	limited nitrogen tolerance screen	6 or 7 leaves appeared vs. not
Flower bud formation at day 21	limited nitrogen tolerance screen	flower buds appear vs. not

[0108] Plants were grouped into transgenic and reference groups and were scored as success or failure according to Table 14. First, the risk (R) was calculated, which is the proportion of plants that were scored as of failure plants within the group. Then the relative risk (RR) was calculated as the ratio of R (transgenic) to R (reference). Risk score (RS) was calculated as $-\log_2 {}^{RR}$. Subsequently the risk scores from multiple events for each transgene of interest were evaluated for statistical significance by t-test using SAS statistical software (SAS 9, SAS/STAT User's Guide, SAS Institute Inc, Cary, NC, USA). RS with a value greater than 0 indicates that the transgenic plants perform better than the reference. RS with a value less than 0 indicates that the transgenic plants perform worse than the reference. The RS with a value equal to 0 indicates that the performance of the transgenic plants and the reference don't show any difference.

M. Statistic analysis for quantitative responses

[0109] A list of responses that were analyzed as quantitative responses illustrated in Table 15.

Table 15

response	screen
seed yield	Soil drought stress tolerance screen
seedling weight at day 14	heat stress tolerance screen
root length at dav 14	heat stress tolerance screen
seedling weight at day 14	salt stress tolerance screen
root length at dav 14	salt stress tolerance screen
root length at dav 11	salt stress tolerance screen
seedling weight at day 14	PEG induced osmotic stress tolerance screen
root length at day 11	PEG induced osmotic stress tolerance screen
root length at day 14	PEG induced osmotic stress tolerance screen
rosette area at day 8	cold shock tolerance screen
rosette area at day 28	cold shock tolerance screen
difference in rosette area from day 8 to day 28	cold shock tolerance screen
root length at day 28	cold germination tolerance screen
seedling weight at day 23	Shade tolerance screen
petiole length at day 23	Shade tolerance screen
root length at day 14	Early plant growth and development screen
Seedling weight at day 14	Early plant growth and development screen
Rosette dry weight at day 53	Late plant growth and development screen
rosette radius at day 25	Late plant growth and development screen
seed dry weight at day 58	Late plant growth and development screen
silique dry weight at day 53	Late plant growth and development screen
silique length at day 40	Late plant growth and development screen
Seedling weight at day 21	Limited nitrogen tolerance screen
Root length at day 21	Limited nitrogen tolerance screen

[0110] The measurements (M) of each plant were transformed by $\log_2$ calculation. The Delta was calculated as $\log_2$M(transgenic)- $\log_2$M(reference). Subsequently the mean delta from multiple events of the transgene of interest was evaluated for statistical significance by t-test using SAS statistical software (SAS 9, SAS/STAT User's Guide, SAS Institute Inc, Cary, NC, USA). The Delta with a value greater than 0 indicates that the transgenic plants perform better than the reference. The Delta with a value less than 0 indicates that the transgenic plants perform worse than the reference. The Delta with a value equal to 0 indicates that the performance of the transgenic plants and the reference don't show any difference.

Example 2 Identification of Homologs

[0111] A BLAST searchable "All Protein Database" is constructed of known protein sequences using a proprietary sequence database and the National Center for Biotechnology Information (NCBI) non-redundant amino acid database (nr.aa). For each organism from which a DNA sequence provided herein was obtained, an "Organism Protein Database" is constructed of known protein sequences of the organism; the Organism Protein Database is a subset of the All Protein Database based on the NCBI taxonomy ID for the organism.

[0112] The All Protein Database is queried using amino acid sequence of cognate protein for gene DNA used in trait-improving recombinant DNA, *i.e.,* sequences of SEQ ID NO: 760 through SEQ ID NO: 1518 using "blastp" with E-value cutoff of le-8. Up to 1000 top hits were kept, and separated by organism names. For each organism other than that of the query sequence, a list is kept for hits from the query organism itself with a more significant E-value than the best hit of the organism. The list contains likely duplicated genes, and is referred to as the Core List. Another list was kept for all the hits from each organism, sorted by E-value, and referred to as the Hit List.

[0113] The Organism Protein Database is queried using amino acid sequences of SEQ ID NO: 760 through SEQ ID NO: 1518 using "blastp" with E-value cutoff of 1e-4. Up to 1000 top hits are kept. A BLAST searchable database is constructed based on these hits, and is referred to as "SubDB". SubDB was queried with each sequence in the Hit List using "blastp" with E-value cutoff of 1e-8. The hit with the best E-value is compared with the Core List from the corresponding organism. The hit is deemed a likely ortholog if it belongs to the Core List, otherwise it is deemed not a likely ortholog and there is no further search of sequences in the Hit List for the same organism. Likely orthologs from a large number of distinct organisms were identified and are reported by amino acid sequences of SEQ ID NO: 1519 to SEQ ID NO: 67778. These orthologs are reported in Tables 16 as homologs to the proteins cognate to genes used in trait-improving recombinant DNA.

Example 3 Consensus sequence build

[0114] ClustalW program is selected for multiple sequence alignments of an amino acid sequence of SEQ ID NO: 760 and its homologs, through SEQ ID NO: 1518 and its homologs. Three major factors affecting the sequence alignments dramatically are (1) protein weight matrices; (2) gap open penalty; (3) gap extension penalty. Protein weight matrices available for ClustalW program include Blosum, Pam and Gonnet series. Those parameters with gap open penalty and gap extension penalty were extensively tested. On the basis of the test results, Blosum weight matrix, gap open penalty of 10 and gap extension penalty of 1 were chosen for multiple sequence alignment. The consensus sequence of SEQ ID NO: 768 and its 17 homologs were derived according to the procedure described above and is displayed in Figure 4.

Example 4. Pfam module annoation

[0115] This example illustrates the identification of domain and domain module by Pfam analysis.

[0116] The amino acid sequence of the expressed proteins that were shown to be associated with an enhanced trait were analyzed for Pfam protein family against the current Pfam collection of multiple sequence alignments and hidden Markov models using the HMMER software. The Pfam domain modules and individual protein domain for the proteins of SEQ ID NO: 760 through 1518 are shown in Table 17 and Table 18 respectively. The Hidden Markov model databases for the identified patent families allow identification of other homologous proteins and their cognate encoding DNA to enable the full breadth of the invention for a person of ordinary skill in the art. Certain proteins are identified by a single Pfam domain and others by multiple Pfam domains. For instance, the protein with amino acids of SEQ ID NO: 766 is characterized by two Pfam domains, i.e. "FHA" and "PP2C". See also the protein with amino acids of SEQ ID NO: 1515 which is characterized by seven copies of

the Pfam domain "WD40". In Table 18 "score" is the gathering score for the Hidden Markov Model of the domain which exceeds the gathering cutoff reported in Table 19.

Table 17.

PEP SEQ ID	Construct ID	Module	Position
760	CGPG1022.pep	RRM_1	95-165
761	CGPG1035.pep	Peptidase_C54	82-373
763	CGPG105.pep	AP2	48-112
764	CGPG1060.pep	DUF788	1-169
765	CGPG1069.pep	NDUF_B7	2-81
766	CGPG108.pep	FHA::PP2C	208-284::309-570
771	CGPG1136.pep	RRM_1	22-87
774	CGPG1145.pep	NUDIX	24-160
776	CGPG1173.pep	adh_short	6-181
777	CGPG1176.pep	F-box	2-50
779	CGPG122.pep	PTR2	113-517
780	CGPG126.pep	Response_reg	34-158
781	CGPG1262.pep	Gar1	51-152
782	CGPG128.pep	Response_reg	25-149
783	CGPG1280.pep	DUF676	515-717
784	CGPG1291.pep	DUF862	2-156
785	CGPG1295.pep	TMEM14	7-104
787	CGPG1315.pep	Brix	60-255
788	CGPG 1335.pep	LRR_1	424-447
789	CGPG 1344.pep	Pkinase	496-767
790	CGPG1352.pep	Pkinase_Tyr	154-425
791	CGPG 1364.pep	Pkinase	38-416
793	CGPG1396.pep	malic::Malic_M	106-295::297-550
794	CGPG1398.pep	Glycolytic	11-358
795	CGPG1399.pep	Metallophos	161-360
796	CGPG1429.pep	NTP _transferase::Hexapep::Hexap ep	86-365::413-430::466-483
797	CGPG1430.pep	E1_dh	89-393
798	CGPG1445.pep	Pkinase	33-294
799	CGPG146.pep	p450	38-482
800	CGPG1492.pep	Aldedh	29-491
801	CGPG1528.pep	ATP_synt_H	1-70
802	CGPG1530.pep	ArfGap::C2	15-137::183-262
803	CGPG1535.pep	SPT2	230-329
804	CGPG1546.pep	CTP_transf_1	101-300
805	CGPG1567.pep	Ribosomal_L19	107-212
806	CGPG 1568.pep	FAD_binding_4	82-221
807	CGPG1575.pep	DUF740	24-595
808	CGPG1619.pep	Pyr_redox_2::Pyr_redox_dim	27-343::373-483
810	CGPG1641.pep	Di19	11-219
811	CGPG1651.pep	DEAD::Helicase_C::DSHCT	69-220::378-462::800-988
812	CGPG1656.pep	Cyt-b5::FA_desaturase	9-82::145-399
813	CGPG1668.pep	DUF791::MFS_1	4-358::42-406
815	CGPG1740.pep	DUF860	25-364

PEP SEQ ID	Construct ID	Module	Position
816	CGPG177.pep	WD40::WD40	168-205::257-296
817	CGPG1785.pep	PB1::Pkinase_Tyr	179-266::863-1126
818	CGPG182.pep	LRR_1::LRR_1::LRR_1::LRR_1::L RR_1::LRR_1::LRR_1::LRR_1::LR R_1:: LRR_1 ::LRR_1::LRR_1::LRR_1	46-67::69-90::115-136::161-183::208-229:: 231-252::276-297::382-403::405-427:: 429-451::477-498::500-521::523-544
819	CGPG1837.pep	TFIIS_M::SPOC	328-445::656-762
820	CGPG1873.pep	Pkinase::NAF	20-275::314-374
823	CGPG1899.pep	F-box::Kelch_1::Kelch_1	18-65::139-186::189-235
824	CGPG1913.pep	F-box::FBA_1	31-78::268-416
825	CGPG1918.pep	F-box	30-77
826	CGPG1919.pep	F-box	65-112
827	CGPG1922.pep	F-box::Kelch_1 ::Kelch_1	25-72::118-163::165-210
828	CGPG1929.pep	F-box	1-44
829	CGPG1938.pep	F-box::LRR_2	8-55::159-185
830	CGPG1956.pep	Pre-SET::SET	409-558::560-702
831	CGPG1964.pep	zf-C3HC4::YDG_SRA	109-147::228-345
832	CGPG1973.pep	zf-UBR	40-109
833	CGPG1977.pep	TFIIF_alpha	18-542
834	CGPG1996.pep	Pkinase	3-286
835	CGPG2005.pep	NADPH_Ox::Ferric_reduct::FAD_b inding_8::NAD_binding_6	130-229::352-511::552-671::677-850
837	CGPG2044.pep	PTR2	99-507
838	CGPG2059.pep	Nuc_sug_transp	104-340
839	CGPG2065.pep	PEARLI-4	342-611
841	CGPG2072.pep	DUF1639	264-300
842	CGPG2074.pep	HMA::HMA	75-138::173-235
843	CGPG2116.pep	NOI	1-67
845	CGPG2142.pep	MATH::MATH	101-233::258-375
847	CGPG2190.pep	DJ-1_Pfpl::DJ-1_Pfpl	34-174::240-378
849	CGPG221.pep	DnaJ::DnaJ_CXXCXGXG::DnaJ_C	35-96::160-243::256-378
850	CGPG2213.pep	RNA_pol_I_A49	83-441
851	CGPG2247.pep	DUF23	256-497
852	CGPG228.pep	p450	67-511
853	CGPG2301.pep	PC_rep::PC_rep::PC_rep:: PC_rep::PC_rep::PC_rep	414-447::448-484::485-519::523-557:: 671-705::706-740
854	CGPG2304.pep	Phi_1	32-309
856	CGPG2348.pep	Gal-bind_lectin::Galactosyl_T	165-343::385-580
857	CGPG2349.pep	IQ::IQ	120-140::142-162
858	CGPG2354.pep	ABC1	183-306
859	CGPG2369.pep	DAGK_cat	228-368
860	CGPG2382.pep	WD40::WD40::WD40::WD40	65-103::106-144::197-235::240-278
861	CGPG2392.pep	UBX	311-392
862	CGPG2397.pep	AA_permease	64-510
863	CGPG240.pep	Hydrolase	22-210
865	CGPG2433.pep	DUF23	289-544

PEP SEQ ID	Construct ID	Module	Position
868	CGPG2464.pep	Glyco_transf_8	83-345
869	CGPG2472.pep	Band_7	35-227
870	CGPG2480.pep	Prefoldin	53-175
871	CGPG253.pep	HEAT::HEAT::HEAT::HEAT:: HEAT::HEAT::HEAT::HEAT::HEAT :: HEAT::HEAT::HEAT	82-117::158-194::197-233::236-272::275-311::314-350::353-389::392-428::431-467::470-506::509-545::548-584
872	CGPG2538.pep	PfkB	7-297
873	CGPG2567.pep	zf-C3HC4	372-412
874	CGPG2571.pep	zf-C3HC4	146-187
875	CGPG258.pep	Cyclin_N::Cyclin_C	185-310::312-433
876	CGPG268.pep	PTR2	97-514
877	CGPG274.pep	WD40::WD40::WD40	259-298::303-342::350-389
878	CGPG275.pep	PP2C	32-271
879	CGPG277.pep	IGPD	103-247
880	CGPG2785.pep	SIR2	52-216
881	CGPG2832.pep	Myb_DNA-binding	195-243
883	CGPG2865.pep	SRF-TF	17-67
884	CGPG2874.pep	polyprenyl_synt	123-383
885	CGPG2914.pep	AP2	84-142
886	CGPG295.pep	Pro_isomerase	96-256
888	CGPG3009.pep	Art	4-184
889	CGPG3030.pep	Pkinase	4-301
890	CGPG3048.pep	adh_short	18-186
891	CGPG3056.pep	PP2C	76-341
893	CGPG309.pep	Cyclin_N	4-143
894	CGPG3094.pep	C2	6- 87
895	CGPG3095.pep	F-box::LRR_2::FBD	5-52::163-188::374-426
896	CGPG3137.pep	Spermine_synth	54-313
897	CGPG3156.pep	DEAD::Helicase_C	33-212::279-355
898	CGPG3157.pep	DEAD::Helicase_C	175-355::427-503
899	CGPG3205.pep	F-box::Kelch_1::Kelch_1	130-177::220-269::347-389
900	CGPG3236.pep	Thioredoxin	4-108
901	CGPG3248.pep	Copine	102-250
902	CGPG3255.pep	NTP_transferase::Hexapep::Hexapep::Hexapep::Hexapep	10-246::294-311::312-329::335-352::379-396
903	CGPG3258.pep	UDPGT	23-484
904	CGPG3261.pep	Pkinase	79-334
907	CGPG3283.pep	Mo25	1-339
908	CGPG3302.pep	SRF-TF::K-box	9-59::76-174
909	CGPG3334.pep	GRP	1-113
910	CGPG3361.pep	DUF1644	38-255
911	CGPG337.pep	Glyco_transf_8	19-264
912	CGPG3400.pep	IQ	304-324
914	CGPG3424.pep	TFIIS_C	79-117
915	CGPG3428.pep	DUF914	136-435

PEP SEQ ID	Construct ID	Module	Position
916	CGPG3465.pep	zf-MYND::UCH	57-94::326-630
917	CGPG347.pep	DREPP	1-225
919	CGPG3567.pep	DUF581	63-121
920	CGPG3575.pep	Mago-bind	22-48
921	CGPG3579.pep	SNARE	141-203
926	CGPG365.pep	MATH::BTB	53-182::206-328
927	CGPG3665.pep	BNR::BNR::BNR	138-149::189-200::239-250
928	CGPG3684.pep	Pro_dh	113-464
929	CGPG3690.pep	MtN3_slv::MtN3_slv	10-97::131-217
930	CGPG3717.pep	OTU	219-331
931	CGPG372.pep	SET	83-212
934	CGPG3781.pep	SRF-TF	11-65
935	CGPG380.pep	Histone	25-94
936	CGPG3821.pep	F-box::FBA_3	5-52::205-281
937	CGPG3824.pep	WRKY	107-169
938	CGPG3901.pep	2OG-FeII_Oxy	166-271
939	CGPG391.pep	Histone	58-132
941	CGPG394.pep	DUF6::TPT	11-152::170-319
942	CGPG3964.pep	Pyr_redox	174-248
943	CGPG397.pep	SOR_SNZ::ThiG	24-229::123-290
945	CGPG3983.pep	DUF6::DUF6	31-164::213-342
946	CGPG3986.pep	WD40::WD40	160-197::249-288
947	CGPG3991.pep	SNARE_assoc	111-232
948	CGPG4050.pep	PP2C	49-327
949	CGPG4070.pep	Not3::NOT2_3_5	2-246::693-881
950	CGPG4071.pep	Pkinase_Tyr	135-389
951	CGPG4099.pep	14-3-3	6-243
952	CGPG4138.pep	adh_short	44-217
953	CGPG4152.pep	RRM_1	11-78
954	CGPG4153.pep	HMG-CoA_red	190-583
955	CGPG4164.pep	PP2C	22-322
956	CGPG4169.pep	WD40::WD40::WD40::WD40	253-291::298-336::340-378::510-549
957	CGPG421 .pep	Pkinase::efhand::efhand::efhand::e fhand	22-280::327-355::363-391::399-427::433-461
958	CGPG422.pep	Pkinase	73-331
959	CGPG4223.pep	SRF-TF	23-76
960	CGPG4240.pep	F-box	8-56
961	CGPG4242.pep	PP2C	58-341
962	CGPG4248.pep	efhand::efhand::efhand	10-38::89-117::127-155
963	CGPG425.pep	Pkinase_Tyr	8-260
964	CGPG4265.pep	Cys_Met_Meta_PP	42-432
965	CGPG4283.pep	Dehydrin	36-183
966	CGPG4297.pep	Globin	10-149
967	CGPG43.pep	Aa_trans	46-481
968	CGPG430.pep	Pkinase	8-264

PEP SEQ ID	Construct ID	Module	Position
969	CGPG4305.pep	Rib_5-P_isom_A	85-273
970	CGPG4307.pep	Orn_Arg_deC_N::Orn_DAP_Arg_d eC	98-348::351-459
971	CGPG4315.pep	PPR::PPR::PPR::PPR::PPR::PPR	139-173::209-243::286-320::321-355:: 356-390::391-425
972	CGPG4320.pep	DUF6::DUF6	20-153::190-319
973	CGPG4344.pep	Mito_carr::Mito_carr::Mito_carr	13-98::104-199::203-297
975	CGPG4349.pep	Aha1_N::AHSA1	29-165::233-291
976	CGPG4365.pep	CCT	220-258
978	CGPG4389.pep	Aminotran_1_2	23-376
979	CGPG4404.pep	p450	37-514
980	CGPG4405.pep	p450	69-504
981	CGPG4419.pep	p450	33-477
982	CGPG4432.pep	p450	70-528
984	CGPG4443.pep	p450	32-551
985	CGPG445.pep	PLAT::Lipoxygenase	54-159::171-843
986	CGPG4453.pep	p450	40-500
987	CGPG4481.pep	Glyco_hydro_17	34-352
988	CGPG4490.pep	AMP-binding	42-473
989	CGPG4498.pep	Glyco_hydro_1	40-516
990	CGPG4506.pep	RRM_1	18-89
991	CGPG4553.pep	DUF313	158-265
992	CGPG4583.pep	HIT	43-142
993	CGPG4643.pep	Pkinase	400-656
994	CGPG4650.pep	Pkinase	141-425
996	CGPG468.pep	Fer4::Fer4	116-139::155-178
997	CGPG4684.pep	MIP	11-232
998	CGPG4689.pep	LRRNT_2::LRR_1::LRR_1::Pkinas e	29-70::120-142::144-165::261-532
999	CGPG4691.pep	PCI	281-385
1000	CGPG4702.pep	DUF6::TPT	106-231::240-385
1001	CGPG4703.pep	TPT	205-349
1002	CGPG4710.pep	CPSase_L_chain::CPSase_L_D2:: CPSase_L_D3::CPSase_L_chain:: CPSase_L_D2::MGS	97-217::219-455::515-638::648-775:: 777-989::1061-1148
1003	CGPG4713.pep	DUF231	241-420
1004	CGPG4730.pep	DHquinase_I::Shikimate_dh_N::Sh ikimate_DH	96-313::328-408::440-558
1005	CGPG4747.pep	UQ_con	8-145
1006	CGPG4755.pep	Cpn60_TCP1	30-520
1008	CGPG4779.pep	Peptidase_M22	27-305
1009	CGPG4848.pep	PGAM	77-246
1010	CGPG4879.pep	SIS::CBS	64-197::229-350
1011	CGPG4882.pep	TFIIS	121-206
1012	CGPG4892.pep	DUF260	5-105
1013	CGPG4903.pep	DUF260	7-108
1014	CGPG4925.pep	WD40::WD40::WD40::WD40	74-112::116-153::207-245::249-287
1015	CGPG4937.pep	NLE::WD40::WD40::WD40::WD40	11-79::140-182::195-233::262-299::348-387

PEP SEQ ID	Construct ID	Module	Position
1016	CGPG4949.pep	Pkinase	208-470
1017	CGPG4971.pep	SKI	11-177
1018	CGPG499.pep	Voltage_CLC::CBS	138-560::593-759
1019	CGPG5004.pep	Adh_short	53-224
1020	CGPG5028.pep	Adh_short	42-200
1021	CGPG5032.pep	Adh_short	48-216
1022	CGPG5038.pep	DUF26::DUF26::Pkinase	74-134::200-254::345-620
1023	CGPG5045.pep	LRRNT_2::LRR_1::LRR_1::LRR_1 :: LRR_1 ::Pkinase	24-67::97-119::122-144::146-168::170-192:: 306-576
1024	CGPG5048.pep	LRRNT_2::LRR_1::LRR_1::LRR_1 ::LRR_1::LRR_1::Pkinase	22-59::89-111::113-135::137-159::161-182::183-205::307-578
1025	CGPG5051.pep	AOX	45-323
1026	CGPG5061.pep	Fibrillarin	1-99
1027	CGPG5062.pep	Skp1_POZ::Skp1	6-66::86-163
1028	CGPG5069.pep	Skp1_POZ::Skp1	4-64::89-167
1029	CGPG5070.pep	Skp1_POZ::Skp1	4-64::72-150
1030	CGPG5097.pep	Pkinase	295-579
1031	CGPG510.pep	Rho_GDI	20-223
1032	CGPG5100.pep	Pkinase	353-615
1033	CGPG5117.pep	efhand_like::PI-PLC-X::PI-PLC-Y::C2	25-105::107-251::294-412::430-523
1034	CGPG5151.pep	p450	1-282
1035	CGPG5155.pep	p450	27-493
1036	CGPG5159.pep	p450	26-520
1037	CGPG516.pep	HD::RelA_SpoT	233-337::427-537
1038	CGPG5161.pep	p450	31-503
1039	CGPG5186.pep	Thioredoxin	70-172
1040	CGPG519.pep	Abhydrolase_1	59-279
1041	CGPG5190.pep	Ribosomal_L37	15-125
1042	CGPG5191.pep	TPR_2	166-199
1044	CGPG521.pep	Abhydrolase_1	65-282
1045	CGPG5211.pep	DUF827	16-271
1047	CGPG5213.pep	DUF623	143-203
1048	CGPG522.pep	FA_desaturase	62-277
1049	CGPG5223.pep	PGM_PMM_I::PGM_PMM_II::PGM_PMM_III::PGM_PMM_IV	79-222::251-360::362-486::507-612
1050	CGPG5224.pep	LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1::LRR_1	231-252::254-275::277-298::300-321:: 323-344::369-390::392-413::440-461
1051	CGPG5225.pep	p450	37-452
1052	CGPG5254.pep	2OG-FeII_Oxy	162-279
1053	CGPG5257.pep	SpoIIE	130-374
1054	CGPG5262.pep	SH3_1	303-359
1056	CGPG5282.pep	F-box::Sel1::Sel1::zf-MYND	17-69::129-167::168-203::273-317
1058	CGPG532.pep	Transket_pyr::Transketolase_C	30-207::222-342
1059	CGPG5336.pep	adh_short	19-188
1060	CGPG5350.pep	Aminotran_4	107-395

PEP SEQ ID	Construct ID	Module	Position
1061	CGPG5355.pep	GRAM	95-173
1062	CGPG5376.pep	DUF21::CBS	14-191::210-326
1063	CGPG5377.pep	CBS	81-226
1064	CGPG5382.pep	B56	93-416
1065	CGPG5385.pep	Pyridoxal_deC	146-452
1066	CGPG539.pep	Citrate_synt	78-455
1067	CGPG5437.pep	IQ	115-135
1068	CGPG5450.pep	DHDPS	64-341
1069	CGPG5473.pep	Xan_ur_permease	31-438
1070	CGPG55.pep	Sugar_tr	6-719
1071	CGPG5505.pep	AlaDh_PNT_N::AlaDh_PNT_C::Sa ccharop_dh_N::Saccharop_dh	18-154::194-400::477-583::589-1060
1073	CGPG5514.pep	Cyclin_N::Cyclin_C	165-294::296-422
1074	CGPG5541.pep	Pkinase	316-590
1075	CGPG5546.pep	Cyclin	108-264
1076	CGPG5552.pep	Cornichon	2-125
1077	CGPG5556.pep	SAC3_GANP	20-211
1078	CGPG557.pep	Chitin_bind_1::Barwin	21-62::73-191
1079	CGPG5576.pep	zf-PARP::zf-PARP::PADR1::BRCT::WGR:: PARP _reg::PARP	11-88::117-195::290-343::394-471::517-605:: 633-765::767-979
1080	CGPG5596.pep	Response_reg	9-143
1081	CGPG5605.pep	DEAD::Helicase_C	52-221::290-366
1082	CGPG5606.pep	LRRNT_2::LRR_1::LRR_1::LRR_1 ::LRR_1::LRR_1::LRR_1::LRR_1:: LRR_1::LRR_1::LRR_1::LRR_1::L RR_1::LRR_1::LRR_1::LRR_1::LR R_1::LRR_1:: LRR_1::LRR_1::Pkinase	21-62::90-113::115-137::140-162::164-186::188-211::213-235::237-259::261-283::308-330::332-354::356-375::380-402::404-426::428-450::452-474::500-522::524-546::548-570::571-592::683-964
1083	CGPG561.pep	XG_FTase	54-532
1084	CGPG5618.pep	Lectin_legB::Pkinase	20-247::376-651
1085	CGPG5642.pep	Aldedh	18-477
1086	CGPG5644.pep	ELFV _dehydrog_N::ELFV _dehydr og	51-181::197-428
1087	CGPG5647.pep	Aldedh	46-511
1088	CGPG5655.pep	Glutaminase	23-309
1089	CGPG5660.pep	Glutaminase	24-308
1090	CGPG5662.pep	Aminotran_3	47-381
1091	CGPG568.pep	FTHFS	14-634
1092	CGPG5686.pep	Aminotran_3	31-387
1093	CGPG5702.pep	Gln-synt_N::Gln-synt_C	28-109::116-397
1094	CGPG5712.pep	Pribosyltran	22-158
1095	CGPG5713.pep	Rib_5-P_isom_A	55-229
1096	CGPG5715.pep	Pribosyltran	27-163
1097	CGPG5723.pep	NDK	4-138
1098	CGPG5729.pep	Cyclin_N::Cyclin_C	210-336::338-457
1099	CGPG5730.pep	Lung_7-TM_R	151-444
1101	CGPG5741.pep	NIF	165-344
1102	CGPG5752.pep	CAF1	161-404

PEP SEQ ID	Construct ID	Module	Position
1103	CGPG5771.pep	Acyltransferase	84-277
1104	CGPG5778.pep	Aa_trans	51-498
1105	CGPG5782.pep	Sugar_tr	65-525
1106	CGPG5785.pep	Sugar_tr	69-530
1107	CGPG5797.pep	AA_permease	94-562
1108	CGPG580.pep	MGDG_synth::Glyco_tran_28_C	155-323::349-512
1109	CGPG5805.pep	AA_permease	57-511
1110	CGPG5810.pep	Ank::Ank::Pkinase_Tyr	74-106::107-139::200-468
1111	CGPG5822.pep	Pkinase	131-418
1112	CGPG5837.pep	Pkinase	14-275
1113	CGPG5855.pep	Pkinase	81-363
1114	CGPG5868.pep	Pkinase_Tyr	45-312
1115	CGPG587.pep	FKBP_C	104-208
1117	CGPG5893.pep	Pkinase	52-314
1118	CGPG5909.pep	ADH_zinc_N	163-310
1119	CGPG5914.pep	ADH_N::ADH_zinc_N	54-188::219-362
1123	CGPG5930.pep	Mov34	328-437
1124	CGPG5945.pep	Pyr_redox_2	8-305
1125	CGPG5958.pep	Pyr_redox_2	8-304
1126	CGPG5977.pep	Ank::Ank::Ank::Pkinase	48-80::81-113::114-146::166-424
1127	CGPG598.pep	Nramp	66-429
1128	CGPG5986.pep	Pkinase	43-329
11 29	CGPG5994.pep	F-box::LRR_2	62-108::314-340
1130	CGPG5996.pep	Tetraspannin	4-230
1131	CGPG6021.pep	RRM_1::RRM_1	8-77::108-178
1132	CGPG6027.pep	RRM_1	42-113
1133	CGPG6035.pep	Pyr_redox_2::efhand	51-370::376-404
1134	CGPG604.pep	PSI_PsaH	6-145
1136	CGPG606.pep	Phytochelatin::DUF1984	46-178::179-259
1137	CGPG6069.pep	RNA_pol_A_bac	124-268
1138	CGPG608.pep	TB2_DP1_HVA22	11-108
1139	CGPG6080.pep	Str_synth	144-232
1140	CGPG6082.pep	Ras	8-179
1141	CGPG6089.pep	NicO	153-372
1143	CGPG6128.pep	Reticulon	22-197
1144	CGPG614.pep	cobW	74-246
1145	CGPG6149.pep	Glutaredoxin	84-148
1146	CGPG6172.pep	Ras	11-173
1147	CGPG6174.pep	Ras	19-180
1148	CGPG6176.pep	Ras	15-177
1149	CGPG6197.pep	Phi_1	55-334
1150	CGPG620.pep	tRNA-synt_1g	71-430
1152	CGPG6204.pep	mTERF	75-357
1153	CGPG621.pep	RRM_1	19-90
1154	CGPG6210.pep	Sugar_tr	29-459

PEP SEQ ID	Construct ID	Module	Position
1155	CGPG6211.pep	Sugar _tr	24-479
1156	CGPG6214.pep	Sugar_tr	26-487
1157	CGPG6215.pep	PTR2	93-486
1158	CGPG6222.pep	Sugar_tr	27-490
1159	CGPG6229.pep	Sugar_tr	28-490
1160	CGPG6233.pep	MFS_1	37-473
1161	CGPG6237.pep	Sugar_tr	25-483
1162	CGPG6243.pep	Pkinase	25-333
1163	CGPG6248.pep	Pkinase::NAF	22-276::306-366
1164	CGPG6252.pep	Pkinase::NAF	12-266::298-358
1165	CGPG6267.pep	Pkinase	68-306
1166	CGPG6272.pep	Pkinase	74-349
1167	CGPG6294.pep	Pkinase	75-352
1168	CGPG63.pep	p450	44-511
1170	CGPG6317.pep	PTR2	101-488
1171	CGPG6328.pep	Trehalose_PPase	121-354
1172	CGPG6334.pep	Sterol_desat	34-245
1173	CGPG6336.pep	Sterol_desat	38-247
1174	CGPG6349.pep	LRR_1::LRR_1::LRR_1::LRR_1::L RR_1::LRR_1::LRR_1	42-62::64-84::108-128::130-151::153-174:: 176-197::199-219
1175	CGPG6352.pep	zf-CCHC	81-98
1177	CGPG6364.pep	Gp_dh_N::Gp_dh_C	3-152::157-313
1178	CGPG6366.pep	Gp_dh_N::Gp_dh_C	3-153::158-314
1179	CGPG6375.pep	Aminotran_1_2	36-390
1180	CGPG6388.pep	NTP_transferase	15-285
1181	CGPG6391.pep	ADH_N::ADH_zinc_N	32-143::172-312
1182	CGPG6399.pep	ADH_N::ADH_zinc_N	27-155::186-332
1183	CGPG6407.pep	Glucokinase	5-341
1184	CGPG6418.pep	ADH_N::ADH_zinc_N	28-156::187-333
1185	CGPG6430.pep	Iso_dh	6-355
1186	CGPG6432.pep	ADH_N::ADH_zinc_N	25-135::166-305
1187	CGPG6437.pep	TPT	205-388
1188	CGPG6445.pep	Aldedh	45-511
1189	CGPG6450.pep	Aldedh	26-491
1190	CGPG6458.pep	Aldedh	22-480
1191	CGPG6465.pep	PfkB	10-314
1192	CGPG6476.pep	PFK	3-278
1193	CGPG6505.pep	Aminotran_3	123-449
1194	CGPG6507.pep	Gln-synt_N::Gln-synt_C	105-187::193-446
1195	CGPG6509.pep	Glutaminase	112-396
1196	CGPG6510.pep	Aldedh	17-476
1197	CGPG6515.pep	Aldedh	19-476
1198	CGPG6520.pep	Aldedh	29-491
1199	CGPG6531.pep	Enolase_N::Enolase_C	3-133::138-425
1200	CGPG6553.pep	Aldedh	103-563

PEP SEQ ID	Construct ID	Module	Position
1201	CGPG6557.pep	ELFV_dehydrog_N::ELFV_dehydr og	145-275::290-533
1202	CGPG6563.pep	Aminotran_1_2	120-472
1203	CGPG6564.pep	iPGM_N::Metalloenzyme	90-451::461-576
1204	CGPG6572.pep	Gp_dh_N::Gp_dh_C	91-241::246-402
1205	CGPG6577.pep	iPGM_N::Metalloenzyme	92-451::461-577
1206	CGPG6588.pep	Pyr_redox_2::Pyr_redox_dim	92-409::437-546
1207	CGPG6596.pep	Biotin_lipoyl::E3_binding::2-oxoacid_dh	91-164::228-264::296-521
1209	CGPG6619.pep	Transketolase_N::Transket_pyr::Tr ansketolase_C	101-435::450-627::639-754
1210	CGPG6623.pep	PGAM	96-330
1211	CGPG6626.pep	OstA	109-219
1212	CGPG663.pep	Pro_CA	155-325
1213	CGPG6635.pep	Cytochrom_C	126-204
1215	CGPG6641.pep	AstE_AspA	93-372
1216	CGPG6642.pep	Transket_pyr::Transketolase_C	125-303::319-443
1217	CGPG6645.pep	TIM	95-336
1218	CGPG6660.pep	CBS	97-214
1219	CGPG6671.pep	NTP_transferase	102-374
1220	CGPG6697.pep	Transaldolase	100-400
1221	CGPG6706.pep	iPGM_N::Metalloenzyme	90-451::461-576
1222	CGPG6723.pep	Aminotran_1_2	124-478
1223	CGPG6729.pep	Gln-synt_N::Gln-synt_C	100-182::189-470
1224	CGPG6738.pep	Aminotran_1_2	123-473
1225	CGPG6742.pep	Aldedh	105-563
1226	CGPG6752.pep	TIM	92-334
1227	CGPG6760.pep	GATase_2::Asn_synthase	2-164::241-531
1228	CGPG6768.pep	PGI	55-545
1229	CGPG6779.pep	Isoamylase_N::Alpha-amylase	105-182::219-613
1230	CGPG6785.pep	Molybdop_Fe4S4::Molybdopterin:: Molydop_binding	44-105::108-660::892-1011
1231	CGPG6800.pep	PGI	52-541
1232	CGPG686.pep	RRM_1::zf-CCHC	9-80::118-135
1233	CGPG6898.pep	Hin1	28-163
1234	CGPG6900.pep	Pkinase	97-365
1236	CGPG6920.pep	Dehydrin	14-128
1237	CGPG6921.pep	CorA	48-440
1240	CGPG6945.pep	SNARE	37-99
1241	CGPG6946.pep	MATH	13-133
1242	CGPG6948.pep	PAP2	100-233
1243	CGPG6974.pep	DUF538	7-146
1244	CGPG6976.pep	DUF926	293-406
1245	CGPG6996.pep	CPDase	1-179
1246	CGPG7002.pep	zf-C3HC4	123-157
1247	CGPG7013.pep	zf-C3HC4	115-156
1248	CGPG7021.pep	Invertase_neut	98-564
1251	CGPG7075.pep	DUF1749	77-349

PEP SEQ ID	Construct ID	Module	Position
1252	CGPG7080.pep	Glutaredoxin	44-106
1253	CGPG7094.pep	DUF300	6-281
1254	CGPG7095.pep	Abhydrolase_3	107-321
1255	CGPG7104.pep	Saccharop_dh	13-445
1256	CGPG7118.pep	F-box	25-73
1257	CGPG7122.pep	Pkinase	20-280
1258	CGPG713.pep	Cyclin_N	5-135
1259	CGPG7130.pep	CS	145-220
1260	CGPG7145.pep	Transthyretin	191-310
1261	CGPG7166.pep	DnaJ	79-141
1262	CGPG7179.pep	Bystin	127-423
1263	CGPG7184.pep	PBD	27-127
1264	CGPG7185.pep	GAF::HisKA	190-346::382-445
1265	CGPG7192.pep	2OG-FeII_Oxy	201-301
1266	CGPG7199.pep	RWD	3-122
1267	CGPG72.pep	Amino_oxidase	66-528
1268	CGPG7231.pep	B3_4::B5	118-280::305-378
1269	CGPG7241.pep	Peptidase_C26	58-281
1272	CGPG7265.pep	ARM_1	12-296
1273	CGPG7274.pep	DUF640	36-168
1274	CGPG7291.pep	eIF-1a	20-91
1275	CGPG7303.pep	Aldedh	20-484
1276	CGPG7315.pep	Y_phosphatase2	116-280
1278	CGPG7327.pep	Actin	2-470
1280	CGPG7347.pep	Tcp11	648-1133
1281	CGPG7348.pep	CorA	90-467
1283	CGPG7356.pep	Metallophos	2-120
1284	CGPG7359.pep	Methyltransf_12	38-133
1286	CGPG7372.pep	zf-C3HC4	119-160
1287	CGPG7379.pep	zf-C3HC4	36-76
1288	CGPG7398.pep	DUF212	22-167
1289	CGPG7403.pep	TLD	203-341
1290	CGPG7404.pep	PBP	25-170
1291	CGPG7410.pep	HLH	36-83
1292	CGPG7417.pep	MMR_HSR1	131-252
1293	CGPG7423.pep	Gln-synt_N::Gln-synt_C	102-183::190-471
1294	CGPG7424.pep	FBPase	92-424
1297	CGPG7443.pep	DUF1001	92-274
1298	CGPG7449.pep	ScpA_ScpB	104-347
1301	CGPG7459.pep	DUF1350	90-360
1303	CGPG7481.pep	Abhydrolase_1	113-361
1304	CGPG7483.pep	GTP_EFTU::GTP_EFTU_D2::EFG _C	62-260::281-355::461-551
1306	CGPG7503.pep	PBP	19-170
1307	CGPG7504.pep	MSF1	15-187
1309	CGPG7516.pep	DUF783	25-229

PEP SEQ ID	Construct ID	Module	Position
1312	CGPG7524.pep	Isy1	1-292
1313	CGPG7525.pep	UFD1	10-184
1315	CGPG7537.pep	KTI12	1-291
1317	CGPG7575.pep	Efhand	95-123
1318	CGPG7577.pep	TP_methylase	1-213
1319	CGPG7590.pep	Ribonuc_L-PSP	61-179
1321	CGPG7601.pep	CCT	237-275
1322	CGPG7605.pep	RRM_1	88-158
1323	CGPG7607.pep	Amidohydro_2	10-289
1325	CGPG7632.pep	zf-Tim10_DDP	12-77
1326	CGPG7673.pep	zf-MYND::UCH	76-113::468-774
1327	CGPG7683.pep	zf-LSD1::zf-LSD1::zf-LSD1	28-52::67-91::105-129
1328	CGPG773.pep	H_PPase	64-798
1329	CGPG7776.pep	DUF525	311-445
1330	CGPG7781.pep	SapB_1::SapB_2::SapB_1::SapB_ 2	45-83::86-119::131-169::172-206
1331	CGPG7785.pep	LRRNT_2::LRR_1::LRR_1::LRR_1 ::LRR_1::LRR_1::LRR_1::Pkinase	24-65::93-115::117-139::141-163::165-187:: 189-211::213-235::415-682
1332	CGPG7787.pep	Aldose_epim	26-301
1334	CGPG7796.pep	WD40::WD40::WD40::WD40::WD40::WD40::WD40::WD40::WD40::W D40::Utp13	50-88::92-130::134-174::182-220::391-432:: 436-475::489-527::531-569::573-611::615-653::674-809
1335	CGPG7797.pep	GILT	35-144
1336	CGPG7801.pep	LRR_1::LRR_1::LRR_1::LRR_1::L RR_1::LRR_1::LRR_1::LRR_1::Pki nase	106-129::132-154::156-178::180-199::201-223::225-246::249-272::273-294::456-716
1337	CGPG7813.pep	WD40::WD40::WD40::WD40::PWP 2	379-417::421-459::507-545::549-587::785-900
1341	CGPG7863.pep	zf-CW::MBD	100-153::162-237
1342	CGPG7868.pep	BCNT	165-244
1343	CGPG7881.pep	Aldedh	99-558
1344	CGPG7887.pep	HEAT::Arm::HEAT::Arm	191-222::262-302::389-424::423-463
1345	CGPG7899.pep	RRM_1	225-295
1346	CGPG7901.pep	IQ::IQ	107-127::129-149
1347	CGPG7909.pep	DUF383::DUF384	92-271::272-330
1348	CGPG7911.pep	AAA	245-447
1349	CGPG7919.pep	Cullin	30-191
1350	CGPG7935.pep	IQ::IQ	93-113::115-135
1351	CGPG7940.pep	RRM_1	96-161
1352	CGPG7959.pep	Cyclin_N::Cyclin_C	180-306::308-428
1353	CGPG7967.pep	IQ::IQ	106-126::128-148
1354	CGPG7975.pep	Arm::Arm	28-68::70-110
1355	CGPG7996.pep	efhand	136-164
1356	CGPG8006.pep	AAA	241-440
1357	CGPG801.pep	Cyt-b5	74-171
1358	CGPG8023.pep	RRM_1	11 - 82

PEP SEQ ID	Construct ID	Module	Position
1359	CGPG8025.pep	IQ::IQ	93-113::115-135
1360	CGPG8038.pep	MFS_1	36-433
1361	CGPG8053.pep	DUF246	182-525
1364	CGPG8070.pep	GILT	32-136
1365	CGPG8073.pep	Dirigent	17-183
1366	CGPG8076.pep	Tryp_alpha_amyl	32-107
1369	CGPG8095.pep	IPK	16-279
1370	CGPG8096.pep	60KD_IMP	151-348
1374	CGPG8129.pep	Ank::Ank::Ank	49-81::82-114::115-147
1378	CGPG8165.pep	Glutaredoxin	44-106
1379	CGPG8169.pep	Nol1_Nop2_Fmu	226-505
1380	CGPG8203.pep	Uricase::Uricase	11-140::147-300
1381	CGPG8205.pep	DZC	113-148
1383	CGPG8213.pep	Phosphoesterase	27-388
1384	CGPG8225.pep	FBPase	25-348
1385	CGPG8227.pep	NIR_SIR_ferr::NIR_SIR::NIR_SIR_ ferr::NIR_SIR	44-111::119-275::331-399::405-553
1386	CGPG8235.pep	Aldedh	12-471
1387	CGPG8236.pep	Molybdop_Fe4S4::Molybdopterin:: Molydop_binding::Fer2_BFD	9-63::66-495::593-703::852-903
1388	CGPG8244.pep	PAS_2::GAF::Phytochrome::HisKA::HATPase_c	15-125::152-320::331-513::528-596::637-747
1389	CGPG8254.pep	NIR_SIR_ferr::NIR_SIR::NIR_SIR_ ferr::NIR_SIR	66-133::166-347::362-434::443-591
1390	CGPG8255.pep	PPDK_N::PEP-utilizers::PEP-utilizers_C	16-384::439-531::559-914
1391	CGPG8262.pep	ELFV _dehydrog_N::ELFV_dehydr og	33-163::179-420
1392	CGPG8264.pep	Aldedh	17-480
1393	CGPG8269.pep	PGK	1-396
1394	CGPG8271.pep	Gln-synt_N::Gln-synt_C	16-97::104-386
1395	CGPG8305.pep	Sulfotransfer_1	70-336
1396	CGPG8320.pep	DUF1005	282-487
1397	CGPG8326.pep	Senescence	35-369
1398	CGPG8344.pep	PPR::PPR::PPR::PPR::PPR::PPR: : PPR	173-207::208-242::243-277::279-312::314-348::349-383::384-418
1399	CGPG8347.pep	Ribosomal_S8	5-130
1400	CGPG8359.pep	Tryp_alpha_amyl	85-167
1401	CGPG8370.pep	Tim17	40-156
1402	CGPG8371.pep	PseudoU_synth_1::PseudoU_synt h_1	62-167::324-431
1404	CGPG8378.pep	LysM	78-121
1406	CGPG841.pep	ArfGap	4-120
1408	CGPG8438.pep	DUF239	174-368
1409	CGPG8450.pep	DUF793	1-390
1410	CGPG8451.pep	IQ::IQ	105-125::127-147
1411	CGPG8459.pep	ubiquitin::UBA::XPC-binding::UBA	6-78::145-187::242-298::322-361
1412	CGPG8461.pep	Ribosomal_S8	5-130
1413	CGPG8463.pep	PI3_PI4_kinase	163-421
1414	CGPG8471.pep	F-box::FBA_1	1-46::211-383

PEP SEQ ID	Construct ID	Module	Position
1415	CGPG8474.pep	Metallothio_PEC	12- 85
1416	CGPG8475.pep	DAO	10-372
1417	CGPG8476.pep	IQ::IQ	84-104::106-126
1418	CGPG8490.pep	ACT::ACT	21-85::110-174
1419	CGPG8510.pep	DUF538	9-149
1420	CGPG8530.pep	Radical_SAM	119-283
1421	CGPG8533.pep	DUF212	27-172
1425	CGPG8555.pep	NUDIX	59-196
1426	CGPG8561.pep	zf-C3HC4	154-191
1427	CGPG8569.pep	2OG-Fell_Oxy	159-282
1428	CGPG8573.pep	DUF617	83-242
1431	CGPG8607.pep	DUF862	69-219
1432	CGPG8611.pep	Stig1	13-154
1434	CGPG8632.pep	Sina	86-273
1435	CGPG8634.pep	FA_desaturase	55-278
1436	CGPG8635.pep	DUF59	36-117
1438	CGPG8640.pep	DUF581	119-176
1439	CGPG8642.pep	CRAL_TRIO_N::CRAL_TRIO	5-80::93-266
1441	CGPG8666.pep	PetM	69-120
1443	CGPG8688.pep	Polyketide_cyc	60-191
1444	CGPG8689.pep	DUF506	74-282
1445	CGPG8704.pep	GHMP_kinases_N::GHMP_kinase s_C	24-93::166-249
1448	CGPG8769.pep	Self-incomp_S1	35-144
1449	CGPG8774.pep	Maf	1-207
1450	CGPG8778.pep	PPR::PPR::PPR::PPR::PPR::PPR	13-47::115-149::249-283::284-318:: 320-354::386-420
1451	CGPG8784.pep	Snf7	16-189
1452	CGPG879.pep	ABC_tran::ABC2_membrane::PDR _assoc::ABC_tran::ABC2_membra ne	195-418::520-733::738-812::887-1077:: 1174-1388
1453	CGPG8797.pep	AMP-binding	67-488
1454	CGPG8810.pep	DUF1645	80-252
1455	CGPG8827.pep	DUF623	199-263
1456	CGPG8853.pep	DUF1635	1-218
1457	CGPG8873.pep	p450	72-518
1458	CGPG8877.pep	Exo_endo_phos	33-310
1459	CGPG8878.pep	Pkinase::efhand::efhand	79-337::400-428::434-462
1460	CGPG8881.pep	DUF1677	3-107
1461	CGPG8895.pep	RNA_poll_A14	1-137
1462	CGPG8906.pep	MCM	272-635
1463	CGPG8917.pep	Pkinase	363-697
1464	CGPG8919.pep	Usp::Pkinase	11-141::405-676
1465	CGPG8925.pep	DUF617	82-260
1466	CGPG8930.pep	Lectin_legB::Pkinase	26-261::347-617
1467	CGPG8937.pep	LRR_1::LRR_1::LRR_1::Pkinase	440-461::463-485::487-510::602-873
1468	CGPG8942.pep	RRM_1	23-94

PEP SEQ ID	Construct ID	Module	Position
1469	CGPG8946.pep	Pkinase	516-786
1470	CGPG8990.pep	V-SNARE	71-221
1472	CGPG9008.pep	TPK_catalytic::TPK_B1_binding	40-180::191-259
1473	CGPG9016.pep	ETC_C1_NDUFA4	54-156
1474	CGPG9036.pep	MSP	93-329
1475	CGPG9060.pep	LSM	22-101
1477	CGPG908.pep	PPR::PPR::PPR::PPR::PPR::PPR: :PPR::PPR	62-96::125-158::187-221::250-284:: 351-385::386-419::422-456::488-522
1478	CGPG9093.pep	AWPM-19	15-156
1479	CGPG9096.pep	OTU	11-121
1482	CGPG9111.pep	TB2_DP1_HVA22	4-101
1483	CGPG9112.pep	DUF778	10-177
1484	CGPG9123.pep	DUF833	1-264
1485	CGPG9124.pep	Exo_endo_phos	20-427
1486	CGPG9138.pep	ThiC	165-588
1488	CGPG9150.pep	Pkinase	56-326
1489	CGPG9152.pep	eIF2A	217-410
1490	CGPG9162.pep	AAA	211-398
1491	CGPG9165.pep	GATase::GMP_synt_C	11-201::432-524
1492	CGPG9166.pep	GATase::GMP_synt_C	28-210::447-539
1493	CGPG9171.pep	Zip	5-266
1494	CGPG9177.pep	Complex1_30kDa::Complex1_49k Da	113-181::329-600
1495	CGPG9178.pep	PRA-CH::PRA-PH	54-129::142-230
1496	CGPG9179.pep	Pkinase	4-283
1497	CGPG9181.pep	P21-Arc	17-187
1499	CGPG9189.pep	SAC3_GANP	19-164
1500	CGPG9201.pep	TPT	201-350
1501	CGPG9222.pep	YjeF_N::Carb_kinase	34-199::257-496
1502	CGPG9234.pep	DUF393	65-183
1503	CGPG9237.pep	Tim17	18-146
1504	CGPG9244.pep	TOM20_plant	9-200
1506	CGPG9249.pep	Pkinase	46-330
1507	CGPG9251.pep	Cyclin_N::Cyclin_C	54-186::188-314
1508	CGPG9280.pep	DUF1000	53-168
1510	CGPG9302.pep	Diphthamide_syn	30-398
1511	CGPG931.pep	Pkinase	114-398
1512	CGPG9313.pep	CN_hydrolase::NAD_synthase	5-200::338-652
1514	CGPG9327.pep	OPT	74-729
1515	CGPG933.pep	WD40::WD40::WD40::WD40::WD40::WD40::WD40	46-84::134-173::177-215::222-260::314-353:: 524-562::568-605
1516	CGPG9334.pep	Sugar_tr	7-720
1517	CGPG967.pep	BTB::NPH3	38-135::218-460
1518	CGPG988.pep	Cystatin	36-124

Table 18

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
760	CGPG1022	RRM_1	95	165	58.4	2.40E-14
761	CGPG1035	Peptidase_C54	82	373	558.5	6.50E-165
763	CGPG105	AP2	48	112	146.2	8.50E-41
764	CGPG1060	DUF788	1	169	339.1	7.70E-99
765	CGPG1069	NDUF_B7	2	81	20.4	9.50E-08
766	CGPG108	FHA	208	284	59.7	9.90E-15
766	CGPG108	PP2C	309	570	282.3	9.50E-82
771	CGPG1136	RRM_1	22	87	32.4	1.60E-06
774	CGPG1145	NUDIX	24	160	79.2	1.30E-20
776	CGPG1173	adh_short	6	181	-32	0.00071
777	CGPG1176	F-box	2	50	21.6	0.0027
779	CGPG122	PTR2	113	517	661.3	7.40E-196
780	CGPG126	Response_reg	34	158	86	1.10E-22
781	CGPG1262	Gar1	51	152	251.2	2.10E-72
782	CGPG128	Response_reg	25	149	84.9	2.50E-22
783	CGPG1280	DUF676	515	717	301.1	2.10E-87
784	CGPG1291	DUF862	2	156	209.3	8.70E-60
785	CGPG1295	TMEM14	7	104	166.9	5.20E-47
787	CGPG1315	Brix	60	255	139.3	1.00E-38
788	CGPG1335	LRR_1	424	447	10.1	3.6
789	CGPG1344	Pkinase	496	767	132.9	8.60E-37
789	CGPG1344	Pkinase_Tyr	497	767	81.2	3.30E-21
790	CGPG1352	Pkinase	154	425	140.3	5.20E-39
790	CGPG1352	Pkinase_Tyr	154	425	142.1	1.50E-39
791	CGPG1364	Pkinase	38	416	177.6	3.00E-50
793	CGPG1396	malic	106	295	422.9	4.50E-124
793	CGPG1396	Malic_M	297	550	466.9	2.50E-137
794	CGPG1398	Glycolytic	11	358	877.1	8.10E-261
795	CGPG1399	Metallophos	161	360	87.4	4.50E-23
796	CGPG1429	NTP_transferase	86	365	444	2.00E-130
796	CGPG1429	Hexapep	413	430	3.5	55
796	CGPG1429	Hexapep	466	483	19.6	0.011
797	CGPG1430	E1_dh	89	393	468.9	6.30E-138
798	CGPG1445	Pkinase	33	294	257.4	2.90E-74
798	CGPG1445	Pkinase_Tyr	33	294	99.8	8.00E-27
799	CGPG146	p450	38	482	75.2	2.00E-19
800	CGPG1492	Aldedh	29	491	535.5	5.80E-158
801	CGPG1528	ATP_synt_H	1	70	128.2	2.30E-35
802	CGPG1530	ArfGap	15	137	169.4	9.00E-48
802	CGPG1530	C2	183	262	103	8.90E-28
803	CGPG1535	SPT2	230	329	31.1	9.80E-07
804	CGPG1546	CTP_transf_1	101	300	20	2.00E-07
805	CGPG1567	Ribosomal_L19	107	212	72.7	1.20E-18
806	CGPG1568	FAD_binding_4	82	221	53.1	9.10E-13
807	CGPG1575	DUF740	24	595	626.7	1.90E-185
808	CGPG1619	Pyr_redox_2	27	343	213.2	5.80E-61

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
808	CGPG1619	Pyr_redox	205	297	93.6	6.00E-25
808	CGPG1619	Pyr_redox_dim	373	483	158.2	2.10E-44
810	CGPG1641	Di19	11	219	487.1	2.10E-143
811	CGPG1651	DEAD	69	220	110.3	5.50E-30
811	CGPG1651	Helicase_C	378	462	45.3	2.00E-10
811	CGPG1651	DSHCT	800	988	358.6	1.00E-104
812	CGPG1656	Cyt-b5	9	82	94.5	3.30E-25
812	CGPG1656	FA_desaturase	145	399	256.9	4.10E-74
813	CGPG1668	DUF791	4	358	877.2	7.80E-261
813	CGPG1668	MFS_1	42	406	33.6	6.70E-07
815	CGPG1740	DUF860	25	364	615	6.40E-182
816	CGPG177	WD40	168	205	23.2	0.00096
816	CGPG177	WD40	257	296	36	1.30E-07
817	CGPG1785	PB1	179	266	108.9	1.40E-29
817	CGPG1785	Pkinase	863	1126	202.7	8.80E-58
817	CGPG1785	Pkinase_Tyr	863	1126	253	6.30E-73
818	CGPG182	LRR_1	46	67	11.1	2.3
818	CGPG182	LRR_1	69	90	12.4	1.4
818	CGPG182	LRR_1	115	136	11.8	1.8
818	CGPG182	LRR_1	161	183	8.6	7
818	CGPG182	LRR_1	208	229	12.9	1.1
818	CGPG182	LRR_1	231	252	9.4	4.9
818	CGPG182	LRR_1	276	297	18.4	0.026
818	CGPG182	LRR_1	382	403	8.8	6.5
818	CGPG182	LRR_1	405	427	10.2	3.5
818	CGPG182	LRR_1	429	451	8.8	6.5
818	CGPG182	LRR_1	477	498	9.9	3.9
818	CGPG182	LRR_1	500	521	17	0.069
818	CGPG182	LRR_1	523	544	20.7	0.0052
819	CGPG1837	TFIIS_M	328	445	155	1.90E-43
819	CGPG1837	SPOC	656	762	92.5	1.30E-24
820	CGPG1873	Pkinase	20	275	323.7	3.20E-94
820	CGPG1873	NAF	314	374	112	1.70E-30
823	CGPG1899	F-box	18	65	34.8	3.00E-07
823	CGPG1899	Kelch_1	139	186	33.7	6.30E-07
823	CGPG1899	Kelch_2	188	235	16.7	0.082
823	CGPG1899	Kelch_1	189	235	51.4	3.00E-12
824	CGPG1913	F-box	31	78	39.4	1.20E-08
824	CGPG1913	FBA_1	268	416	-16.6	6.10E-05
825	CGPG1918	F-box	30	77	36	1.30E-07
826	CGPG1919	F-box	65	112	43.1	9.70E-10
827	CGPG1922	F-box	25	72	46.6	8.30E-11
827	CGPG1922	Kelch_2	118	163	24.4	0.0004
827	CGPG1922	Kelch_1	118	163	39.1	1.50E-08
827	CGPG1922	Kelch_2	165	208	26.7	8.10E-05
827	CGPG1922	Kelch_1	165	210	49.6	1.00E-11
828	CGPG1929	F-box	1	44	14.8	0.31

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
829	CGPG1938	F-box	8	55	35.4	2.00E-07
829	CGPG1938	LRR_2	159	185	29.1	1.60E-05
830	CGPG1956	Pre-SET	409	558	20.9	5.60E-06
830	CGPG1956	SET	560	702	157.5	3.40E-44
831	CGPG1964	zf-C3HC4	109	147	35.2	2.30E-07
831	CGPG1964	YDG_SRA	228	345	212.8	8.10E-61
832	CGPG1973	zf-UBR	40	109	73.4	7.10E-19
833	CGPG1977	TFIIF_alpha	18	542	984.3	4.60E-293
834	CGPG1996	Pkinase	3	286	373.9	2.50E-109
835	CGPG2005	NADPH_Ox	130	229	245.7	9.80E-71
835	CGPG2005	Ferric_reduct	352	511	177.6	3.00E-50
835	CGPG2005	FAD_binding_8	552	671	227.3	3.40E-65
835	CGPG2005	NAD_binding_6	677	850	271.5	1.60E-78
837	CGPG2044	PTR2	99	507	587.7	1.10E-173
838	CGPG2059	Nuc_sug_transp	104	340	26.5	4.50E-15
839	CGPG2065	PEARLI-4	342	611	652.6	3.30E-193
841	CGPG2072	DUF1639	264	300	60.4	5.90E-15
842	CGPG2074	HMA	75	138	46.4	9.40E-11
842	CGPG2074	HMA	173	235	50.6	5.40E-12
843	CGPG2116	NOI	1	67	147.8	2.80E-41
845	CGPG2142	MATH	101	233	5.3	0.028
845	CGPG2142	MATH	258	375	33	1.00E-06
847	CGPG2190	DJ-1_Pfpl	34	174	110.4	5.10E-30
847	CGPG2190	DJ-1_Pfpl	240	378	129.9	6.90E-36
849	CGPG221	DnaJ	35	96	137.6	3.30E-38
849	CGPG221	DnaJ_CXXCXGXG	160	243	101	3.60E-27
849	CGPG221	DnaJ_C	256	378	210.4	4.00E-60
850	CGPG2213	RNA_pol_I_A49	83	441	629.1	3.80E-186
851	CGPG2247	DUF23	256	497	99.8	8.20E-27
852	CGPG228	p450	67	511	252.1	1.10E-72
853	CGPG2301	PC_rep	414	447	28.8	1.90E-05
853	CGPG2301	PC_rep	448	484	28	3.20E-05
853	CGPG2301	PC_rep	485	519	33.7	6.30E-07
853	CGPG2301	PC_rep	523	557	10.4	0.45
853	CGPG2301	PC_rep	671	705	11.9	0.28
853	CGPG2301	PC_rep	706	740	32.7	1.30E-06
854	CGPG2304	Phi_1	32	309	680.3	1.40E-201
856	CGPG2348	Gal-bind_lectin	165	343	143.9	4.40E-40
856	CGPG2348	Galactosyl_T	385	580	105.4	1.60E-28
857	CGPG2349	IQ	120	140	33.4	7.70E-07
857	CGPG2349	IQ	142	162	13.6	0.74
858	CGPG2354	ABC1	183	306	132.6	1.00E-36
859	CGPG2369	DAGK_cat	228	368	129.9	7.20E-36
860	CGPG2382	WD40	65	103	48.6	2.2O E-11
860	CGPG2382	WD40	106	144	32.1	2.00E-06
860	CGPG2382	WD40	197	235	34.5	3.70E-07

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
860	CGPG2382	WD40	240	278	47.3	5.30E-11
861	CGPG2392	UBX	311	392	104	4.40E-28
862	CGPG2397	AA_permease	64	510	34.5	3.70E-07
863	CGPG240	Hydrolase	22	210	118.1	2.50E-32
865	CGPG2433	DUF23	289	544	209.9	6.00E-60
868	CGPG2464	Glyco_transf_8	83	345	341.2	1.70E-99
869	CGPG2472	Band_7	35	227	90.6	4.80E-24
870	CGPG2480	Prefoldin	53	175	140.5	4.40E-39
871	CGPG253	HEAT	82	117	18.6	0.022
871	CGPG253	HEAT	158	194	22.9	0.0012
871	CGPG253	HEAT	197	233	15.3	0.22
871	CGPG253	HEAT	236	272	31.1	3.80E-06
871	CGPG253	HEAT	275	311	27.5	4.80E-05
871	CGPG253	HEAT	314	350	26.6	8.60E-05
871	CGPG253	HEAT	353	389	27.9	3.60E-05
871	CGPG253	HEAT	392	428	24.6	0.00035
871	CGPG253	HEAT	431	467	24.2	0.00045
871	CGPG253	HEAT	470	506	21.3	0.0036
871	CGPG253	HEAT	509	545	18.9	0.019
871	CGPG253	HEAT	548	584	17.9	0.036
872	CGPG2538	PfkB	7	297	115.6	1.40E-31
873	CGPG2567	zf-C3HC4	372	412	42.6	1.40E-09
874	CGPG2571	zf-C3HC4	146	187	39.3	1.30E-08
875	CGPG258	Cyclin_N	185	310	240.4	3.70E-69
875	CGPG258	Cyclin_C	312	433	188.8	1.30E-53
876	CGPG268	PTR2	97	514	458.7	7.20E-135
877	CGPG274	WD40	259	298	36.8	7.40E-08
877	CGPG274	WD40	303	342	26.9	7.30E-05
877	CGPG274	WD40	350	389	26.6	9.10E-05
878	CGPG275	PP2C	32	271	205.2	1.50E-58
879	CGPG277	IGPD	103	247	372.6	6.20E-109
880	CGPG2785	SIR2	52	216	107.2	4.70E-29
881	CGPG2832	Myb_DNA-binding	195	243	33.6	6.80E-07
883	CGPG2865	SRF-TF	17	67	94.4	3.50E-25
884	CGPG2874	polyprenyl_synt	123	383	275.6	9.70E-80
885	CGPG2914	AP2	84	142	18	5.20E-06
886	CGPG295	Pro_isomerase	96	256	405.8	6.30E-119
888	CGPG3009	Arf	4	184	165.1	1.80E-46
889	CGPG3030	Pkinase	4	301	322.2	9.20E-94
890	CGPG3048	adh_short	18	186	135.3	1.60E-37
890	CGPG3048	KR	18	188	-35.3	2.60E-05
891	CGPG3056	PP2C	76	341	261.8	1.40E-75
893	CGPG309	Cyclin_N	4	143	8.9	2.50E-05
894	CGPG3094	C2	6	87	73.4	7.30E-19
895	CGPG3095	F-box	5	52	34.8	2.90E-07
895	CGPG3095	LRR_2	163	188	34.7	3.30E-07
895	CGPG3095	FBD	374	426	83.7	5.60E-22

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
896	CGPG3137	Spermine_synth	54	313	429.1	6.20E-126
897	CGPG3156	DEAD	33	212	223	6.80E-64
897	CGPG3156	Helicase_C	279	355	131.8	1.90E-36
898	CGPG3157	DEAD	175	355	231.2	2.30E-66
898	CGPG3157	Helicase_C	427	503	130.3	5.40E-36
899	CGPG3205	F-box	130	177	35.8	1.50E-07
899	CGPG3205	Kelch_1	220	269	34.4	4.00E-07
899	CGPG3205	Kelch_2	220	269	16.3	0.11
899	CGPG3205	Kelch_1	347	389	11.8	0.18
900	CGPG3236	Thioredoxin	4	108	67.2	5.20E-17
901	CGPG3248	Copine	102	250	294.3	2.20E-85
902	CGPG3255	NTP_transferase	10	246	50.6	2.10E-13
902	CGPG3255	Hexapep	294	311	4.4	42
902	CGPG3255	Hexapep	312	329	16.7	0.083
902	CGPG3255	Hexapep	335	352	10.7	5.2
902	CGPG3255	Hexapep	379	396	1.8	85
903	CGPG3258	UDPGT	23	484	-66	2.70E-07
904	CGPG3261	Pkinase	79	334	261.2	2.00E-75
907	CGPG3283	Mo25	1	339	584.5	1.00E-172
908	CGPG3302	SRF-TF	9	59	118.3	2.20E-32
908	CGPG3302	K-box	76	174	130.2	5.60E-36
909	CGPG3334	GRP	1	113	129.8	7.40E-36
910	CGPG3361	DUF1644	38	255	215.2	1.50E-61
911	CGPG337	Glyco_transf_8	19	264	298.7	1.10E-86
912	CGPG3400	IQ	304	324	14.7	0.33
914	CGPG3424	TFIIS_C	79	117	31.8	2.40E-06
915	CGPG3428	DUF914	136	435	-191.9	0.0045
916	CGPG3465	zf-MYND	57	94	50.2	6.80E-12
916	CGPG3465	UCH	326	630	175.9	1.00E-49
917	CGPG347	DREPP	1	225	483.5	2.50E-142
917	CGPG347	PPAK	172	197	0.5	17
919	CGPG3567	DUF581	63	121	135.5	1.40E-37
920	CGPG3575	Mago-bind	22	48	58.7	2.00E-14
921	CGPG3579	SNARE	141	203	59.8	8.90E-15
926	CGPG365	MATH	53	182	59.9	8.30E-15
926	CGPG365	BTB	206	328	86.5	7.90E-23
927	CGPG3665	BNR	138	149	10.5	5.1
927	CGPG3665	BNR	189	200	8.4	9.7
927	CGPG3665	BNR	239	250	10.7	4.8
928	CGPG3684	Pro_dh	113	464	472.8	4.30E-139
929	CGPG3690	MtN3_slv	10	97	116	1.10E-31
929	CGPG3690	MtN3_slv	131	217	119	1.30E-32
930	CGPG3717	OTU	219	331	154.2	3.50E-43
931	CGPG372	SET	83	212	181.8	1.70E-51
934	CGPG3781	SRF-TF	11	65	30.5	6.00E-06
935	CGPG380	Histone	25	94	67.1	5.70E-17

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
936	CGPG3821	F-box	5	52	36.5	9.50E-08
936	CGPG3821	FBA_3	205	281	-0.8	0.00013
937	CGPG3824	WRKY	107	169	89.8	8.20E-24
938	CGPG3901	2OG-FeII_Oxy	166	271	67.5	4.30E-17
939	CGPG391	Histone	58	132	144.1	3.60E-40
941	CGPG394	DUF6	11	152	22.3	0.0018
941	CGPG394	TPT	170	319	165.1	1.80E-46
942	CGPG3964	Pyr_redox	174	248	7.9	0.0034
943	CGPG397	SOR_SNZ	24	229	449.4	4.60E-132
943	CGPG397	ThiG	123	290	-178.1	0.0011
945	CGPG3983	DUF6	31	164	50.3	6.60E-12
945	CGPG3983	DUF6	213	342	60.5	5.40E-15
946	CGPG3986	WD40	160	197	27.3	5.50E-05
946	CGPG3986	WD40	249	288	33.1	9.60E-07
947	CGPG3991	SNARE_assoc	111	232	91.5	2.60E-24
948	CGPG4050	PP2C	49	327	107	5.40E-29
949	CGPG4070	Not3	2	246	527.4	1.50E-155
949	CGPG4070	NOT2_3_5	693	881	217	4.30E-62
950	CGPG4071	Pkinase_Tyr	135	389	256.4	5.90E-74
950	CGPG4071	Pkinase	135	389	221.3	2.20E-63
951	CGPG4099	14-3-3	6	243	509.5	3.80E-150
952	CGPG4138	adh_short	44	217	55.7	1.60E-13
953	CGPG4152	RRM_1	11	78	44.3	4.00E-10
954	CGPG4153	HMG-CoA_red	190	583	1044.7	0
955	CGPG4164	PP2C	22	322	276.7	4.60E-80
956	CGPG4169	WD40	253	291	38.4	2.40E-08
956	CGPG4169	WD40	298	336	30.8	4.80E-06
956	CGPG4169	WD40	340	378	24.8	0.00031
956	CGPG4169	WD40	510	549	55.3	2.00E-13
957	CGPG421	Pkinase	22	280	354.8	1.40E-103
957	CGPG421	efhand	327	355	39.1	1.50E-08
957	CGPG421	efhand	363	391	26.9	7.30E-05
957	CGPG421	efhand	399	427	30.3	6.70E-06
957	CGPG421	efhand	433	461	37.9	3.50E-08
958	CGPG422	Pkinase	73	331	363.9	2.50E-106
959	CGPG4223	SRF-TF	23	76	25.8	0.00015
960	CGPG4240	F-box	8	56	30.1	7.90E-06
961	CGPG4242	PP2C	58	341	195.8	1.00E-55
962	CGPG4248	efhand	10	38	30.5	6.00E-06
962	CGPG4248	efhand	89	117	37	6.70E-08
962	CGPG4248	efhand	127	155	27.1	6.10E-05
963	CGPG425	Pkinase_Tyr	8	260	238.9	1.10E-68
963	CGPG425	Pkinase	8	260	224.7	2.00E-64
964	CGPG4265	Cys_Met_Meta_PP	42	432	263.8	3.50E-76
965	CGPG4283	Dehydrin	36	183	171.1	2.70E-48
966	CGPG4297	Globin	10	149	102.6	1.10E-27
967	CGPG43	Aa_trans	46	481	587.5	1.30E-173

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
968	CGPG430	Pkinase_Tyr	8	264	127.5	3.70E-35
968	CGPG430	Pkinase	8	264	297.5	2.50E-86
969	CGPG4305	Rib_5-P_isom_A	85	273	-27.7	1.60E-07
970	CGPG4307	Orn_Arg_deC_N	98	348	174.8	2.20E-49
970	CGPG4307	Orn_DAP_Arg_deC	351	459	125.2	1.80E-34
971	CGPG4315	PPR	139	173	7.5	0.97
971	CGPG4315	PPR	209	243	26.1	0.00013
971	CGPG4315	PPR	286	320	36.6	8.60E-08
971	CGPG4315	PPR	321	355	11.6	0.32
971	CGPG4315	PPR	356	390	3.1	3.2
971	CGPG4315	PPR	391	425	11.4	0.33
972	CGPG4320	DUF6	20	153	52.8	1.20E-12
972	CGPG4320	DUF6	190	319	40.8	4.70E-09
973	CGPG4344	Mito_carr	13	98	65.1	2.30E-16
973	CGPG4344	Mito_carr	104	199	103.1	8.20E-28
973	CGPG4344	Mito_carr	203	297	83.2	8.20E-22
975	CGPG4349	Aha1_N	29	165	185	1.80E-52
975	CGPG4349	AHSA1	233	291	17.7	0.0027
976	CGPG4365	CCT	220	258	75.3	2.00E-19
978	CGPG4389	Aminotran_1_2	23	376	250.1	4.70E-72
979	CGPG4404	p450	37	514	135.5	1.40E-37
980	CGPG4405	p450	69	504	265.7	9.60E-77
981	CGPG4419	p450	33	477	342.6	6.60E-100
982	CGPG4432	p450	70	528	261.7	1.50E-75
984	CGPG4443	p450	32	551	268.9	1.00E-77
985	CGPG445	PLAT	54	159	137.1	4.70E-38
985	CGPG445	Lipoxygenase	171	843	1610.6	0
986	CGPG4453	p450	40	500	373.2	4.20E-109
987	CGPG4481	Glyco_hydro_17	34	352	365.3	9.40E-107
988	CGPG4490	AMP-binding	42	473	358	1.50E-104
989	CGPG4498	Glyco_hydro_1	40	516	757.2	1.10E-224
990	CGPG4506	RRM_1	18	89	95.5	1.60E-25
991	CGPG4553	DUF313	158	265	219	1.10E-62
992	CGPG4583	HIT	43	142	152.5	1.10E-42
993	CGPG4643	Pkinase	400	656	303.4	4.20E-88
993	CGPG4643	Pkinase_Tyr	400	656	149.3	1.00E-41
994	CGPG4650	Pkinase	141	425	320.1	4.00E-93
996	CGPG468	Fer4	116	139	30.6	5.60E-06
996	CGPG468	Fer4	155	178	38.5	2.30E-08
997	CGPG4684	MIP	11	232	407.1	2.60E-119
998	CGPG4689	LRRNT_2	29	70	63.6	6.40E-16
998	CGPG4689	LRR_1	120	142	10.7	2.8
998	CGPG4689	LRR_1	144	165	8.2	8.5
998	CGPG4689	Pkinase	261	532	154.6	2.70E-43
998	CGPG4689	Pkinase_Tyr	261	532	77.7	3.80E-20
999	CGPG4691	PCI	281	385	116.6	6.90E-32

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
1000	CGPG4702	UAA	92	388	-129.1	0.00058
1000	CGPG4702	DUF6	106	231	27.4	5.10E-05
1000	CGPG4702	TPT	240	385	193.4	5.60E-55
1001	CGPG4703	UAA	55	355	-71.5	7.60E-07
1001	CGPG4703	TPT	205	349	160.4	4.80E-45
1002	CGPG4710	CPSase_L_chain	97	217	196.1	8.20E-56
1002	CGPG4710	CPSase_L_D2	219	455	449.7	3.80E-132
1002	CGPG4710	CPSase_L_D3	515	638	255.2	1.30E-73
1002	CGPG4710	CPSase_L_chain	648	775	68.2	2.60E-17
1002	CGPG4710	CPSase_L_D2	777	989	118.2	2.40E-32
1002	CGPG4710	MGS	1061	1148	105.9	1.20E-28
1003	CGPG4713	DUF231	241	420	229.6	6.60E-66
1004	CGPG4730	DHquinase_I	96	313	281.4	1.80E-81
1004	CGPG4730	Shikimate_dh_N	328	408	148.1	2.40E-41
1004	CGPG4730	Shikimate_DH	440	558	118.7	1.60E-32
1005	CGPG4747	UQ_con	8	145	267.3	3.00E-77
1006	CGPG4755	Cpn60_TCP1	30	520	556.6	2.60E-164
1008	CGPG4779	Peptidase_M22	27	305	238.7	1.20E-68
1009	CGPG4848	PGAM	77	246	22.5	4.10E-05
1010	CGPG4879	SIS	64	197	71.5	2.60E-18
1010	CGPG4879	CBS	229	350	83.4	6.80E-22
1011	CGPG4882	TFIIS	121	206	127	5.10E-35
1012	CGPG4892	DUF260	5	105	193.4	5.60E-55
1013	CGPG4903	DUF260	7	108	237	4.20E-68
1014	CGPG4925	WD40	74	112	34.3	4.30E-07
1014	CGPG4925	WD40	116	153	27.5	4.60E-05
1014	CGPG4925	WD40	207	245	42.3	1.60E-09
1014	CGPG4925	WD40	249	287	47.1	6.10E-11
1015	CGPG4937	NLE	11	79	115.3	1.70E-31
1015	CGPG4937	WD40	140	182	33.3	8.30E-07
1015	CGPG4937	WD40	195	233	31.2	3.50E-06
1015	CGPG4937	WD40	262	299	29.4	1.20E-05
1015	CGPG4937	WD40	348	387	34.5	3.70E-07
1016	CGPG4949	Pkinase	208	470	-29.3	8.10E-07
1017	CGPG4971	SKI	11	177	104	4.30E-28
1018	CGPG499	Voltage_CLC	138	560	690.2	1.50E-204
1018	CGPG499	CBS	593	759	42.9	1.10E-09
1019	CGPG5004	adh_short	53	224	50.1	7.30E-12
1020	CGPG5028	adh_short	42	200	-2.3	7.90E-06
1021	CGPG5032	adh_short	48	216	81.4	2.80E-21
1022	CGPG5038	DUF26	74	134	74.3	3.90E-19
1022	CGPG5038	DUF26	200	254	94	4.40E-25
1022	CGPG5038	Pkinase	345	620	172.1	1.40E-48
1022	CGPG5038	Pkinase_Tyr	345	620	130.8	3.70E-36
1023	CGPG5045	LRRNT_2	24	67	38.3	2.70E-08
1023	CGPG5045	LRR_1	97	119	16.6	0.092
1023	CGPG5045	LRR_1	122	144	10.9	2.6

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
1023	CGPG5045	LRR_1	146	168	12.9	1.1
1023	CGPG5045	LRR_1	170	192	14.8	0.31
1023	CGPG5045	Pkinase	306	576	6.1	6.30E-09
1024	CGPG5048	LRRNT_2	22	59	39.5	1.20E-08
1024	CGPG5048	LRR_1	89	111	16.8	0.08
1024	CGPG5048	LRR_1	113	135	13.6	0.72
1024	CGPG5048	LRR_1	137	159	20.2	0.0076
1024	CGPG5048	LRR_1	161	182	14.5	0.4
1024	CGPG5048	LRR_1	183	205	14.1	0.49
1024	CGPG5048	Pkinase	307	578	47.4	2.20E-11
1025	CGPG5051	AOX	45	323	739.1	3.00E-219
1026	CGPG5061	Fibrillarin	1	99	56.9	6.50E-14
1027	CGPG5062	Skp1_POZ	6	66	115.7	1.30E-31
1027	CGPG5062	Skp1	86	163	168.3	2.00E-47
1028	CGPG5069	Skp1_POZ	4	64	108.8	1.60E-29
1028	CGPG5069	Skp1	89	167	169.2	1.10E-47
1029	CGPG5070	Skp1_POZ	4	64	93.5	6.40E-25
1029	CGPG5070	Skp1	72	150	113.9	4.50E-31
1030	CGPG5097	Pkinase	295	579	140.1	5.90E-39
1030	CGPG5097	Pkinase_Tyr	295	579	68.2	2.60E-17
1031	CGPG510	Rho_GDI	20	223	44	6.20E-12
1032	CGPG5100	Pkinase	353	615	-2.8	2.10E-08
1033	CGPG5117	efhand_like	25	105	66.7	7.50E-17
1033	CGPG5117	PI-PLC-X	107	251	133	8.30E-37
1033	CGPG5117	PI-PLC-Y	294	412	87.5	4.20E-23
1033	CGPG5117	C2	430	523	64.2	4.10E-16
1034	CGPG5151	p450	1	282	11.9	1.60E-11
1035	CGPG5155	p450	27	493	112.9	9.10E-31
1036	CGPG5159	p450	26	520	145.4	1.50E-40
1037	CGPG516	HD	233	337	53.7	6.00E-13
1037	CGPG516	RelA_SpoT	427	537	165	1.90E-46
1037	CGPG516	p450	31	503	89.9	8.00E-24
1039	CGPG5186	Thioredoxin	70	172	137.3	4.20E-38
1040	CGPG519	Abhydrolase_1	59	279	29.7	1.10E-05
1041	CGPG5190	Ribosomal_L37	15	125	143.9	4.40E-40
1042	CGPG5191	TPR_2	166	199	22	0.0022
1044	CGPG521	Abhydrolase_1	65	282	21	0.00018
1044	CGPG521	DUF827	16	271	333.9	2.80E-97
1047	CGPG5213	DUF623	143	203	116.7	6.40E-32
1048	CGPG522	FA_desaturase	62	277	200.7	3.50E-57
1049	CGPG5223	PGM_PMM_I	79	222	166.1	8.80E-47
1049	CGPG5223	PGM_PMM_II	251	360	96.4	8.30E-26
1049	CGPG5223	PGM_PMM_III	362	486	138.1	2.50E-38
1049	CGPG5223	PGM_PMM_IV	507	612	75.4	1.80E-19
1050	CGPG5224	LRR_1	231	252	9.5	4.7
1050	CGPG5224	LRR_1	254	275	15.2	0.24

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
1050	CGPG5224	LRR_1	277	298	18.3	0.027
1050	CGPG5224	LRR_1	300	321	17.8	0.039
1050	CGPG5224	LRR_1	323	344	12.7	1.2
1050	CGPG5224	LRR_1	369	390	7.8	10
1050	CGPG5224	LRR_1	392	413	13.5	0.75
1050	CGPG5224	LRR_1	440	461	17.7	0.041
1051	CGPG5225	p450	37	452	209.6	7.00E-60
1052	CGPG5254	2OG-Fell_Oxy	162	279	65.3	1.90E-16
1053	CGPG5257	SpoIIE	130	374	52.9	1.00E-12
1054	CGPG5262	SH3_1	303	359	75.4	1.80E-19
1054	CGPG5262	SH3_2	304	359	35.8	1.50E-07
1056	CGPG5282	F-box	17	69	14.5	0.39
1056	CGPG5282	Sel1	129	167	19.9	0.0091
1056	CGPG5282	Sel1	168	203	12.2	0.47
1056	CGPG5282	zf-MYND	273	317	38.2	2.80E-08
1058	CGPG532	Transket_pyr	30	207	261.4	1.90E-75
1058	CGPG532	Transketolase_C	222	342	175.3	1.50E-49
1059	CGPG5336	adh_short	19	188	81.3	3.10E-21
1059	CGPG5336	KR	19	205	-66.7	0.0017
1060	CGPG5350	Aminotran_4	107	395	353.2	4.30E-103
1061	CGPG5355	GRAM	95	173	41.4	3.20E-09
1062	CGPG5376	DUF21	14	191	162.9	8.00E-46
1062	CGPG5376	CBS	210	326	27	6.60E-05
1063	CGPG5377	CBS	81	226	138.6	1.70E-38
1064	CGPG5382	B56	93	416	759.8	1.80E-225
1065	CGPG5385	Pyridoxal_deC	146	452	-54.5	1.00E-10
1065	CGPG5385	Aminotran_5	150	491	-148.7	7.00E-05
1066	CGPG539	Citrate_synt	78	455	764.2	8.10E-227
1067	CGPG5437	IQ	115	135	31.3	3.40E-06
1068	CGPG5450	DHDPS	64	341	486.2	4.00E-143
1069	CGPG5473	Xan_ur_permease	31	438	164.5	2.70E-46
1070	CGPG55	Sugar_tr	6	719	208.1	2.10E-59
1070	CGPG55	MFS_1	11	678	137.1	4.70E-38
1071	CGPG5505	AlaDh_PNT_N	18	154	81.4	2.80E-21
1071	CGPG5505	AlaDh_PNT_C	194	400	134	4.10E-37
1071	CGPG5505	Saccharop_dh_N	477	583	228.5	1.50E-65
1071	CGPG5505	ThiF	585	714	-36.3	0.0039
1071	CGPG5505	Saccharop_dh	589	1060	377.2	2.50E-110
1073	CGPG5514	Cyclin_N	165	294	211.1	2.60E-60
1073	CGPG5514	Cyclin_C	296	422	111.3	2.70E-30
1074	CGPG5541	Pkinase	316	590	319.8	4.80E-93
1075	CGPG5546	Cyclin	108	264	289.2	7.70E-84
1076	CGPG5552	Cornichon	2	125	268.7	1.20E-77
1077	CGPG5556	SAC3_GANP	20	211	214.5	2.30E-61
1078	CGPG557	Chitin_bind_1	21	62	72.3	1.50E-18
1078	CGPG557	Barwin	73	191	311.7	1.30E-90
1079	CGPG5576	zf-PARP	11	88	88.5	2.10E-23

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
1079	CGPG5576	zf-PARP	117	195	65.3	2.00E-16
1079	CGPG5576	PADR1	290	343	120.6	4.40E-33
1079	CGPG5576	BRCT	394	471	47.4	4.80E-11
1079	CGPG5576	WGR	517	605	153	7.90E-43
1079	CGPG5576	PARP_reg	633	765	87.7	3.60E-23
1079	CGPG5576	PARP	767	979	434.2	1.80E-127
1080	CGPG5596	Response_reg	9	143	77.4	4.60E-20
1081	CGPG5605	DEAD	52	221	246.1	7.20E-71
1081	CGPG5605	Helicase_C	290	366	89.9	7.50E-24
1082	CGPG5606	LRRNT_2	21	62	49.4	1.20E-11
1082	CGPG5606	LRR_1	90	113	14.1	0.52
1082	CGPG5606	LRR_1	115	137	14.7	0.35
1082	CGPG5606	LRR_1	140	162	19.3	0.014
1082	CGPG5606	LRR_1	164	186	17.2	0.059
1082	CGPG5606	LRR_1	188	211	11.7	1.9
1082	CGPG5606	LRR_1	213	235	14.2	0.47
1082	CGPG5606	LRR_1	237	259	16.1	0.13
1082	CGPG5606	LRR_1	261	283	8.9	6.3
1082	CGPG5606	LRR_1	308	330	12	1.6
1082	CGPG5606	LRR_1	332	354	11.1	2.4
1082	CGPG5606	LRR_1	356	375	9.3	5.1
1082	CGPG5606	LRR_1	380	402	10.8	2.7
1082	CGPG5606	LRR_1	404	426	17.1	0.065
1082	CGPG5606	LRR_1	428	450	12	1.6
1082	CGPG5606	LRR_1	452	474	14.6	0.36
1082	CGPG5606	LRR_1	500	522	14.3	0.44
1082	CGPG5606	LRR_1	524	546	14.9	0.28
1082	CGPG5606	LRR_1	548	570	15.1	0.25
1082	CGPG5606	LRR_1	571	592	15.6	0.18
1082	CGPG5606	Pkinase	683	964	125.6	1.40E-34
1082	CGPG5606	Pkinase_Tyr	683	964	85	2.30E-22
1083	CGPG561	XG_FTase	54	532	1264.7	0
1084	CGPG5618	Lectin_legB	20	247	260.2	4.30E-75
1084	CGPG5618	Pkinase	376	651	185.1	1.70E-52
1084	CGPG5618	Pkinase_Tyr	376	651	141.6	2.10E-39
1085	CGPG5642	Aldedh	18	477	674.3	9.50E-200
1086	CGPG5644	ELFV_dehydrog_N	51	181	278.1	1.80E-80
1086	CGPG5644	ELFV_dehydrog	197	428	394.9	1.20E-115
1087	CGPG5647	Aldedh	46	511	669.6	2.50E-198
1088	CGPG5655	Glutaminase	23	309	642.2	4.30E-190
1089	CGPG5660	Glutaminase	24	308	599	4.30E-177
1090	CGPG5662	Aminotran_3	47	381	473.1	3.30E-139
1091	CGPG568	FTHFS	14	634	1422.6	0
1092	CGPG5686	Aminotran_3	31	387	365.8	7.00E-107
1093	CGPG5702	Gln-synt_N	28	109	171.5	2.10E-48
1093	CGPG5702	Gln-synt_C	116	397	581.1	1.10E-171

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
1094	CGPG5712	Pribosyltran	22	158	167.1	4.50E-47
1095	CGPG5713	Rib_5-P_isom_A	55	229	353.2	4.30E-103
1096	CGPG5715	Pribosyltran	27	163	131.6	2.20E-36
1097	CGPG5723	NDK	4	138	304.7	1.80E-88
1098	CGPG5729	Cyclin_N	210	336	218.9	1.20E-62
1098	CGPG5729	Cyclin_C	338	457	133.1	7.50E-37
1099	CGPG5730	Lung_7-TM_R	151	444	474.5	1.30E-139
1101	CGPG5741	NIF	165	344	184.2	3.20E-52
1102	CGPG5752	CAF1	161	404	356.1	5.80E-104
1103	CGPG5771	Acyltransferase	84	277	123.8	4.90E-34
1104	CGPG5778	Aa_trans	51	498	498.7	6.60E-147
1105	CGPG5782	Sugar_tr	65	525	819.5	1.80E-243
1105	CGPG5782	MFS_1	69	485	103.5	6.40E-28
1106	CGPG5785	Sugar_tr	69	530	791.6	4.50E-235
1106	CGPG5785	MFS_1	73	490	88.2	2.50E-23
1107	CGPG5797	AA_permease	94	562	588.2	7.60E-174
1108	CGPG580	MGDG_synth	155	323	316.4	5.00E-92
1108	CGPG580	Glyco_tran_28_C	349	512	5.9	0.0004
1109	CGPG5805	AA_permease	57	511	619.8	2.40E-183
1110	CGPG5810	Ank	74	106	1.8	17
1110	CGPG5810	Ank	107	139	51.9	2.10E-12
1110	CGPG5810	Pkinase	197	468	93.7	5.40E-25
1110	CGPG5810	Pkinase_Tyr	200	468	100.3	5.80E-27
1111	CGPG5822	Pkinase	131	418	302.6	7.40E-88
1112	CGPG5837	Pkinase	14	275	128.1	2.50E-35
1113	CGPG5855	Pkinase_Tyr	81	363	133.4	6.10E-37
1113	CGPG5855	Pkinase	81	363	158.3	2.00E-44
1114	CGPG5868	Pkinase_Tyr	45	312	154.4	3.00E-43
1114	CGPG5868	Pkinase	45	312	150.1	6.00E-42
1115	CGPG587	FKBP_C	104	208	138.8	1.50E-38
1117	CGPG5893	Pkinase	52	314	-49.3	1.30E-05
1118	CGPG5909	ADH_zinc_N	163	310	104.41	3.40E-28
1119	CGPG5914	ADH_N	54	188	144.5	2.80E-40
1119	CGPG5914	ADH_zinc_N	219	362	157.2	4.30E-44
1123	CGPG5930	Mov34	328	437	81.7	2.30E-21
1124	CGPG5945	Pyr_redox_2	8	305	125.3	1.70E-34
1124	CGPG5945	Pyr_redox	167	262	104.5	3.00E-28
1125	CGPG5958	Pyr_redox_2	8	304	126.4	8.20E-35
1125	CGPG5958	Pyr_redox	166	261	115.1	2.00E-31
1126	CGPG5977	Ank	48	80	1.7	18
1126	CGPG5977	Ank	81	113	39.4	1.30E-08
1126	CGPG5977	Ank	114	146	18.6	0.023
1126	CGPG5977	Pkinase	166	424	186.4	6.90E-53
1126	CGPG5977	Pkinase_Tyr	166	424	172.3	1.20E-48
1127	CGPG598	Nramp	66	429	644.5	8.90E-191
1128	CGPG5986	Pkinase	43	329	323.5	3.60E-94
1129	CGPG5994	F-box	62	108	15.1	0.26

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
1129	CGPG5994	LRR_2	314	340	17.1	0.063
1130	CGPG5996	Tetraspannin	4	230	244.3	2.60E-70
1131	CGPG6021	RRM_1	8	77	73.1	8.60E-19
1131	CGPG6021	RRM_1	108	178	81.2	3.20E-21
1132	CGPG6027	RRM_1	42	113	104.5	3.10E-28
1133	CGPG6035	Pyr_redox_2	51	370	86.5	8.30E-23
1133	CGPG6035	Pyr_redox	216	323	55.5	1.80E-13
1133	CGPG6035	efhand	376	404	23.3	0.00087
1134	CGPG604	PSI_PsaH	6	145	342.9	5.50E-100
1136	CGPG606	Phytochelatin	46	178	381.8	1.10E-111
1136	CGPG606	DUF1984	179	259	206.3	7.10E-59
1137	CGPG6069	RNA_pol_L	90	382	75.5	1.60E-19
1137	CGPG6069	RNA_pol_A_bac	124	268	113	8.80E-31
1138	CGPG608	TB2_DP1_HVA22	11	108	188.4	1.70E-53
1139	CGPG6080	Str_synth	144	232	164.7	2.40E-46
1140	CGPG6082	Miro	8	121	62.7	1.20E-15
1140	CGPG6082	Ras	8	179	254	3.00E-73
1141	CGPG6089	NicO	153	372	147.1	4.70E-41
1143	CGPG6128	Reticulon	22	197	303.7	3.40E-88
1144	CGPG614	cobW	74	246	232.9	6.80E-67
1145	CGPG6149	Glutaredoxin	84	148	115.9	1.10E-31
1146	CGPG6172	Miro	11	126	74.1	4.60E-19
1146	CGPG6172	Ras	11	173	288.8	1.00E-83
1147	CGPG6174	Miro	19	133	75.8	1.30E-19
1147	CGPG6174	Ras	19	180	326.5	4.80E-95
1148	CGPG6176	Miro	15	130	63.8	5.50E-16
1148	CGPG6176	Ras	15	177	285.5	1.00E-82
1149	CGPG6197	Phi_1	55	334	656.6	2.00E-194
1150	CGPG620	tRNA-synt_1g	71	430	627.4	1.20E-185
1152	CGPG6204	mTERF	75	357	69.9	8.00E-18
1153	CGPG621	RRM_1	19	90	20.7	0.0017
1154	CGPG6210	MFS_1	26	419	55.8	1.40E-13
1154	CGPG6210	Sugar_tr	29	459	239.3	8.30E-69
1155	CGPG6211	Sugar_tr	24	479	469.9	3.00E-138
1155	CGPG6211	MFS_1	30	443	98.8	1.60E-26
1156	CGPG6214	Sugar_tr	26	487	541.1	1.20E-159
1156	CGPG6214	MFS_1	32	448	89.3	1.20E-23
1157	CGPG6215	MFS_1	34	498	52.2	1.80E-12
1157	CGPG6215	PTR2	93	486	181.3	2.40E-51
1158	CGPG6222	Sugar_tr	27	490	523.9	1.70E-154
1158	CGPG6222	MFS_1	31	447	92.4	1.40E-24
1159	CGPG6229	MFS_1	23	447	97.4	4.40E-26
1159	CGPG6229	Sugar_tr	28	490	565.7	4.40E-167
1160	CGPG6233	Sugar_tr	22	512	23.1	1.30E-07
1160	CGPG6233	MFS_1	37	473	69.1	1.40E-17
1161	CGPG6237	Sugar_tr	25	483	398.5	1.00E-116

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
1161	CGPG6237	MFS_1	29	442	110	6.80E-30
1162	CGPG6243	Pkinase	25	333	289.3	7.40E-84
1163	CGPG6248	Pkinase	22	276	338.1	1.50E-98
1163	CGPG6248	NAF	306	366	64.3	3.90E-16
1164	CGPG6252	Pkinase	12	266	340.3	3.20E-99
1164	CGPG6252	NAF	298	358	110.9	3.70E-30
1165	CGPG6267	Pkinase	68	306	-7.3	4.00E-08
1166	CGPG6272	Pkinase	74	349	167.4	3.70E-47
1166	CGPG6272	Pkinase_Tyr	74	349	134.3	3.20E-37
1167	CGPG6294	Pkinase	75	352	-1.8	1.90E-08
1168	CGPG63	p450	44	511	425.2	8.90E-125
1170	CGPG6317	MFS_1	39	504	44.5	3.50E-10
1170	CGPG6317	PTR2	101	488	297.8	2.00E-86
1171	CGPG6328	Trehalose_PPase	121	354	380.5	2.60E-111
1172	CGPG6334	Sterol_desat	34	245	281.2	2.00E-81
1173	CGPG6336	Sterol_desat	38	247	261.6	1.60E-75
1174	CGPG6349	LRR_1	42	62	15.7	0.17
1174	CGPG6349	LRR_1	64	84	7.9	9.3
1174	CGPG6349	LRR_1	108	128	11.6	1.9
1174	CGPG6349	LRR_1	130	151	12.5	1.3
1174	CGPG6349	LRR_1	153	174	10.7	2.9
1174	CGPG6349	LRR_1	176	197	11.9	1.7
1174	CGPG6349	LRR_1	199	219	7.9	9.6
1175	CGPG6352	zf-CCHC	81	98	18.4	0.00091
1177	CGPG6364	Gp_dh_N	3	152	341.6	1.30E-99
1177	CGPG6364	Gp_dh_C	157	313	381.4	1.40E-111
1178	CGPG6366	Gp_dh_N	3	153	301.7	1.40E-87
1178	CGPG6366	Gp_dh_C	158	314	334	2.60E-97
1179	CGPG6375	Aminotran_1_2	36	390	217	4.30E-62
1180	CGPG6388	NTP_transferase	15	285	397.9	1.50E-116
1181	CGPG6391	ADH_N	32	143	172.7	9.30E-49
1181	CGPG6391	ADH_zinc_N	172	312	193.2	6.00E-55
1182	CGPG6399	ADH_N	27	155	135.6	1.30E-37
1182	CGPG6399	ADH_zinc_N	186	332	115.4	1.70E-31
1183	CGPG6407	Glucokinase	5	341	569.2	4.00E-168
1184	CGPG6418	ADH_N	28	156	128.2	2.40E-35
1184	CGPG6418	ADH_zinc_N	187	333	135.1	2.00E-37
1185	CGPG6430	Iso_dh	6	355	346.2	5.40E-101
1186	CGPG6432	ADH_N	25	135	157.5	3.40E-44
1186	CGPG6432	ADH_zinc_N	166	305	114.8	2.40E-31
1187	CGPG6437	TPT	205	388	167.3	4.00E-47
1188	CGPG6445	Aldedh	45	511	720.6	1.10E-213
1189	CGPG6450	Aldedh	26	491	797.6	7.00E-237
1190	CGPG6458	Aldedh	22	480	796.6	1.40E-236
1191	CGPG6465	PfkB	10	314	274.5	2.10E-79
1192	CGPG6476	PFK	3	278	659.8	2.20E-195
1193	CGPG6505	Aminotran_3	123	449	321.7	1.30E-93

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
1194	CGPG6507	Gln-synt_N	105	187	85.7	1.50E-22
1194	CGPG6507	Gln-synt_C	193	446	528.1	9.40E-156
1195	CGPG6509	Glutaminase	112	396	599	4.30E-177
1196	CGPG6510	Aldedh	17	476	689.2	3.10E-204
1197	CGPG6515	Aldedh	19	476	789.7	1.70E-234
1198	CGPG6520	Aldedh	29	491	790.7	8.30E-235
1199	CGPG6531	Enolase_N	3	133	215.5	1.20E-61
1199	CGPG6531	Enolase_C	138	425	571.7	7.20E-169
1200	CGPG6553	Aldedh	103	563	768.4	4.40E-228
1201	CGPG6557	ELFV_dehydrog_N	145	275	294.9	1.50E-85
1201	CGPG6557	ELFV_dehydrog	290	533	486.7	2.80E-143
1202	CGPG6563	Aminotran_1_2	120	472	403.3	3.50E-118
1203	CGPG6564	iPGM_N	90	451	876.8	1.00E-260
1203	CGPG6564	Metalloenzyme	461	576	173.3	5.90E-49
1204	CGPG6572	Gp_dh_N	91	241	301.7	1.40E-87
1204	CGPG6572	Gp_dh_C	246	402	334	2.60E-97
1205	CGPG6577	iPGM_N	92	451	863.6	9.30E-257
1205	CGPG6577	Metalloenzyme	461	577	195.7	1.10E-55
1206	CGPG6588	DAO	92	493	-24.3	0.00021
1206	CGPG6588	FAD_binding_2	92	421	-110.2	0.0013
1206	CGPG6588	GIDA	92	418	-223.3	0.0021
1206	CGPG6588	Pyr_redox_2	92	409	252.3	9.90E-73
1206	CGPG6588	Pyr_redox	265	362	125.3	1.70E-34
1206	CGPG6588	Pyr_redox_dim	437	546	222.4	9.80E-64
1207	CGPG6596	Biotin_lipoyl	91	164	76	1.20E-19
1207	CGPG6596	E3_binding	228	264	68.1	2.70E-17
1207	CGPG6596	2-oxoacid_dh	296	521	326.6	4.20E-95
1209	CGPG6619	Transketolase_N	101	435	777.9	5.90E-231
1209	CGPG6619	Transket_pyr	450	627	245.4	1.20E-70
1209	CGPG6619	Transketolase_C	639	754	36.1	1.30E-07
1210	CGPG6623	PGAM	96	330	130.8	3.80E-36
1211	CGPG6626	OstA	109	219	106.8	6.20E-29
1212	CGPG663	Pro_CA	155	325	357.7	1.90E-104
1213	CGPG6635	Cytochrom_C	126	204	55.4	1.90E-13
1215	CGPG6641	AstE_AspA	93	372	312.6	7.00E-91
1216	CGPG6642	Transket_pyr	125	303	234.2	2.70E-67
1216	CGPG6642	Transketolase_C	319	443	196.1	8.20E-56
1217	CGPG6645	TIM	95	336	398.9	7.60E-117
1218	CGPG6660	CBS	97	214	118.4	2.00E-32
1219	CGPG6671	NTP_transferase	102	374	277.3	2.90E-80
1220	CGPG6697	Transaldolase	100	400	657.9	7.90E-195
1221	CGPG6706	iPGM_N	90	451	870.1	1.00E-258
1221	CGPG6706	Metalloenzyme	461	576	191.4	2.10E-54
1222	CGPG6723	Aminotran_1_2	124	478	217	4.30E-62
1223	CGPG6729	Gln-synt_N	100	182	148.3	2.00E-41
1223	CGPG6729	Gln-synt_C	189	470	568.5	6.70E-168

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
1224	CGPG6738	Aminotran_1_2	123	473	205.6	1.10E-58
1225	CGPG6742	Aldedh	105	563	730.5	1.10E-216
1226	CGPG6752	TIM	92	334	465.9	5.00E-137
1227	CGPG6760	GATase_2	2	164	-6.7	1.70E-10
1227	CGPG6760	Asn_synthase	241	531	383.2	3.80E-112
1228	CGPG6768	PGI	55	545	770.6	9.60E-229
1229	CGPG6779	Isoamylase_N	105	182	91.3	2.90E-24
1229	CGPG6779	Alpha-amylase	219	613	30.3	8.20E-08
1230	CGPG6785	Molybdop_Fe4S4	44	105	86.1	1.10E-22
1230	CGPG6785	Molybdopterin	108	660	93.7	5.70E-25
1230	CGPG6785	Molydop_binding	892	1011	60.2	6.90E-15
1231	CGPG6800	PGI	52	541	1093.7	0
1232	CGPG686	RRM_1	9	80	101	3.50E-27
1232	CGPG686	zf-CCHC	118	135	37.8	3.90E-08
1233	CGPG6898	Hin1	28	163	112.4	1.30E-30
1234	CGPG6900	Pkinase	97	365	172.1	1.40E-48
1236	CGPG6920	Dehydrin	14	128	165.3	1.50E-46
1237	CGPG6921	CorA	48	440	576.8	2.10E-170
1240	CGPG6945	SNARE	37	99	67.1	5.60E-17
1241	CGPG6946	MATH	13	133	30.7	5.10E-06
1242	CGPG6948	PAP2	100	233	71.2	3.40E-18
1243	CGPG6974	DUF538	7	146	248.7	1.20E-71
1244	CGPG6976	DUF926	293	406	220	5.20E-63
1245	CGPG6996	CPDase	1	179	275.9	7.80E-80
1246	CGPG7002	zf-C3HC4	123	157	25	0.00026
1247	CGPG7013	zf-C3HC4	115	156	26.2	0.00011
1248	CGPG7021	Invertase_neut	98	564	1154	0
1248	CGPG7021	GDE_C	151	537	-212.6	0.0022
1251	CGPG7075	DUF1749	77	349	217.1	3.80E-62
1252	CGPG7080	Glutaredoxin	44	106	97.2	5.10E-26
1253	CGPG7094	DUF300	6	281	574.1	1.40E-169
1254	CGPG7095	Abhydrolase_3	107	321	295.6	9.10E-86
1255	CGPG7104	Saccharop_dh	13	445	35.1	6.50E-09
1256	CGPG7118	F-box	25	73	25	0.00026
1257	CGPG7122	Pkinase	20	280	206.6	5.70E-59
1257	CGPG7122	Pkinase_Tyr	20	280	199.1	1.10E-56
1258	CGPG713	Cyclin_N	5	135	6.2	4.30E-05
1259	CGPG7130	CS	145	220	109.9	7.50E-30
1260	CGPG7145	Transthyretin	191	310	185.5	1.30E-52
1261	CGPG7166	DnaJ	79	141	29.6	5.80E-06
1262	CGPG7179	Bystin	127	423	795.6	2.90E-236
1263	CGPG7184	PBD	27	127	24	0.0002
1264	CGPG7185	GAF	190	3461	32.9	1.10E-06
1264	CGPG7185	HisKA	382	4451	24.6	0.00036
1265	CGPG7192	2OG-FeII_Oxy	201	3011	136.6	6.60E-38
1266	CGPG7199	RWD	3	1221	126.7	6.30E-35
1267	CGPG72	Amino_oxidase	66	5281	217.5	3.10E-62

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
1268	CGPG7231	B3_4	118	280	89.3	1.10E-23
1268	CGPG7231	B5	305	378	94.9	2.40E-25
1269	CGPG7241	Peptidase_C26	58	2811	149	1.20E-41
1272	CGPG7265	ARM_1	12	2961	531.9	6.60E-157
1273	CGPG7274	DUF640	36	168	312.1	1.00E-90
1274	CGPG7291	eIF-1a	20	91	71.9	2.00E-18
1275	CGPG7303	Aldedh	20	4841	779	2.80E-231
1276	CGPG7315	Y_phosphatase2	116	2801	346.6	4.00E-101
1278	CGPG7327	Actin	2	4701	33.2	5.40E-16
1280	CGPG7347	Tcp11	648	1133	261.8	1.40E-75
1281	CGPG7348	CorA	90	4671	408.2	1.20E-119
1283	CGPG7356	Metallophos	2	120	28.1	3.10E-05
1284	CGPG7359	Methyltransf_11	38	135	43.8	5.80E-10
1284	CGPG7359	Methyltransf_12	38	133	46	1.30E-10
1286	CGPG7372	zf-C3HC4	119	160	38.8	1.90E-08
1287	CGPG7379	zf-C3HC4	36	76	39.6	1.10E-08
1288	CGPG7398	DUF212	22	167	141.6	2.10E-39
1289	CGPG7403	TLD	203	341	176.8	5.30E-50
1290	CGPG7404	PBP	25	170	217.5	2.90E-62
1291	CGPG7410	HLH	36	83	14	0.0047
1292	CGPG7417	MMR_HSR1	131	252	120.2	6.00E-33
1293	CGPG7423	Gln-synt_N	102	183	171.5	2.10E-48
1293	CGPG7423	Gln-synt_C	190	471	581.1	1.10E-171
1294	CGPG7424	FBPase	92	424	521.2	1.20E-153
1297	CGPG7443	DUF1001	92	274	425.2	9.10E-125
1298	CGPG7449	ScpA_ScpB	104	347	405	1.10E-118
1301	CGPG7459	DUF1350	90	360	812.2	2.80E-241
1303	CGPG7481	Abhydrolase_1	113	361	29.1	1.50E-05
1304	CGPG7483	GTP_EFTU	62	260	227.2	3.70E-65
1304	CGPG7483	GTP_EFTU_D2	281	355	38.5	2.30E-08
1304	CGPG7483	EFG_C	461	551	54.5	3.60E-13
1306	CGPG7503	PBP	19	170	159.9	6.70E-45
1307	CGPG7504	MSF1	15	187	125.9	1.10E-34
1309	CGPG7516	DUF783	25	229	255.1	1.40E-73
1312	CGPG7524	Isy1	1	292	519.5	3.70E-153
1313	CGPG7525	UFD1	10	184	417.5	1.90E-122
1315	CGPG7537	KTI12	1	2911	406.2	4.80E-119
1317	CGPG7575	efhand	95	123	31.4	3.20E-06
1318	CGPG7577	TP_methylase	1	213	89.5	1.00E-23
1319	CGPG7590	Ribonuc_L-PSP	61	179	210.1	5.20E-60
1321	CGPG7601	CCT	237	275	74	4.80E-19
1322	CGPG7605	RRM_1	88	158	65	2.40E-16
1323	CGPG7607	Amidohydro_2	10	289	102.2	1.50E-27
1325	CGPG7632	zf-Tim10_DDP	12	77	105	2.30E-28
1326	CGPG7673	zf-MYND	76	113	47.5	4.40E-11
1326	CGPG7673	UCH	468	774	192.5	1.00E-54

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
1327	CGPG7683	zf-LSD1	28	52	40.3	6.70E-09
1327	CGPG7683	zf-LSD1	67	91	54.8	2.80E-13
1327	CGPG7683	zf-LSD1	105	129	54.1	4.70E-13
1328	CGPG773	H_PPase	64	798	1699.2	0
1329	CGPG7776	DUF525	311	445	155.8	1.10E-43
1330	CGPG7781	SapB_1	45	83	37.9	3.60E-08
1330	CGPG7781	SapB_2	86	119	18.1	0.025
1330	CGPG7781	SapB_1	131	169	27.7	4.20E-05
1330	CGPG7781	SapB_2	172	206	20.8	0.0049
1331	CGPG7785	LRRNT_2	24	65	39.3	1.30E-08
1331	CGPG7785	LRR_1	93	115	11.4	2.1
1331	CGPG7785	LRR_1	117	139	8.8	6.4
1331	CGPG7785	LRR_1	141	163	12.5	1.3
1331	CGPG7785	LRR_1	165	187	15.6	0.18
1331	CGPG7785	LRR_1	189	211	8.7	6.8
1331	CGPG7785	LRR_1	213	235	16.9	0.075
1331	CGPG7785	Pkinase	415	682	18.7	1.10E-09
1332	CGPG7787	Aldose_epim	26	301	257.4	3.00E-74
1334	CGPG7796	WD40	50	88	32	2.10E-06
1334	CGPG7796	WD40	92	130	43	1.00E-09
1334	CGPG7796	WD40	134	174	47.8	3.70E-11
1334	CGPG7796	WD40	182	220	37.9	3.40E-08
1334	CGPG7796	WD40	391	432	33.3	8.40E-07
1334	CGPG7796	WD40	436	475	40.4	6.20E-09
1334	CGPG7796	WD40	489	527	28.9	1.80E-05
1334	CGPG7796	WD40	531	569	31	4.30E-06
1334	CGPG7796	WD40	573	611	43.9	5.30E-10
1334	CGPG7796	WD40	615	653	28.6	2.20E-05
1334	CGPG7796	Utp13	674	809	231.1	2.40E-66
1335	CGPG7797	GILT	35	144	133.6	5.40E-37
1336	CGPG7801	LRR_1	106	129	8.1	8.7
1336	CGPG7801	LRR_1	132	154	16.9	0.071
1336	CGPG7801	LRR_1	156	178	10.9	2.6
1336	CGPG7801	LRR_1	180	199	9.2	5.4
1336	CGPG7801	LRR_1	201	223	9.4	4.9
1336	CGPG7801	LRR_1	225	246	17.1	0.062
1336	CGPG7801	LRR_1	249	272	12.8	1.1
1336	CGPG7801	LRR_1	273	294	10.3	3.4
1336	CGPG7801	Pkinase	456	716	-45.5	7.60E-06
1337	CGPG7813	WD40	379	417	43.1	9.20E-10
1337	CGPG7813	WD40	421	459	39.8	9.60E-09
1337	CGPG7813	WD40	507	545	46.9	6.80E-11
1337	CGPG7813	WD40	549	587	29.5	1.20E-05
1337	CGPG7813	PWP2	785	900	243.1	5.70E-70
1341	CGPG7863	zf-CW	100	153	85.7	1.40E-22
1341	CGPG7863	MBD	162	237	43.4	7.80E-10
1342	CGPG7868	BCNT	165	244	123.2	7.40E-34

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
1343	CGPG7881	Aldedh	99	558	694.8	6.40E-206
1344	CGPG7887	HEAT	191	222	12	1.5
1344	CGPG7887	Arm	262	302	27.2	6.00E-05
1344	CGPG7887	HEAT	389	424	14.1	0.52
1344	CGPG7887	Arm	423	463	32.8	1.20E-06
1345	CGPG7899	RRM_1	225	295	27.8	3.80E-05
1346	CGPG7901	IQ	107	127	30.9	4.40E-06
1346	CGPG7901	IQ	129	149	18.8	0.02
1347	CGPG7909	DUF383	92	271	353	4.90E-103
1347	CGPG7909	DUF384	272	330	107.8	3.20E-29
1348	CGPG7911	AAA	245	447	58.7	1.90E-14
1349	CGPG7919	Cullin	30	191	-9.6	7.00E-09
1350	CGPG7935	IQ	93	113	26.3	0.00011
1350	CGPG7935	IQ	115	135	17.6	0.046
1351	CGPG7940	RRM_1	96	161	37.7	3.90E-08
1352	CGPG7959	Cyclin_N	180	306	218.1	2.00E-62
1352	CGPG7959	Cyclin_C	308	428	179	1.20E-50
1353	CGPG7967	IQ	106	126	30.4	6.50E-06
1353	CGPG7967	IQ	128	148	15.1	0.26
1354	CGPG7975	Arm	28	68	23.4	0.00079
1354	CGPG7975	Arm	70	110	17.4	0.052
1355	CGPG7996	efhand	136	164	22.7	0.0013
1356	CGPG8006	AAA	241	440	50.9	4.10E-12
1357	CGPG801	Cyt-b5	74	171	81.3	3.00E-21
1358	CGPG8023	RRM_1	11	82	114.5	3.00E-31
1359	CGPG8025	IQ	93	113	27	6.80E-05
1359	CGPG8025	IQ	115	135	20.6	0.0056
1360	CGPG8038	MFS_1	36	433	124.8	2.40E-34
1361	CGPG8053	DUF246	182	525	691.9	4.70E-205
1364	CGPG8070	GILT	32	136	193.2	6.30E-55
1365	CGPG8073	Dirigent	17	183	330.8	2.30E-96
1366	CGPG8076	Tryp_alpha_amyl	32	107	47.1	5.90E-11
1369	CGPG8095	IPK	16	279	434.8	1.20E-127
1370	CGPG8096	60KD_IMP	151	348	35.5	1.70E-13
1374	CGPG8129	Ank	49	81	32.1	1.90E-06
1374	CGPG8129	Ank	82	114	24.1	0.00049
1374	CGPG8129	Ank	115	147	43.2	8.90E-10
1378	CGPG8165	Glutaredoxin	44	106	97.2	5.10E-26
1379	CGPG8169	Nol1_Nop2_Fmu	226	505	21.9	3.60E-09
1380	CGPG8203	Uricase	11	140	134.3	3.40E-37
1380	CGPG8203	Uricase	147	300	177.6	3.00E-50
1381	CGPG8205	DZC	113	148	81	3.70E-21
1383	CGPG8213	Phosphoesterase	27	388	519.9	2.70E-153
1384	CGPG8225	FBPase	25	348	464.4	1.40E-136
1385	CGPG8227	NIR_SIR_ferr	44	111	90.7	4.50E-24
1385	CGPG8227	NIR_SIR	119	275	207.5	3.00E-59

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
1385	CGPG8227	NIR_SIR_ferr	331	399	57.3	5.00E-14
1385	CGPG8227	NIR_SIR	405	553	28.9	1.40E-05
1386	CGPG8235	Aldedh	12	471	791.5	4.70E-235
1387	CGPG8236	Molvbdop_Fe4S4	9	63	76	1.20E-19
1387	CGPG8236	Molybdopterin	66	495	428.7	8.00E-126
1387	CGPG8236	Molydop_binding	593	703	111.8	2.00E-30
1387	CGPG8236	Fer2_BFD	852	903	50.3	6.50E-12
1388	CGPG8244	PAS_2	15	125	151.7	2.00E-42
1388	CGPG8244	GAF	152	320	93.4	7.10E-25
1388	CGPG8244	Phytochrome	331	513	88.8	1.70E-23
1388	CGPG8244	HisKA	528	596	43.1	9.40E-10
1388	CGPG8244	HATPase_c	637	747	127	5.20E-35
1389	CGPG8254	NIR_SIR_ferr	66	133	48.1	2.90E-11
1389	CGPG8254	NIR_SIR	166	347	198.6	1.40E-56
1389	CGPG8254	NIR_SIR_ferr	362	434	77.4	4.50E-20
1389	CGPG8254	NIR_SIR	443	591	15.1	0.00014
1390	CGPG8255	PPDK_N	16	384	620.2	1.80E-183
1390	CGPG8255	PEP-utilizers	439	531	141.1	3.00E-39
1390	CGPG8255	PEP-utilizers_C	559	914	485.9	4.80E-143
1391	CGPG8262	ELFV_dehydrog_N	33	163	239.1	9.20E-69
1391	CGPG8262	ELFV_dehydrog	179	420	400.7	2.10E-117
1392	CGPG8264	Aldedh	17	480	795.7	2.70E-236
1393	CGPG8269	PGK	1	396	769.8	1.70E-228
1394	CGPG8271	Gln-synt_N	16	97	149.9	6.70E-42
1394	CGPG8271	Gln-synt_C	104	386	584.6	9.60E-173
1395	CGPG8305	Sulfotransfer_1	70	336	352.4	7.40E-103
1396	CGPG8320	DUF1005	282	487	545.7	4.80E-161
1397	CGPG8326	Senescence	35	369	791.4	5.30E-235
1398	CGPG8344	PPR	173	207	17.6	0.046
1398	CGPG8344	PPR	208	242	19.4	0.013
1398	CGPG8344	PPR	243	277	10.4	0.44
1398	CGPG8344	PPR	279	312	13.4	0.19
1398	CGPG8344	PPR	314	348	2	4.3
1398	CGPG8344	PPR	349	383	8.3	0.79
1398	CGPG8344	PPR	384	418	2.3	4
1399	CGPG8347	Ribosomal_S8	5	130	214.4	2.60E-61
1400	CGPG8359	Tryp_alpha_amyl	85	167	93.5	6.40E-25
1401	CGPG8370	Tim17	40	156	129.2	1.10E-35
1402	CGPG8371	PseudoU_synth_1	62	167	44.3	4.10E-10
1402	CGPG8371	PseudoU_synth_1	324	431	18.3	0.00016
1404	CGPG8378	LysM	78	121	22	0.0021
1406	CGPG841	ArfGap	4	120	173.8	4.20E-49
1405	CGPG8383	DUF239	174	368	401.1	1.60E-117
1409	CGPG8450	DUF793	1	390	976.4	1.10E-290
1410	CGPG8451	IQ	105	125	21.2	0.0038
1410	CGPG8451	IQ	127	147	21.5	0.0031
1411	CGPG8459	ubiquitin	6	78	58.1	2.90E-14

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
1411	CGPG8459	UBA	145	187	49.6	1.10E-11
1411	CGPG8459	XPC-binding	242	298	56.4	9.40E-14
1411	CGPG8459	UBA	322	361	46	1.20E-10
1412	CGPG8461	Ribosomal_S8	5	130	219	1.10E-62
1413	CGPG8463	PI3_PI4_kinase	163	421	280.6	3.00E-81
1414	CGPG8471	F-box	1	46	36.9	6.90E-08
1414	CGPG8471	FBA_1	211	383	295.9	7.50E-86
1415	CGPG8474	Metallothio_PEC	12	85	150	6.10E-42
1416	CGPG8475	DAO	10	372	186.6	5.80E-53
1417	CGPG8476	IQ	84	104	30	8.20E-06
1417	CGPG8476	IQ	106	126	14.4	0.41
1418	CGPG8490	ACT	21	85	3.9	1.3
1418	CGPG8490	ACT	110	174	36.6	8.60E-08
1419	CGPG8510	DUF538	9	149	250.2	4.20E-72
1420	CGPG8530	Radical_SAM	119	283	51.3	3.30E-12
1421	CGPG8533	DUF212	27	172	104.1	4.20E-28
1425	CGPG8555	NUDIX	59	196	82	1.90E-21
1426	CGPG8561	zf-C3HC4	154	191	34	5.30E-07
1427	CGPG8569	2OG-FeII_Oxy	159	282	61.8	2.20E-15
1428	CGPG8573	DUF617	83	242	392.1	8.40E-115
1431	CGPG8607	DUF862	69	219	244	3.20E-70
1432	CGPG8611	Stig1	13	154	165.9	1.00E-46
1434	CGPG8632	Sina	86	273	-41.1	0.00037
1435	CGPG8634	FA_desaturase	55	278	132.1	1.60E-36
1436	CGPG8635	DUF59	36	117	47	6.30E-11
1438	CGPG8640	DUF581	119	176	133.1	7.60E-37
1439	CGPG8642	CRAL_TRIO_N	5	80	30.8	4.60E-06
1439	CGPG8642	CRAL_TRIO	93	266	84.7	2.80E-22
1441	CGPG8666	PetM	69	120	81.9	2.00E-21
1443	CGPG8688	Bet_v_I	55	192	-31.7	0.0014
1443	CGPG8688	Polyketide_cyc	60	191	28.7	2.00E-05
1444	CGPG8689	DUF506	74	282	436	5.20E-128
1445	CGPG8704	GHMP_kinases_N	24	93	39.2	1.40E-08
1445	CGPG8704	GHMP_kinases_C	166	249	32.3	1.70E-06
1448	CGPG8769	Self-incomp_S1	35	144	175.9	9.80E-50
1449	CGPG8774	Maf	1	207	-0.7	4.20E-09
1450	CGPG8778	PPR	13	47	5.4	1.7
1450	CGPG8778	PPR	115	149	24.7	0.00032
1450	CGPG8778	PPR	249	283	40.8	4.70E-09
1450	CGPG8778	PPR	284	318	12.2	0.27
1450	CGPG8778	PPR	320	354	16.7	0.078
1450	CGPG8778	PPR	386	420	9.5	0.56
1451	CGPG8784	Snf7	16	189	208.6	1.50E-59
1452	CGPG879	ABC_tran	195	418	49.2	7.50E-12
1452	CGPG879	ABC2_membrane	520	733	231.7	1.60E-66
1452	CGPG879	PDR_assoc	738	812	107.4	4.30E-29

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
1452	CGPG879	ABC_tran	887	1077	109	1.40E-29
1452	CGPG879	ABC2_membrane	1174	1388	249.2	8.80E-72
1453	CGPG8797	AMP-binding	67	488	430.1	3.10E-126
1454	CGPG8810	DUF1645	80	252	310.1	4.00E-90
1455	CGPG8827	DUF623	199	263	128.8	1.50E-35
1456	CGPG8853	DUF1635	1	218	517	2.10E-152
1457	CGPG8873	p450	72	518	236.2	6.90E-68
1458	CGPG8877	Exo_endo_phos	33	310	121.7	2.10E-33
1459	CGPG8878	Pkinase	79	337	343.8	2.80E-100
1459	CGPG8878	efhand	400	428	24.9	0.00028
1459	CGPG8878	efhand	434	462	34.5	3.60E-07
1460	CGPG8881	DUF1677	3	107	192.2	1.30E-54
1461	CGPG8895	RNA_poll_A14	1	137	277.8	2.20E-80
1462	CGPG8906	MCM	272	635	641.9	5.40E-190
1463	CGPG8917	Pkinase	363	697	244	3.20E-70
1464	CGPG8919	Usp	11	141	43.4	8.00E-10
1464	CGPG8919	Pkinase_Tyr	405	676	88.6	1.90E-23
1464	CGPG8919	Pkinase	405	676	138.8	1.50E-38
1465	CGPG8925	DUF617	82	260	262.9	6.60E-76
1466	CGPG8930	Lectin_legB	26	261	232.7	8.20E-67
1466	CGPG8930	Pkinase	347	617	166.9	5.30E-47
1466	CGPG8930	Pkinase_Tyr	347	617	115.3	1.80E-31
1467	CGPG8937	LRR_1	440	461	13.9	0.57
1467	CGPG8937	LRR_1	463	485	18.7	0.022
1467	CGPG8937	LRR_1	487	510	14.6	0.36
1467	CGPG8937	Pkinase	602	873	111.2	3.00E-30
1467	CGPG8937	Pkinase_Tyr	603	873	110.1	6.30E-30
1468	CGPG8942	RRM_1	23	94	105.3	1.80E-28
1469	CGPG8946	Pkinase	516	786	150.8	3.60E-42
1469	CGPG8946	Pkinase_Tyr	516	786	129.6	8.70E-36
1470	CGPG8990	V-SNARE	71	221	154.1	3.70E-43
1472	CGPG9008	TPK_catalytic	40	180	114.5	3.00E-31
1472	CGPG9008	TPK_B1_binding	191	259	94.4	3.40E-25
1473	CGPG9016	ETC_C1_NDUFA4	54	156	176.6	6.20E-50
1474	CGPG9036	MSP	93	329	549	4.70E-162
1475	CGPG9060	LSM	22	101	66.3	1.00E-16
1477	CGPG908	PPR	62	96	9.9	0.5
1477	CGPG908	PPR	125	158	20.9	0.0047
1477	CGPG908	PPR	187	221	27	6.50E-05
1477	CGPG908	PPR	250	284	50.4	6.20E-12
1477	CGPG908	PPR	351	385	53.9	5.30E-13
1477	CGPG908	PPR	386	419	2.2	4
1477	CGPG908	PPR	422	456	17.9	0.035
1477	CGPG908	PPR	488	522	3.4	3
1478	CGPG9093	AWPM-19	15	156	325.5	9.00E-95
1479	CGPG9096	OTU	11	121	104.8	2.50E-28
1482	CGPG9111	TB2_DP1_HVA22	4	101	157	5.10E-44

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
1483	CGPG9112	DUF778	10	177	350.3	3.20E-102
1484	CGPG9123	DUF833	1	264	236.7	4.90E-68
1485	CGPG9124	Exo_endo_phos	20	427	39.2	1.40E-08
1485	CGPG9124	efhand	337	365	31.2	3.70E-06
1486	CGPG9138	ThiC	165	588	1118.5	0
1488	CGPG9150	Pkinase	56	326	144.9	2.20E-40
1488	CGPG9150	Pkinase_Tyr	56	326	129.9	6.90E-36
1489	CGPG9152	eIF2A	217	410	382.7	5.60E-112
1490	CGPG9162	AAA_5	211	346	6.5	0.00057
1490	CGPG9162	AAA	211	398	309.1	8.00E-90
1491	CGPG9165	GATase	11	201	185.4	1.40E-52
1491	CGPG9165	GMP_synt_C	432	524	210.5	3.80E-60
1492	CGPG9166	GATase	28	210	194.9	1.90E-55
1492	CGPG9166	GMP_synt_C	447	539	211.2	2.30E-60
1493	CGPG9171	Zip	5	266	60.5	5.40E-15
1494	CGPG9177	Complex1_30kDa	113	181	146.8	5.60E-41
1494	CGPG9177	Complex1_49kDa	329	600	639.1	3.70E-189
1495	CGPG9178	PRA-CH	54	129	201	2.90E-57
1495	CGPG9178	PRA-PH	142	230	175.7	1.20E-49
1496	CGPG9179	Pkinase	4	283	341.9	1.10E-99
1496	CGPG9179	Pkinase_Tyr	4	283	96.5	7.90E-26
1497	CGPG9181	P21-Arc	17	187	370.6	2.40E-108
1499	CGPG9189	SAC3_GANP	19	164	152.8	9.30E-43
1500	CGPG9201	TPT	201	350	168.8	1.40E-47
1501	CGPG9222	YjeF_N	34	199	271.5	1.70E-78
1501	CGPG9222	Carb_kinase	257	496	426.9	2.70E-125
1502	CGPG9234	DUF393	65	183	109.6	9.00E-30
1503	CGPG9237	Tim17	18	146	112.4	1.30E-30
1504	CGPG9244	TOM20_plant	9	200	435.3	8.30E-128
1506	CGPG9249	Pkinase	46	330	137.7	3.20E-38
1506	CGPG9249	Pkinase_Tyr	46	330	94.3	3.60E-25
1507	CGPG9251	Cyclin_N	54	186	115.8	1.30E-31
1507	CGPG9251	Cyclin_C	188	314	23.7	0.00055
1508	CGPG9280	DUF1000	53	168	192	1.40E-54
1510	CGPG9302	Diphthamide_syn	30	398	118.1	2.50E-32
1511	CGPG931	Pkinase	114	398	303.3	4.30E-88
1512	CGPG9313	CN_hydrolase	5	200	75.3	2.00E-19
1512	CGPG9313	NAD_synthase	338	652	-11.3	1.20E-11
1514	CGPG9327	OPT	74	729	779.8	1.60E-231
1515	CGPG933	WD40	46	84	23.2	0.00093
1515	CGPG933	WD40	134	173	22.9	0.0012
1515	CGPG933	WD40	177	215	33.6	7.00E-07
1515	CGPG933	WD40	222	260	42.8	1.10E-09
1515	CGPG933	WD40	314	353	21.7	0.0026
1515	CGPG933	WD40	524	562	31.5	3.00E-06
1515	CGPG933	WD40	568	605	23.3	0.00085

PEP SEQ ID	Construct ID	Pfam domain name	begin	start	score	E-value
1516	CGPG9334	Sugar_tr	7	720	205.2	1.50E-58
1516	CGPG9334	MFS_1	11	679	116.5	7.90E-32
1517	CGPG967	BTB	38	135	7.2	0.00091
1517	CGPG967	NPH3	218	460	370.2	3.20E-108
1518	CGPG988	Cystatin	36	124	86.1	1.10E-22

Table 19

Pfam domain name	accession number	gathering cutoff	domain description
14-3-3	PF00244.10	25	14-3-3 protein
2-oxoacid_dh	PF00198.13	-112	2-oxoacid dehydrogenases acyltransferase (catalytic domain)
2OG-FeII_Oxy	PF03171.10	11.5	2OG-Fe(II) oxygenase superfamily
60KD_IMP	PF02096.11	-95	60Kd inner membrane protein
AAA	PF00004.19	12.3	ATPase family associated with various cellular activities (AAA)
AAA_5	PF07728.4	4	ATPase family associated with various cellular activities (AAA)
AA_permease	PF00324.11	-120.8	Amino acid permease
ABC1	PF03109.7	-27.6	ABC1 family
ABC2_membrane	PF01061.14	-17.9	ABC-2 type transporter
ABC_tran	PF00005.17	9.5	ABC transporter
ACT	PF01842.15	0	ACT domain
ADH_N	PF08240.2	-14.5	Alcohol dehydrogenase GroES-like domain
ADH_zinc_N	PF00107.16	23.8	Zinc-binding dehydrogenase
AHSA1	PF08327.1	16.3	Activator of Hsp90 ATPase homolog 1-like protein
AMP-binding	PF00501.18	0	AMP-binding enzyme
AOX	PF01786.8	25	Alternative oxidase
AP2	PF00847.10	0	AP2 domain
ARM_1	PF04683.4	25	Adhesion regulating molecule conserved region
ATP_synt_H	PF05493.3	25	ATP synthase subunit H
AWPM-19	PF05512.2	25	AWPM-19-like family
Aa_trans	PF01490.8	-128.4	Transmembrane amino acid transporter protein
Abhydrolase_1	PF00561.10	10.3	alpha/beta hydrolase fold
Abhvdrolase_3	PF07859.3	25.8	alpha/beta hydrolase fold
Actin	PF00022.9	-144	Actin
Acyltransferase	PF01553.11	-0.4	Acyltransferase
Ahal_N	PF09229.1	-19.7	Activator of Hsp90 ATPase, N-terminal
AlaDh_PNT_C	PF01262.12	-43.4	Alanine dehydrogenase/PNT, C-terminal domain
AlaDh_PNT_N	PF05222.5	25	Alanine dehydrogenase/PNT, N-terminal domain
Aldedh	PF00171.12	-209.3	Aldehyde dehydrogenase family
Aldose_epim	PF01263.10	-70.5	Aldose 1-epimerase
Alpha-amylase	PF00128.14	-92.6	Alpha amylase, catalytic domain
Amidohydro_2	PF04909.4	-1.7	Amidohvdrolase
Amino_oxidase	PF01593.14	-11.4	Flavin containing amine oxidoreductase
Aminotran_1_2	PF00155.11	-57.5	Aminotransferase class I and II
Aminotran_3	PF00202.11	-206.1	Aminotransferase class-III
Aminotran_4	PF01063.9	-50	Aminotransferase class IV
Aminotran_5	PF00266.9	-164.4	Aminotransferase class-V

Pfam domain name	accession number	gathering cutoff	domain description
Ank	PF00023.20	0	Ankyrin repeat
Arf	PF00025.11	40	ADP-ribosylation factor family
ArfGap	PF01412.9	-17	Putative GTPase activating protein for Arf
Arm	PF00514.13	17	Armadillo/beta-catenin-like repeat
Asn_synthase	PF00733.11	-52.8	Asparagine synthase
AstE_AspA	PF04952.5	-36.8	Succinylglutamate desuccinylase / Aspartoacylase family
B3_4	PF03483.7	10	B3/4 domain
B5	PF03484.5	25	tRNA synthetase B5 domain
B56	PF01603.10	-210	Protein phosphatase 2A regulatory B subunit (B56 family)
BCNT	PF07572.3	25	Bucentaur or craniofacial development
BNR	PF02012.10	0.7	BNR/Asp-box repeat
BRCT	PF00533.16	27.8	BRCA1 C Terminus (BRCT) domain
BTB	PF00651.21	6.2	BTB/POZ domain
Band_7	PF01145.15	-5	SPFH domain / Band 7 family
Barwin	PF00967.8	25	Barwin family
Bet_v_I	PF00407.9	-33	Pathogenesis-related protein Bet v I family
Biotin_lipoyl	PF00364.12	-2.3	Biotin-requiring enzyme
Brix	PF04427.8	11.4	Brix domain
Bystin	PF05291.2	25	Bystin
C2	PF00168.20	3.7	C2 domain
CAF1	PF04857.10	-100.5	CAF1 family ribonuclease
CBS	PF00571.18	17.5	CBS domain pair
CCT	PF06203.4	25	CCT motif
CN_hydrolase	PF00795.12	-13.9	Carbon-nitrogen hydrolase
CPDase	PF07823.2	-14.5	Cyclic phosphodiesterase-like protein
CPSase_L_D2	PF02786.7	-48.9	Carbamoyl-phosphate synthase L chain, ATP binding domain
CPSase_L_D3	PF02787.9	-56	Carbamoyl-phosphate synthetase large chain, oligomerisation domain
CPSase_L_chain	PF00289.12	14	Carbamoyl-phosphate synthase L chain, N-terminal domain
CRAL_TRIO	PF00650.10	-26	CRAL/TRIO domain
CRAL_TRIO_N	PF03765.5	16	CRAL/TRIO, N-terminus
CS	PF04969.6	8.6	CS domain
CTP_transf_1	PF01148.10	-38.5	Cytidylyltransferase family
Carb_kinase	PF01256.8	-66.3	Carbohydrate kinase
Chitin_bind_1	PF00187.9	25.1	Chitin recognition protein
Citrate_synt	PF00285.11	-101.5	Citrate svnthase
Complex1_30kDa	PF00329.9	-3	Respiratory-chain NADH dehydrogenase, 30 Kd subunit
Complex1_49kDa	PF00346.9	-108	Respiratory-chain NADH dehydrogenase, 49 Kd subunit
Copine	PF07002.6	-36.5	Copine
CorA	PF01544.9	-61.3	CorA-like Mg2+ transporter protein
Cornichon	PF03311.4	25	Cornichon protein
Cpn60_ TCP1	PF00118.14	-223.4	TCP-1/cpn60 chaperonin family
Cullin	PF00888.12	-33.3	Cullin family
Cyclin	PF08613.1	-34.2	Cyclin

Pfam domain name	accession number	gathering cutoff	domain description
Cyclin_C	PF02984.9	-13	Cyclin, C-terminal domain
Cyclin_N	PF00134.13	-14.7	Cyclin, N-terminal domain
Cys_Met_Meta_PP	PF01053.10	-278.4	Cys/Met metabolism PLP-dependent enzyme
Cystatin	PF00031.11	17.5	Cystatin domain
Cyt-b5	PF00173.18	4	Cytochrome b5-like Heme/Steroid binding domain
Cytochrom_C	PF00034.11	11.7	Cytochrome c
DAGK_cat	PF00781.14	-5.7	Diacylglycerol kinase catalytic domain (presumed)
DAO	PF01266.14	-35	FAD dependent oxidoreductase
DEAD	PF00270.19	7.2	DEAD/DEAH box helicase
DHDPS	PF00701.12	-90	Dihydrodipicolinate synthetase family
DHquinase_I	PF01487.6	25	Type I 3-dehydroquinase
DJ-1_PfpI	PF01965.14	-7	DJ-1/PfpI family
DREPP	PF05558.3	25	DREPP plasma membrane polypeptide
DSHCT	PF08148.2	-86.9	DSHCT (NUC185) domain
DUF1000	PF06201.4	-20.8	Domain of Unknown Function (DUF1000)
DUF1001	PF06206.2	-63.3	Protein of unknown function (DUF1001)
DUF1005	PF06219.3	25	Protein of unknown function (DUF1005)
DUF1350	PF07082.2	-145.7	Protein of unknown function (DUF1350)
DUF1635	PF07795.2	-27.2	Protein of unknown function (DUF1635)
DUF1639	PF07797.4	25	Protein of unknown function (DUF1639)
DUF1644	PF07800.3	25	Protein of unknown function (DUF1644)
DUF1645	PF07816.2	-35.3	Protein of unknown function (DUF1645)
DUF1677	PF07911.4	25	Protein of unknown function (DUF1677)
DUF1749	PF08538.1	-181.1	Protein of unknown function (DUF1749)
DUF1984	PF09328.1	12.8	Domain of unknown function (DUF1984)
DUF21	PF01595.10	-28.2	Domain of unknown function DUF21
DUF212	PF02681.5	-30	Divergent PAP2 family
DUF23	PF01697.17	-18.5	Domain of unknown function
DUF231	PF03005.6	-58	Arabidopsis proteins of unknown function
DUF239	PF03080.5	25	Arabidopsis proteins of unknown function
DUF246	PF03138.5	-15	Plant protein family
DUF26	PF01657.8	0	Domain of unknown function DUF26
DUF260	PF03195.5	0.8	Protein of unknown function DUF260
DUF300	PF03619.7	25	Domain of unknown function
DUF313	PF03754.4	25	Domain of unknown function (DUF313)
DUF383	PF04063.4	25	Domain of unknown function (DUF383)
DUF384	PF04064.4	25	Domain of unknown function (DUF384)
DUF393	PF04134.3	25	Protein of unknown function, DUF393
DUF506	PF04720.3	25	Protein of unknown function (DUF506)
DUF525	PF04379.5	25	Protein of unknown function (DUF525)
DUF538	PF04398.3	25	Protein of unknown function, DUF538
DUF581	PF04570.5	-3.1	Protein of unknown function (DUF581)
DUF59	PF01883.9	-7.9	Domain of unknown function DUF59
DUF6	PF00892.11	20.8	Integral membrane protein DUF6
DUF617	PF04759.4	25	Protein of unknown function, DUF617
DUF623	PF04844.4	25	Protein of unknown function, DUF623

Pfam domain name	accession number	gathering cutoff	domain description
DUF640	PF04852.3	2.4	Protein of unknown function (DUF640)
DUF676	PF05057.5	-60.7	Putative serine esterase (DUF676)
DUF740	PF05340.3	25	Protein of unknown function (DUF740)
DUF778	PF05608.2	25	Protein of unknown function (DUF778)
DUF783	PF05615.3	25	Protein of unknown function (DUF783)
DUF788	PF05620.2	25	Protein of unknown function (DUF788)
DUF791	PF05631.4	-136.8	Protein of unknown function (DUF791)
DUF793	PF05633.2	25	Protein of unknown function (DUF793)
DUF827	PF05701.2	25	Plant protein of unknown function (DUF827)
DUF833	PF05742.2	-63.1	Protein of unknown function (DUF833)
DUF860	PF05898.4	25	Plant specific of unknown function (DUF860)
DUF862	PF05903.5	-21.4	PPPDE putative peptidase domain
DUF914	PF06027.3	-193	Eukaryotic protein of unknown function (DUF914)
DUF926	PF06047.2	25	Domain of Unknown Function (DUF926)
DZC	PF08381.1	15.3	Disease resistance/zinc finger/chromosome condensation-like region
Dehydrin	PF00257.10	-4.4	Dehydrin
Di19	PF05605.3	25	Drought induced 19 protein (Di19)
Diphthamide_syn	PF01866.8	25	Putative diphthamide synthesis protein
Dirigent	PF03018.5	25	Dirigent-like protein
DnaJ	PF00226.21	-8	DnaJ domain
DnaJ_C	PF01556.9	-24	DnaJ C terminal region
DnaJ_CXXCXGXG	PF00684.9	1	DnaJ central domain (4 repeats)
E1_dh	PF00676.10	-90	Dehydrogenase E1 component
E3_binding	PF02817.7	10	e3 binding domain
EFG_C	PF00679.14	6	Elongation factor G C-terminus
ELFV_dehydrog	PF00208.11	-27	Glutamate/Leucine/Phenylalanine/Valine dehydrogenase
ELFV_dehydrog_N	PF02812.8	31.8	Glu/Leu/Phe/Val dehydrogenase, dimerisation domain
ETC_C1_NDUFA4	PF04800.3	25	ETC complex I subunit conserved region
Enolase_C	PF00113.12	-71.2	Enolase, C-terminal TIM barrel domain
Enolase_N	PF03952.6	11.3	Enolase, N-terminal domain
Exo_endo_phos	PF03372.13	11	Endonuclease/Exonuclease/phosphatase family
F-box	PF00646.23	13.9	F-box domain
FAD_binding_2	PF00890.14	-124.8	FAD binding domain
FAD_binding_4	PF01565.13	-8.1	FAD binding domain
FAD_binding_8	PF08022.2	-10.4	FAD-binding domain
FA_desaturase	PF00487.14	-46	Fatty acid desaturase
FBA_1	PF07734.3	-39.4	F-box associated
FBA_3	PF08268.2	-17.1	F-box associated
FBD	PF08387.1	25	FBD
FBPase	PF00316.10	-170.3	Fructose-1-6-bisphosphatase
FHA	PF00498.16	25	FHA domain
FKBP_C	PF00254.18	-7.6	FKBP-type peptidyl-prolyl cis-trans isomerase
FTHFS	PF01268.9	-167	Formate--tetrahydrofolate ligase
Fer2_BFD	PF04324.5	25	BFD-like [2Fe-2S] binding domain
Fer4	PF00037.17	9.3	4Fe-4S binding domain

Pfam domain name	accession number	gathering cutoff	domain description
Ferric_reduct	PF01794.9	-7	Ferric reductase like transmembrane component
Fibrillarin	PF01269.8	-86.6	Fibrillarin
GAF	PF01590.16	23	GAF domain
GATase	PF00117.18	-38.1	Glutamine amidotransferase class-I
GATase_2	PF00310.11	-95.1	Glutamine amidotransferases class-II
GDE_C	PF06202.4	-218.8	Amylo-alpha-1,6-glucosidase
GHMP_kinases_C	PF08544.3	20.8	GHMP kinases C terminal
GHMP_kinases_N	PF00288.16	17.1	GHMP kinases N terminal domain
GIDA	PF01134.12	-226.7	Glucose inhibited division protein A
GILT	PF03227.6	25	Gamma interferon inducible lysosomal thiol reductase (GILT)
GMP_synt_C	PF00958.12	25	GMP synthase C terminal domain
GRAM	PF02893.10	24.4	GRAM domain
GRP	PF07172.2	16.8	Glycine rich protein family
GTP_EFTU	PF00009.17	8	Elongation factor Tu GTP binding domain
GTP_EFTU_D2	PF03144.15	25	Elongation factor Tu domain 2
Gal-bind_lectin	PF00337.12	-30	Galactoside-binding lectin
Galactosyl_T	PF01762.12	-46	Galactosyl transferase
Garl	PF04410.5	25	Garl protein RNA binding region
Gln-synt_C	PF00120.14	-124	Glutamine synthetase, catalytic domain
Gln-synt_N	PF03951.9	9	Glutamine synthetase, beta-Grasp domain
Globin	PF00042.12	-8.8	Globin
Glucokinase	PF02685.6	-157.6	Glucokinase
Glutaminase	PF04960.6	-143.6	Glutaminase
Glutaredoxin	PF00462.14	17.2	Glutaredoxin
Glyco_hydro_1	PF00232.9	-301.8	Glycosyl hydrolase family 1
Glvco_hydro_17	PF00332.9	-152.3	Glycosyl hydrolases family 17
Glyco_tran_28_C	PF04101.6	-10.4	Glycosyltransferase family 28 C-terminal domain
G)vco_transf_8	PF01501.10	-43.2	Glycosyl transferase family 8
Glycolytic	PF00274.9	-174.5	Fructose-bisphosphate aldolase class-I
Gp_dh_C	PF02800.10	-64.1	Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain
Gp_dh_N	PF00044.14	-74.2	Glyceraldehyde 3-phosphate dehydrogenase, NAD binding domain
HATPase_c	PF02518.16	22.4	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase
HD	PF01966.12	15.3	HD domain
HEAT	PF02985.12	11.5	HEAT repeat
HIT	PF01230.13	-4.5	HIT domain
HLH	PF00010.16	8.3	Helix-loop-helix DNA-binding domain
HMA	PF00403.16	19.5	Heavy-metal-associated domain
HMG-CoA_red	PF00368.9	-242	Hydroxymethylglutaryl-coenzyme A reductase
H_PPase	PF03030.7	-377	Inorganic H+ pyrophosphatase
Helicase_C	PF00271.21	2.1	Helicase conserved C-terminal domain
Hexapep	PF00132.14	0.3	Bacterial transferase hexapeptide (three repeats)
Hin1	PF07320.4	25	Harpin-induced protein 1 (Hin1)
HisKA	PF00512.15	10.3	His Kinase A (phosphoacceptor) domain

Pfam domain name	accession number	gathering cutoff	domain description
Histone	PF00125.14	17.4	Core histone H2A/H2B/H3/H4
Hydrolase	PF00702.16	13.6	haloacid dehalogenase-like hydrolase
IGPD	PF00475.9	25	Imidazoleglycerol-phosphate dehydratase
IPK	PF03770.7	25	Inositol polyphosphate kinase
IQ	PF00612.17	11.9	IQ calmodulin-binding motif
Invertase_neut	PF04853.3	-233.6	Plant neutral invertase
Iso_dh	PF00180.10	-97	Isocitrate/isopropylmalate dehydrogenase
Isoamylase_N	PF02922.8	-6.5	Isoamylase N-terminal domain
Isy1	PF06246.3	25	Is1-like splicing family
K-box	PF01486.8	0	K-box region
KR	PF08659.1	-74.3	KR domain
KTI12	PF08433.1	-109.1	Chromatin associated protein KTI12
Kelch_1	PF01344.15	7.8	Kelch motif
Kelch_2	PF07646.5	14	Kelch motif
LRRNT_2	PF08263.3	18.6	Leucine rich repeat N-terminal domain
LRR_1	PF00560.23	7.7	Leucine Rich Repeat
LRR_2	PF07723.3	6	Leucine Rich Repeat
LSM	PF01423.12	13.7	LSM domain
Lectin_legB	PF00139.10	-110.1	Legume lectin domain
Lipoxygenase	PF00305.9	-211	Lipoxygenase
Lung_7-TM_R	PF06814.3	25	Lung seven transmembrane receptor
LysM	PF01476.10	20	LysM domain
MATH	PF00917.16	0.5	MATH domain
MBD	PF01429.10	12.9	Methyl-CpG binding domain
MCM	PF00493.13	25	MCM2/3/5 family
MFS_1	PF07690.6	23.5	Major Facilitator Superfamily
MGDG_synth	PF06925.2	25	Monogalactosyldiacylglycerol (MGDG) synthase
MGS	PF02142.12	3	MGS-like domain
MIP	PF00230.10	-62	Major intrinsic protein
MMR_HSR1	PF01926.13	31.2	GTPase of unknown function
MSF1	PF04707.4	25	MSF1-like conserved region
MSP	PF01716.9	-71	Manganese-stabilising protein / photosystem II polypeptide
Maf	PF02545.5	-42	Maf-like protein
Mago-bind	PF09282.1	25	Mago binding
Malic_M	PF03949.5	-143.9	Malic enzyme, NAD binding domain
Metalloenzyme	PF01676.8	-14.4	Metalloenzyme superfamily
Metallophos	PF00149.18	22	Calcineurin-like phosphoesterase
Metallothio_PEC	PF02068.6	25	Plant PEC family metallothionein
Methyltransf_11	PF08241.2	20.9	Methyltransferase domain
Methyltransf_12	PF08242.2	23	Methyltransferase domain
Miro	PF08477.3	10.8	Miro-like protein
Mito_carr	PF00153.17	0	Mitochondrial carrier protein
Mo25	PF08569.1	-73.5	Mo25-like
Molybdop_Fe4S4	PF04879.6	13.6	Molybdopterin oxidoreductase Fe4S4 domain
Molybdopterin	PF00384.12	-50	Molybdopterin oxidoreductase

Pfam domain name	accession number	gathering cutoff	domain description
Molydop_binding	PF01568.11	1.1	Molydopterin dinucleotide binding domain
Mov34	PF01398.11	-4	Mov34/MPN/PAD-1 family
MtN3_slv	PF03083.6	9.7	MtN3/saliva family
Myb_DNA-binding	PF00249.21	14	Myb-like DNA-binding domain
NADPH_Ox	PF08414.1	25	Respiratory burst NADPH oxidase
NAD_binding_6	PF08030.2	-23.6	Ferric reductase NAD binding domain
NAD_synthase	PF02540.7	-93.3	NAD synthase
NAF	PF03822.5	4.5	NAF domain
NDK	PF00334.9	-59.9	Nucleoside diphosphate kinase
NDUF_B7	PF05676.3	-25.7	NADH-ubiquinone oxidoreductase B18 subunit (NDUFB7)
NIF	PF03031.8	-77.9	NLI interacting factor-like phosphatase
NIR_SIR	PF01077.12	-19.6	Nitrite and sulphite reductase 4Fe-4S domain
NIR_SIR_ferr	PF03460.7	2.4	Nitrite/Sulfite reductase ferredoxin-like half domain
NLE	PF08154.2	14	NLE (NUC135) domain
NOI	PF05627.2	0.3	Nitrate-induced NOI protein
NOT2_3_5	PF04153.8	25	NOT2 / NOT3 / NOT5 family
NPH3	PF03000.5	25	NPH3 family
NTP_transferase	PF00483.13	-90.5	Nucleotidyl transferase
NUDIX	PF00293.18	0.2	NUDIX domain
NicO	PF03824.6	-17	High-affinity nickel-transport protein
Nol1_Nop2_Fmu	PF01189.8	-68.2	NOL1/NOP2/sun family
Not3	PF04065.5	25	Not1 N-terminal domain, CCR4-Not complex component
Nramp	PF01566.9	-217	Natural resistance-associated macrophage protein
Nuc_sug_transp	PF04142.6	-158.6	Nucleotide-sugar transporter
OPT	PF03169.6	-238.6	OPT oligopeptide transporter protein
OUT	PF02338.9	10	OTU-like cysteine protease
Orn_Arg_deC_N	PF02784.7	-76	Pyridoxal-dependent decarboxylase, pyridoxal binding domain
Orn_DAP_Arg_deC	PF00278.12	6.7	pyridoxal-dependent decarboxylase, C-terminal sheet domain
OstA	PF03968.5	-12.1	OstA-like protein
P21-Arc	PF04062.5	-74.5	P21-ARC (ARP2/3 complex 21 kDa subunit)
PADR1	PF08063.2	25	PADR1 (NUC008) domain
PAP2	PF01569.12	8.3	PAP2 superfamily
PARP	PF00644.10	-55.5	Poly(ADP-ribose) polymerase catalytic domain
PARP_reg	PF02877.5	52.8	Poly(ADP-ribose) polymerase, regulatory domain
PAS_2	PF08446.1	-2.1	PAS fold
PB1	PF00564.15	12.3	PB1 domain
PBD	PF00786.18	12.2	P21-Rho-binding domain
PBP	PF01161.10	-20.6	Phosphatidylethanolamine-binding protein
PCI	PF01399.17	25	PCI domain
PC_rep	PF01851.12	0	Proteasome/cyclosome repeat
PDR_assoc	PF08370.2	25	Plant PDR ABC transporter associated
PEARLI-4	PF05278.3	25	Arabidopsis phospholipase-like protein (PEARLI 4)
PEP-utilizers	PF00391.13	0.6	PEP-utilising enzyme, mobile domain
PEP-utilizers_C	PF02896.8	-173	PEP-utilising enzyme, TIM barrel domain

Pfam domain name	accession number	gathering cutoff	domain description
PFK	PF00365.10	-132	Phosphofructokinase
PGAM	PF00300.12	-3	Phosphoglycerate mutase family
PGI	PF00342.9	-168.9	Phosphoglucose isomerase
PGK	PF00162.9	-39.9	Phosphoglycerate kinase
PGM_PMM_I	PF02878.6	-37.5	Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain I
PGM_PMM_II	PF02879.6	-20	Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain II
PGM_PMM_III	PF02880.6	-7.1	Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain III
PGM_PMM_IV	PF00408.10	7.4	Phosphoglucomutase/phosphomannomutase, C-terminal domain
PI-PLC-X	PF00388.9	18.8	Phosphatidylinositol-specific phospholipase C, X domain
PI-PLC-Y	PF00387.9	-11	Phosphatidylinositol-specific phospholipase C, Y domain
PI3_PI4_kinase	PF00454.17	14.8	Phosphatidylinositol 3- and 4-kinase
PLAT	PF01477.13	36.3	PLAT/LH2 domain
PP2C	PF00481.12	-44	Protein phosphatase 2C
PPAK	PF02818.5	0	PPAK motif
PPDK_N	PF01326.9	-150.2	Pyruvate phosphate dikinase, PEP/pyruvate binding domain
PPR	PF01535.11	0	PPR repeat
PRA-CH	PF01502.9	25	Phosphoribosyl-AMP cyclohydrolase
PRA-PH	PF01503.8	-18.3	Phosphoribosyl-ATP pyrophosphohydrolase
PSI_PsaH	PF03244.4	25	Photosystem I reaction centre subunit VI
PTR2	PF00854.12	-50	POT family
PWP2	PF04047.4	25	Periodic tryptophan protein 2 WD repeat associated presumed domain
Peptidase_C26	PF07722.3	25	Peptidase C26
Peptidase_C54	PF03416.9	-153.2	Peptidase family C54
Peptidase_M22	PF00814.15	-53	Glycoprotease family
PetM	PF08041.2	25	PetM family of cytochrome b6f complex subunit 7
PfkB	PF00294.14	-67.8	pfkB family carbohydrate kinase
Phi_1	PF04674.3	25	Phosphate-induced protein 1 conserved region
Phosphoesterase	PF04185.5	-71.5	Phosphoesterase family
Phytochelatin	PF05023.5	25	Phytochelatin synthase
Phvtochrome	PF00360.10	13	Phytochrome region
Pkinase	PF00069.15	-70.3	Protein kinase domain
Pkinase_Tvr	PF07714.7	65	Protein tyrosine kinase
Polyketide_cyc	PF03364.10	20.6	Polyketide cyclase / dehydrase and lipid transport
Pre-SET	PF05033.6	3.9	Pre-SET motif
Prefoldin	PF02996.8	9.3	Prefoldin subunit
Pribosyltran	PF00156.17	2	Phosphoribosyl transferase domain
Pro_CA	PF00484.9	-45	Carbonic anhydrase
Pro_dh	PF01619.8	-120.5	Proline dehydrogenase
Pro_isomerase	PF00160.11	-37	Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD
PseudoU_synth_1	PF01416.10	11	tRNA pseudouridine synthase
Pvr_redox	PF00070.17	5	Pyridine nucleotide-disulphide oxidoreductase
Pyr_redox_2	PF07992.4	-20	Pyridine nucleotide-disulphide oxidoreductase

Pfam domain name	accession number	gathering cutoff	domain description
Pyr_redox_dim	PF02852.12	-13	Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain
Pyridoxal_deC	PF00282.9	-158.6	Pyridoxal-dependent decarboxylase conserved domain
RNA_polI_A14	PF08203.2	25	Yeast RNA polymerase I subunit RPA14
RNA pol_A_bac	PF01000.16	10	RNA polymerase Rpb3/RpoA insert domain
RNA-pol-I-A49	PF06870.3	25	A49-like RNA polymerase I associated factor
RNA_pol_L	PF01193.14	16.9	RNA polymerase Rpb3/Rpb11 dimerisation domain
RRM_1	PF00076.12	17.7	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
RWD	PF05773.12	18.4	RWD domain
Radical_SAM	PF04055.11	8.5	Radical SAM superfamily
Ras	PF00071.12	-69.9	Ras family
RelA_SpoT	PF04607.7	-6.7	Region found in RelA / SpoT proteins
Response_reg	PF00072.14	4	Response regulator receiver domain
Reticulon	PF02453.8	-40	Reticulon
Rho_GDI	PF02115.7	-55	RHO protein GDP dissociation inhibitor
Rib_5-P_isom_A	PF06026.5	-84.5	Ribose 5-phosphate isomerase A (phosphoriboisomerase A)
Ribonuc_L-PSP	PF01042.11	-25	Endoribonuclease L-PSP
Ribosomal_L19	PF01245.10	-31	Ribosomal protein L19
Ribosomal_L37	PF08561.1	25	Mitochondrial ribosomal protein L37
Ribosomal_S8	PF00410.9	-27	Ribosomal protein S8
SAC3_GANP	PF03399.6	-15.2	SAC3/GANP/Ninl/mts3/eIF-3 p25 family
SET	PF00856.18	23.5	SET domain
SH3_1	PF00018.18	-8	SH3 domain
SH3_2	PF07653.7	0	Variant SH3 domain
SIR2	PF02146.8	-95	Sir2 family
SIS	PF01380.12	0	SIS domain
SKI	PF01202.12	-9.2	Shikimate kinase
SNARE	PF05739.9	23.8	SNARE domain
SNARE_assoc	PF09335.1	-12.1	SNARE associated Golgi protein
SOR_SNZ	PF01680.7	25	SOR/SNZ family
SPOC	PF07744.3	12.3	SPOC domain
SPT2	PF08243.2	25	SPT2 chromatin protein
SRF-TF	PF00319.9	11	SRF-type transcription factor (DNA-binding and dimerisation domain)
Saccharop_dh	PF03435.8	-77.9	Saccharopine dehydrogenase
Saccharop_dh_N	PF04455.3	25	LOR/SDH bifunctional enzyme conserved region
SapB_1	PF05184.5	3	Saposin-like type B, region 1
SapB_2	PF03489.7	10.8	Saposin-like type B, region 2
ScpA_ScpB	PF02616.5	-39	ScpA/B protein
Sell	PF08238.2	6.2	Sell repeat
Self-incomp_S1	PF05938.2	-12.7	Plant self-incompatibility protein S1
Senescence	PF06911.3	-53.5	Senescence-associated protein
Shikimate_DH	PF01488.10	-4.4	Shikimate / quinate 5-dehydrogenase
Shikimate_dh_N	PF08501.1	-12.2	Shikimate dehydrogenase substrate binding domain
Sina	PF03145.7	-48.4	Seven in absentia protein family

Pfam domain name	accession number	gathering cutoff	domain description
Skp1	PF01466.9	-2	Skp1 family, dimerisation domain
Skp1_POZ	PF03931.5	14.9	Skp1 family, tetramerisation domain
Snf7	PF03357.11	-22.9	Snf7
Spermine_svnth	PF01564.7	-93.8	Spermine/spermidine svnthase
SpoIIE	PF07228.3	-13.7	Stage II sporulation protein E (SpoIIE)
Sterol_desat	PF01598.8	-13	Sterol desaturase
	PF04885.4	25	Stigma-specific protein, Stig1
Stig1 Str_synth	PF03088.7	4.7	Strictosidine synthase
Sugar_tr	PF00083.14	-85	Sugar (and other) transporter
Sulfotransfer_1	PF00685.17	-53.1	Sulfotransferase domain
TB2_DP1_HVA22	PF03134.9	-25.1	TB2/DP1, HVA22 family
TFIIF_alpha	PF05793.3	25	Transcription initiation factor IIF, alpha subunit (TFIIF-alpha)
TFIIS	PF08711.1	3	Transcription elongation factor S-II protein N terminal
TFIIS_C	PF01096.9	15	Transcription factor S-II (TFIIS)
TFIIS_M	PF07500.4	7.4	Transcription factor S-II (TFIIS), central domain
TIM	PF00121.9	-97	Triosephosphate isomerase
TLD	PF07534.6	25	TLD
TMEM14	PF03647.4	-1	Transmembrane proteins 14C
TOM20_plant	PF06552.3	25	Plant specific mitochondrial import receptor subunit TOM20
TPK_B1_binding	PF04265.5	25	Thiamin pyrophosphokinase, vitamin B1 binding domain
TPK_catalytic	PF04263.7	-23.8	Thiamin pyrophosphokinase, catalytic domain
TPR_2	PF07719.7	20.1	Tetratricopeptide repeat
TPT	PF03151.7	-15.3	Triose-phosphate Transporter family
TP_methylase	PF00590.10	-38	Tetrapyrrole (Corrin/Porphyrin) Methylases
Tcp11	PF05794.4	25	T-complex protein 11
Tetraspannin	PF00335.10	-15.4	Tetraspanin family
ThiC	PF01964.9	25	ThiC family
ThiF	PF00899.11	-38.4	ThiF family
ThiG	PF05690.4	-186.9	Thiazole biosynthesis protein ThiG
Thioredoxin	PF00085.10	-25.7	Thioredoxin
Tim17	PF02466.9	2.7	Tim17/Tim22/Tim23 family
Transaldolase	PF00923.9	-49	Transaldolase
Transket_pyr	PF02779.14	-49	Transketolase, pyrimidine binding domain
Transketolase_C	PF02780.10	-15.5	Transketolase, C-terminal domain
Transketolase_N	PF00456.11	-98	Transketolase, thiamine diphosphate binding domain
Transthyretin	PF00576.11	25	Transthyretin precursor (formerly prealbumin)
Trehalose_PPase	PF02358.7	-49.4	Trehalose-phosphatase
Tryp_alpha_amyl	PF00234.12	-4	Protease inhibitor/seed storage/LTP family
UAA	PF08449.2	-146.2	UAA transporter family
UBA	PF00627.21	20.7	UBA/TS-N domain
UBX	PF00789.11	10	UBX domain
UCH	PF00443.19	-8.6	Ubiquitin carboxyl-terminal hydrolase
UDPGT	PF00201.9	-151	UDP-glucoronosyl and UDP-glucosyl transferase
UFD1	PF03152.5	25	Ubiquitin fusion degradation protein UFD1

Pfam domain name	accession number	gathering cutoff	domain description
UQ_con	PF00179.16	-30	Ubiquitin-conjugating enzyme
Uricase	PF01014.9	-10.6	Uricase
Usp	PF00582.16	21.6	Universal stress protein family
Utp13	PF08625.1	-12.4	Utp13 specific WD40 associated domain
V-SNARE	PF05008.5	-16	Vesicle transport v-SNARE protein
Voltage_CLC	PF00654.10	-148	Voltage gated chloride channel
WD40	PF00400.22	21.5	WD domain, G-beta repeat
WGR	PF05406.5	5.8	WGR domain
WRKY	PF03106.6	25	WRKY DNA -binding domain
XG_FTase	PF03254.4	25	Xyloglucan fucosyltransferase
XPC-binding	PF09280.1	27.6	XPC-binding domain
Xan_ur_permease	PF00860.11	-151.2	Permease family
YDG_SRA	PF02182.8	25	YDG/SRA domain
Y_phosphatase2	PF03162.4	-47.6	Tyrosine phosphatase family
YjeF_N	PF03853.5	25	YjeF-related protein N-terminus
Zip	PF02535.12	-25.6	ZIP Zinc transporter
adh_short	PF00106.15	-40.2	short chain dehydrogenase
cobW	PF02492.9	-10	CobW/HypB/UreG, nucleotide-binding domain
eIF-1a	PF01176.9	20	Translation initiation factor IA / IF-1
eIF2A	PF08662.1	0	Eukaryotic translation initiation factor eIF2A
efhand	PF00036.22	21.7	EF hand
efhand_like	PF09279.1	17.8	Phosphoinositide-specific phospholipase C, efhand-like
iPGM_N	PF06415.4	-263.4	BPG-independent PGAM N-terminus (iPGM_N)
mTERF	PF02536.5	-60	mTERF
malic	PF00390.9	25	Malic enzyme, N-terminal domain
p450	PF00067.12	-105	Cytochrome P450
polyprenyl_synt	PF00348.8	-43	Polyprenyl synthetase
tRNA-synt_1g	PF09334.1	-272.5	tRNA synthetases class I (M)
ubiquitin	PF00240.13	19.4	Ubiquitin family
zf-C3HC4	PF00097.15	16	Zinc finger, C3HC4 type (RING finger)
zf-CCHC	PF00098.13	17.9	Zinc knuckle
zf-CW	PF07496.5	25	CW-type Zinc Finger
zf-LSD1	PF06943.3	25	LSD1 zinc finger
zf-MYND	PF01753.9	11	MYND finger
zf-PARP	PF00645.8	25	Poly(ADP-ribose) polymerase and DNA-Ligase Zn-finger region
zf-Tim10_DDP	PF02953.6	-5	Tim10/DDP family zinc finger
zf-UBR	PF02207.10	25	Putative zinc finger in N-recognin (UBR box)

Example 5. Plasmid contruction for transferring recombinant DNA

[0117] This example illustrates the construction of plasmids for transferring recombinant DNA into the nucleus of a plant cell which can be regenerated into a transgenic crop plant of this invention. Primers for PCR amplification of protein coding nucleotides of recombinant DNA are designed at or near the start and stop codons of the coding sequence, in order to eliminate most of the 5' and 3' untranslated regions. DNA of interest, i.e. each DNA identified in Table 2 and the DNA for the identified homologous genes, are cloned and amplified by PCR prior to insertion into the insertion site the base vector.

A. Plant expression constructs for corn transformation

[0118] Elements of an exemplary common expression vector, pMON93039 are illustrated in Table 20. The exemplary base vector which is especially useful for corn transformation is illustrated in Figure 1 and assembled using technology known in the art.

Table 20. pMON93039

function	name	annotation	Coordinates of SEQ ID NO: 67779
Agrobacterium T-DNA trabsfer	B-AGRtu.right border	Agro right border sequence, essential for transfer of T-DNA.	11364-11720
Gene of interest expression cassette	E-Os.Act1	upstream promoter region of the rice actin 1 gene	19-775
	E-CaMV.35S.2xA1-B3	duplicated35S A1-B3 domain without TATA box	788-1120
	P-Os.Act1	promoter region of the rice actin 1 gene	1125-1204
	L-Ta.Lhcb1	5' untranslated leader of wheat major chlorophyll a/b binding protein	1210-1270
	I-Os.Act1	first intron and flanking UTR exon sequences from the rice actin 1 gene	1287-1766
	T-St.Pis4	3' non-translated region of the potato proteinase inhibitor II gene which functions to direct polyadenylation of the mRNA	1838-2780
Plant selectable marker expression cassette	P-Os.Act1	Promoter from the rice actin 1 gene	2830-3670
	L-Os.Act1	first exon of the rice actin 1 gene	3671-3750
	I-Os.Act1	first intron and flanking UTR exon sequences from the rice actin 1 gene	3751-4228
	TS-At.ShkG-CTP2	Transit peptide region of Arabidopsis EPSPS	4238-4465
	CR-AGRtu.aroA-CP4.nat	coding region for bacterial strain CP4 native arogA gene	4466-5833
	T-AGRtu.nos	A 3' non-translated region of the nopaline synthase gene of Agrobacterium tumefaciens Ti plasmid which functions to direct polyadenylation of the mRNA.	5849-6101
Agrobacterium T-DNA transfer	B-AGRtu.left border	Agro left border sequence, essential for transfer of T-DNA.	6168-6609
Maintenance in E. coli	OR-Ec.oriV-RK2	The vegetative origin of replication from plasmid RK2.	6696-7092
	CR-Ec.rop	Coding region for repressor of primer from the ColE1 plasmid. Expression of this gene product interferes with primer binding at the origin of replication, keeping plasmid copy number low.	8601-8792
	OR-Ec.ori-ColEI	The minimal origin of replication from the E. coli plasmid ColEI.	9220-9808
	P-Ec.aadA-SPC/STR	romoter for Tn7 adenylyltransferase (AAD(3"))	10339-10380
	CR-Ec.aadA-SPC/STR	Coding region for Tn7 adenylyltransferase (AAD(3")) conferring spectinomycin and streptomycin resistance.	10381-11169
	T-Ec.aadA-SPC/STR	3' UTR from the Tn7 adenylyltransferase (AAD(3")) gene of E. coli.	11170-11227

B. Plant expression constructs for soybean or canola transformation

[0119] Plasmids for use in transformation of soybean are also prepared. Elements of an exemplary common expression vector plasmid pMON82053 are shown in Table 21 below. This exemplary soybean transformation base vector illustrated in Figure 2 is assembled using the technology known in the art. DNA of interest, i.e. each DNA identified in Table 2 and the DNA for the identified homologous genes, is cloned and amplified by PCR prior to insertion into the insertion site the base vector at the insertion site between the enhanced 35S CaMV promoter and the termination sequence of cotton E6 gene.

Table 21. pMON82053

function	name	annotation	Coordinates of SEQ ID NO: 67780
Agrobacterium T-DNA transfer	B-AGRtu.left border	Agro left border sequence, essential for transfer of T-DNA.	6144-6585
Plant selectable marker expression cassette	P-At.Act7	Promoter from the arabidopsis actin 7 gene	6624-7861
	L-At.Act7	5'UTR of Arabidopsis Act7 gene	
	I-At.Act7	Intron from the Arabidopsis actin7 gene	
	TS-At.ShkG-CTP2	Transit peptide region of Arabidopsis EPSPS	7864-8091
	CR-AGRtu.aroA-CP4.nno_At	Synthetic CP4 coding region with dicot preferred codon usage.	8092-9459
	T-AGRtu.nos	A 3' non-translated region of the nopaline synthase gene of Agrobacterium tumefaciens Ti plasmid which functions to direct polyadenylation of the mRNA.	9466-9718
Gene of interest expression cassette	P-CaMV.35S-enh	Promoter for 35S RNA from CaMV containing a duplication of the -90 to -350 region.	1-613
	T-Gb.E6-3b	3' untranslated region from the fiber protein E6 gene of sea-island cotton;	688-1002
Agrobaterium T-DNA transfer	B-AGRtu.right border	Agro right border sequence, essential for transfer of T-DNA.	1033-1389
Maintenance in E. coli	OR-Ec.oriV-RK2	The vegetative origin of replication from plasmid RK2.	5661-6057
	CR-Ec.rop	Coding region for repressor of primer from the ColE1 plasmid. Expression of this gene product interferes with primer binding at the origin of replication, keeping plasmid copy number low.	3961-4152
	OR-Ec.ori-ColEl	The minimal origin of replication from the E. coli plasmid ColE1.	2945-3533
	P-Ec.aadA-SPC/STR	romoter for Tn7 adenylyltransferase (AAD(3"))	2373-2414
	CR-Ec.aadA-SPC/STR	Coding region for Tn7 adenylyltransferase (AAD(3")) conferring spectinomycin and streptomycin resistance.	1584-2372
	T-Ec.aadA-SPC/STR	3' UTR from the Tn7 adenylyltransferase (AAD(3")) gene of E. coli.	1526-1583

C. Plant expression constructs for cotton transformation

[0120] Plasmids for use in transformation of cotton are also prepared. Elements of an exemplary common expression vector plasmid pMON99053 are shown in Table 22 below and Figure 3. Primers for PCR amplification of protein coding nucleotides of recombinant DNA are designed at or near the start and stop codons of the coding sequence, in order to eliminate most of the 5' and 3' untranslated regions. Each recombinant DNA coding for a protein identified in Table 2 is amplified by PCR prior to insertion into the insertion site within the gene of interest expression cassette of one of the base.

Table 22. pMON99053

function	name	annotation	Coordinates of SEQ ID NO: 67781
Agrobacterium T-DNA transfer	B-AGRtu.right border	Agro right border sequence, essential for transfer of T-DNA.	11364-11720
Gene of interest expression cassette	Exp-CaMV.35S-enh+ph.DnaK	Enhanced version of the 35S RNA promoter from CaMV plus the petunia hsp70 5' untranslated region	7794-8497
	T-Ps.RbcS2-E9	The 3' non-translated region of the pea RbcS2 gene which functions to direct polyadenylation of the mRNA.	67-699
Plant selectable marker expression cassette	Exp-CaMV.35S	Promoter and 5' untranslated region of the 35S RNA from CaMV	730-1053
	CR-Ec.nptII-Tn5	Neomycin Phosphotransferase II gene that confers resistance to neomycin and kanamycin	1087-1881
	T-AGRtu.nos	A 3' non-translated region of the nopaline synthase gene of Agrobacterium tumefaciens Ti plasmid which functions to direct polyadenylation of the mRNA.	1913-2165
Agrobacterium T-DNA transfer	B-AGRtu.left border	Agro left border sequence, essential for transfer of T-DNA.	2211-2652
Maintenance in E. coli	OR-Ec.oriV-RK2	The vegetative origin of replication from plasmid RK2.	2739-3135
	CR-Ec.rop	Coding region for repressor of primer from the ColE1 plasmid. Expression of this gene product interferes with primer binding at the origin of replication, keeping plasmid copy number low.	4644-4835
	OR-Ec.ori-ColE1	The minimal origin of replication from the E. coli plasmid ColEI.	5263-5851
	P-Ec.aadA-SPC/STR	romoter for Tn7 adenylyltransferase (AAD(3"))	6382-6423
	CR-Ec.aadA-SPC/STR	Coding region for Tn7 adenylyltransferase (AAD(3")) conferring spectinomycin and streptomycin resistance.	6424-7212
	T-Ec.aadA-SPC/STR	3' UTR from the Tn7 adenylyltransferase (AAD(3")) gene of E. coli.	7213-7270

Example 6. Corn plant tranformation

[0121] This example illustrates the production and identification of transgenic corn cells in seed of transgenic corn plants having an enhanced agronomic trait, i.e. enhanced nitrogen use efficiency, increased yield, enhanced water use efficiency, enhanced tolerance to cold and/or enhanced seed compositions as compared to control plants. Transgenic corn cells are prepared with recombinant DNA expressing each of the protein encoding DNAs listed in Table 2 by *Agrobacterium*-mediated transformation using the corn transformation constructs as disclosed in Example 5.

[0122] Corn transformation is effected using methods disclosed in U.S. Patent Application Publication 2004/0344075 A1 where corn embryos are inoculated and co-cultured with the *Agrobacterium tumefaciens* strain ABI and the corn transformation vector. To regenerate transgenic corn plants the transgenic callus resulting from transformation is placed on media to initiate shoot development in plantlets which are transferred to potting soil for initial growth in a growth chamber followed by a mist bench before transplanting to pots where plants are grown to maturity. The plants are self fertilized and seed is harvested for screening as seed, seedlings or progeny R2 plants or hybrids, *e.g.,* for yield trials in the screens indicated above.

[0123] Many transgenic events which survive to fertile transgenic plants that produce seeds and progeny plants do not exhibit an enhanced agronomic trait. The transgenic plants and seeds having the transgenic cells of this invention which have recombinant DNA imparting the enhanced agronomic traits are identified by screening for nitrogen use efficiency, yield, water use efficiency, cold tolerance and enhanced seed composition.

Example 7. Soybean plant transformation

[0124] This example illustrates the production and identification of transgenic soybean cells in seed of transgenic soybean plants having an enhanced agronomic trait, i.e. enhanced nitrogen use efficiency, increased yield, enhanced water use efficiency, enhanced tolerance to cold and/or enhanced seed compositions as compared to control plants. Transgenic soybean cells are prepared with recombinant DNA expressing each of the protein encoding DNAs listed in Table 1 by *Agrobacterium*-mediated transformation using the soybean transformation constructs disclosed in Example 5. Soybean transformation is effected using methods disclosed in U.S. Patent 6,384,301 where soybean meristem explants are wounded then inoculated and co-cultured with the soybean transformation vector, then transferred to selection media for 6-8 weeks to allow selection and growth of transgenic shoots.

[0125] The transformation is repeated for each of the protein encoding DNAs identified in Table 2.

[0126] Transgenic shoots producing roots are transferred to the greenhouse and potted in soil. Many transgenic events which survive to fertile transgenic plants that produce seeds and progeny plants do not exhibit an enhanced agronomic trait. The transgenic plants and seeds having the transgenic cells of this invention which have recombinant DNA imparting the enhanced agronomic traits are identified by screening for nitrogen use efficiency, yield, water use efficiency, cold tolerance and enhanced seed composition.

Example 8. Selection of transgenic plants with enhanced agronomic trait(s)

[0127] This example illustrates identification of plant cells of the invention by screening derived plants and seeds for enhanced trait. Transgenic seed and plants in corn, soybean, cotton or canola with recombinant DNA identified in Table 2 are prepared by plant cells transformed with DNA that is stably integrated into the genome of the corn cell. Transgenic corn plant cells are transformed with recombinant DNA from each of the genes identified in Table 2. Progeny transgenic plants and seed of the transformed plant cells are screened for enhanced water use efficiency, enhanced cold tolerance, increased yield, enhanced nitrogen use efficiency, enhanced seed protein and enhanced seed oil as compared to control plants

A. Selection for enhanced Nitrogen Use Efficiency

[0128] Transgenic corn seeds provided by the present invention are planted in fields with three levels of nitrogen (N) fertilizer being applied, i.e. low level (0 N), medium level (80 lb/ac) and high level (180 lb/ac). A variety of physiological traits are monitored. Plants with enhanced NUE provide higher yield as compared to control plants.

B. Selection for increased yield

[0129] Effective selection of enhanced yielding transgenic plants uses hybrid progeny of the transgenic plants for corn, cotton, and canola, or inbred progeny of transgenic plants for soybeanplants plant such as corn, cotton, canola, or inbred plant such as soy, canola and cottoncotton over multiple locations with plants grown under optimal production management practices, and maximum pest control. A useful target for improved yield is a 5% to 10% increase in yield as compared to yield produced by plants grown from seed for a control plant. Selection methods may be applied in multiple and diverse geographic locations, for example up to 16 or more locations, over one or more planting seasons, for example at least two planting seasons, to statistically distinguish yield improvement from natural environmental effects

C. Selection for enhanced water use efficiency (WUE)

[0130] The selection process imposes a water withholding period to induce stressdrought followed by watering. For for example, for corn, a useful selection process imposes 3 drought/re-water cycles on plants over a total period of 15 days after an initial stress free growth period of 11 days. Each cycle consists of 5 days, with no water being applied for the first four days and a water quenching on the 5th day of the cycle. The primary phenotypes analyzed by the selection method are the changes in plant growth rate as determined by height and biomass during a vegetative drought treatment.

D. Selection for Growth Under Cold Stress

[0131]

1. (1) Cold germination assay - Trays of transgenic and control seeds are placed in a growth chamber at 9.7°C for 24 days (no light). Seeds having higher germination rates as compared to the control are identified.
2. (2) Cold field efficacy trial - A cold field efficacy trial is used to identify gene constructs that confer enhanced cold vigor at germination and early seedling growth under early spring planting field conditions in conventional-till and simulated no-till environments. Seeds are planted into the ground around two weeks before local farmers begin to plant corn so that a significant cold stress is exerted onto the crop, named as cold treatment. Seeds also are planted under local optimal planting conditions such that the crop has little or no exposure to cold condition, named as normal treatment. At each location, seeds are planted under both cold and normal conditions with 3 repetitions per treatment. Two temperature monitors are set up at each location to monitor both air and soil temperature daily.

[0132] Seed emergence is defined as the point when the growing shoot breaks the soil surface. The number of emerged seedlings in each plot is counted everyday from the day the earliest plot begins to emerge until no significant changes in emergence occur. In addition, for each planting date, the latest date when emergence is 0 in all plots is also recorded. Seedling vigor is also rated at V3-V4 stage before the average of corn plant height reaches 10 inches, with 1=excellent early growth, 5=Average growth and 9=poor growth. Days to 50% emergence, maximum percent emergence and seedling vigor are used to determine plants with enhanced cold tolerance.

E. Screens for transgenic plant seeds with increased protein and/or oil levels

[0133] This example sets forth a high-throughput selection for identifying plant seeds with improvement in seed composition using the Infratec 1200 series Grain Analyzer, which is a near-infrared transmittance spectrometer used to determine the composition of a bulk seed sample (Table 23). Near infrared analysis is a non-destructive, high-throughput method that can analyze multiple traits in a single sample scan. An NIR calibration for the analytes of interest is used to predict the values of an unknown sample. The NIR spectrum is obtained for the sample and compared to the calibration using a complex chemometric software package that provides predicted values as well as information on how well the sample fits in the calibration.

[0134] Infratec Model 1221, 1225, or 1227 with transport module by Foss North America is used with cuvette, item # 1000-4033, Foss North America or for small samples with small cell cuvette, Foss standard cuvette modified by Leon Girard Co. Corn and soy check samples of varying composition maintained in check cell cuvettes are supplied by Leon Girard Co. NIT collection software is provided by Maximum Consulting Inc.Software. Calculations are performed automatically by the software. Seed samples are received in packets or containers with barcode labels from the customer. The seed is poured into the cuvettes and analyzed as received.

Table 23

Typical sample(s):	Whole grain corn and soybean seeds
Analytical time to run method:	Less than 0.75 min per sample
Total elapsed time per run:	1.5 minute per sample
Typical and minimum sample size:	Corn typical: 50cc; minimum 30cc Soybean typical: 50cc; minimum 5cc
Typical analytical range:	Determined in part by the specific calibration.
	Corn - moisture 5-15%, oil 5-20%, protein 5-30%, starch 50-75%, and density 1.0-1.3%.
	Soybean - moisture 5-15%, oil 15-25%, and protein 35-50%.

Example 9. Cotton transgenic plants with enhanced agronomic traits

[0135] Cotton transformation is performed as generally described in WO0036911 and in U.S. Pat. No. 5,846,797. Transgenic cotton plants containing each of the recombinant DNA having a sequence of SEQ ID NO: 1 through SEQ ID NO: 759 are

obtained by transforming with recombinant DNA from each of the genes identified in Table 1. Progeny transgenic plants are selected from a population of transgenic cotton events under specified growing conditions and are compared with control cotton plants. Control cotton plants are substantially the same cotton genotype but without the recombinant DNA, for example, either a parental cotton plant of the same genotype that was not transformed with the identical recombinant DNA or a negative isoline of the transformed plant. Additionally, a commercial cotton cultivar adapted to the geographical region and cultivation conditions, i.e. cotton variety ST474, cotton variety FM 958, and cotton variety Siokra L-23, are used to compare the relative performance of the transgenic cotton plants containing the recombinant DNA. The specified culture conditions are growing a first set of transgenic and control plants under "wet" conditions, i.e. irrigated in the range of 85 to 100 percent of evapotranspiration to provide leaf water potential of -14 to -18 bars, and growing a second set of transgenic and control plants under "dry" conditions, i.e. irrigated in the range of 40 to 60 percent of evapotranspiration to provide a leaf water potential of -21 to -25 bars. Pest control, such as weed and insect control is applied equally to both wet and dry treatments as needed. Data gathered during the trial includes weather records throughout the growing season including detailed records of rainfall; soil characterization information; any herbicide or insecticide applications; any gross agronomic differences observed such as leaf morphology, branching habit, leaf color, time to flowering, and fruiting pattern; plant height at various points during the trial; stand density; node and fruit number including node above white flower and node above crack boll measurements; and visual wilt scoring. Cotton boll samples are taken and analyzed for lint fraction and fiber quality. The cotton is harvested at the normal harvest timeframe for the trial area. Enhanced water use efficiency is indicated by increased yield, improved relative water content, enhanced leaf water potential, increased biomass, enhanced leaf extension rates, and improved fiber parameters.

[0136] The transgenic cotton plants of this invention are identified from among the transgenic cotton plants by agronomic trait screening as having increased yield and enhanced water use efficiency.

Example 10. Canola plants with enhanced agrominic traits

[0137] This example illustrates plant transformation useful in producing the transgenic canola plants of this invention and the production and identification of transgenic seed for transgenic canola having enhanced water use efficiency, enhanced cold tolerance, increased yield, enhanced nitrogen use efficiency, enhanced seed protein and enhanced seed oil.

[0138] Tissues from in vitro grown canola seedlings are prepared and inoculated with a suspension of overnight grown *Agrobacterium* containing plasmid DNA with the gene of interest cassette and a plant selectable marker cassette. Following co-cultivation with Agrobacterium, the infected tissues are allowed to grow on selection to promote growth of transgenic shoots, followed by growth of roots from the transgenic shoots. The selected plantlets are then transferred to the greenhouse and potted in soil. Molecular characterization are performed to confirm the presence of the gene of interest, and its expression in transgenic plants and progenies. Progeny transgenic plants are selected from a population of transgenic canola events under specified growing conditions and are compared with control canola plants. Control canola plants are substantially the same canola genotype but without the recombinant DNA, for example, either a parental canola plant of the same genotype that is not transformed with the identical recombinant DNA or a negative isoline of the transformed plant

[0139] Transgenic canola plant cells are transformed with recombinant DNA from each of the genes identified in Table 2. Transgenic progeny plants and seed of the transformed plant cells are screened for enhanced water use efficiency, enhanced cold tolerance, increased yield, enhanced nitrogen use efficiency, enhanced seed protein and enhanced seed oil.

Example 11. Selection of transgenic plants with enhanced agronomic trait(s)

[0140] This example illustrates the preparation and identification by selection of transgenic seeds and plants derived from transgenic plant cells of this invention where the plants and seed are identified by screening for a transgenic plant having an enhanced agronomic trait imparted by expression or suppression of a protein selected from the group including the homologous proteins identified in Example 2. Transgenic plant cells of corn, soybean, cotton, canola, alfalfa, wheat and rice are transformed with recombinant DNA for expressing or suppressing each of the homologs identified in Example 2. Plants are regenerated from the transformed plant cells and used to produce progeny plants and seed that are screened for enhanced water use efficiency, enhanced cold tolerance, increased yield, enhanced nitrogen use efficiency, enhanced seed protein and enhanced seed oil. Plants are identified exhibiting enhanced traits imparted by expression or suppression of the homologous proteins.

Example 12. Monocot and dicot plant transformation for the suppression of endogeneous protein

[0141] This example illustrates monocot and dicot plant transformation to produce nuclei of this invention in cells of a transgenic plant by transformation where the recombinant DNA suppresses the expression of an endogenous protein identified in Table 24.

[0142] Corn, soybean, cotton, or canola tissue are transformed as described in Examples 2-5 using recombinant DNA in the nucleus with DNA that is transcribed into RNA that forms double- stranded RNA targeted to an endogenous gene with DNA encoding the protein. The genes for which the double-stranded RNAs are targeted are the native gene in corn, soybean, cotton or canola that are homologs of the genes encoding the protein that has the function of the protein in *Arabidopsis* as identified in table 24.

[0143] Populations of transgenic plants prepared in Examples 6, 7, 9, 10 or 11 with DNA for suppressing a gene identified in Table 2 as providing an enhanced trait by gene suppression are screened to identify an event from those plants with a nucleus of the invention by selecting the trait identified in this specification.

Table 24

PEP SEQ ID	Gene_id	Construct ID	Traits				
760	CGPG1022.pep	RRM_1	DS				
761	CGPG1035.pep	Peptidase_C54	SS				
763	CGPG105.pep	AP2	HS	PEG			
764	CGPG1060.pep	DUF788	LN				
771	CGPG1136.pep	RRM_1	DS				
774	CGPG1145.pep	LNDIX	LN				
776	CGPG1173.pep	adh_short	LN				
779	CGPG122.pep	PTR2	LN				
781	CGPG1262.pep	Gar1	CK				
782	CGPG128.pep	Response_reg	LN				
784	CGPG1291.pep	DUF862	DS				
794	CGPG1398.pep	Glycolytic	LN				
795	CGPG1399.pep	Metallophos	LN				
799	CGPG146.pep	p450	CS	PP	SS		
801	CGPG1528.pep	ATP_synt_H	LN				
803	CGPG1535.pep	SPT2	LN				
804	CGPG1546.pep	CTP_transf_1	LN				
805	CGPG1567.pep	Ribosomal_L19	LN				
807	CGPG1575.pep	DUF740	DS				
810	CGPG1641.pep	Di19	SP				
812	CGPG1656.pep	Cyt-b5::FA_desaturase	CS				
813	CGPG1668.pep	DUF791::MFS_1	SS				
817	CGPG1785pep	P81::Pkinase_Tyr	CK				
829	CGPG1938.pep	F-box::LRR_2	CS				
835	CGPG2005.pep	NADPH_Ox::Ferric_reduct::FAD_binding_8::NAD_binding_6	CS	PP	HS	SS	PEG
838	CGPG2059.pep	LNc_sug_transp	SS				
842	CGPG2074.pep	HMA::HMA	CK				
845	CGPG2142.pep	MATH::MATH	DS				
850	CGPG2213.pep	RNA_pol_I_A49	CK	PEG			
851	CGPG2247.pep	DUF23	CK				
852	CGPG228.pep	p450	SP				
858	CGPG2354.pep	ABC1	PP				

PEP SEQ ID	Gene_id	Construct ID	Traits				
863	CGPG240.pep	Hydrolase	DS				
869	CGPG2472.pep	Band_7	LN				
877	CGPG274.pep	WD40::WD40::WD40	PP	LL			
879	CGPG277.pep	IGPD	LN				
893	CGPG309.pep	Cyclin_N	LN				
911	CGPG337.pep	Glyco_transf_8	LN				
917	CGPG347.pep	DREPP	LN				
931	CGPG372.pep	SET	LN				
941	CGPG394.pep	DUF6::TPT	LN				
943	CGPG397.pep	SOR_SNZ::ThiG	CK				
957	CGPG421.pep	Pkinase::efhand::efhand::efhand::efhand	LN				
958	CGPG422.pep	Pkinase	LN				
968	CGPG430.pep	Pkinase	DS				
996	CGPG468.pep	Fer4::Fer4	LN				
1031	CGPG510.pep	Rho_GDI	SS				
1040	CGPG519.pep	Abhydrolase_1	PEG				
1058	CGPG532.pep	Transket_pyr::Transketolase_C	LN				
1078	CGPG557.pep	Chitin_bind_1::Barwin	LN				
1083	CGPG561.pep	XG_FTase	PP				
1091	CGPG568.pep	FTHFS	LN				
1108	CGPG580.pep	MGDG_synth::Glyco_tran_28_C	LN				
1134	CGPG604.pep	PSI_PsaH	LN				
1144	CGPG614.pep	cobW	LN				
1150	CGPG620.pep	tRNA-synt_1g	DS				
1212	CGPG663.pep	Pro_CA	LN				
1232	CGPG686.pep	RRM_1::zf-CCHC	LN				
1258	CGPG713.pep	Cyclin_N	LN				
1267	CGPG72.pep	Amino_oxidase	LN				
1328	CGPG773.pep	H_PPase	PP				
1357	CGPG801.pep	Cyt-b5	LN				
1406	CGPG841.pep	ArfGap	LN				
1452	CGPG879.pep	ABC_tran::ABC2_membrane::PDR_assoc::ABC_tran::ABC2_membrane	LN				
1477	CGPG908.pep	PPR::PPR::PPR::PPR::PPR::PPR::PPR::PPR	LN				
1515	CGPG933.pep	WD40::WD40::WD40::WD40::WD40::WD40::WD40	SP				
1517	CGPG967.pep	BTB::NPH3	CS				

Table 16

SEQ ID NO: homolog SEQ ID NOs

760:27133 58543 37449 15741 23545 40760 20576 8500 58315 30609 8776 42309
21498 64901 58729 32871 17724 56907 23843 8141 46838 60136 9305 61451
34879 66802 27639 11099 6961 61278 47165 8960 52445

761:21925 19679 10928 10340 25265 63687 49344 66929 67029 42524 21089 26303
27640 51892 51897 15690 2938 55813 18650 45273 61649 31888 11456 16368
17129 14918 22083 30415 24582 24583 4533 28424 58898 37353 50706 57290
61656 43016 50371 40077 30586 37110 62557 6352 45504 60824 6333 49368
3638 33531 39854 23524

763:35807 35804 35805 21478 4255 38013 4175 4177 4174 51238 60498 60509
1573 4170 17741 51289 37874 51271 4151 38017 4207 39734 4124 4146
12167 63154 63156 63758 12163 12166 12143 12146 39648 7734 7147 38482
60930 50739 50733 50748 50361 12132 65973 6784 6289 6286 41278 21530
6835 43829 6963 14326 42702 64751 9547 18248 62831 64708 65030 64712
6435 11219 30229 67096 24237 24235 51156 50289 8084 53638 63936 60098
32858 24179 50747 25771 41906 41904 49357 10793 24190 8299 40928 39150
18215 16245 55174 55157 54530 3310 54515 44909 6302 6319 57800 25440
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      35622 25057 43785 67485  4434 25506 25559 25055  8643 38483 25562 48779
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      36326 36321 36311 36312 36327 36334 41950  8553 15475 38048 12270 23947
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      50447 29045  3094 12307 26622 27496 59778  8688 14937 45592 28498 22388
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  771:38888 42457 24584 44183 14229 52493 18549 57066 37863 14476 48729 22127
      26098 25466 11886 34077 41522 33757  9870 53316 41865 50802 58718 56315
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      44838 43536 55663 23537 21904 49120 22191 66363 64005  4029 35152 46284
      30866 41725 56411 49550 67629 66392 45209 39687 25564 11122  6029 54710
      48073


777:63526 18614 37317  7482 58438 35686
778:61324 46060 52076 22112 22110  3381 25834 31691 11951 64455 11457 53900
779:11378 64091 64114 64113 64210 64212 64167 64130 64192 64194 64140 64213
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    6696
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     2248 23561 53441 65514 52292 31179 34249 54853 12639 11470 30095 64913
    17964 66520 33679 53458 34639 55972 54537  4614 39364 11261 56158 67017
    58914 20390  2334 32940 44652 47836  8073 47786 34400
782:57965 18905 26969 14770 53978  2910 13465 46068 24984 31704 41081 38391
    32584 40052 31604 25449 22944 34019 66913 11555 46146 21892 42630 50746
    28757 40291 52247 16062 46834 43077 16549 11209 25909  5368  5372 37905
    15137 41171  2908 55815 17683 38593 45946 64920 66860 59110 63167 15528
    31766 15141  2530 63121 31769 53068 14157 58847 58947 26343  8016 22801
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    63989 66997 55542 57914 54457 62133 40096 64479 25194 16338  5848 65023
    62348 28188 67556 14563 50220 16426 19789 34425 65307 66099 45121 48608
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Patentkrav

1. Plantecellekerne med stabilt integreret, rekombinant DNA, hvor det rekombinante DNA omfatter en promoter, der er funktionel i plantecellen, og som er operabelt forbundet med et protein-kodende DNA, der koder for en aminosyresekvens med mindst 90 % sekvensidentitet i den fulde længde af SEQ ID NO: 1018, hvor transgene planter med det rekombinante DNA i kernerne har en øget varmetolerance sammenlignet med kontrolplanter, der ikke har det rekombinante DNA i kernerne.

2. Rekombinant DNA-konstrukt, som omfatter en promotor, der er funktionel i plantecellen, og som er operabelt forbundet med et protein-kodende DNA, der koder for en aminosyresekvens med mindst 90 % sekvensidentitet i den fulde længde af SEQ ID NO: 1018, hvor transgene planter med det rekombinante DNA i kernerne har en øget varmetolerance sammenlignet med kontrolplanter, der ikke har det rekombinante DNA i kernerne.

3. Plantecellekerne ifølge krav 1, som omfatter det rekombinante DNA-konstrukt, der omfatter en promoter, der er funktionel i plantecellen, og som er operabelt forbundet med et protein-kodende DNA, der koder for en aminosyresekvens med mindst 90 % sekvensidentitet i den fulde længde af SEQ ID NO: 1018, yderligere omfattende DNA, der eksprimerer et protein, der tilvejebringer tolerance over for ukrudtsmiddel til plantecellen.

4. Plantecellekerne ifølge krav 3, hvor midlet i ukrudtsmidlet er en glyphosat-, dicamba- eller glufosinatforbindelse.

5. Transgent frø, omfattende en flerhed af planteceller med en plantecellekerne, omfattende et rekombinant DNA-konstrukt, der omfatter en promoter, der er funktionel i plantecellen, og som er operabelt forbundet med et protein-kodende DNA, der koder for en aminosyresekvens med mindst 90 % sekvensidentitet i den fulde længde af SEQ ID NO: 1018, hvor transgene planter med det rekombinante DNA i kernerne har en øget varmetolerance sammenlignet med kontrolplanter, der ikke har det rekombinante DNA i kernerne.

6. Transgent frø ifølge krav 5, der kan anvendes til at fremstille en afgrøde af transgene planter som resultat af ekspression af rekombinant DNA i en kerne, omfattende et rekombinant DNA-konstrukt, der omfatter en promoter, som er funktionel i plantecellen, og som er operabelt forbundet med et protein-kodende DNA, der koder for en aminosyresekvens med mindst 90 % sekvensidentitet i den fulde længde af SEQ ID NO: 1018, hvor det transgene frø kan opnås ved en fremgangsmåde omfattende:
(a) at screene en population af planter for det rekombinante DNA,
(b) at udvælge fra populationen en eller flere planter, der indeholder det rekombinante DNA, og
(c) at indsamle frø fra planter, der er udvalgt i trin (b).

7. Transgent frø ifølge krav 6, hvor fremgangsmåden til at fremstille det transgene frø yderligere omfatter
(d) verificering af, at det rekombinante DNA er stabilt integreret i den udvalgte plante, og
(e) analyse af væv fra den udvalgte plante for at bestemme ekspressionen eller suppressionen af et protein med funktion af et protein med en aminosyresekvens af SEQ ID NO: 1018.

8. Transgent frø ifølge krav 5 eller 6, hvor frøet er udvalgt fra gruppen bestående af majs-, sojabønne-, bomulds-, alfalfa-, raps-, hvede- og risfrø.

DRAWINGS

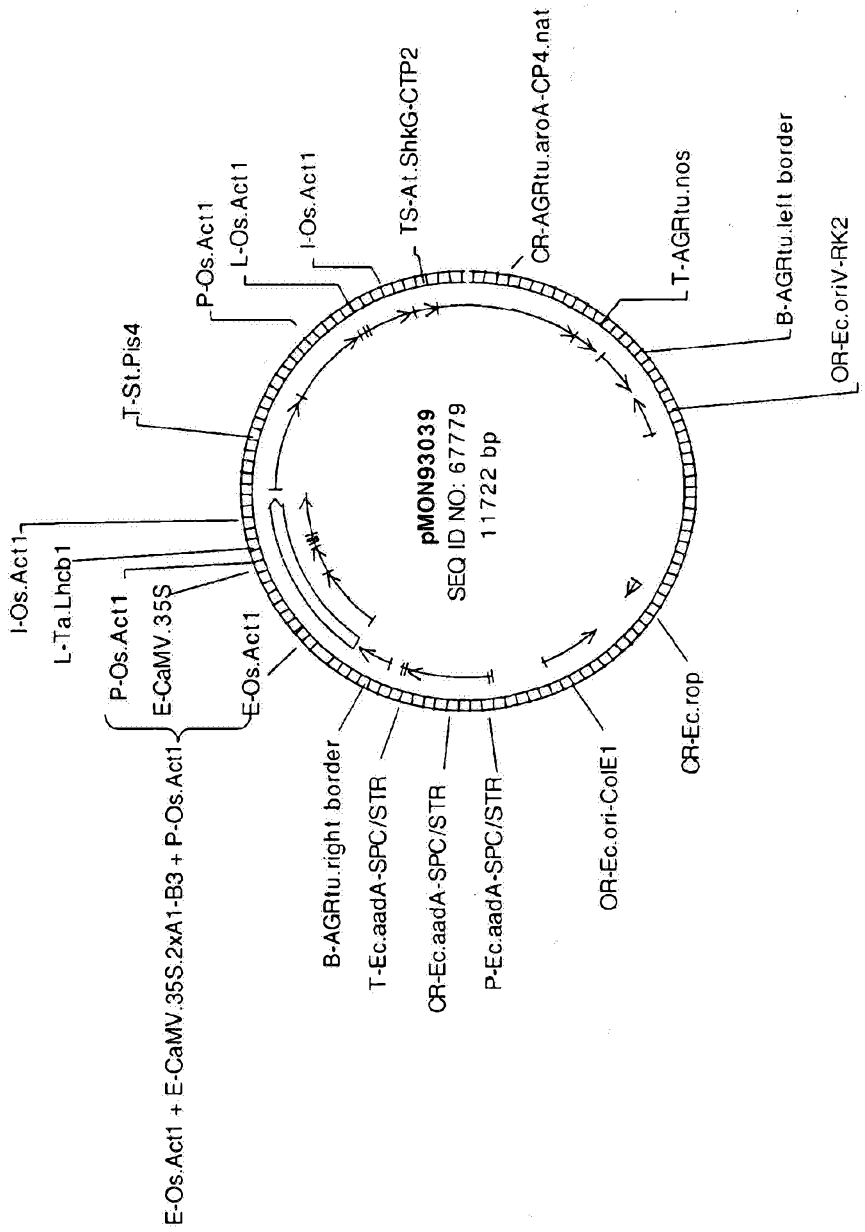
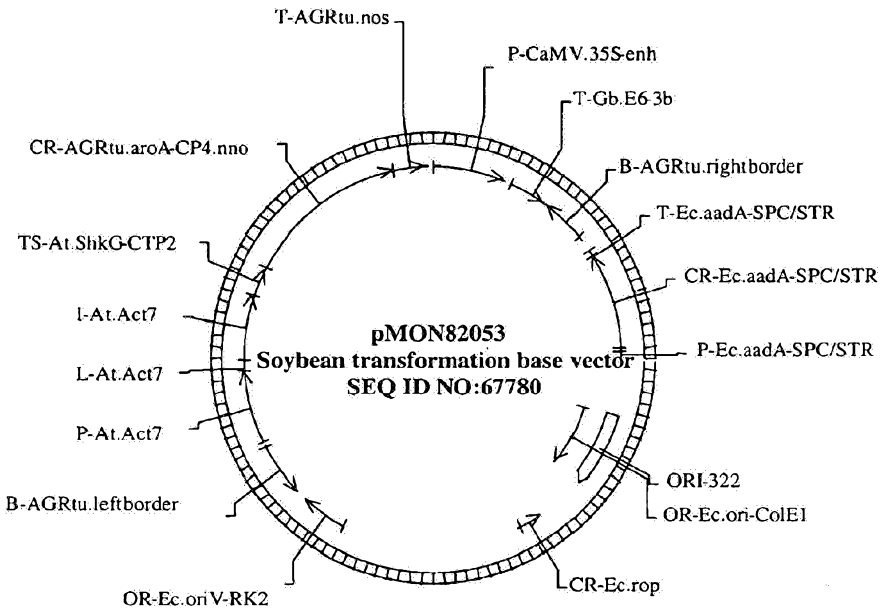


Figure 1. Plasmid map of pMON93039

Figure 2.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OR-Ec.oriV-RK2

Figure 3

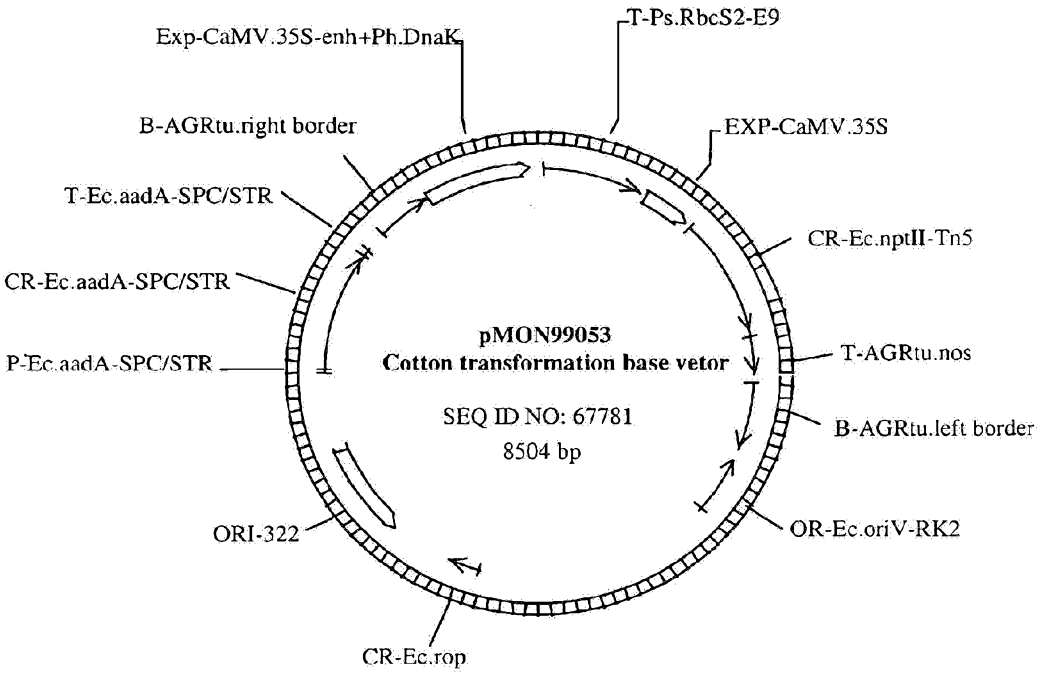
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Figure 4

SEQ ID NO

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21692     ------------------------------------------------------------
57173     ------------------------------------------------------------
57659     ------------------------------------------------------------
4374      ----------------------------MARNPTRTVYIGNLDEKVTERILYEILIQPGR
55005     ------------------------------------------------------------
42612     ------------------------------------------------------------
67783     ------------------------------------------------------------
consensus

------------------------------------------------------------
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------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
TTFIPGNSLSTIELGLSKELREMLPIVVFKESFTVMDSQCSVCLGDYQPNDKLQQIPVCK
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
VVDLCIPRDKETSCPKGYAFAEYETEEIAQYAVQLFSGLVRLYGKTLKFAISGQDKPSSN
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------


--------------MNQDLAKVQTEEDDFLIEISGEAPLTYSTLEGCVPPTFRSMTVGPI
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------MSTVPREFAGLDPRSADFHPALTRCPV
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
HTFHMDCIDLWLTSHTTCPLCRLALIPSRSRQSQDDPVPSLVSPDEEVSSQPESEPVNHR
------------------------------------------------------------
```

Figure 4 continued

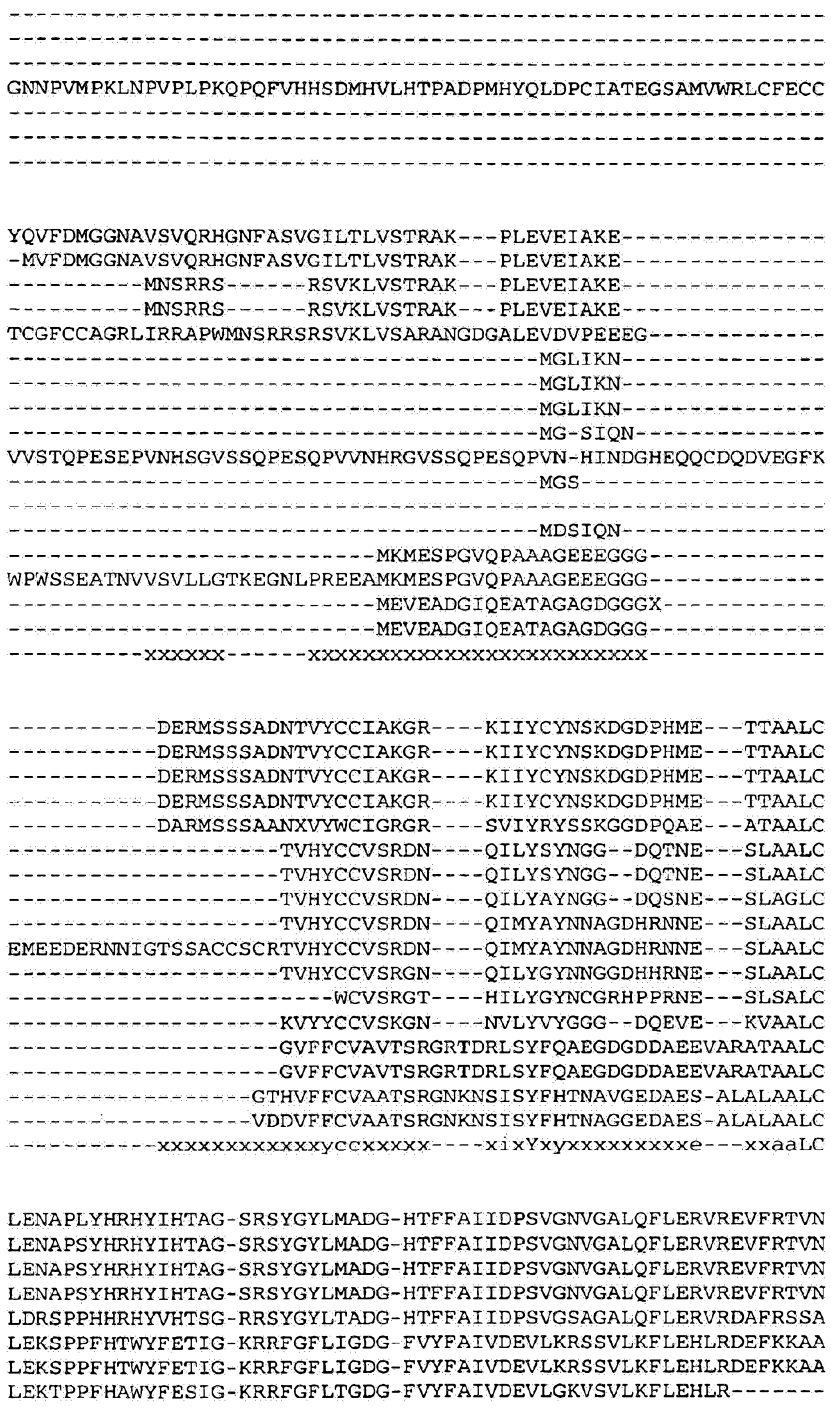

Figure 4 continued

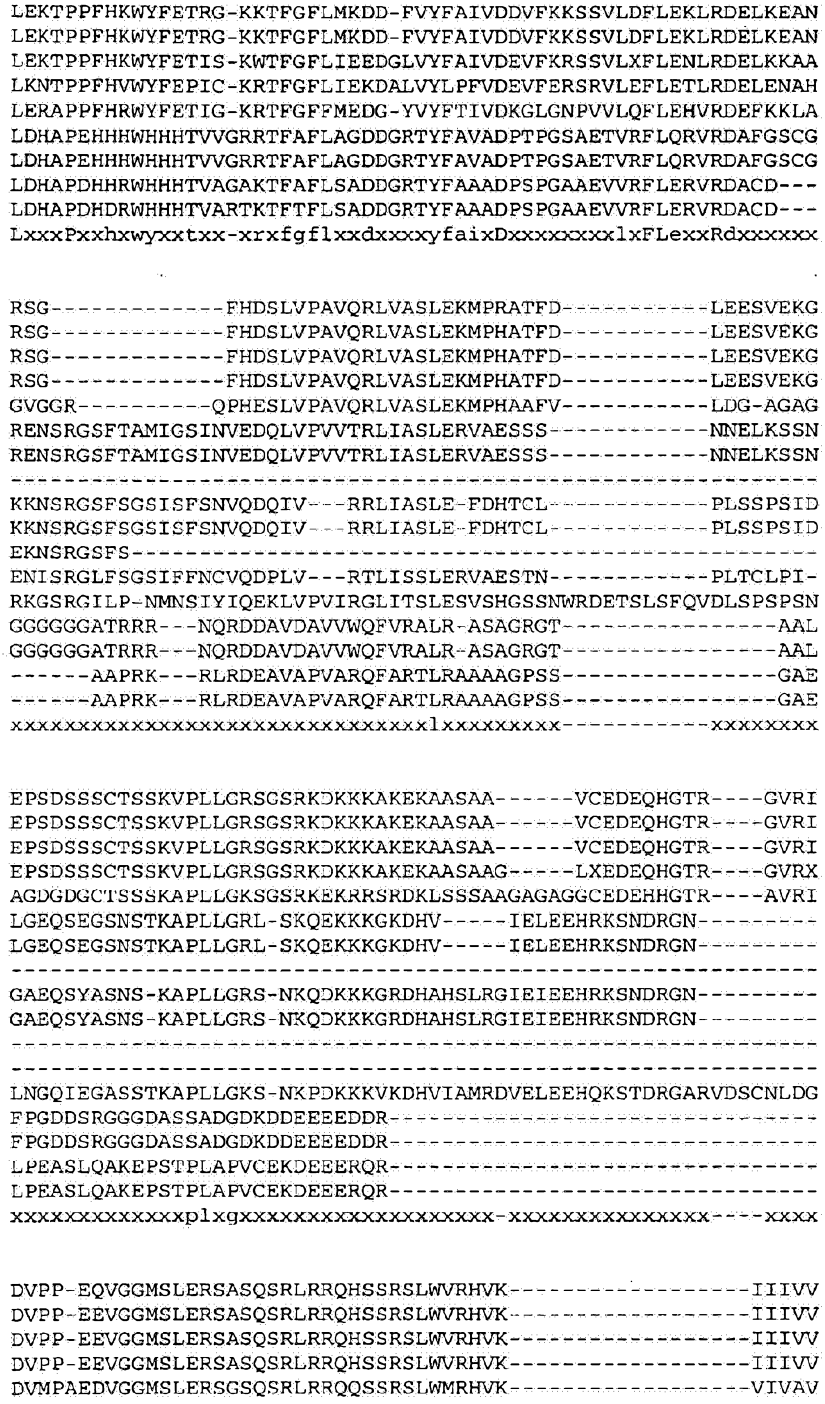

Figure 4 continued