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(54) **GENES AND USES FOR PLANT IMPROVEMENT**

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(57) **ABSTRACT**

Transgenic seed for crops with improved traits are provided by trait-improving recombinant DNA where plants grown from such transgenic seed exhibit one or more improved traits as compared to a control plant. Exemplary recombinant DNA expresses a succinate semialdehyde dehydrogenase.

GENES AND USES FOR PLANT IMPROVEMENT

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims benefit under 35USC § 119(e) of U.S. provisional application Ser. No. 60/592,978, filed Jul. 31, 2004, herein incorporated by reference.

INCORPORATION OF SEQUENCE LISTING

[0002] Two copies of the sequence listing (Copy 1 and Copy 2) and a computer readable form (CRF) of the sequence listing, all on CD-ROMs, each containing the file named "pa01184_53452B.rpt", which is 67,108,864 bytes (measured in MS-WINDOWS, MEDIUM TYPE: CD-ROM (ASCII TEXT) COMPUTER: IBM PC/XT/AT,IBM PS/20R COMPATIBLES. OPERATING SYSTEM: DOS/WINDOWS 2000/NT) and was created on Jul. 18, 2005, are herein incorporated by reference.

FIELD OF THE INVENTION

[0003] Disclosed herein are inventions in the field of plant genetics and developmental biology. More specifically, this invention provides transgenic seeds for crops, wherein the genome of said seed comprises recombinant DNA, the expression of which results in the production of transgenic plants that have improved trait(s).

BACKGROUND OF THE INVENTION

[0004] Transgenic plants with improved traits such as improved yield, environmental stress tolerance, pest resistance, herbicide tolerance, modified seed compositions, and the like are desired by both farmers and consumers. Although considerable efforts in plant breeding have provided significant gains in desired traits, the ability to introduce specific DNA into plant genomes provides further opportunities for generation of plants with improved and/or unique traits. The ability to develop transgenic plants with improved traits depends in part on the identification of genes that are useful in recombinant DNA constructs for production of transformed plants with improved properties.

SUMMARY OF THE INVENTION

[0005] This invention provides transgenic seeds, transgenic plants and DNA constructs with trait-improving recombinant DNA from a gene for a protein having an amino acid sequence with at least 90% identity to a consensus amino acid sequence in the group consisting of SEQ ID NO: 270 and its homologs through SEQ ID NO: 538, where the respective homolog proteins have amino acid sequences SEQ ID NO: 539 through SEQ ID NO: 22568, as indicated in Table 17. In some cases of trait improvement, the recombinant DNA encodes a protein; in other cases, the recombinant DNA suppresses endogenous protein expression. In a broad aspect this invention provides transgenic seeds for growing crop plants with improved traits, such crop plants with improved traits and the plant parts including transgenic seed produced by such crop plants. The improved traits provided by the recombinant DNA in the transgenic crop plant of this invention are identified by comparison to a control plant, i.e., a plant without the trait-improving recombinant DNA. In one aspect of the invention, transgenic crop plant grown from the transgenic seed has improved yield, as compared to the yield of a control plant, e.g., a plant without the recombinant DNA that produces the increased yield. Some plants of this invention exhibit increased yield by producing a yield increase under non-stress conditions. Other plants of this invention exhibit increased yield by producing a yield increase under one or more environmental stress conditions including, but not limited to, water deficit stress, cold stress, heat stress, high salinity stress, shade stress, and low nitrogen availability stress. Still other plants of this invention have other improved phenotypes, such as improved plant development, plant morphology, plant physiology or seed composition as compared to a corresponding trait of a control plant. The various aspects of this invention are especially useful for transgenic seed and transgenic plants having improved traits in corn (maize), soybean, cotton, canola (rape), wheat, sunflower, sorghum, alfalfa, barley, millet, rice, tobacco, fruit and vegetable crops, and turfgrass.

[0006] The invention also comprises recombinant DNA constructs. In one aspect, such recombinant DNA constructs useful for the transgenic seed and transgenic plants of this invention comprise a promoter functional in a plant cell operably linked to a DNA segment for expressing a protein associated with a trait in a model plant or a homologue. In another aspect the recombinant DNA constructs useful for the transgenic seed and transgenic plants of this invention comprise a promoter functional in a plant cell operably linked to a DNA segment for suppressing the level of an endogenous plant protein which is a homologue to a model-plant protein, the suppression of which is associated with an improved trait. Suppression can be effected by any of a variety of methods known in the art, e.g. post transcriptional suppression by anti-sense, sense, dsRNA and the like or by transcriptional suppression.

[0007] This invention also provides a method of producing a transgenic crop plant having at least one improved trait, wherein the method comprises providing to a grower of transgenic seeds comprising recombinant DNA for expression or suppression of a trait-improving gene provided herein, and growing transgenic plant from said transgenic seed. Such methods are used to generate transgenic crop plants having at least one improved trait under one or more environmental stress conditions including, but not limited to, water deficit stress, cold stress, heat stress, high salinity stress, shade stress, and low nitrogen availability stress. In another aspect, such methods are used to generate transgenic crop plants having improved plant development, plant morphology, plant physiology or seed component phenotype as compared to a corresponding phenotype of a control plant. Of particular interest are uses of such methods to generate transgenic crop plants having increased yield under non-stress condition, or under one or more stress conditions.

DETAILED DESCRIPTION OF THE INVENTION

[0008] This invention provides transgenic plant seed having in its genome trait-improving recombinant DNA and transgenic plants grown from such seed which exhibit an improved trait as compared a control plant. In one aspect, the invention provides transgenic plants where the improved trait is one or more of improved drought stress tolerance, improved heat stress tolerance, improved cold stress tolerance, improved high salinity stress tolerance, improved low

nitrogen availability stress tolerance, improved shade stress tolerance, improved plant growth and development at the stages of seed imbibition through early vegetative phase, and improved plant growth and development at the stages of leaf development, flower production and seed maturity. Particular transgenic plants grown from transgenic seeds of this invention exhibit increased seed yield. Recombinant DNA constructs used in this invention comprise recombinant DNA disclosed herein which produces mRNA to modulate gene expression imparting improved traits to plants.

[0009] "Gene" means all or part of the DNA that encodes a protein or mRNA, e.g., chromosomal DNA, plasmid DNA, cDNA, or synthetic DNA, and includes DNA regions flanking the coding sequences, e.g., introns, 5'UTR, 3'UTR, promoters and other DNA involved in the regulation of expression.

[0010] "Transgenic seed" means plant seed having a genome altered by the incorporation of recombinant DNA, e.g., by transformation. "Transgenic plant" means a plant produced from an original transformation event, or progeny from later generations or crosses of a plant to a transformed plant, so long as the progeny contains the recombinant DNA in its genome. "Recombinant DNA" means a DNA molecule having a genetically engineered modification introduced through a combination of endogenous and/or exogenous DNA elements in a transcription unit, manipulation via mutagenesis, restriction enzymes, and the like or simply by inserting multiple copies of a native transcription unit. Recombinant DNA may comprise DNA segments obtained from different sources, or DNA segments obtained from the same source, but which have been manipulated to join DNA segments which do not naturally exist in the joined form. Recombinant DNA can exist outside of a cell, e.g., as a PCR fragment or in a plasmid, or can be integrated into a genome such as a plant genome.

[0011] "Trait" means a physiological, morphological, biochemical, or physical characteristic of a plant or particular plant material or cell. In some instances the characteristic is visible to the human eye, e.g., seed or plant size, or can be measured by biochemical techniques, e.g., detecting the protein, starch, or oil content of seed or leaves, or by observation of a metabolic or physiological process, e.g., by measuring uptake of carbon dioxide, or by the observation of the expression level of a gene or genes, e.g., by employing Northern analysis, RT-PCR, microarray gene expression assays, or reporter gene expression systems, or by agricultural observations such as stress tolerance, yield, or pathogen tolerance.

[0012] "Control plant" is a plant without trait-improving recombinant DNA. A control plant is used to measure and compare trait improvement in a transgenic plant with such trait-improving recombinant DNA. One suitable control plant is a non-transgenic plant of the parental line that was used to generate a transgenic plant. Another suitable control plant is a transgenic plant that comprises recombinant DNA without the specific trait producing DNA, e.g., simply a marker gene. Another suitable control plant is a negative segregant progeny of hemizygous transgenic plant. In certain demonstrations of trait improvement, e.g., in field conditions, the use of a limited number of control plants can cause a wide variation in the control dataset. To minimize the effect of the variation within the control dataset, a "reference" is used, i.e., a trimmed mean of all data from both transgenic and control plants grown under the same conditions and at the same developmental stage. The trimmed mean is calculated by eliminating a specific percentage, i.e., 20%, of the smallest and largest observation from the data set and then calculating the average of the remaining observation.

[0013] "Trait improvement" means a detectable and desirable difference in a characteristic in a transgenic plant relative to a control plant or a reference. In some cases, the trait improvement is measured quantitatively. For example, the trait improvement can entail at least a 2% desirable difference in an observed trait, at least a 5% desirable difference, at least about a 10% desirable difference, at least about a 20% desirable difference, at least about a 30% desirable difference, at least about a 50% desirable difference, at least about a 70% desirable difference, or at least about a 100% difference, or an even greater desirable difference. In other cases, the trait improvement is only measured qualitatively. It is known that there are natural variations in a trait. Therefore, the trait improvement observed entails a change of the normal distribution of the trait in the transgenic plant compared with the trait distribution observed in a control plant or a reference, which is evaluated by statistical methods provided herein. Trait improvement includes, but not limited to, yield increase, including increased yield under non-stress conditions and increased yield under environmental stress conditions. Stress conditions may include, for example, drought, shade, fungal disease, viral disease, bacterial disease, insect infestation, nematode infestation, cold temperature exposure, heat exposure, osmotic stress, reduced nitrogen nutrient availability, reduced phosphorus nutrient availability and high plant density. Many agronomic traits can affect "yield", including without limitation, plant 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. Other traits that can affect yield include, 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. Also of interest is the generation of transgenic plants that demonstrate desirable phenotypic properties that may or may not confer an increase in overall plant yield. Such properties include improved plant morphology, plant physiology or improved components of the mature seed harvested from the transgenic plant.

[0014] "Yield-limiting environment" means a condition under which a plant would have the limitation on yield including environmental stress conditions.

[0015] "Stress condition" means a condition unfavorable for a plant, which adversely affects plant metabolism, growth and/or development. A plant under the stress condition typically shows reduced germination rate, retarded growth and development, reduced photosynthesis rate, and eventually leading to reduction in yield. Specifically, "water deficit stress" means sub-optimal conditions for water and humidity needed for normal growth of natural plants. Relative water content (RWC) is one physiological measure of

plant water deficit. RWC measures the effect of osmotic adjustment in plant water status, when a plant is under stressed conditions. RWC can result from heat, drought, high salinity and induced osmotic stress.

[0016] "Cold stress" means exposure of a plant to temperatures below, e.g., at least two or more degrees Celsius below, those temperatures that are normal for a particular species or particular strain of plant.

[0017] "Sufficient nitrogen growth condition" means a growth condition where the soil or growth medium contains or receives enough amounts of nitrogen nutrient to sustain a healthy plant growth and/or for a plant to reach its typical yield for a particular plant species or a particular strain. "Nitrogen nutrient" means any one or any mix of the nitrate salts commonly used as plant nitrogen fertilizer, including, but not limited to, potassium nitrate, calcium nitrate, sodium nitrate, ammonium nitrate. "Ammonium" means any one or any mix of the ammonium salts commonly used as plant nitrogen fertilizer, e.g., ammonium nitrate, ammonium chloride, ammonium sulfate, etc. Those skilled in the art know what constitutes such soil, media and fertilizer inputs for most plant species. "Low nitrogen availability stress" means a plant growth condition that does not contain sufficient nitrogen nutrient to maintain a healthy plant growth and/or for a plant to reach its typical yield under a sufficient nitrogen growth condition; a useful low nitrogen availability stress is a growth condition with 50% or less of the conventional nitrogen inputs.

[0018] "Shade stress" means a limited light availability that triggers the shade avoidance response in plant. Plants are subject to shade stress when localized at lower part of the canopy, or in close proximity of neighboring vegetation. Shade stress is exacerbated when the planting density exceeds the average prevailing density for a particular plant species. The average prevailing densities per acre of a few other examples of crop plants in the USA in the year 2000 were: wheat 1,000,000-1,500,000; rice 650,000-900,000; soybean 150,000-200,000, canola 260,000-350,000, sunflower 17,000-23,000 and cotton 28,000-55,000 plants per acre.

[0019] "Increased yield" of a transgenic plant of this invention is evidenced and 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, tons per acre, tons per acre, kilo per hectare. For example, corn yield is measured as production of shelled corn kernels per unit of production area, e.g., in bushels per acre or metric tons per hectare, often reported on a moisture adjusted basis, e.g., at 15.5% moisture. Increased yield is often achieved 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. Trait-improving recombinant DNA is used to provide transgenic 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.

[0020] "Expression" means transcription of DNA to produce RNA. The resulting RNA includes mRNA encoding a protein, antisense RNA that is complementary to an mRNA encoding a protein, or an RNA transcript comprising a combination of sense and antisense gene regions, such as for use in RNAi gene suppression. Expression also means production of encoded protein from mRNA.

[0021] "Promoter" means a region of DNA upstream from the start of transcription and involved in recognition and binding of RNA polymerase and other proteins to initiate transcription. A "plant promoter" is a promoter capable of initiating transcription in plant cells whether or not its origin is a plant cell. Exemplary plant promoters include, but are not limited to, those that are obtained from plants, plant viruses, and bacteria which comprise genes expressed in plant cells such as *Agrobacterium* or *Rhizobium*. "Tissue preferred" promoters preferentially regulate expression in certain tissues, such as leaves, roots, or seeds. "Tissue specific" promoters predominately regulate expression only in certain tissues. "Cell type" specific promoter primarily regulate expression in certain cell types in one or more organs, for example, vascular cells in roots or leaves. "Inducible" and "repressible" promoters regulate expression under environmental influences, under the effect of anaerobic conditions, certain chemicals, or the presence of light. Tissue specific, tissue preferred, cell type specific, and inducible promoters constitute a class of "non-constitutive" promoters. "Constitutive" promoters are promoters which are active under most conditions. "Anti-sense orientation" refers to a DNA sequence that is operably linked to a promoter in an orientation where the anti-sense strand is transcribed. "Operably linked" refers to an association of two or more DNA elements in a single construct so that the function of one is affected by the other. For example, a promoter is operably linked with transcribable DNA when it is capable of affecting the expression of that DNA; that is, the coding DNA is under the transcriptional control of the promoter.

[0022] "Consensus sequence" means an artificial, amino acid sequence of conserved parts of the proteins encoded by homologous genes, e.g., as determined by a CLUSTAL W alignment of amino acid sequence of homolog proteins.

[0023] "Homologs" means genes that produce functionally similar proteins, e.g., in the same organism or in different organisms. A gene can be related to a homolog gene by descent from a common ancestral DNA. Homologs include genes where the relationship is by speciation, e.g., often called orthologs, or by genetic duplication, e.g., often called paralogs. More specifically, "orthologs" include homologs in different species that evolved from a common ancestral gene by specification. Normally orthologs retain the same function in the course of evolution. "Paralogs" include homologs in the same species that have diverged from each other as a consequence of genetic duplication.

[0024] "Percent identity" means the extent to which two optimally aligned DNA or protein segments are invariant throughout a window of alignment of components, e.g. nucleotide sequence or amino acid sequence. An "identity fraction" for aligned segments of sequences is the number of identical components which are shared divided by the total number of sequence components in the segment used as a reference over a window of alignment which is the smaller of the sequences. "Percent identity" ("% identity") is the identity fraction times 100. "% identity" to a consensus amino acid sequence" is 100 times the identity fraction in a

window of alignment of an amino acid sequence of a test protein optimally aligned to consensus amino acid sequence of this invention.

[0025] "*Arabidopsis*" means plants of *Arabidopsis thaliana*.

Recombinant DNA Constructs

[0026] This invention provides recombinant DNA constructs comprising DNA elements for imparting one or more improved traits to transgenic plant. Such constructs typically comprise a promoter operatively linked to DNA to provide for expression of a protein or RNA for gene suppression in a target plant. Recombinant DNA constructs can also include additional regulatory elements, such as 5' or 3' untranslated regions (UTRs) such as polyadenylation sites, introns, and transit or signal peptides. Such recombinant DNA constructs are assembled using methods known to those of ordinary skill in the art.

[0027] In certain embodiments, recombinant DNA constructs comprise sense-oriented, trait-imparting DNA operably linked to a promoter that is functional in a plant to provide for expression of the trait-imparting DNA in the sense orientation such that a desired protein is produced. In other embodiments at least a part of the trait-imparting DNA is in an anti-sense orientation for gene suppression activity.

[0028] Recombinant DNA constructs, especially for expressing proteins are typically prepared with a 3' UTR that a polyadenylation site and signal. Recombinant DNA constructs can also include a transit peptide for targeting of a gene target 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. Pat. No. 5,188,642 and U.S. Pat. No. 5,728,925, incorporated herein by reference.

[0029] Table 1 provides a list of genes that can provide trait-imparting DNA for recombinant DNA constructs. DNA from each gene was used in a model plant (*Arabidopsis*) to discover associations with improved traits. The DNA was also used to identify homologs from which a consensus amino acid sequence is defined for characterizing the aspects of the invention where recombinant DNA is incorporated in the transgenic seeds, transgenic plants, DNA constructs and methods of this invention. With reference to Table 1:

[0030] "NUC SEQ ID NO" refers to a SEQ ID NO. for particular DNA sequence in the Sequence Listing.

[0031] "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

[0032] "construct_id" refers to an arbitrary number used to identify a particular recombinant DNA construct comprising the particular DNA.

[0033] "gene" refers to an arbitrary name used to identify the particular DNA.

[0034] "orientation" refers to the orientation of the particular DNA in a recombinant DNA construct relative to the promoter.

[0035] "species" refers to the organism from which the particular DNA was derived.

TABLE 1

Nuc SEQ ID	Pep SEQ ID	construct_id	Gene	orientation	Species
1	270	14324	CGPG1560	SENSE	*Arabidopsis thaliana*
2	271	17484	CGPG2630	SENSE	*Arabidopsis thaliana*
3	272	19109	CGPG1381	ANTI-SENSE	*Arabidopsis thaliana*
4	273	70423	CGPG3165	SENSE	*Arabidopsis thaliana*
5	274	70424	CGPG3180	SENSE	*Arabidopsis thaliana*
6	275	70480	CGPG3833	SENSE	*Arabidopsis thaliana*
7	276	70509	CGPG2420	SENSE	*Arabidopsis thaliana*
8	277	70647	CGPG4334	SENSE	*Arabidopsis thaliana*
9	278	70675	CGPG4519	SENSE	*Arabidopsis thaliana*
10	279	70829	CGPG518	SENSE	*Arabidopsis thaliana*
11	280	70849	CGPG596	SENSE	*Arabidopsis thaliana*
12	281	71627	CGPG1270	SENSE	*Arabidopsis thaliana*
13	282	71934	CGPG2294	SENSE	*Arabidopsis thaliana*
14	283	72615	CGPG4829	SENSE	*Arabidopsis thaliana*
15	284	72927	CGPG1477	SENSE	*Arabidopsis thaliana*
16	285	73014	CGPG5692	SENSE	*Xenorhabdus nematophilus* 85816
17	286	73559	CGPG6535	SENSE	*Bacillus subtilis* 168
18	287	74251	CGPG5489	SENSE	*Arabidopsis thaliana*
19	288	19631	CGPG3627	SENSE	*Arabidopsis thaliana*
20	289	70121	CGPG2380	SENSE	*Saccharomyces cerevisiae*
21	290	70654	CGPG4352	SENSE	*Arabidopsis thaliana*
22	291	70696	CGPG4590	SENSE	*Arabidopsis thaliana*
23	292	70713	CGPG1462	ANTI-SENSE	*Arabidopsis thaliana*
24	293	70740	CGPG3700	SENSE	*Arabidopsis thaliana*
25	294	71321	CGPG4418	SENSE	*Arabidopsis thaliana*
26	295	71835	CGPG4634	SENSE	*Arabidopsis thaliana*
27	296	72934	CGPG5798	SENSE	*Saccharomyces cerevisiae*
28	297	72945	CGPG5787	SENSE	*Saccharomyces cerevisiae*
29	298	72980	CGPG5773	SENSE	*Saccharomyces cerevisiae*
30	299	73504	CGPG6480	SENSE	*Synechocystis* sp. PCC 6803
31	300	73507	CGPG6504	SENSE	*Bacillus subtilis* 168
32	301	73573	CGPG6462	SENSE	*Agrobacterium tumefacians* C58
33	302	73586	CGPG6471	SENSE	*Bacillus subtilis* 168
34	303	73770	CGPG5435	SENSE	*Arabidopsis thaliana*

TABLE 1-continued

Nuc SEQ ID	Pep SEQ ID	construct_id	Gene	orientation	Species
35	304	74105	CGPG6574	SENSE	*Xenorhabdus nematophilus* 86068
36	305	74111	CGPG6622	SENSE	*Escherichia coli* K-12
37	306	74136	CGPG6632	SENSE	*Synechocystis*
38	307	74139	CGPG6561	SENSE	*Escherichia coli* K-12
39	308	74267	CGPG5364	SENSE	*Arabidopsis thaliana*
40	309	74291	CGPG5363	SENSE	*Arabidopsis thaliana*
41	310	74318	CGPG5826	SENSE	*Arabidopsis thaliana*
42	311	74319	CGPG5831	SENSE	*Arabidopsis thaliana*
43	312	74324	CGPG5885	SENSE	*Arabidopsis thaliana*
44	313	74512	CGPG32	SENSE	*Arabidopsis thaliana*
45	314	74583	CGPG6649	SENSE	*Ralstonia metallidurans* CH34
46	315	70427	CGPG3067	SENSE	*Arabidopsis thaliana*
47	316	71811	CGPG4426	SENSE	*Arabidopsis thaliana*
48	317	73463	CGPG6384	SENSE	*Ralstonia metallidurans* CH34
49	318	72081	CGPG5279	SENSE	*Glycine max*
50	319	10139	CGPG101	ANTI-SENSE	*Arabidopsis thaliana*
51	320	11410	CGPG103	SENSE	*Arabidopsis thaliana*
52	321	11604	CGPG48	ANTI-SENSE	*Arabidopsis thaliana*
53	322	12368	CGPG1006	SENSE	*Arabidopsis thaliana*
54	323	13502	CGPG1354	SENSE	*Arabidopsis thaliana*
55	324	13745	CGPG1576	ANTI-SENSE	*Arabidopsis thaliana*
56	325	13821	CGPG1569	SENSE	*Arabidopsis thaliana*
57	326	14240	CGPG1697	SENSE	*Arabidopsis thaliana*
58	327	14718	CGPG1082	SENSE	*Arabidopsis thaliana*
59	328	17022	CGPG1774	SENSE	*Arabidopsis thaliana*
60	329	17924	CGPG2882	SENSE	*Arabidopsis thaliana*
61	330	18259	CGPG3368	SENSE	*Arabidopsis thaliana*
62	331	19171	CGPG2952	SENSE	*Saccharomyces cerevisiae*
63	332	19201	CGPG2332	SENSE	*Arabidopsis thaliana*
64	333	19317	CGPG3662	SENSE	*Xanthomonas*
65	334	70417	CGPG3427	SENSE	*Arabidopsis thaliana*
66	335	70467	CGPG3785	SENSE	*Arabidopsis thaliana*
67	336	70806	CGPG712	SENSE	*Arabidopsis thaliana*
68	337	70818	CGPG479	SENSE	*Arabidopsis thaliana*
69	338	70820	CGPG655	SENSE	*Arabidopsis thaliana*
70	339	70919	CGPG4029	SENSE	*Glycine max*
71	340	71623	CGPG4696	SENSE	*Arabidopsis thaliana*
72	341	71662	CGPG4679	SENSE	*Glycine max*
73	342	71693	CGPG4652	SENSE	*Glycine max*
74	343	72384	CGPG4639	SENSE	*Saccharomyces cerevisiae*
75	344	72439	CGPG5075	SENSE	*Arabidopsis thaliana*
76	345	72619	CGPG4835	SENSE	*Arabidopsis thaliana*
77	346	72624	CGPG4842	SENSE	*Arabidopsis thaliana*
78	347	72715	CGPG5521	SENSE	*Saccharomyces cerevisiae*
79	348	72754	CGPG5548	SENSE	*Saccharomyces cerevisiae*
80	349	72819	CGPG4989	SENSE	*Arabidopsis thaliana*
81	350	75516	CGPG7689	SENSE	*Glycine max*
82	351	75701	CGPG7856	SENSE	*Glycine max*
83	352	73515	CGPG6473	SENSE	*Bacillus subtilis* 168
84	353	74684	CGPG6360	SENSE	*Arabidopsis thaliana*
85	354	19542	CGPG3069	SENSE	*Arabidopsis thaliana*
86	355	19618	CGPG3574	SENSE	*Arabidopsis thaliana*
87	356	19649	CGPG3140	SENSE	*Arabidopsis thaliana*
88	357	19745	CGPG3973	SENSE	*Glycine max*
89	358	19768	CGPG4096	SENSE	*Glycine max*
90	359	19772	CGPG3939	SENSE	*Glycine max*
91	360	19779	CGPG4113	SENSE	*Glycine max*
92	361	19833	CGPG4074	SENSE	*Glycine max*
93	362	19862	CGPG3961	SENSE	*Glycine max*
94	363	19879	CGPG4009	SENSE	*Glycine max*
95	364	70445	CGPG3728	SENSE	*Arabidopsis thaliana*
96	365	70738	CGPG3195	SENSE	*Arabidopsis thaliana*
97	366	71437	CGPG4043	SENSE	*Glycine max*
98	367	71572	CGPG4520	SENSE	*Arabidopsis thaliana*
99	368	71617	CGPG1227	SENSE	*Arabidopsis thaliana*
100	369	72532	CGPG4780	SENSE	*Arabidopsis thaliana*
101	370	72757	CGPG5572	SENSE	*Arabidopsis thaliana*
102	371	73412	CGPG6448	SENSE	*Pseudomonas syringae* var tomato DC3000
103	372	74102	CGPG6550	SENSE	*Bacillus halodurans* C-125
104	373	72633	CGPG4853	SENSE	*Arabidopsis thaliana*
105	374	72456	CGPG4745	SENSE	*Arabidopsis thaliana*
106	375	72963	CGPG1746	SENSE	*Arabidopsis thaliana*
107	376	70426	CGPG3199	SENSE	*Arabidopsis thaliana*
108	377	70772	CGPG4627	SENSE	*Arabidopsis thaliana*

TABLE 1-continued

Nuc SEQ ID	Pep SEQ ID	construct_id	Gene	orientation	Species
109	378	71137	CGPG125	SENSE	*Arabidopsis thaliana*
110	379	71529	CGPG2808	SENSE	*Arabidopsis thaliana*
111	380	71601	CGPG1858	SENSE	*Arabidopsis thaliana*
112	381	72362	CGPG983	SENSE	*Arabidopsis thaliana*
113	382	72466	CGPG4767	SENSE	*Arabidopsis thaliana*
114	383	72524	CGPG4770	SENSE	*Arabidopsis thaliana*
115	384	73085	CGPG5689	SENSE	*Synechocystis* sp. PCC 6803
116	385	74241	CGPG5457	SENSE	*Arabidopsis thaliana*
117	386	74247	CGPG5475	SENSE	*Arabidopsis thaliana*
118	387	74284	CGPG5413	SENSE	*Arabidopsis thaliana*
119	388	74652	CGPG6168	SENSE	*Arabidopsis thaliana*
120	389	70437	CGPG3706	SENSE	*Arabidopsis thaliana*
121	390	71633	CGPG857	SENSE	*Arabidopsis thaliana*
122	391	72948	CGPG5617	SENSE	*Arabidopsis thaliana*
123	392	72519	CGPG4749	SENSE	*Arabidopsis thaliana*
124	393	10475	CGPG399	SENSE	*Arabidopsis thaliana*
125	394	11120	CGPG459	ANTI-SENSE	*Arabidopsis thaliana*
126	395	19736	CGPG4129	SENSE	*Glycine max*
127	396	71606	CGPG4715	SENSE	*Arabidopsis thaliana*
128	397	71840	CGPG4353	SENSE	*Arabidopsis thaliana*
129	398	74240	CGPG5454	SENSE	*Arabidopsis thaliana*
130	399	74331	CGPG5834	SENSE	*Arabidopsis thaliana*
131	400	74610	CGPG6048	SENSE	*Arabidopsis thaliana*
132	401	75527	CGPG7682	SENSE	*Glycine max*
133	402	70681	CGPG4584	SENSE	*Arabidopsis thaliana*
134	403	71663	CGPG4638	SENSE	*Xanthomonas*
135	404	72769	CGPG5573	SENSE	*Arabidopsis thaliana*
136	405	71508	CGPG1541	SENSE	*Arabidopsis thaliana*
137	406	74248	CGPG5476	SENSE	*Arabidopsis thaliana*
138	407	72771	CGPG2166	SENSE	*Arabidopsis thaliana*
139	408	72085	CGPG5228	SENSE	*Arabidopsis thaliana*
140	409	72744	CGPG5563	SENSE	*Saccharomyces cerevisiae*
141	410	73039	CGPG810	SENSE	*Arabidopsis thaliana*
142	411	73054	CGPG5754	SENSE	*Saccharomyces cerevisiae*
143	412	73501	CGPG6456	SENSE	*Agrobacterium tumefacians* C58
144	413	19707	CGPG4179	SENSE	*Glycine max*
145	414	19951	CGPG3941	SENSE	*Glycine max*
146	415	19967	CGPG4032	SENSE	*Glycine max*
147	416	70543	CGPG3815	SENSE	*Arabidopsis thaliana*
148	417	70707	CGPG1273	ANTI-SENSE	*Arabidopsis thaliana*
149	418	70719	CGPG1712	ANTI-SENSE	*Arabidopsis thaliana*
150	419	71134	CGPG817	SENSE	*Arabidopsis thaliana*
151	420	71146	CGPG2928	SENSE	*Arabidopsis thaliana*
152	421	71660	CGPG4690	SENSE	*Arabidopsis thaliana*
153	422	72086	CGPG5236	SENSE	*Arabidopsis thaliana*
154	423	72632	CGPG4852	SENSE	*Arabidopsis thaliana*
155	424	72716	CGPG5529	SENSE	*Saccharomyces cerevisiae*
156	425	72723	CGPG1848	SENSE	*Arabidopsis thaliana*
157	426	72987	CGPG1787	SENSE	*Arabidopsis thaliana*
158	427	74109	CGPG6606	SENSE	*Xenorhabdus nematophilus* 86068
159	428	74140	CGPG6569	SENSE	*Bacillus halodurans* C-125
160	429	74191	CGPG6597	SENSE	*Rhodobacter sphaeroides* 2.4.1
161	430	74265	CGPG5356	SENSE	*Arabidopsis thaliana*
162	431	74369	CGPG6076	SENSE	*Arabidopsis thaliana*
163	432	70217	CGPG6	SENSE	*Arabidopsis thaliana*
164	433	72711	CGPG1846	SENSE	*Arabidopsis thaliana*
165	434	70932	CGPG4089	SENSE	*Glycine max*
166	435	73518	CGPG6497	SENSE	*Pseudomonas fluorescens* PfO-1
167	436	19771	CGPG4011	SENSE	*Glycine max*
168	437	73549	CGPG6460	SENSE	*Xenorhabdus nematophilus* 85816
169	438	72994	CGPG5803	SENSE	*Saccharomyces cerevisiae*
170	439	71928	CGPG1617	SENSE	*Arabidopsis thaliana*
171	440	72903	CGPG5584	SENSE	*Arabidopsis thaliana*
172	441	73017	CGPG5733	SENSE	*Saccharomyces cerevisiae*
173	442	74587	CGPG6774	SENSE	*Agrobacterium tumefacians* C58
174	443	72453	CGPG4735	SENSE	*Arabidopsis thaliana*
175	444	72967	CGPG5742	SENSE	*Saccharomyces cerevisiae*
176	445	72961	CGPG5591	SENSE	*Arabidopsis thaliana*
177	446	73070	CGPG5627	SENSE	*Arabidopsis thaliana*
178	447	73475	CGPG6385	SENSE	*Rhodopseudomonas palustris* CGA009
179	448	72916	CGPG1814	SENSE	*Arabidopsis thaliana*
180	449	72969	CGPG5789	SENSE	*Saccharomyces cerevisiae*
181	450	74449	CGPG6659	SENSE	*Agrobacterium tumefaciens*
182	451	16615	CGPG2539	SENSE	*Agrobacterium*

TABLE 1-continued

Nuc SEQ ID	Pep SEQ ID	construct_id	Gene	orientation	Species
183	452	19187	CGPG3310	SENSE	*Arabidopsis thaliana*
184	453	19648	CGPG3134	SENSE	*Arabidopsis thaliana*
185	454	70354	CGPG3995	SENSE	*Glycine max*
186	455	70421	CGPG2942	SENSE	*Arabidopsis thaliana*
187	456	70459	CGPG3758	SENSE	*Arabidopsis thaliana*
188	457	70465	CGPG3775	SENSE	*Arabidopsis thaliana*
189	458	70683	CGPG4587	SENSE	*Arabidopsis thaliana*
190	459	70725	CGPG2097	ANTI-SENSE	*Arabidopsis thaliana*
191	460	70852	CGPG1465	SENSE	*Arabidopsis thaliana*
192	461	71112	CGPG934	SENSE	*Arabidopsis thaliana*
193	462	71127	CGPG945	SENSE	*Arabidopsis thaliana*
194	463	71132	CGPG1561	SENSE	*Arabidopsis thaliana*
195	464	71217	CGPG95	SENSE	*Arabidopsis thaliana*
196	465	71645	CGPG4688	SENSE	*Arabidopsis thaliana*
197	466	71726	CGPG3894	SENSE	*Arabidopsis thaliana*
198	467	72432	CGPG4562	SENSE	*Arabidopsis thaliana*
199	468	72450	CGPG4732	SENSE	*Arabidopsis thaliana*
200	469	72455	CGPG4742	SENSE	*Arabidopsis thaliana*
201	470	72727	CGPG5522	SENSE	*Saccharomyces cerevisiae*
202	471	72817	CGPG4987	SENSE	*Arabidopsis thaliana*
203	472	72992	CGPG5777	SENSE	*Saccharomyces cerevisiae*
204	473	73007	CGPG5760	SENSE	*Saccharomyces cerevisiae*
205	474	73073	CGPG5688	SENSE	*Synechocystis* sp. PCC 6803
206	475	73506	CGPG6496	SENSE	*Pseudomonas fluorescens* PfO-1
207	476	74107	CGPG6590	SENSE	*Sinorhizobium meliloti* 1021
208	477	74117	CGPG6575	SENSE	*Xenorhabdus nematophilus* 86068
209	478	74131	CGPG6592	SENSE	*Synechocystis* sp. PCC 6803
210	479	74344	CGPG5929	SENSE	*Arabidopsis thaliana*
211	480	14320	CGPG1229	SENSE	*Arabidopsis thaliana*
212	481	16756	CGPG2117	SENSE	*Arabidopsis thaliana*
213	482	17448	CGPG2673	SENSE	*Arabidopsis thaliana*
214	483	17633	CGPG2839	SENSE	*Arabidopsis thaliana*
215	484	18876	CGPG3096	SENSE	*Arabidopsis thaliana*
216	485	19120	CGPG1976	ANTI-SENSE	*Arabidopsis thaliana*
217	486	19221	CGPG2958	SENSE	*Arabidopsis thaliana*
218	487	70206	CGPG4116	SENSE	*Glycine max*
219	488	70223	CGPG53	SENSE	*Arabidopsis thaliana*
220	489	70347	CGPG3147	SENSE	*Arabidopsis thaliana*
221	490	70406	CGPG1687	SENSE	*Arabidopsis thaliana*
222	491	70469	CGPG3791	SENSE	*Arabidopsis thaliana*
223	492	70564	CGPG1864	SENSE	*Arabidopsis thaliana*
224	493	70601	CGPG2917	SENSE	*Arabidopsis thaliana*
225	494	70612	CGPG3721	SENSE	*Arabidopsis thaliana*
226	495	70720	CGPG1358	ANTI-SENSE	*Arabidopsis thaliana*
227	496	70735	CGPG2661	SENSE	*Arabidopsis thaliana*
228	497	70846	CGPG377	SENSE	*Arabidopsis thaliana*
229	498	70923	CGPG4020	SENSE	*Glycine max*
230	499	71149	CGPG3457	SENSE	*Arabidopsis thaliana*
231	500	71608	CGPG4687	SENSE	*Arabidopsis thaliana*
232	501	71739	CGPG4345	SENSE	*Arabidopsis thaliana*
233	502	72014	CGPG5230	SENSE	*Arabidopsis thaliana*
234	503	72051	CGPG5241	SENSE	*Arabidopsis thaliana*
235	504	74259	CGPG5343	SENSE	*Arabidopsis thaliana*
236	505	72463	CGPG4760	SENSE	*Arabidopsis thaliana*
237	506	72902	CGPG5597	SENSE	*Arabidopsis thaliana*
238	507	74572	CGPG6640	SENSE	*Synechocystis*
239	508	73055	CGPG5768	SENSE	*Saccharomyces cerevisiae*
240	509	74103	CGPG6558	SENSE	*Escherichia coli* K-12
241	510	72921	CGPG5781	SENSE	*Saccharomyces cerevisiae*
242	511	72968	CGPG5772	SENSE	*Saccharomyces cerevisiae*
243	512	19703	CGPG4172	SENSE	*Glycine max*
244	513	19946	CGPG4097	SENSE	*Glycine max*
245	514	19980	CGPG3914	SENSE	*Glycine max*
246	515	70435	CGPG3701	SENSE	*Arabidopsis thaliana*
247	516	71114	CGPG1657	SENSE	*Arabidopsis thaliana*
248	517	72451	CGPG4733	SENSE	*Arabidopsis thaliana*
249	518	72947	CGPG5607	SENSE	*Glycine max*
250	519	73012	CGPG5786	SENSE	*Saccharomyces cerevisiae*
251	520	73022	CGPG5622	SENSE	*Arabidopsis thaliana*
252	521	73488	CGPG6394	SENSE	*Bacillus subtilis* 168
253	522	73901	CGPG5237	SENSE	*Arabidopsis thaliana*
254	523	73964	CGPG5804	SENSE	*Saccharomyces cerevisiae*
255	524	74019	CGPG5706	SENSE	*Bacillus subtilis* 168
256	525	74022	CGPG5724	SENSE	*Arabidopsis thaliana*

TABLE 1-continued

Nuc SEQ ID	Pep SEQ ID	construct_id	Gene	orientation	Species
257	526	74114	CGPG6551	SENSE	*Agrobacterium tumefacians* C58
258	527	74262	CGPG5353	SENSE	*Arabidopsis thaliana*
259	528	74292	CGPG5367	SENSE	*Arabidopsis thaliana*
260	529	74302	CGPG5384	SENSE	*Arabidopsis thaliana*
261	530	74325	CGPG5898	SENSE	*Arabidopsis thaliana*
262	531	74429	CGPG6689	SENSE	*Bacillus subtilis* 168
263	532	74440	CGPG6682	SENSE	*Bacillus halodurans* C-125
264	533	74462	CGPG6668	SENSE	*Synechocystis*
265	534	74465	CGPG6692	SENSE	*Bacillus subtilis* 168
266	535	74474	CGPG6669	SENSE	*Synechocystis*
267	536	74505	CGPG6783	SENSE	*Escherichia coli* K-12
268	537	74507	CGPG6799	SENSE	*Xenorhabdus nematophilus* 85816
269	538	74562	CGPG6764	SENSE	*Bacillus subtilis* 168

Recombinant DNA

[0036] Trait-imparting DNA for use in this invention for improved traits in plants is disclosed herein as having a DNA sequence of SEQ ID NO:1 through SEQ ID NO:269 and any of the respective homologs. A subset of the trait-imparting DNA includes fragments with less than the full DNA sequence, e.g., consisting of oligonucleotides of at least about 15 to 20 or more consecutive nucleotides from one of the disclosed sequences. Such oligonucleotides are fragments of the larger molecules having a sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 269, and find use, for example as probes and primers for detection of the polynucleotides of the invention or for cloning DNA for use in this invention.

[0037] Useful DNA includes variants of the disclosed DNA. Such variants include naturally occurring, including homologous DNA from genes of the same or a different species, or 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 nucleotide of a disclosed DNA without causing the amino acid sequence of the protein produced to be changed. Hence, useful DNA can have any base sequence that has been changed from the sequences provided herein by substitution in accordance with degeneracy of the genetic code.

[0038] Homologs of the trait-imparting DNA generally demonstrate significant identity with the DNA provided herein. Homologous DNA is substantially identical to a trait-imparting DNA if, when the nucleotide sequences are optimally aligned there is at least about 60% nucleotide identity, or higher, e.g., at least 70% or 80% or 85% or even 90% identity or higher, such as 95% or 98% identity over a comparison window of at least 50 to 100 nucleotides, and up to the entire length of the trait-imparting DNA. Optimal alignment of sequences for aligning a comparison window can be conducted by algorithms including computerized implementations of the algorithms (for example, the Wisconsin Genetics Software Package Release 7.0-10.0, Genetics Computer Group, 575 Science Dr., Madison, Wis.). The reference DNA sequence can represent a full-length coding sequence or a portion.

[0039] Proteins useful for imparting improved 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 improved traits include the proteins with an amino acid sequence provided herein as SEQ ID NO: 270 through SEQ ID NO: 538, as well as homologs of such proteins.

[0040] One method to identify homologs of the proteins useful in this invention is by comparison of the amino acid sequence of the trait-imparting protein to amino acid sequences of proteins from the same or different organisms, 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. In one method a local sequence alignment program, e.g., BLAST, is used to search a database of sequences to find similar sequences, and the summary Expectation value (E-value) is 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 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 described 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: 539 through SEQ ID NO: 22568 to the proteins with amino acid sequences of SEQ ID NO: 270 through SEQ ID NO: 538 is found is found in Table 17.

[0041] Aspects of the invention also use DNA encoding functional homolog proteins which differ in one or more amino acids from those of protein encoded by disclosed trait-imparting DNA 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 are 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 are 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 uses DNA encoding proteins that differ in one or more amino acids from those of protein encoded from a described trait-imparting DNA as the result of deletion or insertion of one or more amino acids in a native sequence.

[0042] Homologs of the proteins encoded by disclosed trait-improving DNA will generally demonstrate significant sequence identity, e.g., at least 50% amino acid sequence identity or higher such as at least 70% identity or at least 80% or at least 90% identity with an amino acid sequence of SEQ ID NO:270 through SEQ ID NO:538. Identity of protein homologs is determined by optimally aligning the amino acid sequence of a putative protein homolog with a defined amino acid sequence of a protein encoded by a disclosed trait-imparting DNA 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:270 through SEQ ID NO:538.

[0043] Genes that are homologs to each other can be grouped into families and included in multiple sequence alignments to allow a consensus sequence to 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. A consensus sequence is used to define the full scope of the invention, e.g., to identify proteins with a homolog relationship and the corresponding trait-imparting DNA. Thus, this 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.

Promoters

[0044] 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*, caulimovirus promoters such as the cauliflower mosaic virus or figwort mosaic virus promoters. For instance, see U.S. Pat. Nos. 5,858,742 and 5,322,938 which disclose versions of the constitutive promoter derived from cauliflower mosaic virus (CaMV35S), U.S. Pat. No. 5,378,619 which discloses a Figwort Mosaic Virus (FMV) 35S promoter, U.S. Pat. No. 6,437,217 which discloses a maize RS81 promoter, U.S. Pat. No. 5,641,876 which discloses a rice actin promoter, U.S. Pat. No. 6,426,446 which discloses a maize RS324 promoter, U.S. Pat. No. 6,429,362 which discloses a maize PR-1 promoter, U.S. Pat. No. 6,232,526 which discloses a maize A3 promoter, U.S. Pat. No. 6,177,611 which discloses constitutive maize promoters, U.S. Pat. No. 6,433,252 which discloses a maize L3 oleosin promoter, U.S. Pat. No. 6,429,357 which discloses a rice actin 2 promoter and intron, U.S. Pat. No. 5,837,848 which discloses a root specific promoter, U.S. Pat. No. 6,084,089 which discloses cold inducible promoters, U.S. Pat. No. 6,294,714 which discloses light inducible promoters, U.S. Pat. No. 6,140,078 which discloses salt inducible promoters, U.S. Pat. No. 6,252,138 which discloses pathogen inducible promoters, U.S. Pat. No. 6,175,060 which discloses phosphorus deficiency inducible promoters, U.S. Patent Application Publication 2002/0192813A1 which discloses 5', 3' and intron elements useful in the design of effective plant expression vectors, U.S. patent application Ser. No. 09/078,972 which discloses a coixin promoter, U.S. patent application Ser. No. 09/757,089 which discloses a maize chloroplast aldolase promoter, and U.S. patent application Ser. No. 10/739,565 which discloses water-deficit inducible promoters, 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 DNA to provide for expression of desired genes in transgenic plant cells.

[0045] It is well known in the art that promoters are usefully altered to contain multiple "enhancer sequences" to assist in elevating gene expression. By including an enhancer sequence with such constructs, expression is generally enhanced. These enhancers often are found 5' to the start of transcription in a promoter that functions in eukaryotic cells, and can also be inserted in the forward or reverse orientation 5' or 3' to the coding sequence. In some instances, 5' enhancing elements are introns. Particularly useful enhancers are the 5' introns of the rice actin 1 gene and the rice actin 2 gene. Other enhancers include elements from the CaMV 35S promoter, octopine synthase genes, the maize alcohol dehydrogenase gene, the maize shrunken 1 gene and promoters from non-plant eukaryotes.

[0046] In some aspects of the invention it is preferred that the promoter element in the DNA construct be capable of causing sufficient expression in water deficit conditions. Such promoters can be identified and isolated from the regulatory region of plant genes that are over expressed in water deficit conditions. Specific water-deficit-inducible promoters for use in this invention are derived from the 5' regulatory region of genes identified as a heat shock protein 17.5 gene (HSP17.5), an HVA22 gene (HVA22), a Rab17 gene and a cinnamic acid 4-hydroxylase (CA4H) gene (CA4H) of *Zea maize*. Such water-deficit-inducible promoters are disclosed in U.S. 2004-0123347 A1, incorporated herein by reference.

[0047] In other aspects of the invention, sufficient expression in plant seed tissues is desired to effect improvements in seed composition. Exemplary promoters for use for seed composition modification include promoters from seed genes such as napin (U.S. Pat. No. 5,420,034), maize L3

oleosin (U.S. Pat. No. 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).

[0048] In still 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 SSU (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).

[0049] Gene Overexpression

[0050] "Gene overexpression" means expression, e.g., of a gene at a level in its native host that exceeds levels of expression in a non-transgenic host. In many embodiments of the invention, a recombinant DNA construct provides gene overexpression, e.g., as identified in Table 1.

Gene Suppression

[0051] Gene suppression includes any of the well-known methods for suppressing expression, typically indicated by reduced levels of protein. Posttranscriptional gene suppression is mediated by transcription of integrated recombinant DNA to form double-stranded RNA (dsRNA) having homology to a gene targeted for suppression. This formation of dsRNA most commonly results from transcription of an integrated inverted repeat of an element of a target gene, and is a common feature of gene suppression methods known as anti-sense suppression, co-suppression and RNA interference (RNAi). Transcriptional suppression can be mediated by a transcribed dsRNA having homology to a promoter DNA sequence to effect what is called promoter trans suppression.

[0052] More particularly, posttranscriptional gene suppression by inserting a recombinant DNA construct with one or more copies of anti-sense oriented DNA to regulate gene expression in plant cells is disclosed in U.S. Pat. No. 5,107,065 (Shewmaker, et al.,) and U.S. Pat. No. 5,759,829 (Shewmaker, et al.,). Transgenic plants transformed using such anti-sense oriented DNA constructs for gene suppression can comprise integrated DNA arranged as an inverted repeats that result from insertion of the DNA construct into plants by *Agrobacterium*-mediated transformation, as disclosed by Redenbaugh, et al., in "Safety Assessment of Genetically Engineered Flavr Savrm Tomato, CRC Press, Inc. (1992). Inverted repeat insertions can comprises a part or all of the T-DNA construct, e.g., an inverted repeat of a complete transcription unit or an inverted repeat of transcription terminator sequence. Screening for inserted DNA comprising inverted repeat elements can improve the efficiency of identifying transformation events effective for gene silencing whether the transformation construct is a simple anti-sense DNA construct which must be inserted in multiple copies or a complex inverted repeat DNA construct (e.g., an RNAi construct) which can be inserted as a single copy.

[0053] Posttranscriptional gene suppression by inserting a recombinant DNA construct with sense-oriented DNA to regulate gene expression in plants is disclosed in U.S. Pat. No. 5,283,184 (Jorgensen, et al.) and U.S. Pat. No. 5,231,020 (Jorgensen, et al.). Inserted T-DNA providing gene suppression in plants transformed with such sense constructs by *Agrobacterium* is organized predominately in inverted repeat structures, as disclosed by Jorgensen, et al., Mol. Gen. Genet., 207:471-477 (1987). See also Stam, et al., The Plant Journal, 12(1), 63-82 (1997) who used segregation studies to support Jorgensen's finding that gene silencing is mediated by multimeric transgene T-DNA loci in which the T-DNAs are arranged in inverted repeats. Screening for inserted DNA comprising inverted repeat elements can improve the gene silencing efficiency when transforming with simple sense-orientated DNA constructs. Gene silencing efficiency can also be improved by screening for single insertion events when transforming with an RNAi construct containing inverted repeat elements

[0054] As disclosed by Redenbaugh, et al., gene suppression can be achieved by inserting into a plant genome recombinant DNA that transcribes dsRNA. Such a DNA insert can be transcribed to an RNA element having the 3' region as a double stranded RNA. RNAi constructs are also disclosed in EP 0426195 A1 (Goldbach, et al.,—1991) where recombinant DNA constructs for transcription into hairpin dsRNA for providing transgenic plants with resistance to tobacco spotted wilt virus. Double-stranded RNAs were also disclosed in WO 94/01550 (Agrawal, et al.,) where anti-sense RNA was stabilized with a self-complementary 3' segment. Agrawal, et al., referred to U.S. Pat. No. 5,107,065 for using such self-stabilized anti-sense RNAs for regulating gene expression in plant cells; see International Publication No. 94/01550. Other double-stranded hairpin-forming elements in transcribed RNA are disclosed in International Publication No. 98/05770 (Werner, et al.,) where the anti-sense RNA is stabilized by hairpin forming repeats of poly(CG) nucleotides. See also U.S. Patent Application Publication No. 2003/0175965 A1 (Lowe, et al.,) which discloses gene suppression using and RNAi construct comprising a gene coding sequence preceded by inverted repeats of 5'UTR. See also U.S. Patent Application Publication No. 2002/0048814 A1 (Oeller) where RNAi constructs are transcribed to sense or anti-sense RNA which is stabilized by a poly(T)-poly(A) tail. See also U.S. Patent Application Publication No. 2003/0018993 A1 (Gutterson, et al.,) where sense or anti-sense RNA is stabilized by an inverted repeat of the 3' untranslated region of the NOS gene. See also U.S. Patent Application Publication No. 2003/0036197 A1 (Glassman, et al.,) where RNA having homology to a target is stabilized by two complementary RNA regions.

[0055] Gene silencing can also be affected by transcribing RNA from both a sense and an anti-sense oriented DNA, e.g., as disclosed by Shewmaker, et al., in U.S. Pat. No. 5,107,065 where in Example 1 a binary vector was prepared with both sense and anti-sense aroA genes. See also U.S. Pat. No. 6,326,193 where gene targeted DNA is operably linked to opposing promoters.

[0056] Gene silencing can also be affected by transcribing from contiguous sense and anti-sense DNA. In this regard see Sijen, et al., The Plant Cell, Vol. 8, 2277-2294 (1996) discloses the use of constructs carrying inverted repeats of a cowpea mosaic virus gene in transgenic plants to mediate virus resistance. Such constructs for posttranscriptional gene suppression in plants by double-stranded RNA are also disclosed in International Publication No. WO 99/53050 (Waterhouse, et al.,), International Publication No. WO 99/49029 (Graham, et al.), U.S. 2004-0029283 A1 (Fillatti), U.S. Pat. No. 6,506,559 (Fire, et al.,). See also U.S. 2004-

0006792 A1 (Shewmaker, et al.,) that discloses constructs and methods for simultaneously expressing one or more recombinant genes while simultaneously suppressing one or more native genes in a transgenic plant. See also U.S. Pat. No. 6,448,473 (Mitsky, et al.,) that discloses multi-gene suppression vectors for use in plants. All of the above-described patents, applications and international publications disclosing materials and methods for posttranscriptional gene suppression in plants are incorporated herein by reference. Transcriptional suppression such as promoter trans suppression can be affected by a expressing a DNA construct comprising a promoter operably linked to inverted repeats of promoter DNA for a target gene. Constructs useful for such gene suppression mediated by promoter trans suppression are disclosed by Mette, et al., The EMBO Journal, Vol. 18, No. 1, pp. 241-148, 1999 and by Mette, et al., The EMBO Journal, Vol. 19, No. 19, pp. 5194-5201-148, 2000, both of which are incorporated herein by reference.

[0057] Suppression can also be achieved by insertion mutations created by transposable elements may also prevent gene function. For example, in many dicot plants, transformations with the T-DNA of *Agrobacterium* are readily achieved and large numbers of transformants can be rapidly obtained. Also, some species have lines with active transposable elements that are 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 are identified using the polynucleotides of this invention. For example, a large population of mutated plants are screened to detect mutated plants having an insertion in the gene encoding the polypeptide of interest.

Gene Stacking

[0058] This invention also contemplates that the trait-improving recombinant DNA is used in combination with other recombinant DNA to create plants with a multiple desired traits. The combinations generated include multiple copies of any one or more of the recombinant DNA constructs. These stacked combinations are created by any method, including but not limited to cross breeding of transgenic plants, or multiple genetic transformation.

Plant Transformation Methods

[0059] Numerous methods for transforming plant cells with recombinant DNA are known in the art and are useful in producing the transgenic seeds of this invention. Two commonly used methods for plant transformation are *Agrobacterium*-mediated transformation and microprojectile bombardment. Microprojectile bombardment methods are illustrated in U.S. Pat. No. 5,015,580 (soybean); U.S. Pat. No. 5,550,318 (corn); U.S. Pat. No. 5,538,880 (corn); U.S. Pat. No. 5,914,451 (soybean); U.S. Pat. No. 6,160,208 (corn); U.S. Pat. No. 6,399,861 (corn) and U.S. Pat. No. 6,153,812 (wheat) and *Agrobacterium*-mediated transformation is described in U.S. Pat. No. 5,159,135 (cotton); U.S. Pat. No. 5,824,877 (soybean); U.S. Pat. No. 5,591,616 (corn); and U.S. Pat. No. 6,384,301 (soybean), all of which are incorporated herein by reference. For *Agrobacterium tumefaciens* based plant transformation system, additional elements present on transformation constructs include T-DNA left and right border sequences to facilitate incorporation of the recombinant polynucleotide into the plant genome.

[0060] In general it is preferred to introduce heterologous DNA randomly, i.e., at a non-specific location, in the genome of a target plant line. In special cases it is useful to target heterologous DNA insertion in order to achieve site-specific integration, e.g., to replace an existing gene in the genome, to use an existing promoter in the plant genome, or to insert a recombinant polynucleotide at a predetermined site known to be active for gene expression. Several site specific recombination systems exist which are known to function implants include cre-10× as disclosed in U.S. Pat. No. 4,959,317 and FLP-FRT as disclosed in U.S. Pat. No. 5,527,695, both incorporated herein by reference.

[0061] Transformation methods of this invention are preferably practiced in tissue culture on media and in a controlled environment. "Media" means any of the numerous nutrient mixtures that are used to grow cells in vitro, that is, outside of the intact living organism. Recipient cell targets include, but are not limited to, meristem cells, callus, immature embryos and gametic cells such as microspores, pollen, sperm and egg cells. It is contemplated that any cell from which a fertile plant is regenerated is useful as a recipient cell. Callus is initiated from tissue sources including, but not limited to, immature embryos, seedling apical meristems, microspores and the like. Cells capable of proliferating as callus are also recipient cells for genetic transformation. Practical transformation methods and materials for making transgenic plants of this invention, e.g., various media and recipient target cells, transformation of immature embryos and subsequent regeneration of fertile transgenic plants are disclosed in U.S. Pat. Nos. 6,194,636 and 6,232,526 and U.S. 2004-0216189 A1, which are incorporated herein by reference.

[0062] In practice DNA is introduced into only a small percentage of target cells in any one experiment. Marker genes are used to provide an efficient system for identification of those cells that are stably transformed by receiving and integrating a transgenic DNA construct into their genomes. Preferred marker genes provide selective markers that confer resistance to a selective agent, such as an antibiotic or herbicide. Potentially transformed cells are exposed to the selective agent. In the population of surviving cells are those cells where, generally, the resistance-conferring gene has been integrated and expressed at sufficient levels to permit cell survival. Cells are tested further to confirm stable integration of the exogenous DNA. Useful selective marker genes include those conferring resistance to antibiotics such as kanamycin (nptII), hygromycin B (aph IV) and gentamycin (aac3 and aacC4) or resistance to herbicides such as glufosinate (bar or pat) and glyphosate (EPSPS). Examples of such selectable are illustrated in U.S. Pat. Nos. 5,550,318; 5,633,435; 5,780,708 and 6,118,047, all of which are incorporated herein by reference. Screenable markers which provide an ability to visually identify transformants are also often employed, e.g., 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 uidA gene (GUS) for which various chromogenic substrates are known. It is also contemplated that combinations of screenable and selectable markers will be useful for identification of transformed cells. See PCT publication WO 99/61129 which discloses use of a gene fusion between a selectable marker gene and a screenable marker gene, e.g., an NPTII gene and a GFP gene.

[0063] Cells that survive exposure to the selective agent, or cells that have been scored positive in a screening assay, are cultured in regeneration media and allowed to mature into plants. Developing plantlets are transferred to soil less plant growth mix, and hardened off, e.g., 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 preferably matured either in a growth chamber or greenhouse. Plants are regenerated from about 6 wk to 10 months after a transformant is identified, depending on the initial tissue. During regeneration, cells are grown to plants on solid media at about 19 to 28 degrees C. After regenerating plants have reached the stage of shoot and root development, they are transferred to a greenhouse for further growth and testing. Plants are pollinated using conventional plant breeding methods known to those of skill in the art and seed produced.

[0064] Progeny are recovered from transformed plants and tested for expression of the exogenous recombinant polynucleotide. Useful assays include, for example, "molecular biological" assays, such as Southern and Northern blotting and PCR; "biochemical" assays, such as detecting the presence of RNA, e.g., double stranded RNA, or a protein product, e.g., by immunological means (ELISAs and Western blots) or by enzymatic function; plant part assays, such as leaf or root assays; and also, by analyzing the phenotype of the whole regenerated plant.

Discovery of Trait-Improving Recombinant DNA

[0065] To identify recombinant DNA that confer improved traits to plants, *Arabidopsis* plants were transformed with a large population of recombinant DNA constructs for expressing a large variety of distinct DNA. Transgenic plants were produced and screened to identify those plants having recombinant DNA constructs expressing trait-imparting DNA. 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 improved traits, were further evaluated in the second pass screen to confirm the transgene's ability to impart an improved trait. The following Table 2 summarizes the improved traits that have been confirmed as provided by a recombinant DNA construct.

[0066] In particular, Table 2 reports

[0067] "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.

[0068] "construct_id" is an arbitrary name for the recombinant DNA describe more particularly in Table 1.

[0069] "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.

[0070] "description" refers to the description of the top BLAST hit.

[0071] "e-value" provides the expectation value for the BLAST hit.

[0072] "identity" 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.

[0073] "traits" identified by two letters codes the confirmed improvement in a transgenic plant provided by the recombinant DNA. The codes for improved traits are:

[0074] "CK" which indicates cold tolerance improvement identified under a cold shock tolerance screen;

[0075] "CS" which indicates cold tolerance improvement identified by a cold germination tolerance screen;

[0076] "DS" which indicates drought tolerance improvement identified by a soil drought stress tolerance screen;

[0077] "PEG" which indicates osmotic stress tolerance improvement identified by a PEG induced osmotic stress tolerance screen;

[0078] "HS" which indicates heat stress tolerance improvement identified by a heat stress tolerance screen;

[0079] "SS" which indicates high salinity stress tolerance improvement identified by a salt stress tolerance screen;

[0080] "LN" which indicates nitrogen use efficiency improvement identified by a limited nitrogen tolerance screen;

[0081] "LL" which indicates attenuated shade avoidance response identified by a shade tolerance screen under a low light condition;

[0082] "PP" which indicates improved growth and development at early stages identified by an early plant growth and development screen;

[0083] "SP" which indicates improved growth and development at late stages identified by a late plant growth and development screen provided herein.

TABLE 2

Pep SEQ Id	construct id	gene	annotation e value	% identity	ncbi id	description	traits				
270	14324	CGPG1560	1.00E − 127	86	gi|15232185|	ref|NP_191546.1|expressed protein [*Arabidopsis thaliana*]]	CK	SS			
271	17484	CGPG2630	0	93	gi|15220912|	ref|NP_173239.1|zinc finger (C3HC4-type RING finger) family protein [*Arabidopsis thaliana*]	CK				
272	19109	CGPG1381	9.00E − 31	81	gi|18404521|	ref|NP_565870.1|expressed protein [*Arabidopsis thaliana*]	CK				
273	70423	CGPG3165	1.00E − 134	96	gi|30688808|	ref|NP_850953.1|MADS-box protein (AGL9) [*Arabidopsis thaliana*] gb|AAM65812.1| putative floral homeotic protein, AGL9 [*Arabidopsis thaliana*]	CK	CS	CK	HS	PP
274	70424	CGPG3180	1.00E − 142	81	gi|25405039|	pir||H96827protein F20B17.12 [imported]- *Arabidopsis thaliana* gb|AAF68121.1|F20B17.12 [*Arabidopsis thaliana*]	CK				
275	70480	CGPG3833	1.00E − 122	99	gi|18411867|	ref|NP_565174.1|14-3-3 protein GF14 pi (GRF13) [*Arabidopsis thaliana*]	CK				
276	70509	CGPG2420	1.00E − 113	82	gi|15225186|	ref|NP_180770.1|ovate protein-related [*Arabidopsis thaliana*]	CK				
277	70647	CGPG4334	1.00E − 171	94	gi|15237269|	ref|NP_200093.1|ornithine cyclodeaminase/mu-crystallin family protein [*Arabidopsis thaliana*] dbj|BAB10429.1|	CK				
278	70675	CGPG4519	0	100	gi|15224730|	ref|NP_180115.1|2-oxoglutarate-dependent dioxygenase, putative [*Arabidopsis thaliana*] pir||E84648 probable dioxygenase]	CK				
279	70829	CGPG518	0	92	gi|15232841|	ref|NP_186854.1|potassium transporter (KUP3) [*Arabidopsis thaliana*]	CK				
280	70849	CGPG596	1.00E − 166	96	gi|15224801|	ref|NP_179547.1|cytidine deaminase (CDD)/cytidine aminohydrolase [*Arabidopsis thaliana*]	CK				
281	71627	CGPG1270	0	99	gi|18398032|	ref|NP_566315.1|ABC1 family protein [*Arabidopsis thaliana*]	CK				
282	71934	CGPG2294	1.00E − 154	79	gi|15233973|	ref|NP_195575.1|26S proteasome regulatory subunit S5A (RPN10) [*Arabidopsis thaliana*] sp|P55034|PSD4_ARATH 26S proteasome non-ATPase regulatory subunit 4 (26S proteasome regulatory	CK				
283	72615	CGPG4829	2.00E − 49	88	gi|18422886|	ref|NP_568693.1|expressed protein [*Arabidopsis thaliana*]	CK				
284	72927	CGPG1477	1.00E − 114	81	gi|15234815|	ref|NP_194797.1|MA3 domain-containing protein [*Arabidopsis thaliana*] pir||A85359 translation initiation factor-like protein	CK				
285	73014	CGPG5692	1.00E − 180	93	gi|37528369|	ref|NP_931714.1|Fructose-1,6-bisphosphatase (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase) [*Photorhabdus*	CK	PP			

TABLE 2-continued

Pep SEQ Id	construct id	gene	annotation e value	% identity	ncbi id	description	traits		
						luminescens subsp. laumondii TTO1]			
286	73559	CGPG6535	0	93	gi|16078422|	ref|NP_389241.1|similar to aspartate aminotransferase [*Bacillus subtilis*] sp|O31665|MTNE_BACSU Transaminase mtnE pir||F69863 probable transaminase (EC 2.6.1.-) ykrV	CK		
287	74251	CGPG5489	1.00E − 171	87	gi|15238437|	ref|NP_200760.1|zinc transporter (ZIP2) [*Arabidopsis thaliana*] sp|Q9LTH9|ZIP2_ARATH Zinc transporter 2 precursor (ZRT/IRT-like protein 2)	CK	SP	
288	19631	CGPG3627	1.00E − 94	90	gi|18410249|	ref|NP_565053.1|SNF7 family protein [*Arabidopsis thaliana*] pir||G96755 developmental protein homolog DG1118 [imported] - [*Arabidopsis thaliana*]	CS		
289	70121	CGPG2380	1.00E − 111	100	gi|6323765|	ref|NP_013836.1|Hypothetical ORF; Ymr118cp [*Saccharomyces cerevisiae*] sp|Q04487|YM07_YEAST Putative succinate dehydrogenase cytochrome B subunit, mitochondrial precursor	CS		
290	70654	CGPG4352	2.00E − 63	88	gi|18400941|	ref|NP_566531.1|expressed protein [*Arabidopsis thaliana*]	CS		
291	70696	CGPG4590	8.00E − 92	87	gi|25408379|	pir||E84768hypothetical protein At2g35430	CS	PP	
292	70713	CGPG1462	0	95	gi|30678679|	ref|NP_191966.2|malate oxidoreductase, putative	CS		
293	70740	CGPG3700	0	94	gi|18402759|	ref|NP_566667.1|transcription factor jumonji (jmjC) domain-containing protein	CS	LL	PP
294	71321	CGPG4418	0	91	gi|13878402|	sp|Q9STL0|C71N_ARATH Cytochrome P450 71A23 pir||T06712 probable cytochrome P450 T29H11.180	CS		
295	71835	CGPG4634	0	100	gi|15234361|	ref|NP_192100.1|DC1 domain-containing protein [*Arabidopsis thaliana*] pir||E85024 probable CHP-rich zinc finger protein	CS	SP	
296	72934	CGPG5798	0	98	gi|6323512|	ref|NP_013583.1|High-affinity inorganic phosphate (Pi) transporter and low-affinity manganese transporter; regulated by Pho4p and Spt7p; mutation confers resistance to arsenate; exit from the ER during maturation requires Pho86p; Pho84p [*Saccharomyces cerevisiae*]	CS		
297	72945	CGPG5787	0	94	gi|6319991|	ref|NP_010071.1|GABA-specific transport protein; Uga4p [*Saccharomyces cerevisiae*] sp|P32837|UGA4_YEAST GABA-specific permease	CS		

TABLE 2-continued

Pep SEQ Id	construct id	gene	annotation e value	% identity	ncbi id	description	traits			
298	72980	CGPG5773	0	89	gi|63219690|	(GABA-specific transport protein) ref|NP_012036.1|Subunit of the anaphase-promoting complex/cyclosome (APC/C), which is a ubiquitin-protein ligase required for degradation of anaphase inhibitors, including mitotic cyclins, during the metaphase/anaphase transition; Cdc23p	CS			
299	73504	CGPG6480	1.00E − 178	100	gi|16330153|	ref|NP_440881.1|fructokinase [*Synechocystis* sp. PCC 6803] pir||S77227 fructokinase (EC 2.7.1.4)-*Synechocystis* sp. (strain PCC 6803)	CS	PP		
300	73507	CGPG6504	1.00E − 173	100	gi|16078547|	ref|NP_389366.1|similar to glutaminase [*Bacillus subtilis*]	CS	LL	PP	PEG
301	73573	CGPG6462	0	100	gi|15890038|	ref|NP_355719.1|AGR_C_5 067p [*Agrobacterium tumefaciens* str. C58] ref|NP_533456.1| 3-isopropylmalate dehydrogenase	CS	PP		
302	73586	CGPG6471	1.00E − 177	100	gi|16077684|	ref|NP_388498.1|similar to fructokinase [*Bacillus subtilis*]	CS	DS	PP	
303	73770	CGPG5435	2.00E − 34	68	gi|15235771|	ref|NP_193383.1|cysteine protease inhibitor family protein/cystatin family protein [*Arabidopsis thaliana*]	CS	PP		
304	74105	CGPG6574	0	73	gi|23059330|	ref|ZP_00084307.1|COG1012: NAD-dependent aldehyde dehydrogenases [*Pseudomonas fluorescens* PfO-1]	CS			
305	74111	CGPG6622	0	99	gi|16131442]	ref|NP_418028.1|alpha-amylase [*Escherichia coli* K12]	CS			
306	74136	CGPG6632	9.00E − 81	99	gi|16330993|	ref|NP_441721.1|unknown protein [*Synechocystis* sp. PCC 6803]	CS	CK	HS	
307	74139	CGPG6561	1.00E − 180	95	gi|24112825|	ref|NP_707335.1|glyceraldehyde-3-phosphate dehydrogenase A [*Shigella flexneri* 2a str. 301]	CS	LL		
308	74267	CGPG5364	0	97	gi|18399375|	ref|NP_566402.1|U-box domain-containing protein [*Arabidopsis thaliana*]	CS			
309	74291	CGPG5363	0	94	gi|18401867|	ref|NP_565676.1|armadillo/beta-catenin repeat family protein/U-box domain-containing protein [*Arabidopsis thaliana*]	CS			
310	74318	CGPG5826	0	100	gi|15219730|	ref|NP_176847.1|cell division protein kinase, putative [*Arabidopsis thaliana*]	CS	HS		
311	74319	CGPG5831	0	96	gi|15224359|	ref|NP_181907.1|mitogen-activated protein kinase, putative/MAPK, putative (MPK6) [*Arabidopsis thaliana*]	CS			
312	74324	CGPG5885	1.00E − 174	95	gi|42569304|	ref|NP_180094.2|protein kinase family protein [*Arabidopsis thaliana*]	CS			

TABLE 2-continued

Pep SEQ Id	construct id	gene	annotation e value	% identity	ncbi id	description	traits			
313	74512	CGPG32	0	96	gi|15217945|	ref|NP_176132.1|amino acid permease I (AAP1) [*Arabidopsis thaliana*]	CS	HS	SP	
314	74583	CGPG6649	1.00E − 151	83	gi|22978283|	ref|ZP_00024043.1|COG0252: L-asparaginase/archaeal Glu-tRNAGln amidotransferase subunit D [*Ralstonia metallidurans*]	CS	PP		
315	70427	CGPG3067	0	100	gi|42572771|	ref|NP_974481.1|kelch repeat-containing F-box family protein [*Arabidopsis thaliana*]	CS	DS		
316	71811	CGPG4426	0	97	gi|15223341|	ref|NP_171627.1|cytochrome P450, putative [*Arabidopsis thaliana*]	CS	DS	LL	LN
317	73463	CGPG6384	0	100	gi|22977164|	ref|ZP_00022985.1|COG0538: Isocitrate dehydrogenases [*Ralstonia metallidurans*]	DS			
318	72081	CGPG5279	7.00E − 66	77	gi|42570373|	ref|NP_850277.2|CCAAT-box binding transcription factor, putative [*Arabidopsis thaliana*]	DS	PEG		
319	10139	CGPG101	0	89	gi|15229877|	ref|NP_187154.1|sodium proton exchanger, putative (NHX2) [*Arabidopsis thaliana*]	DS			
320	11410	CGPG103	0	82	gi|15236418|	ref|NP_192555.1|homeobox protein knotted-1 like 1 (KNAT1) [*Arabidopsis thaliana*]	DS			
321	11604	CGPG48	0	92	gi|15233457|	ref|NP_194642.1|hexokinase 1 (HXK1) [*Arabidopsis thaliana*]	DS			
322	12368	CGPG1006	1.00E − 146	85	gi|15231451|	ref|NP_190238.1|epsin N-terminal homology (ENTH) domain-containing protein/ clathrin assembly protein-related [*Arabidopsis thaliana*]	DS			
323	13502	CGPG1354	0	95	gi|15224557|	ref|NP_180632.1|serine/ threonine protein kinase, putative [*Arabidopsis thaliana*]	DS	PP		
324	13745	CGPG1576	1.00E − 112	84	gi|15222987|	ref|NP_177749.1|hypothetical protein [*Arabidopsis thaliana*] gb[AAF17642.1| T23E18.15 [*Arabidopsis thaliana*]	DS			
325	13821	CGPG1569	1.00E − 155	85	gi|18416499|	ref|NP_567716.1|expressed protein [*Arabidopsis thaliana*]	DS			
326	14240	CGPG1697	0	94	gi|15241302|	ref|NP_197527.1|expressed protein [*Arabidopsis thaliana*]	DS			
327	14718	CGPG1082	0	86	gi|18407200|	ref|NP_566090.1|expressed protein [*Arabidopsis thaliana*]	DS			
328	17022	CGPG1774	1.00E − 159	100	gi|15237803|	ref|NP_197755.1|nodulin MtN3 family protein [*Arabidopsis thaliana*]	DS			
329	17924	CGPG2882	3.00E − 92	100	gi|15233350|	ref|NP_192875.1|zinc finger (C3HC4-type RING finger) family protein (RHA1b) [*Arabidopsis thaliana*]	DS			
330	18259	CGPG3368	2.00E − 94	88	gi|30685085|	ref|NP_849549.1|zinc finger protein (LSD1) [*Arabidopsis thaliana*]	DS	PP		
331	19171	CGPG2952	0	91	gi|6320063|	ref|NP_010143.1|plasma membrane glucose sensor; Rgt2p [*Saccharomyces cerevisiae*]	DS			

TABLE 2-continued

Pep SEQ Id	construct id	gene	annotation e value	% identity	ncbi id	description	traits		
332	19201	CGPG2332	0	96	gi|15233948|	ref|NP_194205.1|protein kinase (AFC2) [*Arabidopsis thaliana*] sp|P51567|AFC2_ARATH Protein kinase	DS		
333	19317	CGPG3662	1.00E − 151	91	gi|21232858|	ref|NP_638775.1|conserved hypothetical protein [*Xanthomonas campestris* pv. *campestris* str. ATCC 33913]	DS		
334	70417	CGPG3427	0	81	gi|18396278|	ref|NP_566180.1|integral membrane family protein [*Arabidopsis thaliana*]	DS	PP	SP
335	70467	CGPG3785	0	100	gi|15241416|	ref|NP_196953.1|no apical meristem (NAM) family protein [*Arabidopsis thaliana*]	DS		
336	70806	CGPG712	0	100	gi|15218225|	ref|NP_173010.1|cyclin, putative [*Arabidopsis thaliana*]	DS		
337	70818	CGPG479	1.00E − 157	92	gi|30691978|	ref|NP_568508.2|bZIP transcription factor family protein [*Arabidopsis thaliana*]	DS		
338	70820	CGPG655	0	93	gi|15224342|	ref|NP_181899.1|acyl-[acyl-carrier-protein] desaturase/ stearoyl-ACP desaturase (SSI2) [*Arabidopsis thaliana*]	DS		
339	70919	CGPG4029	1.00E − 169	73	gi|6996560|	emb|CAB75429.1|oligouridylate binding protein [*Nicotiana plumbaginifolia*]	DS		
340	71623	CGPG4696	1.00E − 150	95	gi|15236511|	ref|NP_192588.1|mitogen-activated protein kinase, putative [*Arabidopsis thaliana*] pir||T01835 serine/threonine-specific protein kinase ARA.KIN homolog T15F16.3- *Arabidopsis thaliana*	DS		
341	71662	CGPG4679	1.00E − 173	91	gi|5929964|	gb|AAD56659.1|malate dehydrogenase [*Glycine max*]	DS		
342	71693	CGPG4652	6.00E − 86	56	gi|21553460|	gb|AAM62553.1|snap25a [*Arabidopsis thaliana*]	DS		
343	72384	CGPG4639	0	98	gi|1169548|	sp|P38604|ERG7_YEAST Lanosterol synthase (Oxidosqualene-lanosterol cyclase) (2,3-epoxysqualene-lanosterol cyclase) (OSC) gb|AAA64377.1|2,3-oxidosqualene-lanosterol cyclase	DS		
344	72439	CGPG5075	8.00E − 57	90	gi|22331337|	ref|NP_683594.1|NPR1/NIM1-interacting protein 2 (NIMIN-2)	DS		
345	72619	CGPG4835	6.00E − 83	88	gi|15237317|	ref|NP_200108.1|expressed protein [*Arabidopsis thaliana*]	DS		
346	72624	CGPG4842	0	100	gi|15242148|	ref|NP_200558.1|expressed protein [*Arabidopsis thaliana*]	DS		
347	72715	CGPG5521	0	91	gi|6323933|	ref|NP_014004.1|Carboxy-terminal domain (CTD) phosphatase, essential for dephosphorylation of the repeated C-terminal domain of the RNA polymerase II large subunit (Rpo21p); Fcp1p	DS	SS	

TABLE 2-continued

Pep SEQ Id	construct id	gene	annotation e value	% identity	ncbi id	description			traits
						[*Saccharomyces cerevisiae*]			
348	72754	CGPG5548	1.00E − 169	100	gi|728961|	sp|Q00618|BET4_YEAST Geranylgeranyl transferase type II alpha subunit (Type II protein geranyl-	DS		
349	72819	CGPG4989	0	100	gi|18417026|	ref|NP_567780.1|pfkB-type carbohydrate kinase family protein [*Arabidopsis thaliana*]	DS		
350	75516	CGPG7689	1.00E − 138	70	gi|42568081|	ref|NP_197938.2|zinc finger (C3HC4-type RING finger) family protein [*Arabidopsis thaliana*]	DS		
351	75701	CGPG7856	8.00E − 41	37	gi|15225413|	ref|NP_182037.1|zinc finger (C2H2 type) family protein [*Arabidopsis thaliana*]	DS	LN	
352	73515	CGPG6473	1.00E − 162	100	gi|16079626|	ref|NP_390450.1|similar to 6-phosphogluconate dehydrogenase (pentose phosphate) [*Bacillus subtilis*]	HS	CS	PEG
353	74684	CGPG6360	1.00E − 64	100	gi|18390735|	ref|NP_563782.1|expressed protein [*Arabidopsis thaliana*]	CS	HS	
354	19542	CGPG3069	0	90	gi|18403574|	ref|NP_564592.1|F-box family protein [*Arabidopsis thaliana*]	HS		
355	19618	CGPG3574	1.00E − 121	100	gi|15218423|	ref|NP_177373.1|trypsin and protease inhibitor family protein/Kunitz family protein [*Arabidopsis thaliana*] pir||F96746 probable drought induced protein	HS		
356	19649	CGPG3140	1.00E − 141	87	gi|18412787|	ref|NP_567287.1|vesicle-associated membrane family protein/VAMP family protein	HS		
357	19745	CGPG3973	2.00E − 60	46	gi|15239303|	ref|NP_201424.1|expressed protein [*Arabidopsis thaliana*]	HS		
358	19768	CGPG4096	1.00E − 179	81	gi|25052804|	gb|AAN65180.1|mitogen-activated protein kinase 4 [*Petroselinum crispum*]	HS	SS	
359	19772	CGPG3939	3.00E − 82	79	gi|7488744|	pir||T09700MADS-box protein - alfalfa (fragment) gb|AAB51377.1|MADS-box protein [*Medicago sativa*]	HS		
360	19779	CGPG4113	1.00E − 153	89	gi|30681126|	ref|NP_196201.2|phosphate translocator-related [*Arabidopsis thaliana*]	CS	HS	
361	19833	CGPG4074	1.00E − 107	79	gi|6683777|	gb|AAF23363.1|CAGL2 [*Cucumis sativus*]	CS	HS	PP
362	19862	CGPG3961	2.00E − 89	56	gi|15229637|	ref|NP_188469.1|no apical meristem (NAM) family protein [*Arabidopsis thaliana*] dbj|BAB01106.1| unnamed protein product [*Arabidopsis thaliana*]	HS		
363	19879	CGPG4009	0	75	gi|18401703|	ref|NP_564504.1|protein phosphatase 2C-related/ PP2C-related [*Arabidopsis thaliana*]	HS	CS	SS
364	70445	CGPG3728	2.00E − 51	88	gi|30696602|	ref|NP_200357.2|protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [*Arabidopsis thaliana*]	HS		
365	70738	CGPG3195	1.00E − 96	100	gi|15234797|	ref|NP_194791.1|expressed protein [*Arabidopsis thaliana*]	HS	PP	

TABLE 2-continued

Pep SEQ Id	construct id	gene	annotation e value	% identity	ncbi id	description	traits		
366	71437	CGPG4043	1.00E − 164	81	gi|15241535|	ref|NP_196433.1|serine/threonine protein kinase, putative [*Arabidopsis thaliana*]	HS		
367	71572	CGPG4520	3.00E − 83	92	gi|18403850|	ref|NP_565804.1|expressed protein [*Arabidopsis thaliana*]	HS		
368	71617	CGPG1227	0	100	gi|15236219|	ref|NP_195218.1|1-phosphatidylinositol phosphodiesterase-related [*Arabidopsis thaliana*]	HS	CK	
369	72532	CGPG4780	1.00E − 118	90	gi|15236659|	ref|NP_194120.1|expressed protein [*Arabidopsis thaliana*]	HS		
370	72757	CGPG5572	0	89	gi|15242402|	ref|NP_197088.1|zinc finger protein CONSTANS (CO) [*Arabidopsis thaliana*]	HS	LL	PEG
371	73412	CGPG6448	0	99	gi|28867589|	ref|NP_790208.1|glutamine synthetase, type I [*Pseudomonas syringae* pv. tomato str. DC3000]	HS		
372	74102	CGPG6550	1.00E − 167	94	gi|15614187|	ref|NP_242490.1|L-asparaginase [*Bacillus halodurans* C-125]	HS		
373	72633	CGPG4853	1.00E − 145	86	gi|15238013|	ref|NP_199519.1|casein kinase II beta chain, putative [*Arabidopsis thaliana*]	CS	LL	PEG
374	72456	CGPG4745	1.00E − 75	92	gi|15239846|	ref|NP_196763.1|17.6 kDa class II heat shock protein (HSP17.6-CII) [*Arabidopsis thaliana*]	DS	LL	
375	72963	CGPG1746	1.00E − 151	87	gi|15222239|	ref|NP_172174.1|ovate family protein [*Arabidopsis thaliana*]	LL	LN	
376	70426	CGPG3199	8.00E − 54	88	gi|18397268|	ref|NP_564336.1|double-stranded DNA-binding family protein [*Arabidopsis thaliana*]	LL		
377	70772	CGPG4627	1.00E − 92	80	gi|15220084|	ref|NP_173175.1|MADS-box protein (AGL100) [*Arabidopsis thaliana*] P	LL		
378	71137	CGPG125	1.00E − 111	90	gi|15218957|	ref|NP_176202.1|two-component responsive regulator/response regulator 3 (ARR3) [*Arabidopsis thaliana*]	LL		
379	71529	CGPG2808	1.00E − 131	72	gi|42562375|	ref|NP_174152.3|Dof-type zinc finger domain-containing protein [*Arabidopsis thaliana*]	LL		
380	71601	CGPG1858	1.00E − 168	92	gi|15231425|	ref|NP_187378.1|transcriptional activator, putative [*Arabidopsis thaliana*]	LL		
381	72362	CGPG983	1.00E − 163	95	gi|15242779|	ref|NP_200562.1|xyloglucan: xyloglucosyl transferase, putative/xyloglucan endotransglycosylase, putative/endo-xyloglucan transferase, putative [*Arabidopsis thaliana*]	LL		
382	72466	CGPG4767	3.00E − 60	83	gi|15234046|	ref|NP_195030.1|glutaredoxin family protein [*Arabidopsis thaliana*]	CK	LL	PEG
383	72524	CGPG4770	1.00E − 134	91	gi|18412649|	ref|NP_567140.1|expressed protein [*Arabidopsis thaliana*]	CK	LL	
384	73085	CGPG5689	1.00E − 134	100	gi|16331347|	ref|NP_442075.1|triosephosphate isomerase	LL		

TABLE 2-continued

Pep SEQ Id	construct id	gene	annotation e value	% identity	ncbi id	description	traits		
						[*Synechocystis* sp. PCC 6803]			
385	74241	CGPG5457	0	89	gi|444790|	prf||1908224Anucleotide translocator	LL		
386	74247	CGPG5475	1.00E − 159	100	gi|18411863|	ref|NP_565172.1|protein phosphatase 2C, putative/ PP2C, putative [*Arabidopsis thaliana*]	LL		
387	74284	CGPG5413	0	97	gi|15230577|	ref|NP_190087.1|serine carboxypeptidase III, putative [*Arabidopsis thaliana*]	LL		
388	74652	CGPG6168	1.00E − 90	80	gi|15235970|	ref|NP_194879.1|expressed protein [*Arabidopsis thaliana*]	LL	DS	
389	70437	CGPG3706	1.00E − 172	100	gi|30678824|	ref|NP_186983.2|short-chain dehydrogenase/reductase (SDR) family protein [*Arabidopsis thaliana*]	CK	LN	
390	71633	CGPG857	1.00E − 100	86	gi|6690274|	gb|AAF24061.1|v-SNARE AtVTI1a [*Arabidopsis thaliana*]	DS	LN	
391	72948	CGPG5617	0	94	gi|15225456|	ref|NP_182059.1|leucine-rich repeat transmembrane protein kinase, putative [*Arabidopsis thaliana*]	LN	PEG	
392	72519	CGPG4749					LN	SS	
393	10475	CGPG399	1.00E − 164	96	gi|15240972|	ref|NP_195761.1|stress-responsive protein, putative [*Arabidopsis thaliana*]	LN		
394	11120	CGPG459	0	100	gi|15227169|	ref|NP_179812.1|inositol-3-phosphate synthase isozyme 2/myo-inositol-1-phosphate synthase 2/MI-1-P synthase 2/IPS 2 [*Arabidopsis thaliana*]	LN		
395	19736	CGPG4129	2.00E − 94	67	gi|13346194|	gb|AAK19619.1|GHMYB9 [*Gossypium hirsutum*]	LN		
396	71606	CGPG4715	0	91	gi|15218674|	ref|NP_171800.1|phototropic-responsive NPH3 family protein [*Arabidopsis thaliana*]	LN		
397	71840	CGPG4353	0	96	gi|18401087|	ref|NP_566542.1|mitotic phosphoprotein N' end (MPPN) family protein [*Arabidopsis thaliana*]	DS	LL	LN
398	74240	CGPG5454	1.00E − 155	90	gi|15233884|	ref|NP_194188.1|mitochondrial substrate carrier family protein [*Arabidopsis thaliana*] pir||T05577 uncoupling protein homolog F22K18.230 - *Arabidopsis thaliana*	CK	LN	
399	74331	CGPG5834	0	94	gi|15220416|	ref|NP_172003.1|protein kinase family protein [*Arabidopsis thaliana*]	LN		
400	74610	CGPG6048	1.00E − 117	100	gi|15217568|	ref|NP_172434.1|Ras-related GTP-binding protein, putative [*Arabidopsis thaliana*] sp|O04486|RB1C_ARATH Ras-related protein Rab11C	LL	LN	
401	75527	CGPG7682	1.00E − 55	65	gi|15240946|	ref|NP_195750.1|phosphatidyl-ethanolamine-binding family protein [*Arabidopsis thaliana*]	LN		
402	70681	CGPG4584	9.00E − 64	93	gi|18411465|	ref|NP_567196.1|auxin-responsive family protein [*Arabidopsis thaliana*]	CK	PEG	

TABLE 2-continued

Pep SEQ Id	construct id	gene	annotation e value	% identity	ncbi id	description	traits			
403	71663	CGPG4638	0	93	gi|21230153|	ref|NP_636070.1|conserved hypothetical protein [*Xanthomonas campestris* pv. *campestris* str. ATCC 33913]	CK	PEG		
404	72769	CGPG5573	0	100	gi|15225499|	ref|NP_182075.1|cytochrome P450, putative [*Arabidopsis thaliana*]	CK	PEG		
405	71508	CGPG1541	2.00E − 24	100	gi|15241504|	sp|Q9SD80|OM05_ARATH Mitochondrial import receptor subunit TOM5 homolog (Translocase of outer membrane 5 kDa subunit homolog)	PEG	CS	SP	PEG
406	74248	CGPG5476	0	100	gi|15226152|	ref|NP_180926.1|protein phosphatase 2C, putative/ PP2C, putative [*Arabidopsis thaliana*] p	PEG	CS		
407	72771	CGPG2166	5.00E − 44	100	gi|18395032|	ref|NP_564151.1|expressed protein [*Arabidopsis thaliana*]	PEG	CK	HS	SS
408	72085	CGPG5228	0	94	gi|15241541|	ref|NP_199275.1|cytochrome P450 family protein [*Arabidopsis thaliana*] dbj|BAA98115.1|flavonoid 3',5'-hydroxylase-like; cytochrome P450 [*Arabidopsis thaliana*]	PEG	HS		
409	72744	CGPG5563	1.00E − 136	96	gi|6321574|	ref|NP_011651.1|20S proteasome beta-type subunit; the only nonessential 20S subunit; Pre9p [*Saccharomyces cerevisiae*]	HS	PEG	CK	
410	73039	CGPG810	0	96	gi|15242124|	ref|NP_197599.1|molybdopterin biosynthesis CNX1 protein/molybdenum cofactor biosynthesis enzyme CNX1 (CNX1) [*Arabidopsis thaliana*]	HS	PEG		
411	73054	CGPG5754	2.00E − 98	100	gi|6324827|	ref|NP_014896.1|Nat5p [*Saccharomyces cerevisiae*] pir||S67150 hypothetical protein YOR253w - yeast (*Saccharomyces cerevisiae*)	PEG	HS	SS	PEG
412	73501	CGPG6456	0	97	gi|15888752|	ref|NP_354433.1|AGR_C_2631p [*Agrobacterium tumefaciens* str. C58] sp|Q8UFH1|ENO_AGRT5 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)	HS	PEG		
413	19707	CGPG4179	1.00E − 86	49	gi|15236282|	ref|NP_195242.1|O-methyltransferase family 2 protein [*Arabidopsis thaliana*]	PEG	CS		
414	19951	CGPG3941	5.00E − 91	54	gi|15221582|	ref|NP_177064.1|basic helix-loop-helix (bHLH) family protein [*Arabidopsis thaliana*]	PEG	CK		
415	19967	CGPG4032	1.00E − 127	67	gi|4760710|	dbj|BAA77395.1|SLL2-S9-protein [*Brassica rapa*]	PEG			
416	70543	CGPG3815	0	95	gi|15220994|	ref|NP_175222.1|E2F transcription factor-2 (E2F2)/transcription factor E2Fc (E2Fc) [*Arabidopsis thaliana*]	PEG	CK		
417	70707	CGPG1273	1.00E − 108	100	gi|15219558|	ref|NP_177523.1|Ssu72-like family protein	PEG			

TABLE 2-continued

Pep SEQ Id	construct id	gene	annotation e value	% identity	ncbi id	description	traits			
						[*Arabidopsis thaliana*] pir||F96765 unknown protein F				
418	70719	CGPG1712	0	86	gi|18394560|	ref|NP_564043.1|expressed protein [*Arabidopsis thaliana*]	PEG			
419	71134	CGPG817	8.00E − 55	100	gi|15240471|	ref|NP_200327.1|small ubiquitin-like modifier 2 (SUMO) [*Arabidopsis thaliana*]	PEG	HS	PP	
420	71146	CGPG2928	1.00E − 86	92	gi|29165403|	gb|AAO65311.1|MADS affecting flowering 3 variant II [*Arabidopsis thaliana*]	PEG			
421	71660	CGPG4690	3.00E − 80	100	gi|18415773|	ref|NP_567637.1|methionine sulfoxide reductase domain-containing protein/ SelR domain-containing protein [*Arabidopsis thaliana*]	PEG			
422	72086	CGPG5236	0	100	gi|15232215|	ref|NP_191556.1|methylenetetra-hydrofolate reductase 1 (MTHFR1) [*Arabidopsis thaliana*] -	PEG	PP	PEG	
423	72632	CGPG4852	4.00E − 99	90	gi|18425032|	ref|NP_569028.1|expressed protein [*Arabidopsis thaliana*]	PEG			
424	72716	CGPG5529	2.00E − 85	89	gi|6320196|	ref|NP_010276.1|subunit of the Anaphase Promoting Complex; all known APC subunits co-immunoprecipitate with epitope-tagged Apc11p; Apc11p [*Saccharomyces cerevisiae*]	PEG			
425	72723	CGPG1848	0	97	gi|15237500|	ref|NP_199487.1|human Rev interacting-like family protein/hRIP family protein [*Arabidopsis thaliana*] dbj|BAB08919.1|zinc finger protein Glo3-like [*Arabidopsis thaliana*]	PEG			
426	72987	CGPG1787	5.00E − 81	77	gi|15231568|	ref|NP_189282.1|octicosapep-tide/Phox/Bem1p (PB1) domain-containing protein [*Arabidopsis thaliana*]	PEG	SP		
427	74109	CGPG6606	0	77	gi|37524479|	ref|NP_927823.1|maltodextrin phosphorylase [*Photorhabdus luminescens* subsp. *laumondii* TTO1]	PEG			
428	74140	CGPG6569	0	99	gi|15613102|	ref|NP_241405.1|NADP-dependent aldehyde dehydrogenase [*Bacillus halodurans* C-125]	PEG	PP	PEG	
429	74191	CGPG6597	0	96	gi|22960294|	ref|ZP_00007935.1|COG1850: Ribulose 1,5-bisphosphate carboxylase, large subunit [*Rhodobacter sphaeroides*]	PEG			
430	74265	CGPG5356	1.00E − 117	100	gi|15237288|	ref|NP_197727.1|GRAM domain-containing protein/ ABA-responsive protein-related [*Arabidopsis thaliana*]	PEG	PP	PEG	
431	74369	CGPG6076	2.00E − 86	96	gi|18409647|	ref|NP_564994.1|ubiquitin-conjugating enzyme family protein [*Arabidopsis thaliana*]	PEG	CK	PP	PEG
432	70217	CGPG6	0	97	gi|15231536|	ref|NP_189259.1|cytochrome P450 family protein [*Arabidopsis thaliana*]	CK	PP	SP	

TABLE 2-continued

Pep SEQ Id	construct id	gene	annotation e value	% identity	ncbi id	description	traits				
433	72711	CGPG1846	4.00E − 75	79	gi|15221048|	ref|NP_175816.1|transcription initiation factor IID (TFIID) 31 kDa subunit (TAFII-31) family protein [*Arabidopsis thaliana*]	CK	PP	SP		
434	70932	CGPG4089	1.00E − 129	56	gi|15223134|	ref|NP_177792.1|expressed protein [*Arabidopsis thaliana*]	CS	HS	PP		
435	73518	CGPG6497	1.00E − 177	63	gi|22981996|	ref|ZP_00027327.1|COG1012: NAD-dependent aldehyde dehydrogenases [*Burkholderia fungorum*]	CS	CK	PP		
436	19771	CGPG4011	3.00E − 90	80	gi|18418200|	ref|NP_568342.1|rubredoxin family protein [*Arabidopsis thaliana*] dbj|BAB10504.1| gene_id:MKP11.2~unknown protein [*Arabidopsis thaliana*] g	PP	HS	SS		
437	73549	CGPG6460	0	90	gi|37524978|	ref|NP_928322.1|5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase [*Photorhabdus luminescens* subsp. *laumondii* TTO1]	HS	DS	PP		
438	72994	CGPG5803	0	83	gi|6322702|	ref|NP_012776.1|Vacuolar transporter, exports large neutral amino acids from the vacuole; member of a family of seven *S. cerevisiae* genes (AVT1-7) related to vesicular GABA-glycine transporters; Avt3p [*Saccharomyces cerevisiae*]	CK	PEG	CS	PP	PEG
439	71928	CGPG1617	0	100	gi|18394888|	ref|NP_564120.1|catalase 3 (SEN2) [*Arabidopsis thaliana*]	CS	PEG	CK	PP	PEG
440	72903	CGPG5584	0	91	gi|6322293|	ref|NP_012367.1|Histone methyltransferase with a role in transcriptional elongation, methylates a lysine residue of histone H3; associates with the C-terminal domain of Rpo21p; histone methylation activity is regulated by phosphorylation status of Rpo21p; Set2p [*Saccharomyces cerevisiae*] sp|P46995|SET2_YEAST SET domain protein 2	PEG	PP	SS		
441	73017	CGPG5733	0	94	gi|6325368|	ref|NP_015436.1|kinase required for late nuclear division; Dbf20p [*Saccharomyces cerevisiae*]	PEG	PP	PEG		
442	74587	CGPG6774	0	94	gi|17938451|	ref|NP_535240.1|succinate semialdehyde dehydrogenase [*Agrobacterium tumefaciens* str. C58]	PEG	DS	HS	PP	SS
443	72453	CGPG4735	6.00E − 67	91	gi|15218924|	ref|NP_174236.1|auxin-responsive family protein [*Arabidopsis thaliana*] pir||A86417 probable auxin-induced protein, 45653-45228	CK	PP	SP	SS	
444	72967	CGPG5742	0	99	gi|6321525|	ref|NP_011602.1|Cytosolic catalase T, has a role in	CS	CK	HS	LL	PP	SS

TABLE 2-continued

Pep SEQ Id	construct id	gene	annotation e value	% identity	ncbi id	description	traits			
445	72961	CGPG5591	0	95	gi|15228498|	protection from oxidative damage by hydrogen peroxide; Ctt1p [*Saccharomyces cerevisiae*] ref|NP_186975.1|UTP-glucose-1-phosphate uridylyltransferase, putative/ UDP-glucose pyrophosphorylase, putative/UGPase, putative [*Arabidopsis thaliana*]	PEG	SS	HS	PP
446	73070	CGPG5627	0	90	gi|15225044|	ref|NP_181451.1|protein kinase family protein [*Arabidopsis thaliana*]	PEG	PP	SS	
447	73475	CGPG6385	0	100	gi|39934021|	ref|NP_946297.1|glyceraldehyde-3-phosphate dehydrogenase(GAPDH) [*Rhodopseudomonas palustris* CGA009]	PEG	PP	SS	
448	72916	CGPG1814	0	97	gi|15228871|	ref|NP_188303.1|protein phosphatase 2C, putative/ PP2C, putative [*Arabidopsis thaliana*]	PP	SS		
449	72969	CGPG5789	0	94	gi|6321886|	ref|NP_011962.1|Low-affinity glucose transporter of the major facilitator superfamily, expression is induced by Hxk2p in the presence of glucose and repressed by Rgt1p when glucose is limiting; Hxt1p [*Saccharomyces cerevisiae*]	PP	SP	SS	
450	74449	CGPG6659	0	96	gi|15890426|	ref|NP_356098.1|AGR_L_619p [*Agrobacterium tumefaciens* str. C58] pir||A98170 hypothetical protein AGR_L_619 [imported] - *Agrobacterium*	PP	SS		
451	16615	CGPG2539	0	98	gi|15890896|	ref|NP_356568.1|AGR_L_ 1560p [*Agrobacterium tumefaciens* str. C58] ref|NP_534561.1|glucose-1-phosphate adenylyltransferase [*Agrobacterium tumefaciens* str. C58]	PP			
452	19187	CGPG3310	0	91	gi|18423163|	ref|NP_568731.1|squamosa promoter-binding protein, putative [*Arabidopsis thaliana*]	PP			
453	19648	CGPG3134	1.00E − 179	96	gi|18413950|	ref|NP_568102.1|short-chain dehydrogenase/reductase (SDR) family protein [*Arabidopsis thaliana*]	PP			
454	70354	CGPG3995	0	64	gi|15241312|	ref|NP_196916.1|nodulin family protein [*Arabidopsis thaliana*]	DS	PP	SP	
455	70421	CGPG2942	0	88	gi|30677977|	ref|NP_178317.2|zinc finger (C2H2 type) family protein [*Arabidopsis thaliana*]	PP			
456	70459	CGPG3758	0	95	gi|15233315|	ref|NP_188242.1|F-box family protein [*Arabidopsis thaliana*] dbj|BAB01261.1| unnamed protein product [*Arabidopsis thaliana*]	PP			
457	70465	CGPG3775	1.00E − 155	90	gi|15236937|	ref|NP_195254.1|zinc finger (C2H2 type) family protein [*Arabidopsis thaliana*]	PP	SP		

TABLE 2-continued

Pep SEQ Id	construct id	gene	annotation e value	% identity	ncbi id	description	traits	
458	70683	CGPG4587	3.00E − 65	64	gi|18423239|	ref|NP_568751.1|polyadenylate-binding protein, putative/PABP, putative [*Arabidopsis thaliana*]	PP	
459	70725	CGPG2097	0	91	gi|18420505|	ref|NP_568066.1|expressed protein [*Arabidopsis thaliana*]	CS	PP
460	70852	CGPG1465	0	93	gi|15237075|	ref|NP_195290.1|isocitrate dehydrogenase, putative/ NAD+ isocitrate dehydrogenase, putative [*Arabidopsis thaliana*]	PP	SP
461	71112	CGPG934	1.00E − 130	94	gi|15218701|	ref|NP_171806.1|expressed protein [*Arabidopsis thaliana*] pir||E86161 F1003.11 protein- [*Arabidopsis thaliana*] gb|AAD25802.1|Belongs to the PF|01027 Uncharacterized protein family UPF0005 with 7 transmembrane domains. [*Arabidopsis thaliana*]	CS	PP
462	71127	CGPG945	0	97	gi|15225307|	ref|NP_179604.1|26S protease regulatory complex subunit 4, putative [*Arabidopsis thaliana*] pir||E84585 26S proteasome subunit 4 [imported]- *Arabidopsis thaliana*	PP	
463	71132	CGPG1561	0	98	gi|15232209|	ref|NP_191550.1|expressed protein [*Arabidopsis thaliana*]	PP	
464	71217	CGPG95	0	100	gi|15221476|	ref|NP_172127.1|shaggy-related protein kinase iota/ ASK-iota (ASK9) (GSK1) [*Arabidopsis thaliana*] (EC 2.7.1.-)	PP	
465	71645	CGPG4688	3.00E − 69	100	gi|18401105|	ref|NP_566544.1|phosphotransfer family protein [*Arabidopsis thaliana*]	PP	
466	71726	CGPG3894	0	93	gi|15217677|	ref|NP_171725.1|no apical meristem (NAM) family protein [*Arabidopsis thaliana*]	HS	PP
467	72432	CGPG4562	1.00E − 144	92	gi|20152540|	emb|CAD29662.1|putative auxin response factor 23 [*Arabidopsis thaliana*]	PP	SP
468	72450	CGPG4732	1.00E − 170	100	gi|15238890|	ref|NP_197366.1|zinc finger (C3HC4-type RING finger) family protein [*Arabidopsis thaliana*]	LL	PP
469	72455	CGPG4742	1.00E − 144	93	gi|15242893|	ref|NP_200597.1|anthranilate synthase beta subunit, putative [*Arabidopsis thaliana*]	PP	PEG
470	72727	CGPG5522	1.00E − 118	100	gi|6324107|	ref|NP_014177.1|functionally related to TFIIB, affects start site selection in vivo; Ssu72p [*Saccharomyces cerevisiae*]	PP	
471	72817	CGPG4987	0	96	gi|30679158|	ref|NP_567238.2|AAA-type ATPase family protein [*Arabidopsis*	PP	
472	72992	CGPG5777	0	90	gi|6324981|	ref|NP_015049.1|S-adenosylMethionine Permease; Sam3p [*Saccharomyces cerevisiae*]	PP	PEG

TABLE 2-continued

Pep SEQ Id	construct id	gene	annotation e value	% identity	ncbi id	description	traits	
473	73007	CGPG5760	0	93	gi|6320865|	ref|NP_010944.1|One of three possible beta-subunits of the Snf1 kinase complex, allows nuclear localization of the Snf1 kinase complex in the presence of a nonfermentable carbon source; contains glycogen-binding domain; Gal83p [*Saccharomyces cerevisiae*]	PP	
474	73073	CGPG5688	0	95	gi|16331010|	ref|NP_441738.1|fructose 1,6-bisphosphatase [*Synechocystis* sp. PCC 6803]	PP	
475	73506	CGPG6496	0	96	gi|23062569|	ref|ZP_00087347.1|COG1012: NAD-dependent aldehyde dehydrogenases [*Pseudomonas fluorescens* PfO-1]	PP	
476	74107	CGPG6590	0	95	gi|15965198|	ref|NP_385551.1|PYRUVATE DEHYDROGENASE ALPHA2 SUBUNIT PROTEIN [*Sinorhizobium meliloti* 1021]	PP	SS
477	74117	CGPG6575	0	81	gi|37528116|	ref|NP_931461.1|Phenylacetaldehyde dehydrogenase (PAD) [*Photorhabdus luminescens* subsp. *laumondii* TTO1]	CS	PP
478	74131	CGPG6592	0	96	gi|16329404|	ref|NP_440132.1|transaldolase [*Synechocystis* sp. PCC 6803] B -	PP	SS
479	74344	CGPG5929	1.00E − 111	100	gi|15236410|	ref|NP_193147.1|COP9 signalosome subunit, putative/CSN subunit, putative (CSN8) [*Arabidopsis thaliana*]	HS	PP
480	14320	CGPG1229	0	100	gi|18418018|	ref|NP_567894.1|expressed protein [*Arabidopsis thaliana*]	SP	
481	16756	CGPG2117	1.00E − 142	85	gi|18391249|	ref|NP_563885.1|expressed protein [*Arabidopsis thaliana*]	SP	
482	17448	CGPG2673	1.00E − 102	72	gi|15239624|	ref|NP_197993.1|PHD finger family protein [*Arabidopsis thaliana*] gb|AAM64729.1|nucleic acid binding protein-like [*Arabidopsis thaliana*]	SP	
483	17633	CGPG2839	1.00E − 145	85	gi|18395124|	ref|NP_564171.1|basic helix-loop-helix (bHLH) family protein [*Arabidopsis thaliana*]	SP	
484	18876	CGPG3096	1.00E − 172	89	gi|18394949|	ref|NP_564133.1|transporter-related [*Arabidopsis thaliana*] pir||G86343 hypothetical protein T22I11.10	SP	
485	19120	CGPG1976	0	100	gi|15232345|	ref|NP_188710.1|fertilization-dependent endosperm protein (FIE) [*Arabidopsis thaliana*]	SP	
486	19221	CGPG2958	1.00E − 159	78	gi|30690446|	ref|NP_182182.2|Dof zinc finger protein DAG2/Dof affecting germination 2 (DAG2) [*Arabidopsis thaliana*]	SP	
487	70206	CGPG4116	1.00E − 139	64	gi|18412918|	ref|NP_565249.1|phospholipid/glycerol acyltransferase family protein [*Arabidopsis*	SP	

TABLE 2-continued

Pep SEQ Id	construct id	gene	annotation e value	% identity	ncbi id	description		traits
488	70223	CGPG53	0	93	gi|15240313|	ref|NP_198006.1|hexose transporter, putative [*Arabidopsis thaliana*]	SP	
489	70347	CGPG3147	1.00E − 121	66	gi|18416267|	ref|NP_567693.1|Dof-type zinc finger domain-containing protein [*Arabidopsis thaliana*]	SP	
490	70406	CGPG1687	0	93	gi|18397470|	ref|NP_564354.1|early-responsive to dehydration stress protein (ERD4) [*Arabidopsis thaliana*]	SP	
491	70469	CGPG3791	1.00E − 171	89	gi|15237581|	ref|NP_198936.1|MADS-box family protein [*Arabidopsis thaliana*]	SP	HS
492	70564	CGPG1864	0	89	gi|15219067|	ref|NP_173589.1|SWIRM domain-containing protein/ DNA-binding family protein gb|AAD41423.1|Contains similarity to gb|AF033823 moira protein from *Drosophila melanogaster* and contains a PF|00249 Myb-like DNA-binding domain.	SP	
493	70601	CGPG2917	0	91	gi|15235140|	ref|NP_193702.1|zinc finger (C3HC4-type RING finger) family protein [*Arabidopsis thaliana*] pir||T04748 hypothetical protein T16H5.30 - *Arabidopsis thaliana*	SP	PP
494	70612	CGPG3721	0	96	gi|18416732|	ref|NP_568256.1|conserved oligomeric Golgi complex component-related/COG complex component-related [*Arabidopsis thaliana*]	SP	
495	70720	CGPG1358	0	93	gi|15238483|	ref|NP_198387.1|lectin protein kinase family protein [*Arabidopsis thaliana*]	SP	
496	70735	CGPG2661	1.00E − 109	100	gi|15231241|	ref|NP_187953.1|transcription initiation factor IID-1 (TFIID-1)/TATA-box factor 1/TATA sequence-binding protein 1 (TBP1) [*Arabidopsis thaliana*]	SP	
497	70846	CGPG377	1.00E − 151	100	gi|15221223|	ref|NP_177577.1|zinc finger (C3HC4-type RING finger) family protein [*Arabidopsis* thaliana] pir||D96772 probable RING zinc finger protein	SP	
498	70923	CGPG4020	0	87	gi|8132347|	gb|AAF73257.1|MAP kinase PsMAPK2 [*Pisum sativum*]	SP	
499	71149	CGPG3457	0	83	gi|20141566|	sp|P48001|HKL4_ARATH-Homeobox protein knotted-1 like 4 (KNAT4) pir||T51795 HOMEOBOX PROTEIN KNOTTED-1 LIKE 4 (KNAT4) -		
500	71608	CGPG4687	0	100	gi|15220438|	ref|NP_172008.1|ent-kaurenoic acid hydroxylase (KAO1)/cytochrome P450 88A3, putative (CYP88A3) [*Arabidopsis thaliana*]	SP	
501	71739	CGPG4345	7.00E − 89	80	gi|18406944|	ref|NP_566061.1|expressed protein [*Arabidopsis thaliana*]	SP	
502	72014	CGPG5230	0	100	gi|25410898|	pir||D84423probable WD-40-repeat protein [imported] -	SP	

TABLE 2-continued

Pep SEQ Id	construct id	gene	annotation e value	% identity	ncbi id	description	traits				
503	72051	CGPG5241	0	93	gi|18401606|	*Arabidopsis thaliana* gb|AAD14533.1|putative stress protein [*Arabidopsis thaliana*] ref|NP_566585.1|cyclic nucleotide-binding transporter 1/CNBT1 (CNGC20) [*Arabidopsis thaliana*] sp|Q9LD37|CG20_ARATH Probable cyclic nucleotide-gated ion channel 20, chloroplast precursor (Cyclic nucleotide-binding transporter 1)	SP				
504	74259	CGPG5343	0	96	gi|15222882|	ref|NP_175431.1|branched-chain amino acid aminotransferase 6/ branched-chain amino acid transaminase 6 (BCAT6) [*Arabidopsis thaliana*] s	CS	HS	SS		
505	72463	CGPG4760	8.00E − 48	100	gi|15236351|	ref|NP_193115.1|auxin-responsive protein, putative [*Arabidopsis thaliana*]	CS	SS	HS	LN	PP
506	72902	CGPG5597	0	88	gi|15240576|	ref|NP_199800.1|chloride channel protein (CLC-c) [*Arabidopsis thaliana*] sp|Q96282|CLCC_ARATH Chloride channel protein CLC-c (AtCLC-c)	SS	CS	DS		
507	74572	CGPG6640	1.00E − 109	93	gi|16331001|	ref|NP_441729.1|unknown protein [*Synechocystis* sp. PCC 6803]	CS	PP	SS		
508	73055	CGPG5768	0	97	gi|6321588|	ref|NP_011665.1|Hypothetical ORF; Ygr149wp [*Saccharomyces cerevisiae*]	SS	CS	HS		
509	74103	CGPG6558	0	99	gi|15833050|	ref|NP_311823.1|fructose-bisphosphate aldolase class II [*Escherichia coli* O157:H7] r	HS	PP	SS		
510	72921	CGPG5781	0	93	gi|6322892|	ref|NP_012965.1|general amino acid permease; Gap1p [*Saccharomyces cerevisiae*]	CK	PEG	SS		
511	72968	CGPG5772	0	99	gi|6321546|	ref|NP_011623.1|role in DNA replication during S phase; Clb6p [*Saccharomyces cerevisiae*]	PEG	LL	SS		
512	19703	CGPG4172	0	83	gi|7488676|	pir||T07150G-box binding factor 2A - soybean (fragment) gb|AAB00097.1| G-box binding factor	HS	SS			
513	19946	CGPG4097	1.00E − 46	34	gi|15219099|	ref|NP_175691.1|2-oxoglutarate-dependent dioxygenase, putative [*Arabidopsis thaliana*]	SS				
514	19980	CGPG3914	2.00E − 63	49	gi|28629811|	gb|AAO45179.1|transcription factor Myb1 [*Malus xiaojinensis*]	CS	SS			
515	70435	CGPG3701	1.00E − 150	91	gi|15236597|	ref|NP_193499.1|casein kinase II beta chain, putative [*Arabidopsis thaliana*]	SS	PP	SP		
516	71114	CGPG1657	0	88	gi|30680729|	ref|NP_849990.1|K+ efflux antiporter, putative (KEA4) [*Arabidopsis thaliana*]	SS				
517	72451	CGPG4733	0	94	gi|15239622|	ref|NP_197992.1|mitochondrial substrate carrier family	SS				

TABLE 2-continued

Pep SEQ Id	construct id	gene	annotation e value	% identity	ncbi id	description	traits		
						protein [*Arabidopsis thaliana*]			
518	72947	CGPG5607	3.00E − 62	53	gi|1483230|	emb|CAA67968.1|MADS4 protein [*Betula pendula*]	SS		
519	73012	CGPG5786	0	97	gi|6324187|	ref|NP_014257.1|belongs to a ubiquitous family of cytoplasmic membrane proteins that transport only ammonium (NH(4)(+) + NH(3)).; Mep2p [*Saccharomyces cerevisiae*]	SS		
520	73022	CGPG5622	0	86	gi|15225518|	ref|NP_182083.1|protein kinase family protein [*Arabidopsis thaliana*]	SS		
521	73488	CGPG6394	1.00E − 154	94	gi|16080620|	ref|NP_391447.1|UTP-glucose-1-phosphate uridylyltransferase [*Bacillus subtilis*]	SS	CS	PP
522	73901	CGPG5237	0	92	gi|18400284|	ref|NP_565553.1|extra-large guanine nucleotide binding protein/G-protein (XLG)	SS		
523	73964	CGPG5804	0	88	gi|6319773|	ref|NP_009855.1|Na+/Pi cotransporter, active in early growth phase; similar to phosphate transporters of *Neurospora crassa;* transcription regulated by inorganic phosphate concentrations and Pho4p; Pho89p [	SS		
524	74019	CGPG5706	2.00E − 92	100	gi|16079815|	ref|NP_390639.1|adenine phosphoribosyltransferase [*Bacillus subtilis*]	SS		
525	74022	CGPG5724	0	97	gi|18378991|	ref|NP_563659.1|glycosyl hydrolase family 3 protein [*Arabidopsis thaliana*]	SS	SP	
526	74114	CGPG6551	0	99	gi|15888903|	ref|NP_354584.1|AGR_C_2921p [*Agrobacterium tumefaciens* str. C58] pir||H97551 probable aminotransferase aatc	SS		
527	74262	CGPG5353	0	100	gi|18416245|	ref|NP_568226.1|histidinol-phosphate aminotransferase, putative [*Arabidopsis thaliana*]	SS	PP	
528	74292	CGPG5367	0	96	gi|15239204|	ref|NP_201393.1|U-box domain-containing protein [*Arabidopsis thaliana*]	SS		
529	74302	CGPG5384	1.00E − 59	82	gi|25313155|	pir||A96787protein F10A5.6 [imported] - *Arabidopsis thaliana*	PP	SS	
530	74325	CGPG5898	1.00E − 174	86	gi|15230382|	ref|NP_188576.1|cinnamyl-alcohol dehydrogenase (CAD) [*Arabidopsis thaliana*]	SS		
531	74429	CGPG6689	0	96	gi|16077873|	ref|NP_388687.1|acetoin dehydrogenase E1 component (TPP-dependent alpha subunit) [*Bacillus subtilis*]	SS		
532	74440	CGPG6682	6.00E − 90	82	gi|15613838|	ref|NP_242141.1|uridine kinase [*Bacillus halodurans* C-125]	SS		
533	74462	CGPG6668	5.00E − 67	99	gi|16332127|	ref|NP_442855.1|unknown protein [*Synechocystis* sp. PCC 6803]	HS	SS	
534	74465	CGPG6692	1.00E − 119	99	gi|16078642|	ref|NP_389461.1|similar to ribulose-5-phosphate 3-epimerase [*Bacillus subtilis*]	PP	SS	

TABLE 2-continued

Pep SEQ Id	construct id	gene	annotation e value	% identity	ncbi id	description	traits	
535	74474	CGPG6669	2.00E − 85	82	gi|16331209|	ref|NP_441937.1|unknown protein [*Synechocystis* sp. PCC 6803]	LL	SS
536	74505	CGPG6783	0	100	gi|16129426|	ref|NP_415984.1|cryptic nitrate reductase 2 beta subunit [*Escherichia coli* K12]	SS	
537	74507	CGPG6799	0	82	gi|27479656|	gb|AAO17183.1|Orf17 [*Photorhabdus luminescens*]	SP	SS
538	74562	CGPG6764	0	95	gi|16077501|	ref|NP_388315.1|similar to pyruvate oxidase [*Bacillus subtilis*]	SS	

Please note that this file doesn't have Table 3.

Screens for Identifying Trait Improving Genes

[0084] DS—Improvement of drought tolerance identified by a soil drought stress tolerance screen: Drought is a water deficit condition that imposes 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 drought tolerance-imparting DNA defined for this invention are used in recombinant DNA constructs that improve plant survival rate under drought conditions. Exemplary recombinant DNA which has been identified for conferring such drought tolerance is identified as such in Table 2. Such identified recombinant DNA is useful 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 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.

[0085] PEG-Improvement 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 et al., (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. Certain embodiments of transgenic plants with trait-improving recombinant DNA identified in the PEG-induced osmotic stress tolerance screen survive drought conditions providing a higher yield potential as compared to control plants.

[0086] SS-Improvement 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, (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. Exemplary recombinant DNA which has been identified to help plants maintain biomass, root growth and/or plant development in high salinity conditions are identified as such in Table 2. Since osmotic effect is one of the major components of salt stress, which is common to the drought stress, embodiments of trait-improving recombinant DNA identified in a high salinity stress tolerance screen also provide transgenic crops with improved drought tolerance. Embodiments of transgenic plants with trait-improving recombinant DNA identified in a high salinity stress tolerance screen survive drought conditions and/or high salinity conditions providing a higher yield potential as compared to control plants.

[0087] HS-Improvement 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 as heat stress tolerance conferring genes may also impart improved 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.

[0088] CK and CS-Improvement of tolerance to cold stress: Low temperature may immediately result in mechanical constraints, changes in activities of macromolecules, and reduced osmotic potential. 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 degrees C. from planting until day 28 post planting. 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 degrees

C. until day 8 post planting, and subsequently were placed under 8 degrees C. until day 28 post planting. 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 survive cold conditions providing a higher yield potential as compared to control plants.

[0089] Improvement 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, plants are enabled to react to different kinds of stresses. For examples, DNA for expressing proteins of SEQ ID NO:352 and SEQ ID NO:353 is useful to improve both heat stress tolerance and cold stress tolerance in plants. Plants transformed with DNa for expressing protein of SEQ ID NO:508 resist heat stress, salt stress and cold stress. Thus, the disclosed stress tolerance conferring genes are useful in combinations to generate transgenic plants that resist multiple stress conditions.

[0090] PP-Improvement of early plant growth and development: It is known in the art that to minimize the impact of disease on crop profitability, it is important to start the season with healthy 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" encompasses the stages of seed imbibition through the early vegetative phase. Certain DNA is identified as 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, genes conferring the growth advantage in early stages to plants are used to generate transgenic plants that are more resistant to various stress conditions due to improved early plant development. Exemplary recombinant DNA that confers both stress tolerance and growth advantages to plants, is identified as such in Table 2, e.g., DNA encoding a protein of SEQ ID NO:444 can improve the plant early growth and development, and impart heat and cold tolerance to plants. Embodiments of transgenic plants with trait-improving recombinant DNA identified in the early plant development screen grow better under non-stress conditions and/or stress conditions providing a higher yield potential as compared to control plants.

[0091] SP-Improvement of late plant growth and development: "Late growth and development" encompasses the stages of leaf development, flower production, and seed maturity. Transgenic plants with late growth and development advantages express DNA that is identified as such in Table 2. Such plants 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. For example, 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. 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. Embodiments of transgenic plants with trait-improving recombinant DNA identified in the late development screen grow better and/or have improved development during leaf development and seed maturation providing a higher yield potential as compared to control plants.

[0092] LL-Improvement 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. Recombinant DNA that enables plants to have an attenuated shade avoidance response so that the source of plant can be contributed to reproductive growth efficiently provides embodiments of those plants with higher yield as compared to the wild type plants. Embodiments of transgenic plants with trait-improving recombinant DNA identified in a shade stress tolerance screen have attenuated shade response under shade conditions providing a higher yield potential as compared to control plants. The transgenic plants generated by this invention are suitable for a higher density planting, thereby resulting increased yield per unit area.

[0093] LN-Improvement of Tolerance to Low Nitrogen Availability Stress

[0094] 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.

[0095] Recombinant DNA that imparts enhanced nitrogen use efficiency in transgenic plants is identified in Table 2. Such plants exhibit one or more desirable traits including,

but not limited to, increased seedling weight, increased number of green leaves, increased number of rosette leaves, altered root length and advanced flower bud formation. Such plants can also have altered amino acid or protein compositions, increased yield and/or better seed quality. Embodiments of such transgenic plants are productively cultivated under nitrogen nutrient deficient conditions, i.e., nitrogen-poor soils and low nitrogen fertilizer inputs that cause the growth of wild type plants to cease or to be so diminished as to make the wild type plants practically useless under such conditions. The transgenic plants also are 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.

[0096] Stacked Traits: This invention also provides transgenic plants with stacked engineered traits, e.g., a crop having an improved 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 glyphosate resistance trait, or insect resistance, such as using a gene from *Bacillus thuringiensis* 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. 2003-0106096 A1 and 2002-0112260 A1 and U.S. Pat. Nos. 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. Pat. Nos. 5,250,515 and 5,880,275 which disclose plants expressing an endotoxin of *Bacillus thuringiensis* bacteria, to U.S. Pat. No. 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. Pat. No. 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.

[0097] Once one recombinant DNA has been identified as conferring an improved trait of interest in transgenic *Arabidopsis* plants, several methods are available for using the sequence of that recombinant trait-imparting DNA and knowledge about the protein it encodes to identify homologs of that sequence from the same plant and different plant species or other organisms, e.g., bacteria and yeast. Thus, in one aspect, this invention provides methods for identifying a homologous gene with a DNA sequence homologous to any of SEQ ID NO:1 through SEQ ID NO:269, or a homologous protein with an amino acid sequence homologous to any of SEQ ID NO:270 through SEQ ID NO:538. In another aspect, this invention provides a consensus amino acid sequence for respective homologs for each of SEQ ID NO:270 through SEQ ID NO:538. In yet another aspect, this invention also includes linking or associating one or more desired traits, or gene function with a homolog sequence disclosed herein.

[0098] The trait-improving recombinant DNA and methods of using such trait-improving recombinant DNA for generating transgenic plants with improved traits provided by this invention are not limited to any particular plant species. Indeed, the plants of this invention encompass many species of monocots and dicots and include agriculturally useful plants which are cultivated for purposes of food production or industrial applications, e.g., corn and soybean plants and cotton plants. Recombinant DNA constructs optimized for soybean transformation and recombinant DNA constructs optimized for corn transformation are disclosed in the following examples. Other plants of this invention include canola, wheat, sunflower, sorghum, alfalfa, barley, millet, rice, tobacco, fruit and vegetable crops, and turfgrass.

[0099] Thus, embodiments of this invention include the use of both DNA identified in Table 3 and homologs in recombinant DNA for transgenic crop plants with improved traits. Transgenic crop plants with improved traits are identified from populations of plants grown from transgenic events by screening to segregate the plants of this invention from plants without the improved traits. Preferred screens for transgenic crop plants identify plants with improved responses to stress conditions, e.g., assays using imposed stress conditions to detect improved responses to drought stress, nitrogen deficiency, cold growing conditions, or alternatively, under naturally present stress conditions, for example under field conditions. Biomass measures are made on greenhouse or field grown plants and include such measurements as plant height, stem diameter, root and shoot dry weights, and, for corn plants, ear length and diameter.

[0100] Trait data on morphological changes is 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 are 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, barrenness/prolificacy, green snap, and pest resistance. In addition, trait characteristics of harvested grain are 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.

[0101] To confirm hybrid yield in transgenic corn plants expressing trait-imparting DNA of this invention, it is useful to test hybrid plants over multiple years at multiple locations in a geographical location where corn is conventionally grown, e.g., in Iowa, Illinois and Kansas, under "normal" field conditions as well as under stress conditions, e.g., under drought or population density stress.

[0102] Transgenic crop plants are used to provide other aspects of this invention such as transgenic seeds of crop

plants. Seeds of transgenic plants are used to propagate more progeny plants which contain the trait-improving recombinant DNA constructs of this invention. These progeny plants are within the scope of this invention when 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.

Screening Methods for Crop Transgenic Plants with Enhanced Agronomic Trait

[0103] Due to variability in transformation many transgenic events which survive to fertile transgenic plants that produce seeds and progeny plants do not exhibit an enhanced agronomic trait. Thus, screening is necessary to identify the transgenic events that produce the transgenic plants and seeds of this invention. Transgenic crop plants having enhanced traits are identified from populations of plants transformed as described herein by evaluating the trait in a variety of assays to detect an enhanced agronomic trait. Useful assays include analyses to detect changes in the chemical composition, biomass, physiological properties and morphology of the plant. Changes in chemical compositions such as nutritional composition of grain are detected by analysis of the seed composition and content of protein, free amino acids, oil, free fatty acids, starch or tocopherols. Changes in biomass characteristics are detected in greenhouse or field grown plants and include plant height, stem diameter, root and shoot dry weights; and, for corn plants, ear length and diameter. Changes in physiological properties are identified by evaluating responses to stress conditions, e.g., assays using imposed stress conditions such as water deficit, nitrogen deficiency, cold growing conditions, pathogen or insect attack or light deficiency, or increased plant density. Changes in morphology are measured by visual observation of tendency of a transformed plant with an enhanced agronomic trait to also appear to be a normal plant as compared to changes toward bushy, taller, thicker, narrower leaves, striped leaves, knotted trait, chlorosis, albino, anthocyanin production, or altered tassels, ears or roots. Other screening properties include 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, barrenness/prolificacy, green snap, and pest resistance. In addition, phenotypic characteristics of harvested grain are evaluated, 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.

[0104] Seeds for transgenic crop plants with enhanced agronomic traits of this invention are corn, soybean and cotton seeds, as well as seeds for canola, wheat, sunflower, sorghum, alfalfa, barley, millet, rice, tobacco, fruit and vegetable crops, and turfgrass.

A. Screening for Nitrogen Use Efficiency

[0105] Many transgenic crop plants of this invention exhibit enhanced nitrogen use efficiency as compared to control plants. Higher nitrogen soil applications increase seed protein and starch accumulation, and lead to larger seed weight and larger kernel number per ear. Recent improvements in elite high yielding corn hybrid genotypes include the ability to utilize nitrogen efficiently. DNA causing the enhanced nitrogen use efficiency in crop plants are especially useful, e.g., for improving yield. Enhanced nitrogen use efficiency is assessed by measuring changes in plant growth such as leaf area production, shoot biomass, chlorophyll content in plants grown in nitrogen limiting conditions and/or nitrogen sufficient conditions. It is useful to conduct a first screen in nitrogen limiting conditions and confirm replicate transgenic events in both nitrogen limiting and nitrogen sufficient conditions. Table 4 shows an amount of nutrients in the nutrient solution for nitrogen limiting conditions (low N) and nitrogen sufficient conditions (high N) which are useful for nitrogen use efficiency screening. For example in a greenhouse screen pots of transgenic plants and control plants are treated with 100 ml of nutrient solution three times a week on alternate days starting at 8 and 10 days after planting for high N and low N screening, respectively.

TABLE 4

Nutrient stock	2 mM NH_4NO_3 Low nitrogen	20 mM NH_4NO_3 High nitrogen
1 M NH_4N0_3	2 mL/L	20 mL/L
1 M KH_2PO_4	0.5	0.5
1 M $MgSO_4.7H_2O$	2	2
1 M $CaCl_2$	2.5	2.5
1 M K_2SO_4	1	1

Note:
Adjust pH to 5.6 with HCl or KOH

After 28 days of plant growth for low N screening and 23 days for high N screening, measurements are taken for total shoot fresh mass, leaf chlorophyll, leaf area, leaf fresh mass and leaf dry mass.

B. Screening for Increased Yield

[0106] Many transgenic plants of this invention exhibit improved yield as compared to a control plant. Improved yield can result from a variety or other traits such as enhanced seed sink potential, e.g., the number and size of endosperm cells or kernels, and/or enhanced sink strength, e.g., the rate of starch biosynthesis. Sink potential is established very early during kernel development, as endosperm cell number and cell size are determined within the first few days after pollination.

[0107] Much of the increase in corn yield of the past several decades has resulted from an increase in planting density. During that period, corn yield has been increasing at a rate of 2.1 bushels/acre/year, but the planting density has increased at a rate of 250 plants/acre/year. A characteristic of modern hybrid corn is the ability of these varieties to be planted at high density. Many studies have shown that a higher than current planting density should result in more biomass production, but current germplasm does not perform well at these higher densities. One approach to increasing yield is to increase harvest index (HI), the proportion of biomass that is allocated to the kernel compared to total biomass, in high density plantings.

[0108] Effective yield screening of transgenic corn uses hybrid progeny of the transgenic event 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. Useful screening in multiple and diverse geographic locations, e.g., up to 16 or more locations, over one or more planting seasons, e.g., at least two planting seasons, is useful to statistically distinguish yield improvement from natural environmental effects. Useful hybrid screening includes planting multiple transgenic plants, positive and negative control plants, and pollinator plants in standard plots, e.g., 2 row plots, 20 feet long by 5 feet wide with 30 inches distance between rows and a 3 foot alley between ranges. Plants from separate transgenic events can be grouped by recombinant DNA constructs with groups randomly placed in the field. A pollinator plot of a high quality corn line is planted for every two plots to allow open pollination when using male sterile transgenic events. A useful planting density is about 30,000 plants/acre.

[0109] Surrogate indicators for screening for yield improvement include source capacity (biomass), source output (sucrose and photosynthesis), sink components (kernel size, ear size, starch in the seed), development (light response, height, density tolerance), maturity, early flowering trait and physiological responses to high density planting, e.g., at 45,000 plants per acre.

[0110] When screening for yield improvement a useful statistical measurement approach comprises three components, i.e., modeling spatial autocorrelation of the test field separately for each location, adjusting traits of recombinant DNA events for spatial dependence for each location, and conducting an across location analysis.

[0111] A first step in modeling spatial autocorrelation is estimating the covariance parameters of the semivariogram. A spherical covariance model is assumed to model the spatial autocorrelation. Because of the size and nature of the trial, it is likely that the spatial autocorrelation may change. Therefore, anisotropy is also assumed along with spherical covariance structure. The following set of equations describes the statistical form of the anisotropic spherical covariance model.

$$C(h;\theta) = vI(h=0) + \sigma^2\left(1 - \frac{3}{2}h + \frac{1}{2}h^3\right)I(h<1),$$

where I(•) is the indicator function, $h=\dot{x}^2+\dot{y}^2$, and

$$\dot{x}=[\cos(\rho\pi/180)(x_1-x_2)-\sin(\rho\pi/180)(y_1-y_2)]/\omega_x$$

$$\dot{y}=[\sin(\rho\pi/180)(x_1-x_2)+\cos(\rho\pi/180)(y_1-y_2)]/\omega_y$$

where $s_1=(x_1, y_1)$ are the spatial coordinates of one location and $s_2=(x_2, y_2)$ are the spatial coordinates of the second location. There are 5 covariance parameters, $\theta=(v, \sigma^2, \rho, \omega_n, \omega_j)$, where v is the nugget effect, σ^2 is the partial sill, ρ is a rotation in degrees clockwise from north, ω_n is a scaling parameter for the minor axis and ω_j is a scaling parameter for the major axis of an anisotropical ellipse of equal covariance. The five covariance parameters that define the spatial trend will then be estimated by using data from heavily replicated pollinator plots via restricted maximum likelihood approach. In a multi-location field trial, spatial trend are modeled separately for each location.

[0112] After obtaining the variance parameters of the model, a variance-covariance structure is generated for the data set to be analyzed. This variance-covariance structure contains spatial information required to adjust yield data for spatial dependence. In this case, a nested model that best represents the treatment and experimental design of the study is used along with the variance-covariance structure to adjust the yield data. During this process the nursery or the seed batch effects can also be modeled and estimated to adjust the yields for any yield parity caused by seed batch differences.

[0113] After spatially adjusted data from different locations are generated, all adjusted data is combined and analyzed assuming locations as replications. In this analysis, intra and inter-location variances are combined to estimate the standard error of yield from transgenic plants and control plants. Relative mean comparisons are used to indicate statistically significant yield improvements.

C. Screening for Water Use Efficiency

[0114] Many transgenic crop plants of this invention exhibit improved yield resulting from improved water use efficiency and/or drought tolerance.

[0115] A greenhouse screen for transgenic corn plants for water use efficiency measures changes in plant growth rate, e.g., at least a 10% improvement, in height and biomass during a vegetative drought treatment, as compared to control plants. The hydration status of the shoot tissues following the drought is also measured. Shoot Initial Height (SIH) is plant height after 3 weeks of growth under optimum conditions. Shoot Wilt Height (SWH) is plant height at the end of a 6 day drought. Time course experiments have shown that at about 3 days of drought, wild type plants basically stop growing and begin to wilt. Thus a transgenic plant with improved water use efficiency will continue to grow (probably to a lesser extent than with water) and thereby end up as a significantly taller plant at the end of a drought experiment. Shoot Wilt Mass (SWM) is the amount of wet and dry matter in the shoot (plant separated from root ball at the soil line) at the end of the drought; SDM is measure after 2 to 3 weeks in a drying chamber. Shoot Turgid mass (STM) is the SWM plus the mass of the water that is transported into plant tissues in 3 days of soaking in 40 degree C. water in the dark. Experiments show that most of the water is pulled up in 24 hours but it takes 2 more days before additional increase becomes insignificant. STM-SWM is indicative of water use efficiency in plants where recovery from stress is more important than stress tolerance per se. Relative water content (RWC) is a measurement of how much (%) of the plant is water at harvest. RWC=(SWM−SDM)/(STM−SDM)*100. Fully watered corn plants are about 98% RWC. Typically, in a wilt screen the plants are about 60% RWC. Plants with higher RWC at the end of a drought are considered to be healthier plants and more fit for post-drought recovery and growth.

[0116] Relative Growth Rate (RGR) is calculated for each shoot using the formula RGR=(SWH−SIH)/((SWH+SIH)/2)*100

D. Screening for Growth Under Cold Stress

[0117] Many transgenic crop plants of this invention exhibit improved growth under cold stress, e.g., in a cold germination assay, in a cold shock assay, in an early seedling growth assay and in root-shoot biomass assay.

[0118] In a cold germination assay transgenic seeds from transgenic plants, e.g., R2 inbred seeds or F1 hybrid seeds,

seeds of two types of control plants, e.g., negative segregants from the transgenic event or wild type, non-transgenic seeds of the transformed genotype, are treated with fungicide. A useful fungicide such as Captan fungicide (available from Arvesta Corp as MAESTRO® 80DF Fungicide) is applied at the rate of 0.43 mL Captan per 45 g of corn seeds which are dried to provide fungicide-coated seeds.

[0119] In a useful cold screen for transgenic corn seeds ten seeds per transgenic event are placed on filter paper (e.g., Whatman No. 1) in the lid of a Petri dish with 5 ml of water. A closed Petri dish is placed in a growth chamber set at 11 degrees C. for inbred corn seed or 9.5 degrees C. for hybrid corn seed. 2 ml of water is added on day 3 and day 10. Seeds are considered germinated if the emerged radicle size is 1 cm. Cold seeds are scored every 2 days from day 10 up to day 30. Tissue samples are collected at random on the last day of the experiment for confirmation of RNA expression. A germination index (GI) is calculated as

$$GI=(\Sigma([T+1-n_i]*[P_i-P_{i-1}]))/T$$

where "T" is the number of days for the experiment, "n" is the number of days after start, "i" is number of times germination is counted including the current day, "P" is the percentage of seed germinated during any given rating. Statistical differences are calculated between positive and wild type control.

[0120] In a cold shock assay, seeds are planted in potting media and placed in a growth chamber set at 23 degrees C., relative humidity of 65% with 12 hour day and night photoperiod (300 uE/m2-min). Planted seeds are watered for 20 minute every other day by sub-irrigation and flats are rotated every third day. On day 10 after planting the transgenic positive and wild type control plants are positioned in flats in an alternating pattern. Chlorophyll fluorescence of plants is measured on the tenth day during the dark period of growth by using a Walz PAM-2000 portable fluorometer following manufacturer's instructions. After chlorophyll measurements, leaf samples from each event are collected for confirming the expression of recombinant DNA. The plants are then exposed to temperatures of 5 degrees C. for 4 days. On the fourth day chlorophyll fluorescence is measured and plants are restored to a 23 degrees C. environment for recovery over 3 days. During the recovery period the length of the V3 leaf is measured on the first and third days. After two days of recovery V2 leaf damage is determined visually by estimating percent of green V2 leaf. Statistical differences in V3 leaf growth, V2 leaf necrosis and fluorescence during pre-shock and cold shock can be used for estimation of cold shock damage on corn plants.

[0121] In an early seedling growth assay three sets of seeds are assayed. The first set is a group of transgenic seeds from transgenic plants; the second set is negative segregants of the transgenic seed; and the third seed set is seed from two cold tolerant and two cold sensitive wild-type controls. All seeds are treated with a fungicide as indicated above. Seeds are grown in germination paper (12 inch×18 inch pieces of Anchor Paper #SD7606), wetted in a solution of 0.5% KNO_3 and 0.1% Thyram. For each paper fifteen seeds are placed on the line evenly spaced such that the radicles will grow toward the same edge. The wet paper is rolled up evenly and tight enough to hold the seeds in place. The roll is secured into place with two large paper clips, one at the top and one at the bottom. The rolls are incubated in a growth chamber at 23 degrees C. for three days in a randomized complete block design within an appropriate container. The chamber is set for 65% humidity with no light cycle. For the cold stress treatment the rolls are then incubated in a growth chamber at 12 degrees C. for fourteen days. The chamber is set for 65% humidity with no light cycle. For the warm treatment the rolls are incubated at 23 degrees C. for an additional two days. After the treatment the germination papers are unrolled and the seeds that did not germinate are discarded. The lengths of the radicle and coleoptile for each seed are measured. A coleoptile sample is collected from six individual kernels of each entry for confirming the expression of recombinant DNA. Statistical differences in the length of radicle and shoot during pre-shock and cold shock are used for an estimation of the effect of the cold treatment on corn plants. The analysis is conducted independently for the warm and cold treatments.

[0122] In a root-shoot biomass assay two sets of seeds are used. The first set is transgenic seeds with recombinant DNA, e.g., R2 inbred seeds or F1 hybrid seeds; the second seed set is non-transgenic, wild type negative control made from the same genotypes as the transgenic seeds. All seeds are treated with a fungicide as indicated above. The seeds are planted in potting media in pots arranged in a randomized complete block design with 6 replications. Pots are watered as and when needed by filling water up to the brim of the pot. Plants are grown in a greenhouse to a V6 stage or approximately for 28 days. Greenhouse lights are turned on after emergence of seedlings with 14 hours of light 10 hours of dark. Plants are fertilized twice each week with water-soluble fertilizer containing 200-ppm nitrogen. For measurement of root and shoot dry weight, two pots are separated carefully to remove adhering sand by washing with water. Washed roots are cut at the first node. The roots are placed in a paper bag after squeezing excess water, folded once and stapled. The shoots are then folded up to a convenient size (approximately 15 cm), placed in a paper bag. Bags are placed over a wire shelve to facilitate drying in a ventilated room maintained at 120 degrees F. to a moisture content of about 13% then weighed to determine dried root and shoot biomass.

E. Screen for Enhanced Oil, Starch, or Protein Levels in Plant Seeds

[0123] Oil concentrations are determined in kernels by Near Infrared Transmittance (NIT) from inbred and from hybrid lines. Data are also obtained for protein and starch content from this measurement.

[0124] Inbred Kernel Oil Screen

[0125] The primary transformants are selfed to produce R1 seed which is planted to segregating seed. An untransformed control line is planted every sixth row. All plants are self-pollinated. A molecular assay is conducted to determine zygosity of the transgene in each plant. Ears are harvested at maturity, and well-filled ears are chosen for proximate analysis. Proximate analysis is conducted on up to 5 homozygous ears. If 5 good homozygous ears are not available, then hemizygous ears will be used to obtain 5 good transgene-positive ears. Statistical analysis is conducted to determine whether proximate values for transgenic events are different from controls. Events with an increase in oil with a p-value of less than or equal to 0.1 are termed

"putative leads." Kernel composition is confirmed in an inbred confirmation nursery which is conducted with selected events, and is run with a design similar to that of the Gen2 nursery. A "confirmed lead event" demonstrates an increase in oil with a p-value of less than or equal to 0.1 in two nurseries.

[0126] Hybrid Kernel Oil Screen

[0127] Grain samples from the multilocation hybrid yield trials are collected at the time of harvest and are analyzed by NIT. Controls are negative segregants, untransformed controls, or pollinators. Data from 3 to 12 locations are pooled for the statistical analysis. Putative leads have increased oil with a p-value of less than or equal to 0.1.

[0128] The various aspects of the invention are illustrated by means of the following examples which are in no way intended to limit the full breath and scope of claims.

Example 1

Identification of Recombinant DNA that Confers Improved Trait(s) to Plants

A. Expression Constructs for *Arabidopsis* Plant Transformation

[0129] 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. Pat. No. 5,359,142) directly or indirectly (Moore, et al., PNAS 95:376-381, 1998; Guyer, et al., 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, et al., 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

[0130] 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

[0131] 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.

[0132] 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.

[0133] 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.

[0134] 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-transgenic 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, Wash., USA). Table 5 provides a list of recombinant DNA constructs that improve drought tolerance in transgenic plants.

TABLE 5

Pep				Wilt Response Risk score			Seed Weight/ plant			Survival Analysis of wilt response		
SEQ ID	Construct_id	Gene	Orientation	RS mean	p-value	c	delta	p-value	c	diff time to wilting	p-value	c
319	10139	CGPG101	ANTI-SENSE	0.115	0.024	S	−0.123	0.804	/	−0.01	0.469	/
320	11410	CGPG103	SENSE	0.226	0.003	S	−0.366	0.926	/	0	1	/
321	11604	CGPG48	ANTI-SENSE	0.25	0.034	S	0.257	0.01	S	−0.24	0.38	/

TABLE 5-continued

Pep SEQ ID	Construct_id	Gene	Orientation	Wilt Response Risk score RS mean	p-value	c	Seed Weight/plant delta	p-value	c	Survival Analysis of wilt response diff time to wilting	p-value	c
322	12368	CGPG1006	SENSE	0.148	0.044	S	0.359	0.02	S	−0.06	0.764	/
323	13502	CGPG1354	SENSE	0.431	0	S	0.624	0	S	1.34	0.366	/
324	13745	CGPG1576	ANTI-SENSE	−0.021	0.711	/	0.664	0	S	−0.29	0.453	/
325	13821	CGPG1569	SENSE	0.135	0.025	S	0.128	0.402	/	0.24	0.972	/
326	14240	CGPG1697	SENSE	0.377	0.002	S	−1.305	0.991	/	0	1	/
327	14718	CGPG1082	SENSE	0.168	0.001	S	0.135	0.351	/	0.25	0.208	/
328	17022	CGPG1774	SENSE	0.06	0.124	T	0.563	0.043	S	0	0.961	/
329	17924	CGPG2882	SENSE	−0.093	0.914	/	0.288	0.021	S	0.09	0.935	/
330	18259	CGPG3368	SENSE	0.07	0.28	/	0.391	0.058	T	−0.27	0.591	/
331	19171	CGPG2952	SENSE	0.227	0.005	S	0.846	0.001	S	0.12	0.543	/
332	19201	CGPG2332	SENSE	0.124	0.027	S	−0.435	0.785	/	0.35	0.256	/
333	19317	CGPG3662	SENSE	0.338	0	S	−0.071	0.61	/	0.63	0.106	T
334	70417	CGPG3427	SENSE	0.253	0.016	S	−1.424	0.984	/	0	1	/
315	70427	CGPG3067	SENSE	−0.033	0.818	/	1.004	0.002	S	0.01	0.977	/
335	70467	CGPG3785	SENSE	0.127	0.023	S	−0.448	0.946	/	0.71	0.046	S
336	70806	CGPG712	SENSE	0.246	0.046	S	0.174	0.276	/	0.14	0.07	T
337	70818	CGPG479	SENSE	0.07	0.115	T	0.558	0.009	S	0.61	0.283	/
338	70820	CGPG655	SENSE	0.172	0.048	S	0.036	0.441	/	0.26	0.554	/
339	70919	CGPG4029	SENSE	0.167	0.009	S	−0.565	0.904	/	0.31	0.508	/
340	71623	CGPG4696	SENSE	0.158	0.047	S	0.421	0.04	S	0	1	/
390	71633	CGPG857	SENSE	0.121	0.017	S	−0.823	0.967	/	0.45	0.139	T
341	71662	CGPG4679	SENSE	0.063	0.013	S	−0.037	0.631	/	0.16	0.957	/
342	71693	CGPG4652	SENSE	0.074	0.042	S	0.246	0.06	T	0.34	0.616	/
316	71811	CGPG4426	SENSE	0.359	0.015	S	−0.729	0.903	/	0.15	0.822	/
318	72081	CGPG5279	SENSE	0.269	0.005	S	−0.372	0.987	/	0.17	0.404	/
343	72384	CGPG4639	SENSE	0.133	0.018	S	0.62	0.002	S	0.17	0.359	/
344	72439	CGPG5075	SENSE	0.175	0.013	S	−0.035	0.604	/	0.23	0.244	/
374	72456	CGPG4745	SENSE	0.53	0.01	S	−0.737	0.979	/	−0.08	0.823	/
345	72619	CGPG4835	SENSE	0.178	0.039	S	0.219	0.072	T	0.96	0.691	/
346	72624	CGPG4842	SENSE	0.163	0.021	S	0.356	0.051	T	0.3	0.375	/
347	72715	CGPG5521	SENSE	0.082	0.1	T	0.767	0.002	S	0.12	0.628	/
348	72754	CGPG5548	SENSE	0.131	0.031	S	−0.365	0.974	/	0	0.923	/
349	72819	CGPG4989	SENSE	0.094	0.026	S	0.362	0.069	T	0.03	0.83	/
350	75516	CGPG7689	SENSE	0.067	0.066	T	0.965	0.001	S	0.24	0.464	/
351	75701	CGPG7856	SENSE	0.147	0.006	S	0.986	0.015	S	0.15	0.448	/
317	73463	CGPG6384	SENSE	0.174	0.048	S	−1.359	0.959	/	0.09	0.984	/
454	70354	CGPG3995	SENSE	−0.005	0.563	/	0.444	0.002	S	10.29	0.9	/
397	71840	CGPG4353	SENSE	0.142	0.007	S	−0.212	0.859	/	9.29	0.99	/
506	72902	CGPG5597	SENSE	0.009	0.162	T	0.034	0.2	T	5	1	/
437	73549	CGPG6460	SENSE	0.119	0.037	S	−0.774	0.949	/	6.26	0.25	/
302	73586	CGPG6471	SENSE	0.003	0.451	/	0.588	0.002	S	6.34	0.723	/
442	74587	CGPG6774	SENSE	0.262	0.001	S	−0.117	0.574	/	7.49	0.041	S
388	74652	CGPG6168	SENSE	0.475	0	S	−0.766	0.92	/	7.48	0	S

S: represents that the transgenic plants showed statistically significant trait improvement as compared to the reference ($p < 0.05$, 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)
T: represents that the transgenic plants showed a trend of trait improvement as compared to the reference with $p < 0.2$
/: represents the transgenic plants didn't show any alteration or had unfavorable change in traits examined as compared to the reference in the current dataset.

C. Heat Stress Tolerance Screen

[0135] 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.

[0136] T2 seeds were plated on ½× 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 $\mu mol/m^2/s$. 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.

[0137] 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 1 mm (Boyes, et al., (2001) The Plant Cell 13, 1499-1510). The growth stage data was analyzed as a qualitative response according to example 1L. Table 6 provides a list of recombinant DNA constructs that improve heat tolerance in transgenic plants.

TABLE 6

Pep SEQ ID	Construct_id	Gene	Orientation	Growth stage RS mean	Growth stage p-value	Growth stage c	Root Length delta	Root Length p-value	Root Length c	Seedling Weight delta	Seedling Weight p-value	Seedling Weight c
354	19542	CGPG3069	SENSE	0.842	0.021	S	0.296	0.023	S	1.616	0	S
355	19618	CGPG3574	SENSE	1.072	0.005	S	0.328	0.006	S	1.569	0	S
356	19649	CGPG3140	SENSE	0.72	0.042	S	0.243	0.054	T	1.665	0	S
357	19745	CGPG3973	SENSE	0.65	0.016	S	0.19	0.021	S	1.505	0	S
358	19768	CGPG4096	SENSE	1.06	0.035	S	0.17	0.034	S	1.171	0	S
436	19771	CGPG4011	SENSE	0.822	0.023	S	0.201	0.001	S	1.43	0	S
359	19772	CGPG3939	SENSE	0.247	0.014	S	0.151	0.014	S	1.344	0	S
360	19779	CGPG4113	SENSE	0.605	0.051	T	0.181	0.003	S	1.436	0	S
361	19833	CGPG4074	SENSE	0.965	0.026	S	0.266	0.007	S	1.01	0	S
362	19862	CGPG3961	SENSE	0.341	0.119	T	0.132	0.007	S	1.22	0	S
363	19879	CGPG4009	SENSE	0.734	0.002	S	0.22	0.001	S	1.499	0	S
364	70445	CGPG3728	SENSE	0.413	0.062	T	0.148	0.114	T	1.249	0	S
365	70738	CGPG3195	SENSE	0.687	0.055	T	0.205	0.041	S	1.261	0	S
366	71437	CGPG4043	SENSE	0.094	0.198	T	0.092	0.064	T	1.301	0	S
367	71572	CGPG4520	SENSE	0.938	0.052	T	0.441	0	S	1.633	0	S
368	71617	CGPG1227	SENSE	0.809	0.012	S	0.143	0.029	S	1.05	0.003	S
408	72085	CGPG5228	SENSE	1.234	0.02	S	0.192	0.043	S	1.162	0	S
369	72532	CGPG4780	SENSE	1.028	0.022	S	0.198	0.052	T	1.043	0.001	S
409	72744	CGPG5563	SENSE	0.17	0.146	T	0.04	0.359	/	0.827	0.004	S
370	72757	CGPG5572	SENSE	1.82	0.004	S	0.14	0.091	T	1.121	0	S
407	72771	CGPG2166	SENSE	1.776	0.001	S	0.36	0	S	1.428	0	S
444	72967	CGPG5742	SENSE	0.273	0.063	T	0.147	0.102	T	1.03	0	S
410	73039	CGPG810	SENSE	−0.048	0.774	/	−0.135	0.957	/	0.59	0.022	S
411	73054	CGPG5754	SENSE	0.055	0.312	/	0.236	0.001	S	1.434	0	S
508	73055	CGPG5768	SENSE	0.154	0.123	T	0.269	0	S	1.524	0	S
371	73412	CGPG6448	SENSE	0.187	0.118	T	0.134	0.06	T	1.181	0	S
412	73501	CGPG6456	SENSE	1.6	0.003	S	0.081	0.136	T	1.119	0	S
352	73515	CGPG6473	SENSE	−0.037	0.758	/	−0.024	0.604	/	0.694	0.008	S
437	73549	CGPG6460	SENSE	2.612	0	S	0.199	0.017	S	1.432	0	S
372	74102	CGPG6550	SENSE	0.34	0.035	S	0.268	0.002	S	1.355	0	S
509	74103	CGPG6558	SENSE	−0.013	1	/	−0.021	0.608	/	0.86	0	S
353	74684	CGPG6360	SENSE	0.44	0.018	S	0.254	0.002	S	1.383	0	S
512	19703	CGPG4172	SENSE	0.211	0.079	T	0.059	0.301	/	1.262	0	S
273	70423	CGPG3165	SENSE	1.456	0	S	0.418	0	S	1.912	0	S
491	70469	CGPG3791	SENSE	0.143	0.28	/	0.028	0.349	/	1.001	0.001	S
434	70932	CGPG4089	SENSE	0.354	0.1	T	0.03	0.419	/	1.254	0	S
419	71134	CGPG817	SENSE	0.522	0.106	T	0.077	0.248	/	1.225	0	S
466	71726	CGPG3894	SENSE	0.196	0.225	/	0.082	0.2	T	1.243	0	S
505	72463	CGPG4760	SENSE	1.182	0.003	S	0.202	0.026	/	1.702	0	S
445	72961	CGPG5591	SENSE	1.195	0.013	S	0.106	0.105	T	1.084	0	S
306	74136	CGPG6632	SENSE	0.886	0.012	S	0.306	0.009	S	1.42	0	S
504	74259	CGPG5343	SENSE	1.044	0.023	S	0.081	0.187	T	1.274	0	S
310	74318	CGPG5826	SENSE	0.407	0.075	T	0.116	0.052	T	1.118	0	S
479	74344	CGPG5929	SENSE	1.256	0.018	S	0.118	0.125	T	1.275	0	S
533	74462	CGPG6668	SENSE	0.846	0.022	S	0.26	0.011	S	1.425	0	S
313	74512	CGPG32	SENSE	0.241	0.118	T	0.146	0.044	S	1.062	0	S
442	74587	CGPG6774	SENSE	0	/	/	0.084	0.054	T	1.046	0	S

S: represents the transgenic plants showed statistically significant trait improvement as compared to the reference ($p < 0.05$)
T: represents the transgenic plants showed a trend of trait improvement as compared to the reference with $p < 0.2$
/: represents data points not determined or the transgenic plants didn't show any alteration or had unfavorable change in traits examined as compared to the reference in the current dataset

D. Salt Stress Tolerance Screen

[0138] 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.

[0139] 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 mmol/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.

[0140] 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 1 mm (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. Table 7 provides a list of recombinant DNA constructs that improve high salinity tolerance in transgenic plants

TABLE 7

Pep				Growth Stage			Root Length at day 11			Root Length at day 14			Seedling Weight at day 14		
SEQ ID	Construct id	Gene	Orientation	RS mean	p-value	c	delta	p-value	c	delta	p-value	c	delta	p-value	c
512	19703	CGPG4172	SENSE	1.124	0.139	T	0.198	0.021	S	0.072	0.116	T	0.582	0.023	S
513	19946	CGPG4097	SENSE	1.201	0.072	T	0.02	0.89	/	0.069	0.573	/	0.443	0.266	/
514	19980	CGPG3914	SENSE	0.904	0.146	T	0.101	0.259	/	0.144	0.058	T	0.706	0.016	S
515	70435	CGPG3701	SENSE	1.363	0.031	S	−0.118	0.228	/	0.161	0.038	S	0.053	0.697	/
516	71114	CGPG1657	SENSE	0.138	0.399	/	0.245	0.009	S	0.187	0.025	S	0.472	0.069	T
517	72451	CGPG4733	SENSE	2.226	0.02	S	0.186	0.006	S	0.069	0.23	/	0.466	0.011	S
443	72453	CGPG4735	SENSE	1.539	0.031	S	0.232	0.002	S	0.216	0	S	0.737	0.001	S
505	72463	CGPG4760	SENSE	3.026	0.002	S	0.119	0.269	/	0.202	0.073	T	1.26	0	S
392	72519	CGPG4749	SENSE	0.598	0.041	S	0.126	0.055	T	0.172	0.003	S	0.635	0.008	S
506	72902	CGPG5597	SENSE	1.418	0.039	S	0.114	0.286	/	0.226	0.078	T	0.426	0.091	T
448	72916	CGPG1814	SENSE	0.682	0.181	T	0.07	0.532	/	0.201	0.046	S	0.387	0.079	T
510	72921	CGPG5781	SENSE	1.977	0.029	S	0.163	0.176	T	0.211	0.073	T	0.663	0.006	S
518	72947	CGPG5607	SENSE	1.505	0.028	S	0.024	0.899	/	0.204	0.022	S	0.466	0.216	/
445	72961	CGPG5591	SENSE	1.879	0.007	S	0.228	0.122	T	0.229	0.003	S	0.817	0.04	S
444	72967	CGPG5742	SENSE	2.427	0.004	S	0.386	0.009	S	0.369	0.001	S	1.254	0	S
511	72968	CGPG5772	SENSE	1.531	0.055	T	0.302	0.06	T	0.209	0.073	T	0.761	0.003	S
449	72969	CGPG5789	SENSE	0.67	0.078	T	0.029	0.789	/	0.239	0.008	S	0.603	0.013	S
519	73012	CGPG5786	SENSE	2.371	0.001	S	0.366	0	S	0.342	0	S	1.08	0	S
520	73022	CGPG5622	SENSE	1.408	0.036	S	0.22	0.056	T	0.347	0	S	0.492	0.03	S
508	73055	CGPG5768	SENSE	3.291	0.001	S	0.369	0.087	T	0.417	0.005	S	1.096	0.005	S
446	73070	CGPG5627	SENSE	2.755	0.005	S	0.188	0.392	/	0.275	0.011	S	0.685	0.025	S
447	73475	CGPG6385	SENSE	1.11	0.059	T	0.127	0.361	/	0.216	0.001	S	0.474	0.06	T
521	73488	CGPG6394	SENSE	2.373	0.013	S	0.314	0.006	S	0.262	0.002	S	1.126	0.005	S
522	73901	CGPG5237	SENSE	1.141	0.078	T	0.207	0.197	T	0.202	0.097	T	0.639	0.03	SW
523	73964	CGPG5804	SENSE	1.235	0.043	S	0.428	0.008	S	0.317	0.022	S	0.955	0.002	S
524	74019	CGPG5706	SENSE	0.105	0.168	T	0.074	0.649	/	0.171	0.106	T	0.773	0.011	S
525	74022	CGPG5724	SENSE	0.033	0.327	/	−0.065	0.616	/	0.172	0.032	S	0.484	0.068	T
509	74103	CGPG6558	SENSE	1.225	0.074	T	0.26	0.042	S	0.267	0.004	S	0.543	0.042	S
526	74114	CGPG6551	SENSE	3.627	0	S	0.265	0.119	T	0.26	0	S	0.561	0.063	T
504	74259	CGPG5343	SENSE	2.802	0.003	S	0.249	0.098	T	0.256	0.037	S	0.995	0	S
527	74262	CGPG5353	SENSE	0.225	0.319	/	0.238	0.062	T	0.247	0	S	0.629	0.006	S
528	74292	CGPGS367	SENSE	0.327	0.199	T	0.16	0.067	T	0.105	0.166	T	0.565	0.013	S
529	74302	CGPG5384	SENSE	1.246	0.016	S	0.296	0.004	S	0.25	0	S	0.705	0.004	S
530	74325	CGPG5898	SENSE	1.596	0.021	S	−0.035	0.76	/	0.094	0.106	T	0.685	0.004	S
531	74429	CGPG6689	SENSE	1.796	0.008	S	0.298	0.037	S	0.207	0.006	S	0.496	0.029	S
532	74440	CGPG6682	SENSE	0.223	0.334	/	0.43	0.007	S	0.272	0.01	S	0.744	0.017	S
450	74449	CGPG6659	SENSE	0.693	0.19	T	0.204	0.104	T	0.205	0.022	S	0.451	0.095	T
533	74462	CGPG6668	SENSE	2.14	0.028	S	0.244	0.038	S	0.239	0.001	S	0.64	0.013	S
534	74465	CGPG6692	SENSE	1.245	0.016	S	0.35	0.01	S	0.215	0.001	S	0.575	0.043	S
535	74474	CGPG6669	SENSE	3.312	0.002	S	0.233	0.083	T	0.338	0.003	S	0.589	0.044	S
536	74505	CGPG6783	SENSE	1.731	0.043	S	0.272	0.007	S	0.208	0.01	S	0.493	0.009	S
537	74507	CGPG6799	SENSE	2.32	0.009	S	0.056	0.567	/	0.227	0.035	S	0.476	0.126	T
538	74562	CGPG6764	SENSE	1.405	0.038	S	−0.052	0.776	/	0.215	0.014	S	0.104	0.766	/
507	74572	CGPG6640	SENSE	1.425	0.025	S	0.201	0.009	S	0.267	0.001	S	1.184	0	S
270	14324	CGPG1560	SENSE	1.708	0.017	S	0.307	0.01	S	0.408	0	S	0.995	0.002	S
358	19768	CGPG4096	SENSE	1.496	0.061	T	0.163	0.187	T	0.129	0.013	S	0.66	0.002	S
436	19771	CGPG4011	SENSE	1.666	0.051	T	0.319	0.005	S	0.201	0.028	S	0.68	0.031	S
363	19879	CGPG4009	SENSE	2.117	0.029	S	0.16	0.139	T	0.091	0.202	/	0.545	0.028	S
347	72715	CGPG5521	SENSE	1.078	0.002	S	0.207	0.141	T	0.176	0.014	S	0.519	0.015	S
407	72771	CGPG2166	SENSE	0.564	0.256	/	−0.019	0.857	/	0.206	0.013	S	0.306	0.05	S
440	72903	CGPG5584	SENSE	0.645	0.196	T	−0.031	0.569	/	0.097	0.389	/	0.482	0.015	S
411	73054	CGPG5754	SENSE	1.52	0.035	S	0.198	0.089	T	0.098	0.187	T	0.696	0.004	S
476	74107	CGPG6590	SENSE	0.772	0.036	S	0.411	0	S	0.431	0.001	S	1.579	0	S
478	74131	CGPG6592	SENSE	1.747	0.044	S	0.316	0.004	S	0.115	0.01	S	0.663	0.001	S
442	74587	CGPG6774	SENSE	1.754	0.01	S	0.121	0.243	/	0.194	0.001	S	0.681	0	S

S: represents the transgenic plants showed statistically significant trait improvement as compared to the reference ($p < 0.05$)

T: represents the transgenic plants showed a trend of trait improvement as compared to the reference with $p < 0.2$

/: represents the transgenic plants didn't show any alteration or had unfavorable change in traits examined as compared to the reference in the current dataset

E. Polyethylene Glycol (PEG) Induced Osmotic Stress Tolerance Screen

[0141] 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.

[0142] 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, ½× 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.

[0143] 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 1 mm. The growth stage data was analyzed as a qualitative response according to example 1L. Table 8 provides a list of recombinant DNA constructs that improve osmotic stress tolerance in transgenic plants.

TABLE 8

Pep				Growth Stage			Root Length at day 11			Root Length at day 14			Seedling Weight at day 14		
SEQ ID	Gene	Construct_id	Orientation	RS mean	p-value	c	delta	p-value	c	delta	p-value	c	delta	p-value	c
413	19707	CGPG4179	SENSE	2.653	0.019	S	0.074	0.58	T	−0.031	0.81	/	0.427	0.063	T
414	19951	CGPG3941	SENSE	1.432	0.134	T	0.017	0.864	T	−0.08	0.28	/	0.476	0.054	T
415	19967	CGPG4032	SENSE	2.691	0.014	S	0.01	0.934	T	0.19	0.039	S	0.537	0.056	T
416	70543	CGPG3815	SENSE	1.735	0.077	T	0.084	0.561	T	0.323	0.007	S	0.676	0.006	S
402	70681	CGPG4584	SENSE	2.528	0.006	S	−0.065	0.682	/	−0.179	0.05	/	0.374	0.146	T
417	70707	CGPG1273	ANTI-SENSE	1.42	0.095	T	0.248	0.006	S	0.3	0.002	S	0.331	0.007	S
418	70719	CGPG1712	ANTI-SENSE	1.43	0.106	T	−0.007	0.968	/	0.101	0.255	T	0.155	0.349	T
419	71134	CGPG817	SENSE	1.478	0.13	T	0.119	0.15	T	0.035	0.684	T	0.198	0.277	T
420	71146	CGPG2928	SENSE	2.624	0.016	S	0.227	0.101	T	0.242	0.1	T	0.278	0.296	T
405	71508	CGPG1541	SENSE	3.153	0.001	S	0.446	0.054	T	0.384	0.048	S	0.782	0.003	S
421	71660	CGPG4690	SENSE	2.893	0.005	S	−0.024	0.795	/	0.225	0.074	T	0.165	0.329	T
403	71663	CGPG4638	SENSE	0.116	0.444	T	−0.061	0.536	/	0.358	0.041	S	0.058	0.702	T
439	71928	CGPG1617	SENSE	2.076	0.041	S	0.353	0.013	S	0.289	0.035	S	0.531	0.035	S
318	72081	CGPG5279	SENSE	1.262	0.138	T	0.174	0.243	T	0.2	0.197	T	−0.105	0.714	/
408	72085	CGPG5228	SENSE	4	0	S	0.22	0.046	S	0.371	0.004	S	0.929	0	S
422	72086	CGPG5236	SENSE	2.589	0.022	S	0.281	0.033	S	0.136	0.314	T	0.32	0.043	S
423	72632	CGPG4852	SENSE	1.663	0.053	T	0.254	0.069	T	0.094	0.548	T	0.471	0.015	S
424	72716	CGPG5529	SENSE	2.914	0.004	S	0.146	0.058	T	0.007	0.925	T	0.582	0.016	S
425	72723	CGPG1848	SENSE	2.138	0.066	T	0.043	0.728	T	0.2	0.068	T	−0.326	0.225	/
409	72744	CGPG5563	SENSE	1.636	0.05	/	0.195	0.151	T	0.059	0.751	T	0.539	0.005	S
404	72769	CGPG5573	SENSE	2.207	0.055	T	0.086	0.464	T	−0.134	0.162	/	0.389	0.086	T
407	72771	CGPG2166	SENSE	2.569	0.021	S	0.169	0.221	T	0.192	0.038	S	0.56	0.018	S
440	72903	CGPG5584	SENSE	2.161	0.061	T	0.035	0.856	T	0.245	0.162	T	0.06	0.871	T
510	72921	CGPG5781	SENSE	2.249	0.025	S	0.034	0.788	T	0.225	0.077	T	0.306	0.28	T
391	72948	CGPG5617	SENSE	2.267	0.005	S	0.054	0.495	T	0.117	0.019	S	0.289	0.077	T
445	72961	CGPG5591	SENSE	1.19	0.14	T	0.037	0.76	T	0.136	0.339	T	0.588	0.027	S
511	72968	CGPG5772	SENSE	3.142	0.007	S	0.178	0.072	T	−0.031	0.781	/	0.698	0.016	S
426	72987	CGPG1787	SENSE	2.055	0.078	T	−0.058	0.64	/	0.097	0.144	T	0.325	0.054	T
438	72994	CGPG5803	SENSE	2.674	0.013	S	0.245	0.124	T	0.07	0.657	T	0.599	0.035	S
441	73017	CGPG5733	SENSE	4	0	S	0.343	0.09	T	0.462	0.002	S	0.996	0	S
410	73039	CGPG810	SENSE	4	0	S	0.319	0.019	S	0.237	0.05	/	0.426	0.011	S
411	73054	CGPG5754	SENSE	3.048	0.002	S	0.556	0.003	S	0.26	0.063	T	1.12	0.002	S
446	73070	CGPG5627	SENSE	3.439	0.001	S	0.139	0.49	T	0.19	0.135	T	0.24	0.365	T
447	73475	CGPG6385	SENSE	1.933	0.033	S	0.04	0.476	T	0.009	0.897	T	0.459	0.073	T
412	73501	CGPG6456	SENSE	1.29	0.121	T	0.143	0.118	T	0.043	0.564	T	0.433	0.013	S
427	74109	CGPG6606	SENSE	3.517	0	S	0.159	0.136	T	0.249	0.004	S	0.333	0.025	S
428	74140	CGPG6569	SENSE	2.05	0.039	S	0.168	0.138	T	0.196	0.086	T	0.71	0.012	S
429	74191	CGPG6597	SENSE	2.565	0.019	S	0.336	0.092	T	0.199	0.112	T	0.54	0.02	S
406	74248	CGPG5476	SENSE	3.158	0.007	S	0.14	0.192	T	0.204	0.051	T	0.377	0.037	S
430	74265	CGPG5356	SENSE	2.208	0.023	S	0.317	0.034	S	0.419	0.006	S	0.577	0.008	S
431	74369	CGPG6076	SENSE	3.522	0	S	0.347	0.045	S	0.272	0.107	T	0.624	0.02	S
442	74587	CGPG6774	SENSE	3.325	0.002	S	0.073	0.468	T	0.414	0.002	S	0.577	0.016	S
405	71508	CGPG1541	SENSE	3.153	0.001	S	0.446	0.054	T	0.384	0.048	S	0.782	0.003	S
439	71928	CGPG1617	SENSE	2.076	0.041	S	0.353	0.013	S	0.289	0.035	S	0.531	0.035	S
422	72086	CGPG5236	SENSE	2.589	0.022	S	0.281	0.033	S	0.136	0.314	/	0.32	0.043	S
469	72455	CGPG4742	SENSE	1.367	0.15	T	0.026	0.764	/	0.024	0.786	/	0.255	0.04	S

TABLE 8-continued

Pep SEQ ID	Gene	Construct_id	Orientation	Growth Stage RS mean	Growth Stage p-value	Growth Stage c	Root Length at day 11 delta	Root Length at day 11 p-value	Root Length at day 11 c	Root Length at day 14 delta	Root Length at day 14 p-value	Root Length at day 14 c	Seedling Weight at day 14 delta	Seedling Weight at day 14 p-value	Seedling Weight at day 14 c
382	72466	CGPG4767	SENSE	0.735	0.101	T	0.068	0.333	/	0.249	0.006	S	−0.341	0.278	/
373	72633	CGPG4853	SENSE	1.179	0.122	T	0.227	0.009	S	0.097	0.065	T	0.442	0.013	S
370	72757	CGPG5572	SENSE	2.272	0.017	S	0.125	0.361	/	0.11	0.317	/	0.425	0.047	S
472	72992	CGPG5777	SENSE	2.233	0.056	T	0.176	0.261	/	0.116	0.34	/	0.511	0.019	S
438	72994	CGPG5803	SENSE	2.674	0.013	S	0.245	0.124	T	0.07	0.657	/	0.599	0.035	S
441	73017	CGPG5733	SENSE	4	0	S	0.343	0.09	T	0.462	0.002	S	0.996	0	S
411	73054	CGPG5754	SENSE	3.048	0.002	S	0.556	0.003	S	0.26	0.063	T	1.12	0.002	S
300	73507	CGPG6504	SENSE	0.343	0.334	/	0.347	0.007	S	0.261	0.032	S	0.3	0.122	T
352	73515	CGPG6473	SENSE	3.336	0.002	S	0.279	0.009	S	0.241	0.003	S	0.328	0.05	S
428	74140	CGPG6569	SENSE	2.05	0.039	S	0.168	0.138	T	0.196	0.086	T	0.71	0.012	S
430	74265	CGPG5356	SENSE	2.208	0.023	S	0.317	0.034	S	0.419	0.006	S	0.577	0.008	S
431	74369	CGPG6076	SENSE	3.522	0	S	0.347	0.045	S	0.272	0.107	T	0.624	0.02	S
422	74587	CGPG6774	SENSE	3.325	0.002	S	0.073	0.468	/	0.414	0.002	S	0.577	0.016	S

S: represents the transgenic plants showed statistically significant trait improvement as compared to the reference ($p < 0.05$)
T: represents the transgenic plants showed a trend of trait improvement compared to the reference with $p < 0.2$
/: represents the transgenic plants didn't show any alteration or had unfavorable change in traits examined as compared to the reference in the current dataset

F. Cold Shock Tolerance Screen

[0144] 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.

[0145] Eleven seedlings from T2 seeds of each transgenic line plus one control line were plated together on a plate containing ½× 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. Table 9 provides a list of recombinant nucleotides that improve cold shock stress tolerance in plants.

TABLE 9

Pep SEQ ID	Construct_id	Gene	Orientation	rosette area at day 8 delta	rosette area at day 8 p-value	rosette area at day 8 c	rosette area at day 28 delta	rosette area at day 28 p-value	rosette area at day 28 c	difference in rosette area between day 28 and day 8 delta	difference in rosette area between day 28 and day 8 p-value	difference in rosette area between day 28 and day 8 c
270	14324	CGPG1560	SENSE	0.054	0.429	/	0.258	0.017	S	−0.071	0.631	/
271	17484	CGPG2630	SENSE	−0.189	0.759	/	0.544	0.025	S	0.275	0.121	T
272	19109	CGPG1381	ANTI-SENSE	−0.016	0.523	/	0.541	0.008	S	0.818	0.014	S
273	70423	CGPG3165	SENSE	0.316	0.012	S	0.521	0.022	S	0.89	0.018	S
274	70424	CGPG3180	SENSE	0.474	0.003	S	0.695	0.003	S	0.693	0.043	S
275	70480	CGPG3833	SENSE	−0.066	0.591	/	0.175	0.159	T	0.474	0.059	T
276	70509	CGPG2420	SENSE	0.023	0.438	/	0.117	0.216	/	0.609	0.032	S
277	70647	CGPG4334	SENSE	−0.508	0.894	/	0.604	0.049	S	0.895	0.047	S
278	70675	CGPG4519	SENSE	0.2	0.2	/	0.303	0.153	T	0.507	0.034	S
279	70829	CGPG518	SENSE	−0.319	0.823	/	0.804	0.002	S	1.082	0.002	S
280	70849	CGPG596	SENSE	−0.039	0.564	/	0.698	0.001	S	0.707	0.001	S
281	71627	CGPG1270	SENSE	−0.146	0.748	/	0.349	0.05	T	0.3	0.12	T
282	71934	CGPG2294	SENSE	−0.068	0.796	/	0.757	0	S	0.922	0	S
283	72615	CGPG4829	SENSE	0.477	0.007	S	0.834	0	S	0.979	0.001	S
286	73559	CGPG6535	SENSE	0.143	0.093	T	−0.265	0.878	/	−0.344	0.821	/
287	74251	CGPG5489	SENSE	0.377	0.021	S	0.439	0.045	S	0.45	0.07	T
389	70437	CGPG3706	SENSE	−0.273	0.916	/	0.147	0.165	T	0.682	0.034	S
402	70681	CGPG4584	SENSE	0.352	0.155	T	0.252	0.261	/	0.269	0.328	/
403	71663	CGPG4638	SENSE	0.358	0.013	S	0.032	0.423	/	−0.031	0.585	/

TABLE 9-continued

Pep SEQ ID	Construct_id	Gene	Orientation	rosette area at day 8 delta	rosette area at day 8 p-value	rosette area at day 8 c	rosette area at day 28 delta	rosette area at day 28 p-value	rosette area at day 28 c	difference in rosette area between day 28 and day 8 delta	difference in rosette area between day 28 and day 8 p-value	difference in rosette area between day 28 and day 8 c
404	72769	CGPG5573	SENSE	0.381	0.049	S	0.881	0.006	S	1.102	0.005	S
407	72771	CGPG2166	SENSE	0.993	0	S	1.381	0.003	S	1.536	0.003	S
432	70217	CGPG6	SENSE	0.275	0.067	T	0.126	0.289	/	0.362	0.215	/
433	72711	CGPG1846	SENSE	0.774	0.001	S	0.579	0.004	S	0.429	0.038	S
438	72994	CGPG5803	SENSE	0.116	0.381	/	0.708	0.068	T	0.744	0.069	T
510	72921	CGPG5781	SENSE	0.265	0.057	T	0.31	0.162	T	0.367	0.11	T
414	19951	CGPG3941	SENSE	0.729	0.006	S	0.473	0.017	S	0.846	0.006	S
273	70423	CGPG3165	SENSE	0.316	0.012	S	0.521	0.022	S	0.89	0.018	S
416	70543	CGPG3815	SENSE	1.584	0	S	0.86	0	S	0.82	0.002	S
368	71617	CGPG1227	SENSE	0.204	0.136	T	0.408	0.025	S	0.458	0.057	T
439	71928	CGPG1617	SENSE	0.104	0.265	/	0.786	0	S	0.836	0.001	S
382	72466	CGPG4767	SENSE	0.497	0.017	S	0.565	0.017	S	0.963	0.002	S
383	72524	CGPG4770	SENSE	0.438	0.02	S	0.377	0.025	S	0.385	0.043	S
409	72744	CGPG5563	SENSE	0.52	0.058	T	0.859	0.026	S	0.454	0.189	T
444	72967	CGPG5742	SENSE	0.955	0	S	0.629	0.009	S	0.403	0.189	T
435	73518	CGPG6497	SENSE	0.114	0.278	/	0.319	0.01	S	0.195	0.114	T
306	74136	CGPG6632	SENSE	0.606	0.007	S	0.523	0.036	S	0.598	0.025	S
398	74240	CGPG5454	SENSE	−0.099	0.644	/	1.277	0.003	S	1.498	0.006	S
431	74369	CGPG6076	SENSE	0.623	0.002	S	0.62	0.04	S	0.737	0.096	T

S: represents the transgenic plants showed statistically significant trait improvement as compared to the reference ($p < 0.05$)
T: represents the transgenic plants showed a trend of trait improvement compared to the reference with $p < 0.2$
/: represents the transgenic plants didn't show any alteration or had unfavorable change in traits examined as compared to the reference in the current dataset.

G. Cold Germination Tolerance Screen

[0146] 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.

[0147] 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 ½× 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 mmol/m^2/s. At 28 days post planting, root length was measured, growth stage was observed, the visual color was assessed, and a whole plate photograph was taken.

[0148] 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. Table 10 provides a list of recombinant DNA constructs that improve cold stress tolerance in transgenic plants.

TABLE 10

Pep SEQ ID	Construct_id	Gene	Orientation	Growth stage at day 28 RS mean	Growth stage at day 28 p-value	Growth stage at day 28 c	Root Length at day 28 delta	Root Length at day 28 p-value	Root Length at day 28 c
288	19631	CGPG3627	SENSE	2.229	0.052	T	0.094	0.252	/
289	70121	CGPG2380	SENSE	2.732	0.042	S	0.126	0.238	/
290	70654	CGPG4352	SENSE	2.474	0.026	S	0.263	0.019	S
291	70696	CGPG4590	SENSE	3.092	0.01	S	0.086	0.145	T
292	70713	CGPG1462	ANTI-SENSE	4	0	S	0.268	0.014	S
293	70740	CGPG3700	SENSE	2.485	0.024	S	0.244	0.012	S
294	71321	CGPG4418	SENSE	1.837	0.126	T	0.014	0.474	/
295	71835	CGPG4634	SENSE	3.349	0.002	S	0.353	0.036	S
296	72934	CGPG5798	SENSE	2.222	0.023	S	0.243	0.101	T
297	72945	CGPG5787	SENSE	3.478	0.001	S	0.236	0.011	S
298	72980	CGPG5773	SENSE	3.265	0.003	S	0.239	0.006	S
299	73504	CGPG6480	SENSE	4	0	S	0.521	0	S
300	73507	CGPG6504	SENSE	4	0	S	0.404	0.001	S
301	73573	CGPG6462	SENSE	4	0	S	0.268	0.004	S

TABLE 10-continued

Pep SEQ ID	Construct_id	Gene	Orientation	Growth stage at day 28 RS mean	p-value	c	Root Length at day 28 delta	p-value	c
302	73586	CGPG6471	SENSE	4	0	S	0.314	0.064	T
303	73770	CGPG5435	SENSE	3.091	0.01	S	0.303	0.085	T
304	74105	CGPG6574	SENSE	3.329	0.002	S	0.109	0.116	T
305	74111	CGPG6622	SENSE	2.226	0.021	S	0.445	0.006	S
306	74136	CGPG6632	SENSE	3.192	0.005	S	0.328	0.002	S
307	74139	CGPG6561	SENSE	4	0	S	0.254	0.092	T
308	74267	CGPG5364	SENSE	3.054	0.002	S	0.3	0	S
309	74291	CGPG5363	SENSE	4	0	S	0.142	0.142	T
310	74318	CGPG5826	SENSE	4	0	S	0.272	0.008	S
311	74319	CGPG5831	SENSE	3.207	0.005	S	0.201	0.002	S
312	74324	CGPG5885	SENSE	3.144	0.007	S	0.232	0.017	S
313	74512	CGPG32	SENSE	4	0	S	0.332	0.011	S
314	74583	CGPG6649	SENSE	3.249	0.004	S	0.28	0.001	S
315	70427	CGPG3067	SENSE	1.567	0.108	T	0.222	0.044	S
352	73515	CGPG6473	SENSE	4	0	S	0.324	0.003	S
353	74684	CGPG6360	SENSE	2.927	0.004	S	0.426	0.003	S
373	72633	CGPG4853	SENSE	2.121	0.027	S	0.289	0.048	S
405	71508	CGPG1541	SENSE	1.99	0.039	S	0.263	0.033	S
406	74248	CGPG5476	SENSE	2.385	0.011	S	0.217	0.017	S
434	70932	CGPG4089	SENSE	3.268	0.003	S	0.146	0.067	T
435	73518	CGPG6497	SENSE	3.373	0.002	S	0.352	0.032	S
439	71928	CGPG1617	SENSE	3.062	0.011	S	0.18	0.002	S
504	74259	CGPG5343	SENSE	3.511	0	S	0.308	0.024	S
505	72463	CGPG4760	SENSE	2.736	0.01	S	0.032	0.386	/
506	72902	CGPG5597	SENSE	3.105	0.009	S	0.278	0.037	S
507	74572	CGPG6640	SENSE	4	0	S	0.125	0.155	T
508	73055	CGPG5768	SENSE	3.173	0.006	S	0.407	0.004	S
413	19707	CGPG4179	SENSE	1.829	0.061	T	0.169	0.018	S
360	19779	CGPG4113	SENSE	4	0	S	0.213	0.017	S
361	19833	CGPG4074	SENSE	/	/	/	0.292	0.022	S
363	19879	CGPG4009	SENSE	4	0	S	0.34	0.001	S
514	19980	CGPG3914	SENSE	0.798	0.122	T	0.278	0.011	S
273	70423	CGPG3165	SENSE	2.906	0.004	S	0.105	0.114	T
459	70725	CGPG2097	ANTI-SENSE	1.949	0.044	S	0.122	0.148	T
461	71112	CGPG934	SENSE	2.579	0.018	S	0.185	0.17	T
444	72967	CGPG5742	SENSE	4	0	S	0.287	0.007	S
438	72994	CGPG5803	SENSE	1.072	0.098	T	0.161	0.04	S
521	73488	CGPG6394	SENSE	4	0	S	0.211	0.012	S
477	74117	CGPG6575	SENSE	2.567	0.02	S	0.123	0.04	S

S: represents the transgenic plants showed statistically significant trait improvement as compared to the reference ($p < 0.05$)
T: represents the transgenic plants showed a trend of trait improvement as compared to the reference with $p < 0.2$
/: represents data points not determined or the transgenic plants didn't show any alteration or had unfavorable change in traits examined compared to the reference in the current dataset

H. Shade Tolerance Screen

[0149] 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 are 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.

[0150] T2 seeds were plated on glufosinate selection plates with ½ MS medium. Seeds were sown on ½× 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.

[0151] Table 11 provides a list of recombinant DNA constructs that improve shade tolerance in plants

TABLE 11

Pep			flowerbud formation at day 23			Leaf Angle at day 23			Petiole length at day 23			Number of rosette leaves at day 23			seedling weight at day 23		
SEQ ID	Construct_id	Orientation	RS mean	p-value	c	RS mean	p-value	c	RS mean	p-value	c	RS mean	p-value	c	delta	p-value	c
376	70426	SENSE	0.719	0.09	T	0.163	0.244	/	−0.206	0.185	T	−0.225	0.984	/	0.484	0.003	S
377	70772	SENSE	−0.501	0.858	/	−0.066	0.724	/	−0.692	0.004	S	−0.626	0.983	/	−0.693	0.023	/
378	71137	SENSE	0.26	0.384	/	0.11	0.168	T	−0.869	0.029	S	1.064	0.073	T	−0.453	0.288	/
379	71529	SENSE	0.89	0.108	T	−0.014	1	/	−0.44	0.006	S	1.817	0.024	S	−0.022	0.914	/
380	71601	SENSE	1.79	0.066	T	0.195	0.172	T	−0.057	0.59	/	−0.483	0.961	/	0.264	0.308	/
381	72362	SENSE	1.763	0.072	T	0.218	0.262	/	−0.109	0.242	/	0.003	0.484	/	0.311	0.119	T
374	72456	SENSE	0.563	0.313	/	0.751	0.186	T	−0.848	0.001	S	−0.624	0.999	/	−0.85	0.025	/
382	72466	SENSE	−1.382	1	/	−0.092	0.645	/	−0.894	0	S	1.212	0.122	T	−0.879	0.027	/
383	72524	SENSE	−0.153	1	/	0.152	0.09	T	−0.952	0.002	S	−0.57	1	/	−1.269	0.01	/
373	72633	SENSE	3.513	0	S	−0.431	0.977	/	−0.426	0.001	S	−0.735	0.994	/	0.269	0.129	T
375	72963	SENSE	−0.911	0.988	/	0.236	0.396	/	−0.753	0.003	S	−0.083	0.665	/	−0.485	0.015	/
384	73085	SENSE	−0.073	0.756	/	1.212	0.122	T	0.175	0.097	/	4	0	S	0.51	0.027	S
385	74241	SENSE	−0.195	0.935	/	−0.098	0.64	/	−1.077	0.01	S	−0.821	0.999	/	−1.024	0.002	/
386	74247	SENSE	0.43	0.16	T	0.203	0.095	T	−0.22	0.197	T	1.166	0.07	T	0.483	0.018	S
387	74284	SENSE	0.062	0.22	/	2.077	0.038	S	−0.014	0.943	/	2.348	0.04	S	0.03	0.938	/
388	74652	SENSE	0.015	0.442	/	0.093	0.455	/	−0.073	0.621	/	0.967	0.184	T	0.173	0.569	/
363	19879	SENSE	0.585	/	/	0	/	/	0.152	/	/	0	/	/	0.708	/	/
293	70740	SENSE	0.44	0.137	T	0.609	0.103	T	0.161	0.186	/	/	/	/	0.45	0.001	S
316	71811	SENSE	−0.025	0.637	/	0.725	0.113	T	−0.205	0.01	S	/	/	/	−0.517	0.037	/
397	71840	SENSE	1.498	0.12	T	0.712	0.178	T	−0.379	0.001	S	−0.188	0.765	/	−0.95	0.124	/
468	72450	SENSE	0.068	0.349	/	−0.042	1	/	0.166	0.016	/	1.62	0.049	S	0.501	0.038	S
370	72757	SENSE	3.595	0	S	0.872	0.079	T	0.064	0.138	/	−0.767	0.997	/	0.546	0.001	S
444	72967	SENSE	1.829	0.063	T	1.123	0.065	T	0.133	0.196	/	−0.18	0.794	/	0.509	0.008	S
511	72968	SENSE	0.185	0.005	S	0.48	0.179	T	0.22	0.162	/	1.698	0.085	T	0.382	0.031	S
300	73507	SENSE	0.248	0.086	T	0.307	0.287	/	−0.304	0.031	S	/	/	/	0.05	0.86	/
307	74139	SENSE	−0.011	0.556	/	−0.071	1	/	−0.124	0.068	T	−0.511	1	/	−0.413	0.124	/
535	74474	SENSE	0.755	0.154	T	−0.145	0.857	/	0.142	0.396	/	/	/	/	0.765	0.005	S
400	74610	SENSE	0.572	0.222	/	0.177	0.22	/	−0.18	0.071	T	/	/	/	−0.341	0.173	/

S: represents the transgenic plants showed statistically significant trait improvement as compared to the reference ($p < 0.05$)
T: represents the transgenic plants showed a trend of trait improvement as compared to the reference with $p < 0.2$
/: represents data points not determined or the transgenic plants didn't show any alteration or had unfavorable change in traits examined compared to the reference in the current dataset.

I. Early Plant Growth and Development Screen

[0152] 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 day 14 after seed planting.

[0153] T2 seeds were plated on glufosinate selection plates and grown under standard conditions (~100 □E/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.

[0154] Table 12 provides a list recombinant DNA constructs that improve early plant growth and development.

TABLE 12

Pep				Root Length			Seedling Weight		
SEQ ID	Construct_id	gene	Orientation	delta	p-value	c	delta	p-value	c
432	70217	CGPG6	SENSE	0.038	0.469	/	0.375	0.047	S
433	72711	CGPG1846	SENSE	0.132	0.021	S	0.601	0.001	S
434	70932	CGPG4089	SENSE	0.328	0.005	S	0.473	0.017	S
435	73518	CGPG6497	SENSE	0.287	0	S	0.634	0.036	S
436	19771	CGPG4011	SENSE	0.218	0.076	T	0.581	0.018	S
437	73549	CGPG6460	SENSE	0.139	0.003	S	0.349	0.03	S
438	72994	CGPG5803	SENSE	0.44	0.004	S	0.791	0.001	S
439	71928	CGPG1617	SENSE	0.073	0.427	/	0.494	0.005	S
440	72903	CGPG5584	SENSE	0.298	0.002	S	0.399	0.044	S
441	73017	CGPG5733	SENSE	0.284	0.004	S	0.199	0.488	/
442	74587	CGPG6774	SENSE	0.111	0.075	T	0.538	0.006	S
443	72453	CGPG4735	SENSE	0.215	0.005	S	0.416	0.069	T
444	72967	CGPG5742	SENSE	0.103	0.212	/	0.568	0.008	S
445	72961	CGPG5591	SENSE	0.177	0.046	S	0.548	0.006	S

TABLE 12-continued

Pep				Root Length			Seedling Weight		
SEQ ID	Construct_id	gene	Orientation	delta	p-value	c	delta	p-value	c
446	73070	CGPG5627	SENSE	0.221	0.007	S	0.652	0.005	S
447	73475	CGPG6385	SENSE	0.084	0.014	S	0.336	0.014	S
448	72916	CGPG1814	SENSE	0.182	0.067	T	0.353	0.012	S
449	72965	CGPG5789	SENSE	0.133	0.245	/	0.45	0.069	T
450	74449	CGPG6659	SENSE	0.314	0.002	S	0.579	0.027	S
451	16615	CGPG2539	SENSE	0.223	0.023	S	0.571	0.009	S
452	19187	CGPG3310	SENSE	0.264	0.001	S	0.51	0.08	T
453	19648	CGPG3134	SENSE	0.218	0.013	S	0.27	0.106	T
454	70354	CGPG3995	SENSE	0.152	0.046	S	0.406	0.029	S
455	70421	CGPG2942	SENSE	0.179	0.225	/	0.581	0.013	S
456	70459	CGPG3758	SENSE	0.187	0.036	S	−0.034	0.884	/
457	70465	CGPG3775	SENSE	−0.009	0.899	/	0.188	0.196	T
458	70683	CGPG4587	SENSE	0.133	0.088	T	0.402	0.014	S
459	70725	CGPG2097	ANTI-SENSE	0.326	0.001	S	0.116	0.548	/
460	70852	CGPG1465	SENSE	0.237	0	S	0.297	0.127	T
461	71112	CGPG934	SENSE	0.199	0.013	S	0.316	0.034	S
462	71127	CGPG945	SENSE	0.097	0.02	S	0.4	0.054	T
463	71132	CGPG1561	SENSE	0.195	0.02	S	0.08	0.524	/
464	71217	CGPG95	SENSE	0.234	0	S	0.566	0.036	S
465	71645	CGPG4688	SENSE	0.475	0.003	S	0.361	0.133	T
466	71726	CGPG3894	SENSE	0.223	0.056	T	0.458	0.033	S
467	72432	CGPG4562	SENSE	0.209	0	S	0.581	0.041	S
468	72450	CGPG4732	SENSE	0.335	0	S	0.79	0	S
469	72455	CGPG4742	SENSE	0.278	0.019	S	0.482	0.051	T
470	72727	CGPG5522	SENSE	0.123	0.002	S	0.315	0.004	S
471	72817	CGPG4987	SENSE	0.254	0.023	S	0.485	0	S
472	72992	CGPG5777	SENSE	0.219	0.023	S	0.664	0.015	S
473	73007	CGPG5760	SENSE	0.139	0.093	T	0.462	0.008	S
474	73073	CGPG5688	SENSE	0.164	0.022	S	0.285	0.247	/
475	73506	CGPG6496	SENSE	0.512	0	S	0.986	0	S
476	74107	CGPG6590	SENSE	0.282	0.002	S	0.538	0.057	T
477	74117	CGPG6575	SENSE	0.211	0.002	S	0.449	0.005	S
478	74131	CGPG6592	SENSE	0.142	0.047	S	0.586	0.003	S
479	74344	CGPG5929	SENSE	0.27	0.01	S	0.474	0.105	T
323	13502	CGPG1354	SENSE	0.57	0.002	S	0.625	0	S
330	18259	CGPG3368	SENSE	0.226	0.026	S	0.551	0.021	S
361	19833	CGPG4074	SENSE	0.259	0	S	0.472	0.016	S
334	70417	CGPG3427	SENSE	0.187	0.056	T	0.113	0.65	/
273	70423	CGPG3165	SENSE	0.03	0.747	/	0.185	0.007	S
515	70435	CGPG3701	SENSE	0.131	0.051	T	0.394	0.014	S
493	70601	CGPG2917	SENSE	0.177	0	S	0.365	0.063	T
291	70696	CGPG4590	SENSE	0.079	0.205	/	0.331	0.024	S
365	70738	CGPG3195	SENSE	0.012	0.864	/	0.472	0.003	S
293	70740	CGPG3700	SENSE	0.103	0.082	T	0.387	0.021	S
419	71134	CGPG817	SENSE	0.063	0.548	/	0.279	0.066	T
422	72086	CGPG5236	SENSE	0.083	0.234	/	0.398	0.05	S
505	72463	CGPG4760	SENSE	−0.131	0.416	/	0.422	0.003	S
285	73014	CGPG5692	SENSE	0.11	0.391	/	0.373	0.096	T
521	73488	CGPG6394	SENSE	0.018	0.793	/	0.398	0.1	T
299	73504	CGPG6480	SENSE	−0.152	0.479	/	0.538	0.012	S
300	73507	CGPG6504	SENSE	0.15	0.002	S	0.053	0.854	/
301	73573	CGPG6462	SENSE	0.112	0.07	T	0.375	0.006	S
302	73586	CGPG6471	SENSE	0.309	0	S	0.611	0	S
303	73770	CGPG5435	SENSE	0.21	0.059	T	0.281	0.484	/
509	74103	CGPG6558	SENSE	0.374	0	S	0.561	0.024	S
428	74140	CGPG6569	SENSE	0.16	0.017	S	0.376	0.066	T
527	74262	CGPG5353	SENSE	0.203	0.012	S	0.375	0.045	S
430	74265	CGPG5356	SENSE	0.107	0.259	T	0.432	0.067	T
529	74302	CGPG5384	SENSE	0.115	0.101	T	0.269	0.056	T
431	74369	CGPG6076	SENSE	0.138	0.03	S	0.195	0.21	/
534	74465	CGPG6692	SENSE	0.2	0.02	S	0.688	0.042	S
507	74572	CGPG6640	SENSE	0.162	0.023	S	0.617	0	S
314	74583	CGPG6649	SENSE	0.144	0.023	S	0.403	0.008	S

S: represents the transgenic plants showed statistically significant trait improvement as compared to the reference ($p < 0.05$)
T: represents the transgenic plants showed a trend of trait improvement as compared to the reference with $p < 0.2$
/: represents the transgenic plants didn't show any alteration or had unfavorable change in traits examined as compared to the reference in the current dataset

J. Late Plant Growth and Development Screen

[0155] 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.

[0156] *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 2½" 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.

[0157] 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.

[0158] 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.

[0159] Table 13 provides a list of recombinant DNA constructs that improve late plant growth and development.

TABLE 13

Pep			Rosette Dry Weight			Rosette Radius			Seed Dry Weight			Silique Dry Weight			Silique Length		
SEQ ID	Construct_id	Orientation	delta	p-value	c	delta	p-value	c	delta	p-value	c	delta	p-value	c	delta	p-value	c
480	14320	SENSE	−0.145	0.94	/	0.137	0.038	S	−0.702	1	/	0.477	0.002	S	0.016	0.276	/
481	16756	SENSE	0.485	0.016	S	0.223	0.025	S	0.148	0.042	S	0.481	0.002	S	0.147	0.013	S
482	17448	SENSE	−0.288	0.991	/	−0.054	0.829	/	0.376	0.008	S	0.185	0.034	S	−0.064	0.981	/
483	17633	SENSE	0.018	0.359	/	0.13	0.106	T	0.416	0.055	T	0.399	0.044	S	0.116	0.08	T
484	18876	SENSE	0.257	0.016	S	0.026	0.448	/	−0.213	0.786	/	0.388	0	S	−0.015	0.705	/
485	19120	ANTI-SENSE	−0.252	0.936	/	0.022	0.006	S	−1.042	0.95	/	0.165	0.076	T	0.046	0.021	S
486	19221	SENSE	−0.316	0.986	/	0.153	0.097	T	−0.35	0.903	/	0.394	0.068	T	0.183	0.028	S
487	70206	SENSE	0.125	0	S	0.074	0.18	T	0.712	0.022	S	0.12	0.026	S	0.019	0.403	/
488	70223	SENSE	0.197	0.026	S	0.23	0.018	S	−0.781	0.998	/	0.134	0.039	S	−0.205	0.91S	/
489	70347	SENSE	0.156	0.038	S	−0.082	0.868	/	−0.153	0.752	/	0.405	0.006	S	0.056	0.068	T
490	70406	SENSE	−0.275	0.948	/	−0.245	0.992	/	0.759	0.025	S	−0.282	0.949	/	−0.121	0.939	/
491	70469	SENSE	0.032	0.392	/	0.348	0.004	S	−0.733	0.996	/	0.325	0.059	T	−0.141	0.922	/
492	70564	SENSE	0.17	0.037	S	0.051	0.234	/	0.772	0	S	−0.381	0.977	/	−0.015	0.655	/
493	70601	SENSE	0.231	0.086	T	0.247	0.004	S	−0.257	0.959	/	0.323	0.024	S	0.082	0.03	S
494	70612	SENSE	0.053	0.112	T	0.082	0.096	T	1.049	0.011	S	−0.212	0.992	/	0.07	0.004	S
495	70720	ANTI-SENSE	−0.16	0.898	/	0.028	0.384	/	1.312	0.009	S	0.219	0.121	T	0.128	0.018	S
496	70735	SENSE	−0.058	0.672	/	0.156	0.087	T	0.421	0.036	S	0.532	0.003	S	0.033	0.038	S
497	70846	SENSE	0.086	0.255	/	0.134	0.063	T	−0.33	0.918	/	0.142	0.151	T	0.011	0.439	/
498	70923	SENSE	0.484	0.011	S	0.108	0.081	T	−0.4	0.844	/	0.091	0.198	T	0.099	0.001	S
499	71149	SENSE	−1.085	0.993	/	−0.043	0.681	/	0.346	0.017	S	0.136	0.133	T	0.066	0.077	T
500	71608	SENSE	−0.849	0.907	/	−0.132	0.976	/	0.816	0.006	S	0.279	0.004	S	0.038	0.238	/
501	71739	SENSE	−0.275	0.937	/	−0.107	0.955	/	0.334	0	S	−0.075	0.815	/	−0.119	0.874	/
502	72014	SENSE	−0.038	0.94	/	0.07	0.278	/	0.732	0.06	T	−0.026	0.584	/	−0.013	0.596	/
503	72051	SENSE	0.026	0.28	/	0.311	0.003	S	0.222	0.236	/	0.453	0.009	S	0.052	0.168	T
432	70217	SENSE	−0.202	0.893	/	0.203	0.024	S	−0.079	0.743	/	0.27	0.07	T	−0.063	0.856	/
454	70354	SENSE	0.134	0.147	T	−0.119	0.684	/	0.48	0.02	S	−0.119	0.736	/	0.014	0.3	/
334	70417	SENSE	−0.35	0.988	/	−0.041	0.637	/	0.69	0.012	S	−0.136	0.978	/	0.004	0.411	/
515	70435	SENSE	0.664	0.014	S	0.146	0.036	S	0.138	0.097	T	0.33	0.038	S	0.039	0.16	T
457	70465	SENSE	−0.106	0.79	/	/	/	/	0.883	0.001	S	−0.27	0.945	/	−0.097	0.818	/
460	70852	SENSE	0.178	0.031	S	0.145	0.034	S	−0.525	0.904	/	−0.315	0.861	/	−0.059	0.774	/
405	71508	SENSE	0.195	0.162	T	0.251	0.017	S	−0.515	0.929	/	−0.322	0.997	/	−0.196	0.982	/
295	71835	SENSE	0.139	0.055	T	0.163	0.049	S	0.538	0.019	S	0.27	0.068	T	0	0.496	/
467	72432	SENSE	0.146	0.021	S	0.139	0.02	S	0.325	0.012	S	0.074	0.149	T	−0.106	0.879	/
443	72453	SENSE	0.204	0.037	S	0.116	0.046	S	−2.198	0.995	/	0.016	0.448	/	−0.013	0.534	/
433	72711	SENSE	0.292	0.058	T	0.143	0.024	S	−0.114	0.76	/	−0.04	0.667	/	−0.093	0.946	/
449	72969	SENSE	0.046	0.072	T	−0.158	0.887	/	0.39	0.031	S	0.477	0.001	S	0.095	0.054	T
426	72987	SENSE	0.385	0.006	S	/	/	/	0.098	0.104	T	0.153	0.016	S	0.057	0.061	T
525	74022	SENSE	0.11	0.226	/	−0.069	0.844	/	0.71	0.009	S	−0.05	0.613	/	−0.004	0.544	/
287	74251	SENSE	−0.56	0.961	/	−0.184	0.916	/	0.611	0.001	S	0.174	0.229	/	−0.137	0.923	/

TABLE 13-continued

Pep			Rosette Dry Weight			Rosette Radius			Seed Dry Weight			Silique Dry Weight			Silique Length		
SEQ ID	Construct_id	Orientation	delta	p-value	c	delta	p-value	c	delta	p-value	c	delta	p-value	c	delta	p-value	c
537	74507	SENSE	0.255	0.017	S	0.178	0.03	S	0.318	0.032	S	0.188	0.011	S	0.013	0.078	T
313	74512	SENSE	−0.247	0.953	/	0.107	0.015	S	−0.073	0.86	/	0.113	0.034	S	0.05	0.175	T

S: represents the transgenic plants showed statistically significant trait improvement as compared to the reference ($p < 0.05$)
T: represents data points not determined or the transgenic plants showed a trend of trait improvement compared to the reference with $p < 0.2$
/: represents the transgenic plants didn't show any alteration or had unfavorable change in traits examined as compared to the reference in the current dataset

K. Limited Nitrogen Tolerance Screen

[0160] 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.

[0161] T2 seeds were plated on glufosinate selection plates containing 0.5× 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 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.

[0162] 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.

[0163] Table 14 provides a list of recombinant DNA constructs that improve low nitrogen availability tolerance in plants.

TABLE 14

Pep			Flowerbud formation			Number of green leaves			Root Length			Number of rosette leaves			Seedling Weight		
SEQ ID	Construct_id	Orientation	RS mean	p-value	c	RS mean	p-value	c	delta	p-value	c	RS mean	p-value	c	delta	p-value	c
375	72963	SENSE	1.1	0.004	S	0.293	0.021	S	−0.446	0.002	S	−0.246	0.786	/	0.137	0.001	S
389	70437	SENSE	−0.28	0.982	/	−0.08	0.769	/	0.259	0.006	S	0.5	0.005	S	0.133	0.003	S
390	71633	SENSE	0.26	0.26	/	0.254	0.114	T	−0.1	0.539	/	0.647	0.06	T	0.106	0.023	S
391	72948	SENSE	0.587	0.06	T	0.539	0.029	S	−0.237	0.003	S	0.479	0.1	T	0.078	0.121	T
392	72519	SENSE	0.749	0.033	S	0.209	0.104	T	−0.09	0.274	/	0.276	0.264	/	0.116	0.006	S
393	10475	SENSE	1.256	0.026	S	0.588	0.005	S	−0.378	0.002	S	0.081	0.319	/	0.018	0.75	/
394	11120	ANTI-SENSE	0.795	0.033	S	0.608	0.015	S	−0.45	0.001	S	0.287	0.106	T	−0.041	0.387	/
395	19736	SENSE	−0.24	0.907	/	0.355	0.033	S	0.014	0.864	/	0.64	0.006	S	−0.075	0.005	/
396	71606	SENSE	0.605	0.088	T	0.176	0.11	T	−0.033	0.708	/	1.239	0.005	S	0.133	0.002	S
397	71840	SENSE	0.408	0.235	/	0.879	0.006	S	−0.137	0.248	/	0.524	0.032	S	0.066	0.198	T
398	74240	SENSE	−0.06	0.602	/	0.13	0.076	T	−0.107	0.306	/	0.714	0.034	S	0.108	0.002	S
399	74331	SENSE	−0.44	1	/	0.054	0.203	/	0.132	0.055	T	1.045	0.021	S	0.134	0.003	S
400	74610	SENSE	−0.59	1	/	−0.08	0.922	/	0.289	0	S	1.241	0.017	S	0.137	0.001	S
401	75527	SENSE	0.242	0.228	/	0.376	0.028	S	−0.183	0.045	/	0.352	0.083	T	−0.005	0.8	/
316	71811	SENSE	−0.45	0.91	/	/	/	/	−0.112	0.202	/	0.438	0.014	S	−0.054	0.161	/
505	72463	SENSE	−0.16	0.976	/	/	/	/	0.112	0.109	T	0.366	0.024	S	0.13	0.006	S
351	75701	SENSE	0.736	0.048	S	0.07	0.861	/	−0.4	0.018	S	/	/	/	−0.109	0.193	/

S: represents the transgenic plants showed statistically significant trait improvement as compared to the reference ($p < 0.05$)

T: represents the transgenic plants showed a trend of trait improvement compared than the reference with $p < 0.2$

/: represents data points not determined or the transgenic plants didn't show any alteration or had unfavorable change in traits examined as compared to the reference in the current dataset

L. Statistic Analysis for Qualitative Responses

[0164] Table 15 provides a list of responses that were analyzed as qualitative responses

TABLE 15

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 stage1.03 vs. not
growth stage at day 14	salt stress tolerance screen	50% of plants reach stage1.03 vs. not
growth stage at day 14	PEG induced osmotic stress tolerance screen	50% of plants reach stage1.03 vs. not
growth stage at day 7	cold germination tolerance screen	50% of plants reach stage 0.5 vs. not
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

[0165] Plants were grouped into transgenic and reference groups and were scored as success or failure according to criteria in Table 15. 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 S-PLUS statistical software (S-PLUS 6, Guide to statistics, Insightful, Seattle, Wash., 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

[0166] Table 16 provides a list of responses that were analyzed as quantitative responses.

TABLE 16

response	screen
seed yield	Soil drought stress tolerance screen
seedling weight at day 14	heat stress tolerance screen
root length at day 14	heat stress tolerance screen
seedling weight at day 14	salt stress tolerance screen
root length at day 14	salt stress tolerance screen
root length at day 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 day28	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

TABLE 16-continued

response	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

[0167] 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 S-PLUS statistical software (S-PLUS 6, Guide to statistics, Insightful, Seattle, Wash., 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

[0168] A BLAST searchable "All Protein Database" was 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" was 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.

[0169] The All Protein Database was queried using amino acid sequence of cognate protein for gene DNA used in trait-improving recombinant DNA, i.e., sequences of SEQ ID NO: 240 through SEQ ID NO: 478 using "blastp" with E-value cutoff of 1e-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 was 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.

[0170] The Organism Protein Database was queried using amino acid sequences of SEQ ID NO: 270 through SEQ ID NO: 538 using "blastp" with E-value cutoff of 1e-4. Up to 1000 top hits were kept. A BLAST searchable database was 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 was 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: 539 to SEQ ID NO: 22568. The relationship of the homologs to the identified trait-improving genes on an amino acid sequence basis is found in Table 17 where the amino acid sequence of a protein encoded by a trait-improving DNA, e.g., SEQ ID NO:270, is followed by the amino acid sequences of protein encoded by homologous genes, e.g., SEQ ID NO:19844, 4248, 2761, 15944, etc. The source organism of each homolog is reported in the Sequence Listing.

TABLE 17

Sequence IDs for homolog proteins

Seq ID NO:	homolog Seq ID NOs											
270:	19844	4248	2761	15944	11776	16144	10470	9742	6776	1010	2285	16333
	9154	20620	16454	20025	8388	10646	1208	6001	1706	2448	14768	10226
	12626	19846	9302	17295	17794	6354	5098	1789	6430	17749	821	10109
	7542	17855	15562	17462								
271:	1715	5418	7208	19338	7440	711	8113	17151	17592	18879	4807	8671
	9936	11315	10681	3177	10519	6830	13563	12162	15155	1860	18072	20945
	6715	15032	5192	10928								
272:	0											
273:	13771	8553	4219	10043	10800	8345	17501	13569	954	17197	6188	3760
	13267	16169	8132	2667	11216	15637	4652	2270	10309	5708	18374	9446
	12844	7790	7569	4786	9725	14187	12859	16948	18626	13741	5525	7877
	4550	15544	9706	7616	14358	15163	13182	14560	16722	1129	1472	4261
	10693	20144	6437	21413	17893	17984	17116	9925	19953	20648	983	2837
	5663	2943	10465	1841	12497	6435	14763	13495	12676	7513	8363	16389
	8162	7945	14956	15029	12433	22241	16071	13003	16940	18847	12354	7732
	14013	5735	11505	8833	17658	16048	17609	575	6641	6331	3738	10842
	18927	21518	20097	14117	5309	13744	15880	19484	9648	22509	1221	15515
	6785	852	6466	17423	14164	658	8704	16710	19375	3306	14050	16883
	16322	1722	15481	13636	10680	6347	3552	8885	21794	17703	22557	14777
	21189	13711	3601	3968	3692	4003	20044	12943	19749	1865	6355	14902
	6137	22370	19468	10410	21460	10451	17175	20965	12916	1206	6796	11329
	9139	11008	10569	9058	7988	19743	20088	14111	8231	4522	18497	11952
	2866	15466	3609	2403	16796	13539	14806	5364	12620	20699	12940	15426
	4409	12452	5296	9156	629	12665	20947	3649	7530			
274:	16167	5178	2412	10455	20036	11246	19666	6400	5573	22539	8547	21845
	2413	20290	4036	19351	5886	6071	17184	9738				
275:	14665	16694	12678	14928	21489	7918	1571	3959	2490	2517	14615	3788
	10022	16096	21248	13293	8541	13446	6120	4360	3812	15574	18938	19203
	2284	2215	10054	14052	9653	10183	17752	20776	4240	22343	8270	9192
	17217	7374	12141	20657	7674	6445	2522					
276:	12496	3460	13599	7043	9150	1664						
277:	16949	9640	8150	2014	12188	5779	17876	14612	18293	11053	15958	15263
	18370	20984	13094	18734	7380	10318	21641	12737	13028	20561	7087	10686
	9894	7528	12573	16043	14846	20513	2802	8897	14716	10257	16407	2727
	6151	1484	6831	16916	10146	17756	13193	7670	15946	7750	9397	20046
	12547	5399	18644	11883	12531	12530	17188	2130	3805	17493	16821	10181
	3639	3934	1419	780								
278:	16531	9228	5799	19821	10980	17656	3449	19982	13335	20959	11238	13084
	10281	17610	19623	17614	9736	21375	19978	5859	4943	12390	18806	1349
	8759	21741	20400	13707	9170	15899	11361	4333	10631	12909	2136	12776
	20323	7676	5847	9065	19902	4545	6768	546	9246	14134	4442	20731
	9931	6700	8677	19305	4828	3655	17550	7579	21629	9044	19475	637
	4209	3519	3873	15884	12247	10177	1407	10312	15957	16955	17469	20241
	7267	21862	16864	22192	19599	6365	12324	10985	6424	6449	14564	3115
	14885	10603	911	18609	3359	7059	2851	5801	9613	8391	18695	7987
	14964	1081	15171	1312	14747	3060	13390	22115	5060	16536	19729	13468
	11109	21989	2230	9462	9096	18775	10721	11999	8340	16607	22199	8687

TABLE 17-continued

	Sequence IDs for homolog proteins											
	3652	8147	22073	4090	3491	20506	7835	10890	6781	7839	14478	16371
	579	6442	9721	5423	2566	7876	17580	2023	13164	9424	14096	8115
	15304	14818	7282	6422	4841	10106	1075	12995	9297	21280	2309	895
	12373	5366	22159	4499	737	11369	4308	13974	2794	12771	16584	9250
	6930	8792	10185	17718	13148	5054	22383	9674	9868	21546	15881	20000
	19029	4938	14024	15026	15535	16386	15402	21036	12653	9490	4170	11551
	3711	4179	18619	16370	14161	11294	9094	2689	21881			
279:	13577	10344	17371	5840	13904	12689	11795	21912	17226	14519	8854	14229
	7998	8326	1400	16163	11785	10117	21511	21043	18205	2933	2043	22181
	21628	20090	18018	20578	19081	11011	4768	2834	4635	13475	6306	13119
	1671	21348	16926	20801	6361	4269	4366	15615	941	7046	3166	16526
	6250	4790	825	16541	14270	3574	8127	18015	13147	17950	15243	6671
	20662	3487	11787	6762	5488	7117	9417	15702	4859	20527	19240	17200
	7115	19523	12823	9115	11770	20530	4791	20334	11019	20645	14383	1914
	8945	15358	9347	2496	3098	11604	16441	19352	18451	12451	8877	15655
	791	12609	12588	19785	18328	8143	22185	1488	10212	14002	16826	11779
	1890	3879	20130	21633	20930	17222	2691	18852	7120	7853	644	21495
	14630	21041	5676	8447	16750	10436	4523	2686	8237	2948	13559	19008
	3686	18465	3895	7416	10170	18867	14574	1159				
280:	16310	3796	10205	19486	13581	11022	21960	15598	12604	9662	20210	21764
	8626	17323	11666	21316	6121	7438	982	2135	17499	12340	20711	6553
	10296	17874	914	17716	3723							
281:	20551	21096	13717	4006	19762	10017	14425	17785	6291	3855	15232	11917
	21856	18564	19010	3910	13621	19087	670	10539	851	5698	9112	12694
	14218	11947	18104	21227	22348	14178	1862	9829	9325	14533	13149	8679
	17127	6507	10375	2782	3357	594	7548	9316	5728	7981	8022	13688
	1294	13817	21893	10781	5263	11292	5492	9542	8000	16102	6328	11687
	13695	15807	4068	3478	6486	13660	22165	17881	19166	3613	7013	6393
	15983	17688	5124	4243	19684	17008	12366	7161	20062	12194	15870	14385
	9124	9865	6211	628	6448	700	8869	17941	10697	21134	5586	4469
	21167	855	20538	9251	1036	10678	1977	17337	4575	19974	3520	10195
	14572	3870	21293	19011	12921	20120	11647	15054	13976	21163	20362	12988
	15636	2345	4740	3205	17504	1953	15208	16834	7654	15907	8961	
282:	19261	3860	7076	12616	1790	4886	9735	12611	20478	4501	18874	7032
	18024	7225	4544	11443	2127	19283	7367	1338	4482	15213	20554	3826
	14978	21769	11755	4250	15506	20020	6593	1286	20750	18985	16069	4571
	22536	3773	11152	9745	13196	2190	8120	7914	16863	11987	16172	15399
	14422	12490	8076	17180	19067	14493	13105	16459	18285	15863	14085	18130
	11566	17352	20003	2995	5386	8757	19103	15685	20563	18739	20815	19454
	7820	20771	7972									
283:	0											
284:	10750	5276	3894	3486	12240	18158	12170	15393	9765	11266	5031	2792
	9334	20684	1144	13799	10858	16622	20849	22001	6897	17710	15401	18589
	9550	1757	10249	21993	2001	19689	15058	4297	19990	643	11414	18208
	19995											
285:	17916	15231	15741	15829	4645	21977	10291	1806	21573	474	6018	2663
	8036	9618	16693	3960	15864	14578	17125	15924	21826	13440	17249	8650
	20159	1986	15742	19706	22092	8766	6813	17830	10853	21281	13394	5285
	8139	21004	14220	17563	2086	2488	1597	4698	13233	4654	1250	15737
	2907	1469	9957	13288	6516	22526	16496	14873	10471	18290	3086	11953
	18592	3185	9418	17135	8081	9593	19180	4673	7979	16544	13933	1300
	16782	15551	8460	15960	3405	13997	1566	21046	8636	17134	6512	6596
	13346	15639	14396	9252	12093	21591	15042	6953	18637	16784	22523	6262
	16933	22448	4612	19863	6076	4133	19601	3344	12192	16828	17089	19303
	6118	15088	14986	21070	771	3291	2153	21234	18173	11970	21215	10644
	20638	4377	21183	9519	13810	10948	17764	3781	21029	16613	18091	6526
	5846	22213	22003	20765	3801	21866	21771	14860	861	6743	5007	5529
	14267	14880	21391	10210	5693	5970	3793	15855	1007	13001	6878	9875
	16912	19329	13614	10333	13714	6903	21112	8204	1133	21262	16852	15703
	21338	6248	21547	15242	13567	16788	11020	18655	10528	19496	17440	22414
	17480	8142	7760	20388	2829	16249	12914	2569	14595	7096	6689	12534
	6105	16041	9242	9145	1552	10313	1379	9596	11771	5820	593	15445
	3268	14744	18410	6984	10872	10053	9713	8837	1383	4305	10421	2944
	20363	19120	7463	16753	20969	18430	12905	10227	11066	6057	13677	18640
	4083	1527	19285	5385	17557	20851	15693	17304	1683	14391	15965	19854
	8425	14916										
286:	16099	8075	8242	429	13036	10217	18174	507	11062	15313	16399	14594
	3820	5216	5717	10394	20464	15374	15526	18461	17556	14810	4502	12391
	11462	14924	1652	18690	9504	13188	8137	3327	12056	2537	4030	1064
	15390	6367	19001	8581	6859	7602	14778	7681	18172	18107	12112	7417
	13896	2465	12130	19906	4949	17359	16220	13607	526	20229	16469	10705
	15889	16978	8246	16554	18467	9002	9780	17882	21655	20242	21051	3977
	19627	9063	10810	15051	5705	9204	11991	9915	15840	16148	14589	6171
	6614	20389	6007	6226	5373	19830	9030	14898	11912	16971	18279	19602

TABLE 17-continued

Sequence IDs for homolog proteins												
	13078	18533	1840	4491	7812	8977	13027	6371	15170	21310	6443	9755
	12535	2819	14876	3052	12267	8377	3804	7983	22450	22167	22369	21674
	891	13549	7113	14532	11064	9354	7858	8394	2489	17243	2044	9345
	6836	2341	19148	17763	13516	14240	9032	15489	8304	7822	17083	9993
	8188	5481	11010	1093	7789	21699	21306	11113	8956	18128	7880	3416
	2857	17664	21589	11961	19154	11542	4812	7486	21609	5307	21506	3533
	6663	4677	18511	4730	696	9569	17797	18687	7097	20259	15252	13221
	3425	3261	450	6778	14692	22502	14915	21157	20371	3563	12591	16308
	7626	4212	19798	16130	21296	2832	830	14553	14135	6434	18295	17956
	20230	476	10392	12043	3289	20779	1281	17745	21065	5487	3754	8587
	2882	12578	11548	12705	15830	16586	7955	15449	988	20859	1768	11129
	6547	22518	5552	9854	11376	6669	5359	9132	10964	22087	1879	17298
	13137	3333	20301	13752	19370	2425	6946	19538	14273	8003	15340	6427
	17165	15603	12419	10809	13658	14064	4221	7387	3386	13284	20981	2316
	3116	8418	3578	6508	18217	992	22249	14855	13442	3471	19949	5277
	19885	2816	10917	21954	9436	18538	18659	12816	12308	20364	15943	2649
	2515	14701	9329	8193	17579	22076	8890	21073	8376	15177	10882	859
	5990	9814	16053	12078	3144	5209	13848	22428	19076	9604	5454	3141
	17056	14918	953	4088	6615	15729	11270	5837	14568	12544	17630	2371
	4694	12396	15369	16597	3697	10741	13396	21621	16662	8841	11120	14081
	13456	21472	7487	12898	12787	7866	11748	8692	9484	2336	15204	6565
	14320	2978	9294	7482	9493	1277	4576	15513	21001	3242	4952	7813
	7306	12296	12021	6645	21060	9286	22489	6264	13745	16653	19069	7780
	15219	16969	9271	18873	14762	10802	10479	16663	3678	16713	7751	13703
	3630	4691	9472	10709	8542	7060	6112	22457	21974	20476	7333	6482
	14526	7151	2644	835	10655	12264	17372	788	15452	14361	11678	2754
	15289	14415	9468	1673	2117	17672	3643	6809	9280	22095	18903	3706
	15256	18593	5764	11115	12583	11568	622	13613	2331	5136	8073	15998
	5630	10889	9673	9014	7950	6748	9771	11716	18929	14842	6789	1773
	981	18575	19878	21485	14269	9584	12794	21399	20485	9218	18691	3350
	18263	4846	544	19667	9933	4140	1318	20418	11128	20105	16734	2376
	15699	7061	4232	15357	14036	5339	7107	19030	7165	21370	12103	4848
	13211	22530	15360	12863	9975	6398	14067	16683	21170	1924	890	8155
	15866	10131	7187	4332	1235	20330	12927	7088	5099	2302	12424	8303
	17466	14322	11383	2282	14043	15956	1818	3414	12982	18548	15665	10961
	21084	10824	18440	16819	3730	13940	18821	14864	19607	7969	6546	16771
	5441	8459	18266	5000	15749	13014	14274	8444	4707	13097	15930	6281
	18662	7992	9661	19875	11156	3619	14086	20948	16946	3456	6143	6097
	786	6709	13766	5954	9650	17926	9083	20839	17473	5462	22351	12788
	5453	13277	11817	9672	8255	6463	15113	9053	15528	1319	926	17317
	6368	7704	18694	3644	12154	3794	21257	21638	18386	18111	21498	10731
	13776	5539	14530	20282	7762	9529	17675	15191	12380	14865	15825	2818
	16442	10262	10965	15558	5973	22476	19408	5773	5016	20819	18982	19997
	4572	640	19168	17905	2970	2132	20312	4655	16568	21093	13882	5730
	7976	7079	13035	3505	2800	12522	8939	11219	2155	15905	3206	2017
	15587	6277	1297	1423	9549	6119	18728	12545	2037	11704	9571	21379
	13089	11197	13107	22367	2420	17943	7599	5997	1801	21374	16528	8722
	16672											
287:	8532	19537	5344	9149	21995	6924	15909	4097	11901	8844	7649	2133
	2202	5183	18294	19005	11338	19082	14317					
288:	19787	18784	5642	15617	18773	2850	21740	18774	8659	17768	4774	15786
	13450	5349	3435	11594	3337	19500	18011	5026	20455	17036	22287	17395
	9621	6514	1386	11394	7035	21823	15347	11387	15362	4210	5017	10279
	19441	22361	7943	7642	8141	16188	15181	3603	7428	2749	21346	17018
	10086											
289:	652	22063	8339	21393	2555	8373	21778	11080	15895	10755	10659	16023
	19651	17328	17996	10829								
290:	7684	9445	17343	1187	6793	10461	6245	10467	20367	12284		
291:	19558	4465	12410	21267	12416							
292:	13619	7334	20532	21542	12253	16189	8764	2507	21921	6586	19095	9485
	5381	5599	12372	14529	13331	15295	19004	1397	21520	14556	20510	22236
	2986	7080	8521	6732	13272	16558	4313	20499	22483	14588	9523	7470
	18752	12181	20429	12348	695	10907	14321	14033	18144	3919	8802	20993
	8165	3312	17714	14662	16218	6883	15696	5826	8318	13408	11637	4264
	1882	4226	19194	12589	20866	1376	21972	8106	9328	11225	6391	8315
	20980	16513	6488	21387	10825	871	22553	7860	20986	5123	7178	8148
	19174	5633	3500	7737	17944	19517	19101	2424	1678	1758	16439	22408
	11623	7905	18353	18641	17321	18471	6775	8307	11843	9722	15205	20080
	16600	6416	10161	8449	8858	14419	19903	14156	15652	13343	15817	3739
	12654	14241	7430	8851	6919	22017	6531	1962	3371	18557	2125	6815
	15392	19947	6480	15023	1479	1138	21122	20521	21201	1677	17815	9610
	8319	5949	7617	10353	9342	4915	6495	1682	14875	17940	1204	13538
	16452	19603	8029	2886	14466	19507	12125	6822	10351	4123	9222	9605
	18244	18276	17153	17212	12619	14496	11337	8683	15935	10084	14862	5228

TABLE 17-continued

	Sequence IDs for homolog proteins											
	20909	9138	702	17034	5542	16281	16905	2247	17007	15480	13602	16745
	3223	6163	1245	10228	21595	18522	6698	5750	8543	21981	15735	3961
	16417											
293:	10002	18611	6406	14073	5127	8351	1241	12550	10077	11772	10606	3231
	10112	15857	13002	6686	8210	8327	4270	16125	8696	5110	12311	7006
	19199	6994	12597	5342	12722	21575	5723	2670	6046	12012		
294:	9532	10331	15934	2046	6293	19503	22316	15147	14129	5699	7047	13130
	2151	1110	20162	9143	9176	4233	8431	6088	7434	18942	5356	18099
	10361	3212	21551	20873	2419	8077	3140	13009	21068	6829	20236	14326
	6208	847	2330	15785	1052	14929	4869	4567	16757	19546	10070	1727
	6317	8558	3880	18261	6409	6931	17666	21501	12516	16760	16947	3896
	3358	6554	14909	1974	4835	20560	11275	2659	12987	18209	16896	15952
	20752	15130	15569	7406	13923	1051	11602	3912	10042	4592	22204	2430
	1382	18088	15862	20314	9057	10845	5041	7582	21742	12835	17242	15658
	8522	22493	7831	1594	13654	7414	12151	12808	14165	15368	17979	10215
	8018	22247	22220	7254	654	20380	2845	5061	7274	5018	9568	9818
	1494	3725	11235	6804	8938	12700	17001	19302	11190	4028	3173	
295:	21192											
296:	10114	6052	18680	17170	11936	20081	9148	3938	18585	12840	14672	14951
	1544	20775	4870	8723	3360	19138	1416	1901	18744	2625	951	6936
	16543	3550	9203	11070	9360	21434	3920	1693	10869	11881	12895	1003
	5405	14684	21089	14531	21626	20145	17875	7549	2428	2613	18036	1421
	18003	6973	20577	12790	22102	3375	13691	15302	6589	15430	18154	16596
	19645	21006	17187	14709	19975	1854	17428	11844	10033	1792	934	845
	5533	21419	6582	2314	19307	8902	8278	20861	7030	10654	9636	16002
	2969	15306	5928	1894	592	13534	4985	5623	5150	2342	22174	1686
	2688	10718	20383	19440	19860	618	22308	10355	12565	8585	15993	12725
	22563	5578	14369	13712	9428	20205	10767	1546	5387	8364	18905	18948
	2545	17156	20131	22338	2223	7037	15860	5111	16844	14702	1634	13698
	16173	17860	16802	21238	20479	18313	18815	16556	12453	18481	19778	12153
	19470	20701	1477	19657	2220	5033	6117	12286	12326	6566	16110	13469
	17077	20231	4058	9834	3780	19094	6308	9548	1549	21687	13080	7340
	18746	2266	11139	2005	14735	5543	4941	2921	8468	19501	3139	16192
	10723	6333	11355	3845	11452	19385	14092	1395	5545	2216	10682	21311
	15661	21100	2597	14697	9008	17498	17514	9946	20269	5669	5062	15447
	2775	6975	12793	12639	8185	19766	8932	4278	14889	4981	22471	5952
	6818	16336	21140	14098	21953	4979	13968	16410	18878	9696	4978	16146
	2609	22097	16986	20921	22527	16920	18126	16034	5362	933	15779	16770
	1772	9517	6866	16982	19232	19937						
297:	9912	18441	5938	12696	19188	22233	2840	10426	16052	9508	12778	15536
	19286	9563	19034	20209	15518	6498	21608	11026	14044	10165	12621	12028
	16923	21297	5646	16170	12477	16660	1378	2624	3809	12760	16057	7256
	15500	18959	10317	10326	5977	4830	1143	1499	10983	2571	15543	13839
	12370	9041	1331	8508	16831	13832	4303	18599	21584	9787	1548	8292
	1560	18466	11683	17762	17468	9815	4374	18826	20637	18709	16467	7307
	16512	904	18899	17113	10700	5006	22084	5463	20856	18792	1535	13608
	11312	8634	19381	11435	870	7232	5079	6299	13314	10487	15382	14552
	14878	20590	14820	7911	8924	12070	7581	2122	18063	8338	12227	14479
	3229	17500	9776	16213	12767	17455	5438	1839	9982	4649		
298:	18555	7838	6652	1982	15254	2218	6543	13709	5154	14481	4355	8406
	21382	21663	19102									
299:	19421	10037	3803	5108	3343	20336	11002	8946	12661	9168	15378	18020
	16075	5607	19118	22336	19724	8555	2295	21579	1259	8494	18083	960
	13560	20787	22477	19264	6401	8583	9620	5248	701	10759	22290	2593
	21024	17543	1417	15845	17793	18019	6222	10575	1775	8903	15288	2885
	7993	20494	10001	13641	11853	614	12502	13330	17952	13069	9420	1771
	17636	13434	5588	2165	19494	4998	1751	16904	10306	3123	12413	16515
	21706	9144	19364	2394	2677	15207	13710	9045	11258	1042	11230	13140
	18738	15056	11058	930	22417	8107	16349	7322	16450	15822	16451	6646
	18926	2197	302	8630	17924	14996	19753	4515	10245	7300	6710	21723
	12990	8111	14791	13977	19581	12911	22090	603	15053	14851	21092	14284
	20327	13846	9587	21947	7441	12133	14923	3660	13939	6002	5590	11909
	22216	4929	14884	9941	9040	12896	7903	21683	11508	22006	11550	5658
	2777	9977	15523	5791	21963	16141	18240	5322	2499	19702	9292	20325
	5274	9028	10531	1688	20146	5153	7485	18445	4165	5614	10277	16781
	4563	3161	6533	5957	7089	2687	7105	21351	21515	22453	19592	7173
	1968	19358	11469	8780	17266	7586	12142	3066	7281	14577	9430	3270
	13924	12341	15761	12637	10962	2998	19035	4877	659	9821	20906	12168
	1736	20717	2543	16421	1821	18042	14352	15050	8399	19775	21325	7525
	17680	18001	19979	18487	6598	5555	10444	21216	21128	8987	1493	17533
	16118	1639	12595	68552	20981	8912	3290	5745	6378	9285	11287	14670
	11840	9243	9669	14995	13742	20118	9371	11429	12747	19245	1590	13573
	3695	20005	2712	20008	9988	1732	20129	19987				

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Sequence IDs for homolog proteins												
300:	16422	16652	2702	1006	429	10217	533	507	306	535	478	10780
	18650	18461	13998	11343	7459	5240	10390	15192	6367	19001	17659	17306
	18166	3899	19411	17674	6453	14183	9624	20799	11585	14626	21314	12049
	7812	18212	3745	13797	8320	4940	22404	21496	12527	18023	6674	2559
	15926	17879	9075	14547	21758	1689	16481	15621	18121	13519	12731	5774
	10662	11761	10902	17148	12381	2857	17664	21589	11961	19154	6201	21437
	11195	20933	21506	3533	4677	18511	4730	696	9569	17797	18687	7097
	20259	15252	13221	450	11335	20777	12713	22502	14915	21157	20371	3563
	12591	16308	7626	4212	19798	19458	5691	18292	16130	21296	2832	830
	14553	6434	18295	17956	829	12043	20779	1281	17745	1768	6547	16586
	7955	12705	11376	15449	988	20859	11129	22518	5552	9854	6669	5359
	9132	10964	1879	22087	13137	17298	3333	13752	20301	19370	2425	6946
	19538	14273	17165	15340	6427	15603	12419	10809	8003	13658	14064	4221
	7387	13284	20981	2316	3116	8418	3578	3386	6508	18217	22249	992
	13442	3471	14855	19949	5277	19885	2816	10917	9436	18538	18659	12816
	12308	15943	2515	20364	14701	8193	17579	22076	8890	2649	9329	21073
	8376	15177	10882	859	5990	9814	16053	5209	3144	13848	22428	19076
	5454	17056	14918	4088	11270	5837	9604	22455	19840	801	12234	21301
	1149	953	9960	1656	3755	12278	22119	21098	1005	10264	13037	11702
	20954	5581	5063	1118	6454	20632	1696	19474	14911	9381	4111	13374
	2932	3071	18551	22362	1431	12923	6509	19229	14012	5372	12362	17380
	20272	16391	13395	5132	901	9540	19228	14568	17630	2371	4694	12396
	15369	16597	3697	10741	16309	4927	13396	21621	8841	16662	11120	14081
	8692	9484	15204	6565	14320	2978	9294	7482	9493	1277	4952	7813
	7306	12296	12021	6645	9286	22489	13745	16653	19069	7780	15219	16969
	14762	18330	10802	10479	16663	3678	16713	7751	13703	3630	4691	9472
	10709	8542	7060	6112	22457	21974	20476	7333	6482	14526	7151	2644
	835	10655	12264	9315	2786	16253	9488	5634	17372	788	9280	22095
	18903	3706	15256	18593	5764	11115	12583	11568	13613	2331	5136	8073
	15998	5630	11304	19137	5817	5580	18341	8588	12540	2454	4970	17445
	2401	11869	6193	21516	10889	5190	13207	16465	9673	9771	11716	18575
	9584	12794	21399	20485	9218	18691	3350	18263	4846	544	19667	9933
	4140	1318	20418	11128	20105	16734	2376	15699	7061	4232	15357	14036
	5339	7107	19030	7165	21370	12103	4848	13211	22530	15360	12863	9975
	6398	14067	16683	21170	1924	890	8155	15866	10131	7187	4332	1235
	20330	12927	7088	5099	2302	12424	8303	17466	14322	11383	2282	15956
	3414	12982	18548	15665	10961	21084	10824	18440	16819	3730	13940	18821
	14864	1818	19607	7969	6546	16771	5441	8459	18266	5000	15749	13014
	14274	8444	4707	13097	15930	11872	2621	7158	6942	18502	5408	10837
	21928	13800	5188	19614	16117	4719	19714	1833	13499	3107	21492	12503
	21929	7921	1429	14398	22189	6439	12993	12307	6650	18994	747	5932
	18630	6683	1921	15651	5594	6958	13597	19763	10097	14124	14687	1094
	5780	7770	7688	15110	5797	7907	21169	3329	12627	4065	19882	22067
	19211	2061	7038	8909	16914	13129	19881	13235	16317	1551	14888	1201
	20264	7800	7526	2209	5887	10798	15317	10223	11351	10105	10661	15014
	2908	16412	22277	19851	12003	19616	11003	7768	6166	4620	13850	16231
	7016	20541	3458	1240	15787	20099	9282	11480	4994	6281	18662	7992
	9661	19875	11156	3619	14086	20948	16946	3456	6143	786	6709	5954
	17926	20839	22351	13277	15113	6368	7704	18694	3644	12154	3794	21257
	21638	18386	18111	21498	10731	13776	5539	14530	20282	7762	9529	17675
	15191	12380	14865	15825	2818	16442	5901	8220	18578	13297	2495	21913
	4526	16085	10965	15558	18982	2984	11245	17095	7536	5117	2132	20312
	4655	16568	21093	13882	5730	7976	7079	13035	6801	2800	5619	10126
	12545	2037	11704	9571	21379	3712	7685	4483	18456	22341	11197	13107
	16006	21848	20337									
301:	19000	5175	17102	15893	7025	2120	12938	12299	15442	11496	10074	5733
	14018	4497	12860	17771	17375	8161	11868	22009	7849	15996	13313	6451
	9249	12173	13520	22245	9579	19128	12786	1276	5812	2509	15030	5404
	7335	18498	6363	16355	19266	14084	8908	19966	8863	19169	539	3459
	13467	15720	2898	9093	9837	17258	1976	20125	1460	8614	10175	5871
	15351	6426	7149	12032	11271	8224	11194	11907	4519	3493	18304	22188
	18791	10516	18657	11078	6908	20626	14734	4564	18762	9992	1434	6230
	9846	4840	12934	18658	3437	11327	16354	4241	1568	14609	10156	19085
	969	13387	20299	14003	18420	8635	5706	21190	1432	6124	1526	18029
	16093	11179	1324	22474	8016	22059	5181	15454	1309	4573	20643	18651
	6220	9683	15336	12171	3835	20676	15459	11187	6374	19257	8887	12249
	15479	8309	2813	3769	17901	16142	2063	6092	19535	21118	1210	8401
	7375	9531	10590	7738	17854	1657	9700	15494	7894	15287	1226	6551
	13070	19534	13610	1802	22458	17237	8915	14991	3591	9885	9545	21263
	14344	19754	11799	10504	11873	18078	16699	19633	15816	12846	4878	20466
	21081	22381	17475	18403	21905	22085	18453	5736	17957	4021	7834	14499
	2154	13058	11572	3583	10692	7183	16133	15670	12332	1756	16507	18601
	11306	18332	20634	7994	12919	9064	5045	14968	9551	2414	1646	4753
	1805	1502	18175	18991	19442	17821	1888	18587	10549	18855	4858	7028

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	Sequence IDs for homolog proteins											
	14908	22205	5964	4933	4340	5271	927	8374	3316	9426	12837	20014
	16546	20576	5008	9914	10822	13163	7197	6338	17347	21212	3445	14444
	561	1401	13989	15266	20426	12281	7477	7453	766	14757	19524	4093
	17235	17808	16762	10080	9217	14800	9794	18834	2718	6390	20406	7926
	924	20355	13005	19727	8981	4683	7215	4131	6381	3407	11741	12599
	16185	18844	16344	19195	11057	8355	8958	11977	19693	20196	6610	14503
	22133	4744										
302:	8946	9168	14628	299	6214	4182	16075	11899	18083	13560	20787	22477
	16789	19264	6401	9620	5248	701	22290	21024	4074	1417	17543	11432
	17793	6222	18019	21867	3019	20723	20357	10575	3819	6741	17742	1775
	8903	15288	14774	2885	20494	20292	10001	11853	13330	17952	16001	17214
	1751	16904	10306	20788	12413	1843	16515	21706	2394	15207	18738	15056
	9630	930	15269	6646	18926	4515	7300	14791	6976	603	21092	2483
	21947	7441	14923	3660	12133	22216	4929	5590	11909	14884	9941	6002
	9040	13939	12896	7903	14465	21683	11508	8978	22006	5322	21963	2499
	2777	18240	5791	16141	9977	5658	15523	9292	11550	19702	1688	20325
	5274	10531	9028	20146	5614	7485	10844	2674	18445	4072	7836	5153
	4165	15169	10277	16781	7814	3161	5957	6533	4563	7089	2687	21351
	21515	22453	19592	7105	7173	1968	19358	10994	20056	7763	9851	13457
	8780	11469	7586	17266	3066	12142	9430	14577	13924	7281	3270	19033
	15761	12341	2998	12637	2543	10962	19035	20906	4877	659	9821	12168
	20717	14352	1821	18042	16421	1736	15050	8399	19775	17680	18001	21325
	6598	18487	15537	14525	21216	7525	19979	5555	10444	11512	21128	1493
	8987	17533	22098	6855	12595	18912	15079	5745	6378	9285	11287	14670
	11840	14995	13573	3695	19886	12402	20005	2712	9988	1732	1437	
303:	11613	15600	900	21525	7534	8911	20350	17575	7154	10397	5219	15446
	9261	1171	16015									
304:	14477	14507	15421	17494	18062	2648	7991	15716	18037	11158	2783	2025
	16965	22007	22121	19530	11719	9318	11530	17738	1299	21214	12334	21809
	4864	10621	8796	1194	4280	19732	18120	15953	2967	3266	19426	6571
	6888	17781	1697	10045	1251	7276	7126	12814	4960	7248	3598	17583
	17847	7140	8316	18820	21056	7036	15143	13926	18581	5501	1142	3253
	7339	4338	10287	9635	11127	20511	19012	13060	4347	12691	12055	20545
	21425	3704	15743	19675	16542	16559	21229	11524	9274	11075	8804	17224
	3133	3607	10123	13418	2973	11620	15872	11732	19109	740	1359	17419
	6843	1680	16067	3406	4022	6395	9511	2595	20688	4623	22346	2369
	17333	5395	11866	17305	10611	7631	15733	18432	1959	6814	6323	13183
	9078	3032	21942	3286	13158	20759	22152	18157	1337	3062	16447	2772
	10847	14538	4797	21087	7452	19143	16659	16530	16620	11651	17070	1585
	22147	10166	6601	22431	15463	10652	13842	11862	1897	19136	9220	17946
	12697	22065	3138	16162	17146	7667	19062	9071	11793	11610	7968	7594
	7221	10376	5672	11711	3151	4084	14756	8726	18769	3480	10028	2838
	20595	20275	1292	17594	12254	4853	20642	8186	16379	11759	11502	8591
	4288	11992	15333	9201	14724	3846	15765	5294	9934	3608	4038	2297
	1916	7144	15894	19202	4614	3319	11943	21007	5703	7304	9147	4298
	11434	11341	10440	4734	13768	7039	7695	14607	13737	10493	13662	16005
	5151	2008	20772	4271	19954	15488	16991	11303	17894	5027	7608	5609
	16228	18306	2556	13676	8198	5829	17178	6626	16081	16487	20616	939
	20854	11693	16083	22378	12968	16437	7624	6039	10274	13230	16495	10978
	13806	5631	6912	22114	2955	21137	8847	12918	16985	22400	13954	16430
	1905	19874	9524	6234	15225	4942	7297	20802	5035	10180	21875	20321
	12454	9019	4029	11248	16017	3758	13953	2462	4887	8042	7962	11126
	15081	22027	16352	2791	1889	15457	8559	17058	7622	4393	1128	8437
	21033	5138	12634	1952	5842	21247	15955	3808	10420	14719	17939	4794
	21353	19950	18656	13160	3900	11932	16466	13358	19797	5206	2289	9733
	10875	12426	15784	10942	12064	7723	14341	5120	18048	8171	11041	17196
	16314	20434	21075	20432	4222	8716	4904	18464	630	8403	6184	18819
	17228	16302	10762	9202	16022	17350	15237	12703	11159	17792	4597	7291
	15512	1072	6812	15612	4183	5466	17341	9980	4892	1108	1406	22046
	1630	11923	17859	5617	18198	5043	6967	20318	22123	1264	12469	12218
	10452	13091	8047	6109	14712	428	22157	7745	16695	22271	6934	7635
	18516	6231	1574									
305:	8099	12755	17111	978	1006	1542	15083	18937	12887	2035	10217	535
	533	507	306	478	8894	18461	12108	1501	12486	21909	7034	7130
	11072	14307	10425	15925	19332	1367	13146	7730	1937	9628	18825	609
	18335	21615	4370	7330	8575	15629	12213	5331	3191	19367	4875	5240
	11492	21592	7018	6367	19001	20564	13807	16754	21328	19708	4343	9940
	1066	2399	12207	1629	18478	7812	13667	3746	5720	16976	18312	3470
	5618	19921	17739	4546	14856	18520	3007	531	7912	8917	11529	6283
	8622	8288	17072	4299	7840	5830	6060	19606	3409	7000	8429	19346
	2857	17664	21589	11961	19154	18239	18127	11549	16493	21437	11195	20933
	21506	1079	9281	838	3533	4677	18511	4730	696	9569	17797	18687
	7097	20259	15252	13221	450	11335	20777	12713	22502	14915	21157	20371
	12591	3563	16308	7626	4212	19798	19458	5691	18292	16130	2832	21296

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Sequence IDs for homolog proteins												
	830	14553	6434	18295	17956	829	476	12043	20779	1281	17745	7955
	9854	988	20859	6669	5359	9132	16586	12705	15449	1768	11129	6547
	22518	5552	11376	10964	1879	22087	13137	17298	19370	3333	13752	20301
	2425	6946	19538	14273	15340	6427	17165	15603	12419	8003	10809	13658
	14064	4221	7387	13284	20981	2316	3116	8418	3386	6508	19949	18217
	3578	22249	992	18538	13442	3471	14855	5277	19885	2816	10917	9436
	18659	12816	12308	15943	2515	20364	14701	8193	17579	22076	8890	2649
	9329	21073	8376	15177	10882	859	5990	9814	16053	5454	5209	3144
	9604	13848	22428	19076	17056	14918	4088	9960	11270	5837	22455	19840
	12234	21301	1149	801	953	1656	20632	3755	12278	22119	21098	1005
	10264	13037	11702	20954	5581	5063	1118	14568	17630	2371	4694	12396
	15369	16597	3697	10741	16309	4927	13396	21621	8841	16662	11120	14081
	8692	9484	15514	10745	15204	6565	14320	2978	9294	7482	9493	1277
	4952	7813	7306	12296	12021	6645	9286	22489	13745	16653	19069	7780
	15219	16969	14762	18330	10280	10802	10479	16663	3678	7751	16713	13703
	3630	4691	9472	10709	8542	7060	6112	22457	21974	5278	4682	10694
	19198	20476	7333	6482	14526	7151	2644	10655	12264	835	9315	2786
	16253	9488	5634	17372	788	15256	22095	18903	3706	9280	18593	5764
	12583	11568	13613	2331	5136	8073	5630	11115	11304	15998	19137	5817
	5580	18341	2454	8588	12540	4970	17445	2401	11869	7142	4488	19396
	10889	5190	13207	16465	9673	9771	11716	16290	14313	9218	15665	15699
	5441	20485	18548	18575	18821	3350	18263	20418	11128	16734	19030	21370
	13211	22530	15360	6398	14067	21170	15866	10131	4332	1235	12927	7088
	5099	2302	12424	9584	8303	11383	2282	8459	3414	15749	18691	12982
	12794	10961	10824	18440	16819	9975	21399	8444	4707	13097	15930	11872
	2621	7158	14864	6942	19607	7969	6546	5408	18266	10837	21928	13800
	21492	5339	20330	1833	4846	544	19667	9933	4140	1318	20105	2376
	7061	4232	15357	14036	7107	7165	12103	4848	12863	16683	1924	3730
	890	8155	7187	17466	14322	14398	22189	15956	21084	16117	13940	1818
	19714	16771	6683	1921	5000	13014	14274	18502	6650	13499	19763	10097
	5188	19614	4719	3107	5780	12503	21929	7921	1429	5797	6439	12993
	12307	15651	18994	747	5932	18630	7907	5594	6958	3329	4065	19882
	13597	14124	14687	7770	1094	7688	15110	21169	12627	22067	19211	16914
	2061	1201	19616	7038	8909	13129	19881	16317	1551	13235	14888	20264
	7800	7526	2209	11351	5887	10798	10105	15317	10223	10661	15014	2908
	16412	15519	22277	19851	12003	6166	7768	11003	20541	3458	1240	15787
	20099	9282	11480	4994	6281	18662	3619	7992	9661	19875	14086	11156
	20948	16946	3456	6143	786	6709	5954	17926	20839	22351	13277	13192
	15113	6368	18694	3644	12154	3794	21257	21638	7704	21498	14865	18386
	18111	10731	13776	5539	14530	20282	7762	9529	17675	15191	12380	16442
	15825	2818	8220	5901	18578	13297	2495	21913	4526	16085	10965	15558
	21784	775	7504	10887	3135	11204	15835	17679	3002	18189	7516	6483
	9518	14034	11913	9964	2126	10118	3160	10150	10347	14405	15486	7545
	12799	13960	1340	3431	18982	2984	15366	2275	6738	11245	5295	2132
	20312	4655	16568	21093	13882	5730	7976	7079	13035	18086	2800	4062
	8280	13990	6955	16633	12655	12545	2037	11704	9571	21379	3712	7685
	4483	22341	18456	11197	13107	16006	9320	19090				
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	3122	4403	526	11601	7812	6192	17664	2857	21589	11961	19154	21437
	11195	20933	21506	3533	4677	18511	4730	696	9569	17797	18687	7097
	20259	15252	13221	450	11335	20777	12713	22502	14915	21157	20371	3563
	12591	16308	7626	4212	19798	19458	5691	18292	5019	17572	15704	16130
	21296	2832	830	14553	6434	18295	17956	829	476	12043	20779	1281
	17745	16586	7955	12705	15449	988	20859	1768	11129	6547	22518	5552
	9854	11376	6669	5359	9132	10964	1879	14844	22087	13137	17298	3333
	13752	20301	19370	2425	6946	19538	14273	15340	6427	17165	15603	12419
	18044	10809	8003	13658	14064	4221	7387	13284	20981	19949	2316	3116
	8418	3386	6508	18217	3578	22249	992	14855	13442	3471	5277	19885
	8739	2816	10917	15943	9436	18538	1973	18659	12816	12308	2515	20364
	14701	8193	17579	22076	8890	2649	9329	21073	8376	15177	10882	859
	5990	9814	16053	5209	3144	13848	22428	19076	14918	5454	17056	4088
	11270	5837	9604	953	22455	19840	12234	1149	801	21301	9960	1656
	3755	12278	22119	21098	1005	10264	13037	11702	20954	5581	5063	1118
	6454	20632	1696	19474	14911	9381	22362	4111	13374	2932	3071	18551
	1431	12923	6509	19229	14012	5372	12362	17380	20272	16391	901	13395
	5132	9540	19228	6169	11589	13306	3179	14568	17630	2371	4694	12396
	15369	11784	16597	3697	10741	16309	4927	13396	21621	16662	8841	11120
	14081	8692	9484	15204	6565	14320	2978	9294	7482	9493	1277	4952
	7813	7306	12296	12021	6645	9286	22489	13745	16653	19069	7780	15219
	16969	14762	18330	10280	10802	10479	16663	3678	16713	7751	13703	3630
	4691	9472	10709	8542	7060	6112	22457	21974	20476	7333	6482	14526
	7151	2644	835	10655	12264	9315	2786	16253	9488	5634	17372	788
	18247	9280	22095	18903	3706	15256	18593	5764	11115	12583	11568	13613
	2331	5136	8073	15998	5630	11304	19137	5817	5580	18341	8588	12540

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	Sequence IDs for homolog proteins											
	2454	3016	4970	17445	2401	11869	6193	21516	2447	10889	5190	13207
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	3350	18263	4846	544	19667	9933	4140	1318	20418	11128	20105	16734
	2376	15699	7061	4232	15357	14036	5339	7107	19030	7165	21370	12103
	4848	13211	22530	15360	12863	9975	6398	14067	16683	21170	1924	890
	8155	15866	10131	7187	4332	1235	20330	12927	7088	5099	2302	12424
	8303	17466	14322	11383	2282	14274	15956	3414	12982	18548	15665	10961
	21084	10824	18440	16819	3730	13940	18821	14864	1818	19607	7969	6546
	16771	5441	8459	18266	5000	15749	13014	8444	4707	13097	15930	11872
	2621	7158	6942	18502	5408	10837	21928	13800	5188	19614	16117	4719
	1833	13499	3107	21492	12503	21929	7921	1429	14398	22189	6439	12993
	12307	19714	6650	18994	747	5932	18630	6683	1921	15651	19882	5594
	6958	13597	19763	10097	14124	14687	1094	5780	7770	7688	15110	5797
	7907	21169	3329	4065	12627	22067	19211	2061	13235	7038	8909	16914
	13129	16317	19881	1551	14888	1201	20264	7800	7526	2209	5887	10798
	15317	10223	11351	10105	10661	15014	2908	16412	12003	22277	19851	19616
	11003	7768	6166	13850	4620	16231	7016	2717	20886	14522	5254	15519
	20541	3458	1240	15787	20099	9282	11480	4994	6281	18662	7992	9661
	19875	11156	3619	14086	20948	16946	3456	6143	786	6709	5954	17926
	20839	22351	4726	13277	15113	6368	7704	18694	3644	12154	3794	21257
	21638	18386	18111	21498	10731	13776	5539	14530	20282	7762	9529	17675
	15191	12380	14865	15825	2818	16442	5901	8220	18578	13297	2495	21913
	4526	16085	10965	15558	18982	2984	11245	11137	12977	2132	20312	4655
	16568	21093	13882	5730	7976	7079	13035	2800	7101	509	307	305
	12545	2037	11704	9571	21379	3712	7685	4483	18456	22341	11197	13107
	14927	16006	532	428	372							
307:	3349	11861	16061	5336	12949	18887	6597	3983	22099	2324	447	4512
	11806	9383	17441	7957	16578	12877	12285	6745	8158	22143	14055	16201
	1754	1561	18005	11717	9710	6672	1451	10276	2243	21572	5576	13128
	10885	6027	17037	15496	10454	6068	15308	2899	11018	14627	20697	3974
	7859	15270	15938	5811	2698	16879	8859	21272	14729	18033	840	5497
	13669	21714	19513	5502	16413	15747	1844	4651	13831	22094	8195	21288
	3065	16776	4822	18118	19091	5553	14834	21349	12572	16815	8955	13075
	12733	4648	22049	5403	1029	1877	22486	14277	19152	1410	21143	7372
	21858	17690	6467	9703	12831	4606	4506	19173	2942	1265	17141	18407
	8705	18889	4746	3811	9106	17506	7669	11911	20449	10409	22212	9181
	21792	22305	9003	8407	9234	9976	16656	2745	18946	4081	1944	12668
	7458	13728	15650	11471	11697	10966	5324	9173	19342	21172	9379	17192
	21538	8949	22434	3555	19594	13734	9786	21821	21772	21456	21196	9187
	10524	11998	20944	6938	7779	8979	13537	5360	18851	21252	15297	11734
	1781	17886	3931	16508	9825	5806	12904	4987	1438	8935	16959	16382
	1164	22141	2007	17210	14488	6399	14781	6373	22109	599	9398	9473
	5195	4504	5963	14256	6939	6345	1162	18406	17784	1442	4331	6935
	5879	18326	2240	20428	19414	11272	14731	3444	1809	21833	14869	12121
	5793	8845	20490	14861	12563	4528	17811	1567	9570	733	11892	13985
	11612	1512	1070	2951	19948	9341	9353	1718	16198	8546	15048	9919
	20674	3909	10843	16432	10218	15654	4043	14847	6714	8707	9886	20997
	22088	13038	8037	9178	5352	3851	6484	16180	20444	13259	20733	21480
	17651	22149	13792	13689	6933	21822	7825	13935	22010	15175	7093	21104
	21571	14166	13059	1320	19388	12387	18647	10615	2572	16738	17277	10671
	13485	4638	2352	7397	5048	13275	7941	11316	9127	6631	17029	14783
	5081	2879	3446	12504	11878	2839	3228	19752	1088	1402	6179	16798
	22525	16859	10813	2895	20050	10689	9920	13359	6382	16804	22048	15372
	17024	19135	2131	20708	19186	7679	13583	7611	8668	2471	18443	8080
	14254	18267	2356	17724	10645	21850	7740	18043	7128	21146	15408	8078
	2828	15730	8513	18968	650	14046	3085	13243	11222	15011	1105	3976
	1507	15891	10269	17937	6229	13505	13897	17262	1497	9774	5505	5939
	7480	3041	12199	18054	15132	17133	9987	21835	578	22529	20727	13110
	17553	15284	5186	15066	12304	21091	9863	4969	14128	13927	2253	22173
	20557	7177	21588	7134	20606	17839	15095	21594	19310	4399	21404	1167
	2570	8102	16155	14831	9194	9119	2558	21715	11856	11165	7573	10855
	15158	22322	8996	12383	18252	20458	20237	9891	4099	16104	8881	12231
	2561	647	22387	19765	4615	21305	15139	4964	20281	11812	22153	16216
	18833	21797	7671	15097	11028	2172	17562	12574	2664	9816	12353	2954
	21428	12735	2392	5226	8680	17177	18591	20343	15667	21341	11930	10157
	19825	5210	7091	22444	3844	717	18902	14808	11659	8670	1785	8233
	21693	8835	7167	12659	3869	22226	15589	13405	5280	13156	10456	10253
	16881	14660	15728	6461	7132	8140	20493	14049	12322	15683	846	12989
	4867	5866	20584	15020	1964	20885	21697	12785	2196	12335	15689	9927
	763	1531	20138	11358	1132	19079	14162	5361	7543	18763	17112	21617
	7915	20412	1643	20533	8020	9158	2930	19107	21064	3201	11077	14726
	20135	9411	15348	9402	12669	15995	8168	7755	3112	12219	551	21933
	8916	13876	14513	6877	8597	18116	8268	9085	9769	11890	21961	11709
	10758	12800	8640	1212	10509	21023	11267	21751	1557	18735	18051	21254
	15200	5771	17912	3381	18702	19564	12819	17593	8712	8128	1909	6496

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	Sequence IDs for homolog proteins											
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	12167	17453	9268	11122	12880	13525	21522	5843	7885	10162	18002	13496
	9474	11489	14139	5078	13260	10989	5480	3428	22424	15138	4252	2826
	5882	20175	15811	16116	7879	12274	19326	5318	8325	1069	22306	6156
	14294	21302	22394	4521	10893	5702	4766	568	15271	1077	17778	9726
	14452	21497	5648	10532	15330	3647	8350	19227	17520	19834	16427	12852
	9016	11208	9994	5906	20197	1115	15244	22452	15164	4258	6471	14545
	6910	6417	21796	17471	17991	14998	15383	3215	10382	2580	8289	8452
	12605	11475	6041	3868	2991	13102	15010	21365	21059	6894	21208	11757
308:	13659	8503	5417	2636	18255	14258	18186	14480	2997	12520	20393	16958
	14070	11296	3421	20754	17033	17928						
309:	22368	4230	16648	2237	2516	16152	10415	5473	14703	19022	18480	3997
	17101	4156	10514	13955	12976	4059						
310:	4051	3527	13345	2678	8550	12739	5968	11252	1249	13757	11908	13883
	642	18741	863	15128	20888	14323	4672	8571	16644	10920	8004	22023
	10377	10056	4837	19713	7234	1632	16113	13478	12526	19784	19698	2701
	14658	15220	8365	18917	19359	21121	8529	17053	2009	2989	6906	5789
	4862	8968	21524	13803	21337	5536	3377	936	20910	2445	21144	20276
	15766	10716	15947	17616	7904	2437	12791	8028	5119	21686	20353	6765
	13032	12566	2929	19589	6025	12404	5688	7908	7436	18460	14549	1975
	9403	18910	15871	5414	21648	22373	15001	8960	8512	14839	13626	2150
	18521	4687	4104	15162	19653							
311:	7246	7633	13566	4922	7189	6648	3075	2678	8937	18998	20791	2442
	4593	2102	13757	8484	11908	21901	9697	3719	21432	10971	8004	22023
	10056	4837	6659	9021	8001	9591	4169	18319	12526	20405	19739	12836
	12342	14209	15108	19698	21200	14093	4820	21147	16711	686	18917	21915
	21121	8529	17053	2009	2989	6906	12853	7577	6127	14095	21524	6916
	13803	7336	19598	11276	21713	14811	21337	20910	936	2445	11616	15947
	17616	8331	11034	19471	5916	17862	12115	14492	18721	8414	19179	5371
	9277	5119	17025	20374	3996	5057	1399	16384	9470	18719	18399	3401
	8557	2158	3928	19925	15780	1172	19003	4754	6752	7557	21304	14324
	15694	2929	15268	11094	19589	8713	6025	14222	14987	11178	3467	7373
	1975	9403	2856	8286	16534	8056	9369	2719	15871	5414	22373	21648
	1955	5457	18895	17041	22161	13812	8512	14839	13626	18521	21678	2002
	4687	18560	4104	7854	18098	13647	15831	11038	19653	8205		
312:	12932	12556	10612	8324	20661	21261	10886	21109	3162	13645	12519	14154
	4627	9952	7890	12288	13254	22516	21541	11332	12510	6556	17293	7951
	6797	12554	2010									
313:	15796	4326	10345	13029	13317	20973	19570	14613	13103	3759	11764	3247
	11747	9513	3029	20696	20193	9454	5495	18809	16012	8066	7668	15744
	1836	6499	12779	2481	14822							
314:	7479	533	507	535	306	12575	15642	18461	5073	9804	18997	8666
	3659	6320	6367	19001	6157	11916	2258	21356	9857	2163	2584	3331
	20086	6423	4662	3838	14933	8860	19820	15915	7403	4850	4714	9730
	12137	14919	12016	19643	3913	17315	7812	21939	13951	1478	7199	10536
	9491	3917	15376	4608	20333	7216	21640	8527	16880	19870	10959	4725
	15069	5944	17598	6786	14232	4110	10546	16887	4811	15616	10586	10067
	11756	20433	13391	16270	10468	7655	21719	5755	2857	17664	21589	11961
	18800	19154	879	12644	16878	2030	4833	5428	3533	8904	4677	18511
	4730	696	9569	17797	18687	7097	20259	15252	13221	450	22502	14915
	21157	20371	3563	12591	16308	7626	4212	19798	19458	5691	18292	16130
	21296	2832	830	14553	6434	18295	476	12043	20779	1281	17745	16586
	7955	12705	15449	988	20859	1768	11129	6547	22518	5552	9854	11376
	6669	5359	9132	10964	1879	22087	13137	17298	3333	13752	20301	19370
	2425	6946	19538	14273	15340	6427	17165	15603	12419	10809	8003	13658
	14064	7387	13284	20981	2316	3116	8418	3386	6508	18217	3578	
	4221											
	22249	992	13442	3471	14855	19949	5277	19885	2816	10917	9436	18538
	18659	12816	12308	15943	2515	20364	14701	8193	17579	22076	8890	2649
	9329	21073	8376	15177	10882	859	5990	9814	16053	5209	3144	13848
	22428	19076	14568	4694	12396	15369	16597	3697	10741	13396	21621	8841
	16662	11120	14081	15204	6565	14320	2978	9294	7482	9493	1277	7813
	7306	12296	12021	6645	9286	22489	13745	16653	19069	7780	15219	16969
	14762	10802	10479	16663	3678	16713	7751	13703	3630	4691	9472	10709
	8542	7060	6112	22457	21974	20476	7333	6482	14526	7151	2644	835
	10655	12264	788	9673	9771	11716	18575	9584	12794	21399	6281	18662
	7992	9661	19875	11156	3619	14086	786	20948	16946	3456	6143	6709
	5954	17926	20839	22351	13277	10965	15558	8891	10152	15189	13161	3256
	13226	1748	21271	22258	10136	18982	20726	10154	17115	12652	1426	12623
	4475	16706	17850	21904	545	2132	20312	4655	16568	21093	13882	5730
	7976	7079	13035	7273	14619	2800	12728	15228	19263	10088	305	16894
	6203	22106	19049	10427	11733	8133	372	12866	13782			
315:	3342	12667	2100	12617	1136	6158	17567	4891	9212	13652	2310	14039
	8257	4890	20474	16825	8834	4127	1369	14688	17548			

TABLE 17-continued

Sequence IDs for homolog proteins												
316:	10331	15934	2046	6293	19503	17105	13130	7604	20972	611	2151	19670
	1110	20162	9143	9176	19023	19084	18099	5356	15439	3212	10361	21551
	20873	18300	6915	11130	19131	17963	7910	4920	4372	18216	8334	5551
	11009	21068	13009	6829	20236	2330	15785	1052	14929	4869	4064	14251
	6409	4771	21722	3477	22283	4071	13419	2771	12516	2855	6554	5053
	15301	13629	22091	9959	8014	18394	7184	5437	10014	15912	7764	9611
	13654	12151	12808	1755	10215	21979	12492	8018	7254	20380	2845	654
	5061	7274	9568	5018	11235	6804	8938	12700	17001			
317:	7147	17102	22335	21107	13529	17232	12299	15442	10074	12860	8161	6451
	9249	12173	13520	2381	7179	2397	4681	8032	10026	17837	1679	750
	13467	22304	9093	12920	8746	12849	8975	8614	11049	15351	6414	11194
	18365	22000	10060	950	10516	16860	18657	11078	20626	15349	9992	11321
	16068	13071	20575	10629	4241	12058	21534	18040	574	21837	6124	1526
	12392	2919	22474	21550	1309	19435	13170	2632	14407	19257	15479	17487
	7797	19535	13125	7697	9338	11284	15648	2144	9885	3591	21263	9545
	14344	6947	19431	21279	4756	13704	4125	11670	6044	22381	21905	15904
	14499	10692	12332	1756	4806	18332	7994	9064	18991	17391	20098	22081
	5015	11957	13991	17712	22029	21507	3779	6619	4824	1847	11561	2927
	7497	1618	16567	1625	1011	14504	1983	2353	13906	16938	11796	2922
	13819	606	3676	2458	20599	20531	13948	7520	12498	13705	8646	9042
	9750	14969	563	1092	8562	6341	3562	11565	15599	16895	12974	1939
	16577	1711	21985	5754	19800	15748	4371	12415	2463	4827	5656	6520
	14881	1513	19711	6790	20528	13821	9526	8611	6058	17821	1888	18587
	4858	18855	7028	14908	22205	5964	4340	5271	17773	927	8374	3316
	2666	20014	21527	9914	10822	7197	21212	13163	13989	17347	15266	1401
	6338	14444	3445	561	9349	20565	2095	7453	18711	19524	4093	8735
	14800	9217	16762	10080	19195	11057	11977	21372	20196	6610	14503	22133
	19181											
318:	4562	9606	1444	14309	10107	21463	18996	14333	1334	13632	22339	19891
	15309	3134	19973	17693	15433	13252	20233	7289	15373	8208	21182	21283
	14523	6862	8920	22389	7427	19075	14622	18190	16360	12132	1586	14883
	3538	22299	4909	6348	9295	11703	6913	16728	19809	21668	18897	20235
	616	10625	12272	10812	4295	2449	11240	20715	10788	12331		
319:	11506	8025	19504	17096	9236	5967	13265	13150	20345	2575	15093	720
	9238	20846	7110	18462	16689	3666	13238	20249	22504	5681	15821	11308
	7263	2587	3204	8488	1135	3170	19880	7687	4736	5783	20141	8454
	11622	3641	10121	15474	15016	3635	12476	2148	6474	12754	10278	4251
	2157	17396	18150	5472	2435	9967	3440	12802	21724	16131	7711	10389
	5452	18194	15428	5298	16650	13697	3148	15338	9355	4542	7607	12624
	9835	6871	1450	17202	4346	18156	2256	5469	11562	11593	8125	13465
	21018	14122	6978	1534	5284	19934	13992	9438	9860	16616	13159	22237
	9239	12122	7442	20605	16637	625	10834	2546	3875	5692	13941	
320:	5584	14500	1413	1303	11425	12432	20553	5678	19728	1702	21840	16132
	13978	8053	11638	17005	7048	12602	12897	18092	1532	16921	11347	8929
	2022	22014	21806	20100	17247	5940	13718	10507	20917	13044	3334	11629
	3850	19276	8082	15982	2091	8247	2827	4647	21352	16763	13875	2729
	11068	14988	22366	6081	6500	17279	7348	9062	12873	13199	7794	6832
	16726	7795	12202	12467	5788	10596	12756	21948	11263	10951	13316	8432
	13127	9984	13493	8019	12038	1826	14472	9125	4955	19548	16684	5905
	16785	3169	20313	12232	10211	6536	20084	4322	19294			
321:	11679	7712	4765	2778	10428	15613	13759	8748	15529	4789	4143	22492
	10520	5899	5524	1150	15997	6728	7250	19339	3882	2486	16390	13804
	4361	20834	20825	586	2032	2861	14363	17505	15033	6284	9806	19295
	8378	20979	6962	22356	6126	18081	16902	16016	11797	14905	12294	1932
	4974	560	4872	19916	7886	18272	11004	21567	6122	3929	10292	20964
	14636	4316	16294	16670	6202	3283	3979	708	10683	3722	9024	10315
	7707	21597	12187	21031	11517	17433	1323	3512	20375	12464	21941	10366
	13212	15089	3993	3918	17676	18119	2709	17107	15788			
322:	10548	4897	5425	7818	3878	10642	3310	16365	9020	12789	17219	2142
	13865	19002	946	18211								
323:	12932	12556	10612	8471	9836	7200	3244	4931	6155	11441	5925	9952
	1283	20609	2129	3224	8050	2693	11630	8765	8258	10271	17801	10768
	7008	3010	16997	6501	20840	3978	2010					
324:	10963	8235	5742	21966	17140							
325:	15756	6758	15758	5287	19343	4588	17303	13336	21407	16436	6718	
326:	16712	1166	15865	2733	17246	15303	1381	13492	6572	7728	13605	12382
	9290	21152	7868	21359	6654	2544						
327:	12913	16464	16273	20905	3701	8623	4539	11237	7785	12606	12734	1726
	4555	7538	13748	14436	18787	11199	15234	14408	15929	7578	1919	8057
	11210											
328:	14125	20217	16758	5776	15086	18339	9344	13845	5197	20795	5897	9137
	9973	704	18058	11958	7252	2114	7827	5752	4689	7592	15102	22013
	12505	15413	5397	16345	11067	11445	21494	14366	3450	8189	13758	10214
	21577	10815	1385	19042								

TABLE 17-continued

Sequence IDs for homolog proteins												
329:	3497	2714	8101	4216	8074	1106	1600					
330:	11223	1913	6535	17340	17586	15949	10628	5279	16989	13504	22441	20437
	16847	20368	18727	20627	677	8442	2847	12004	5478			
331:	13633	5900	8539	14672	12233	964	10478	20775	5875	5805	1804	1598
	8760	4906	10137	12276	20894	3902	1838	1416	13999	8927	20239	21067
	2846	1536	951	9346	9547	21436	4596	12781	4010	11786	8601	10761
	6187	19637	20291	12933	1404	16680	16262	4172	6985	11107	10370	17700
	13722	7971	3488	17731	14386	6750	13862	2765	17564	11582	6358	16691
	21558	16323	14350	16234	10634	8984	7275	21757	12586	15643	921	10884
	20529	8362	4086	15778	8213	645	8641	14759	21903	9293	2872	7350
	12282	7277	21911	19806	10064	12113	15339	20238	1645	15286	17911	15808
	9799	12685	4914	19213	10728	2852	4839	20536	7995	7379	15240	12971
	591	20690	5666	5145	10145	1126	13494	13052	13798	22187	6567	2224
	22255	22276	19919	8963	4880	11857	15344	20168	20601	21712	7009	15363
	10724	8126	7044	2098	12067	13898	7690	17967	22554			
332:	4051	7246	14199	4757	2211	19939	7119	18627	18219	10672	19725	20509
	7686	2989	10561	7284	936	20910	3464	21563	5884	11537	21063	1972
	3103	11411	17085	21614	20041	6920	896	19271	21101	6679	18617	19003
	7557	2937	8512									
333:	11864	1840	17916	16388	781	8033	2364	22015	9748	2475	765	14146
	13993	16445	7070	19406	13139	11260	21048	22437	16423	12388	15277	9405
	13452	21701	15472	21519	18268	18140	17189	10852	15461	8741	9641	20297
	21384	9522	16319	4702	6436	9574	18726	3628	16593	18634	13820	16639
	4189	17966	3524	13210	12214	13114	18483	11648	5974	15580	4570	17225
	19309	11814	7466	15434	16431	13455	9128	17770	17597	11744	5668	18077
	20332	12252	6487	5722	19526	13902	14620	19013	12349	14056	3612	8715
	15923	4913	11247	1777	16114	9983	8124	7153	20006	10025	1074	21879
	4977	19631	8517	5456	9877	4139	21162	4364	7696	9702	1769	9365
	5341	7159	5323	19419	19967	19719	15541	14191	10391	612	17071	22520
	2596	16797	826	17040	18360	6069	16301	22129	12523	19596	3074	6712
	12666	21205	18284	21965								
334:	22427	862	20385	6265	12399	22070	17740	7828	4067	1153	11326	2935
	9841	19586	16621	4285	4474	5816	1468	12636	2870	12256	15396	20978
	13936	20481	9196	15850	17759	14083	17877	11918	14099	22052	4350	14967
	3030	4936	6573	20255	16179	17938	6661	14748	18841	8544	17559	16186
	13096	10817	20956	15131	16981	20307	6896	9262	16287	14784	4658	18310
	6506	1358	8689	18061	6280	1214	4418	13166	8421	2972	19253	6332
	1033	16181	10378	16100	12772	1621	974	9705	11370	21857	9111	13663
	6502	15769	18274	20182	18579	16062	18202	10290	15049	10207	10284	15057
	16286	790	10968	5513	1193	17665	4712	12568	13764	17032	778	11095
	19866	6900	21331	931	14040	5675	18493	5449	2779	10498	12780	10602
	10664	9704	2890	2696	4265	20376	6349	5782	11580	15846	4001	15619
	21400	16911	11079	4939	15709	14567	17601	14494	2988	2987	3279	14867
	3013	15708										
335:	15578	12136	19850	745	14354	11893	10400	16221	5102	12842	19938	8836
	6356											
336:	1655	8875	17969	16217	19832	4954	10256	13907	2280	7705	2896	5571
	6016	2423	14230	7769	16575	6956	11570	638	22347	12730	3084	7136
	21153	979	18133	14470	4762	13775	13517	18643	14115	20989	4195	14211
	17841	21732	2378	6456	2604	16482	9054	9876	6696	20958	9729	13852
	22311	12997	5664	17434	511	11309	2192	7514	21788	10558	17846	13447
	19287	9827	17314	19480	8685	19289	9913	16783	7798	15355	21362	
337:	16000	2106	21931	7956	15630	12717	10346	15324	20316	3593	13203	3167
	2799	12590	13815	4459	3056	18383	12953	14071	22160	2913	15509	16846
	14685	8814	5931	19964	20780	14871	13615	6779	997			
338:	20669	3012	4857	6538	14648	21791	21544	15892	20656	17483	5020	19379
	16363	12470	5494	9395	17737	5910	3081	8480	20365	7510	1412	19099
	8801	14807	16161	2393	10298	8123	1239	10701	8769	20670	18966	739
	17909	2578	9830	13785	17449	6339	13378	17851	10673	17975	18270	18869
	20842	16312	5144	8392	13794	20142	22008	4642	7811	9505	7022	21431
	7054	13460	4715	13880	15813	16187	18556	12071	5168	4445	8109	6238
	19089	10095	2361	20340	16200	16747	6028	22386	10599	2796	3476	14418
	7731	5135	20971	13422	21726							
339:	2298	2436	19901	14207	19971	5786	15380	16523	17629	1543	2607	3939
	13893	13623	19506	1858	2400	20267	18864	3159	17867	6744	4520	5184
	1289	5953	16468	8962	5695	6006	21230	5243	4876	2057	22012	13975
	18334											
340:	5094	13921	9689	10104	19369	17978	21082	2690	17645	3853	21213	17435
	20373	10839	8089	4282	11406	17050	9439	11816	3709	8068	13476	14133
	17945	20398	2090	4164	2229	4799	13949	13578	8589	10573	17122	18689
	4604	7491	11399	9657	1351	17934	21685	9266	20395	18832	4616	13018
	17935	782	21358	4923	2048	7355	19368	10540	3418	15391	6352	1454
	584	6023	7278	13416	7550	12889	8632	13053	6040	1583	16498	7544
	2590	9046	601	4785	7174	3594	18195	11021	9022	8275	1685	3624

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	Sequence IDs for homolog proteins											
341:	13668	15794	6342	14448	9278	20512	8200	16696	13521	1647	7170	15662
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	4810	16842	15999	3541	7952	9937	1893	9025	19963	10155	18805	2652
	3473	21709	10794	17386	16395	9463	14603	17255	17919	4407	21734	1453
	17376	5269	14505	22325	7898	5201	11700	7509	3737	5907	11800	14887
	18221	3408	1391	6603	945	2741	11668	22559	13979	16492	19717	12052
	13678	12316	20893	10627	18110	9396	17457	12447	17706	4188	12736	10213
	5657	1361	17750	2164	20757	10342	5557	13427	1459	5874	11035	14177
	18713	8770	13138	12686	12216	4228	12420	12044	4116	20177	7717	20582
	6544	20287	13392	5213	21383	20420	12277	610	7242	13209	21266	15605
	17695	1713	6386	7399	3771	15478	14510	14171	22266	6037	14656	20179
	7964	7223	20189	1994	21418	7850	8756	18014	14079	726	12260	21444
	10406	2633	8511	11121	10904	3092	2853	17906	16524	8187	17998	20778
	2286	20199	3729	6145	21008	2565	12962	1257	15354	10610	7157	1796
	6315	17300	22423	14435	16471	16628	6594	21171	9956	9842	18573	17327
	8572	9431	16077	13255	10967	18428	7421	19940	17552	22215	6311	22128
	15501	21897	19865	6983	7587	17139	17241	18872	10791	18810	8812	5978
	20019	19994	6664	13673	2650	8721	16038	14722	18896	21111	2762	17606
	10806	18027	9130	18559	12287	11513	6131	3172	1990	4027	5292	3287
	13481	11191	19301	11297	10021	9171	14682	17190	14540	1140	8118	
342:	2631	10657	18699	2536	6440	2600	16629	20719	4729	7634	14681	5022
	8936	10883	18494	6327	9575	8157	8096	14112	2076	9896	11151	16731
	2204	9035										
343:	2755	21932	4777	6313	21861	12723	19508	1200	15989	16994	5687	6685
	14644	15427	18561	20955	5319	10512	18861	4752	4558	9237	14495	2731
	18748	20853	21624	4158	6682	15121	13328	11123	17204	3588	8417	12524
	14426	12139	5914	22397	13082	3579	4217	4229	10653	20451	3376	17804
	6004	10303	2139	15227	11831	18631	19845	12159	11935	18000	18066	13477
	5998	16773	6555	6113	18981	769	10905	22461	18369	7501	12698	17209
	22284	15974	3000	1328	15319	13157	21846	21899	1244	17408	7057	674
	11714	14760	3856	22403	13952	5958	18866	16803	5945	7999	10446	17518
	21309	12969	5105	10656	10777	18972	14634	7566	9182	10453	6623	6029
	3857	1041	17997	10387	10643	1035	3246	9229	18431	9219	13687	4600
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	4206	8608	11403	21291	15104	9577	22470	10395	7106	18085	1045	18438
	20164	5627	6989	3125	20664	9899	17477	20384	8914	13339	21568	14346
	15753	18139	2610	22040	12680	1930	10147	11672	21762	14042	4281	8445
	18322	7765	11544	8117	10562	17367	2534	14153	16918	7771	16968	14118
	14857	20095	4419	15545	5134	11331	9802	4911	9938	3150	22321	8071
	13544	4128	7168	8967	22547	3271	5965	9073	16529	16953	7176	17918
	1026	16418	11579	13510	11163	21202	11509	15037	10348	12555	7467	9767
	15877	20472	13410	15361	12759	10511	8273	5946	3774	8121		
344:	0											
345:	11342	13022	13189	13375	19355	4603	9001	693	10423	19460	11989	3379
	20654	19018	22196									
346:	4152	1714	20305	10236	21335	10203	4070	20587	13194	15640	10242	11539
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	17513	7821	7744	10704	11320	3178	16909	21864	9099	11919		
347:	15403	7222	17930	22425	8943	8767	5431	9412	9840	7098	10706	20039
	19399	18679	3063	13922	12891	19177	14765	8888	3766	15264	15112	8346
	19249	9496	8467	12097	7066	13354	10438	19683	1867	13713	11392	20463
	8419	9530	13590	19828	17789	3181	19673	20308	20048			
348:	22289	699	7239	11768	21811	2946	15818	18586	10674	14308	3720	10934
	14107	19528	13730	3925	20977	22047	4398	22391	16849	20631		
349:	6607	11545	4182	16789	10863	11170	7754	13889	17668	6741	14774	8116
	16721	683	13808	10075	2147	13320	7970	20540	8978	11576	16025	12292
	10319	5002	13246	7075	22235	11091	9999	20403	14955	7021	7400	15424
	1403	1576	15201	1547	21389	2191	20891	18977	17393	11512	10958	14007
	6534	12539	20887	4792								
350:	21637	9766	13473	10430	2373	10229	22472	2533	8573	9183		
351:	21639	6558	15717	6583	1489	21115	14590	22491	22170	13729	14708	11897
	9169	16003	16657	18303	2503	7619	9667	19462				
352:	14832	4680	730	8944	19323	9756	8807	16549	6800	8830	14997	16942
	1293	1086	19167	624	11497	15185	11336	10574	6438	21022	10877	3498
	1533	10113	8352	18565	10340	12363	3314	18700	8755	21000	5888	14051
	11660	10255	20975	16898	1028	4899	9807	15549	1039	16373	21500	3757
	4390	13334	5158	7861	19157	5010	21692	13142	13526	12155	3025	15524
	4634	18132	20879	11836	6517	5390	6944	17642	10919	12777	22312	12374
	12089	2107	8665	10063	15827	10534	19377	14693	4078	16983	7351	21180
353:	9803	5872	20880	7736	9394	19214	20066	4813	3867	8129	6810	8821
	14360	9758	10208	22542	16794	8724	2461	5260	11314	17374	20064	22105
	20232	17121	17288	16874	14516	1119	2781	15198	20079	14792	3439	22298
	12105	21450										

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Sequence IDs for homolog proteins												
354:	6321	5225	13406	4040	4448	20067	13787	8883	20377	876	9126	21945
	4701	11644										
355:	8510	12886	3986	1767	22183	9676	17318	13827	6552	22440	15136	22229
	15255	8556										
356:	20329	7584	18151	12782	19780	869	1234	4543	4443	6003	10879	6195
	14766	2261	5303	18455	14900	13423	4770	7064	4996			
357:	1090	22239	4778	3892	10096	3089	20675	8225	3300	3785	10016	16285
358:	7246	7633	13566	4922	7189	8550	21432	6659	8001	9021	4169	9591
	18319	13478	12836	12342	14209	15108	19698	21556	16875	20650	5851	17486
	6249	13780	15776	11726	21200	14093	18917	21915	21121	8529	17053	2009
	2989	6906	7928	14192	7577	6127	6916	13803	19598	11276	7336	21713
	21337	2445	11616	17616	21069	3827	12208	819	16095	11103	17030	6075
	5459	17025	20374	5057	1399	3996	16384	3401	8557	9470	18719	18399
	2158	3928	19925	15780	1172	19003	4754	6752	7557	15694	2929	15268
	8286	16534	8056	2719	1955	18895	5457	17041	22161	8512	21678	7854
	13647	18098	15831	11038	15162	8205						
359:	11518	14223	17501	6542	13569	4821	16169	8132	15637	2270	10309	5708
	18374	9446	7790	12784	7569	14187	5525	7188	21691	15258	4550	7616
	5261	15163	14560	20144	10693	12244	21413	6135	7464	11142	13491	17655
	15676	14174	18333	13472	20648	6435	14763	13495	12676	18906	12036	16066
	21593	21667	14370	16048	17609	19658	5604	575	21518	5309	13744	15880
	19484	6704	658	8704	16710	12907	19375	3306	19468	11042	3984	17175
	20965	1206	9155	20970	6796	17057	11008	18605	3353	4650	9058	7988
	19743	8369	3654	18497	11952	2866	16796	8504	20034	19086	4409	12452
	12908	7530										
360:	13327	3981	5070	16490	20204	5909	15321	10310	12746	5760	6045	1730
	1018	15233	13486	17387	20991	5406	13208	21716	9902	21763	22315	6472
	824	1364	18250	18767	12499	21700	3665	8788	19915	12114	17927	19363
361:	13771	10043	10800	17501	13569	6854	4637	16169	8132	2667	15637	2270
	10309	18374	5708	9446	9291	12844	7790	12784	10720	9725	13741	5525
	15920	7877	7188	21691	15258	6705	4550	14008	15544	9706	7616	14358
	13182	14560	16722	1472	4000	1388	4261	10984	9823	21413	4976	9514
	16806	9972	9224	13061	15247	17984	9925	19953	10247	2676	11680	9751
	7643	12752	14983	15727	20648	3200	6435	14763	13495	13003	16940	7214
	15976	5735	6270	22352	12931	14053	16048	17609	575	18286	21834	10842
	18927	21518	20097	5309	13744	15880	19484	658	8704	16710	19375	3306
	6347	19468	10410	10451	11618	20965	12916	1206	20970	11008	1237	7988
	19743	20088	8231	4522	18497	11952	2866	15466	3609	2403	16796	13539
	14806	5364	12620	20699	15426	4409	12452	5296	3102	20918	9156	12665
	629	20947	3649	7530								
362:	1670	8427	4513	13628	17835	1981	20663	1254	19692	11385	11148	18372
	18636	1663	18409	21940	17744	17838	14190	16086	18411	682		
363:	2344	7205	10404	18090	3530	22282	2138	1522	5878	7220	18971	21529
	18900	21077	6911	22318	1047	9881	13404	7614	13515	13092	13300	20784
	3818	8910	19715	892	11279	3262						
364:	7108	14914	4339	11633	1095	18100	17413	19557	4087	5710	14536	8563
365:	16767	7229	7241	19193	14780	8455	1669	2113	16394	13341	4965	20987
	21669	16094	13151	2242	9452	6246	4432	1828	6419	11839	6713	3448
	5129	7881	21433	18954	18710	15718	12146	16149	12186	2849	17256	2464
	11803	21181	15484	8463								
366:	6504	7524	14750	15585	13755	6170	12273	16565	1049	12336	18307	21260
	18677	18863	18346	15597	19755	3751	19920	2278	12086	1347	858	13286
	14325	1020	15133	10620	2444	3050	16139	16876	1573			
367:	16254	15810	10496									
368:	4014	5426	1644	4368	10252	8347	14623	6336	3143	17492	2883	8191
	13701	14972	3068	11055	13245	907	1811	17743	3222	22379	5180	8300
	10258	19899	11656	9989								
369:	12917	22561	8545	4583	16643	6177	17097	3916	4541	14252	13870	6493
	5606	20188	10820	20279	8970	21193						
370:	4823	10748	15527	15435	796	14678	9764	10076	11244	9175	7609	5115
	21377	11924	10595	20985	18928	3164	9788	11682	14840	9374	7368	12999
	6258	1876	19771	13726	657	7929	12344	4713	4417	19488	11641	3883
	6787	11345	16897	10763	19559	1322						
371:	7873	16841	5024	667	14126	19489	20718	20114	6307	13749	4296	12328
	20713	14817	9449	17512	12753	3363	11373	19490	20600	14723	1330	10565
	10981	22124	10789	16941	4863	19070	12635	18547	1307	13095	22242	5955
	10082	21555	19391	1056	17810	15497	12220	6532	15511	7786	2790	6035
	18667	7196	17474	2121	6729	19563	5810	3048	746	3566	16497	12050
	8774	22138	1519	13512	22303	2143	10708	12991	12651	3454	16182	10091
	18474	18979	19291	18720	9390	8536	17155	6630	10710	15964	7870	4033
	10458	1637	16790	15145	11065	1445	18055	8688	19251	19006	13222	19365
	2339	7595	4454	13908	19220	15364	18914	10062	2726	22250	16571	5841
	19972	14541	2092	17011	19981	20191	13421	15044	15913	3884	17551	14501
	21005	6049	4670	18512	20116	22469	12494	12091	21526	21355	8895	11631
	16944	11810	10807	21779	906	756	15963	10502	12400	1579	15470	8436

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Sequence IDs for homolog proteins											
8930	2675	20539	7266	19290	13829	1855	2679	8784	9380	16462	6530
22546	22416	17960	15631	1720	21887	5290	18327	18553	4590	7391	7917
14645	15614	13247	14642	12300	11299	19418	1740	14311	18764	7547	14528
635	9762	6404	17436	12422	16799	6528	15127	16603	13586	8483	3332
2647	22390	2094	17405	13174	3330	5025	17812	3810	19126	12711	9225
18885	11043	21479	7774	21789	17915	1800	13040	16606	13023	2103	2956
11730	6062	11525	15548	21598	14233	4710	17481	6481	20502	21631	14591
703	7865	21847	18542	17238	15120	19632	2874	12903	20473	16809	19278
15968	14351	21898	19284	8790	7247	6870	19794	764	16079	17554	10015
14157	5749	18287	4764	3645	13045	14959	2521	18913	21473	9257	12508
4304	1449	12138	6240	11499	7386	10591	20874	4447	5379	5272	10120
8267	6643	6108	22137	17643	4910	15972	4782	15186	2068	5528	12337
11658	13756	3142	15763	12030	13236	17079	5380	18622	5896	4307	3158
17067	12487	14339	613	6726	15106	15675	11379	7371	5597	12017	17274
14824	18417	20721	11498	16295	15954	12677	9580	12641	17409	19499	9907
10576	21600	1559	1247	18152	17273	13554	16429	16780	20611	10103	3507
20153	6861	13556	3496	16183	11289	3492	3006	5273	3374	9357	22451
22004	19394	18283	11166	15318	8768	18770	9309	16332	16630	17527	9479
8561	16576	10695	18749	17951	10930	9616	3752	10469	2422	4538	18515
20865	7082	1739	12250	6190	16535	9858	7630	15712	2642	22497	1808
8526	18181	7296	21659	16761	14816	21998	13413	14852	10402	11131	6668
16521	11910	2019	5412	11257	11346	4369	17646	5667	12585	1224	11092
5532	10200	16673	17220	17006	6359	17169	14019	20289	17599	5659	9944
9538	3683	3521	19933	16463	13655	5686	21698	20758	784	11603	2553
8439	21559	7563	14314	13522	15633	1741	1518	15412	5891	1375	2785
14686	15611	21250	11653	21545	17884	18298	2764	3864	12813	11218	5410
16378	1570	7383	9592	15460	16787	1050	10032	6964	19685	13788	11507
3504	17418	3664	20387	12935	8777	20035	14635	11626	3618	6519	743
1923	12738	13872	12436	5348	10557	14330	1015	17903	15405	4174	2069
16438	1021	19206	4166	13172	10851	2780	1326	13679	7285	11220	4129
8228	10294	19721	22543	1447	5468	4193	6618	3849	14474	3736	3595
18582											
372: 1006	429	14179	7479	10217	535	533	507	306	478	12575	314
2254	5697	5950	15642	18461	5073	9804	18997	8666	5240	3659	6320
6367	19001	6157	11916	21356	2258	11071	9857	2163	2584	3331	526
15153	20086	6423	4662	3838	14933	8860	19820	15915	7403	13646	4850
4714	9730	12137	14919	12016	19643	3913	17315	7812	21939	13951	1478
7199	10536	9491	3917	18676	15376	4608	16936	20333	1999	7216	1589
17342	21640	8527	5069	16880	19870	10959	4725	15069	13329	20496	5944
17598	6786	7612	14232	18318	534	531	286	4110	10546	16887	4811
15616	10586	10067	4095	692	11756	20433	13391	9954	10468	16270	7655
21719	5755	4146	2857	17664	21589	11961	18800	19154	879	12644	16878
2030	4833	21437	5428	11195	20933	21506	3533	8904	13072	4677	18511
4730	696	9569	17797	18687	7097	20259	15252	13221	450	11335	20777
12713	22502	14915	21157	20371	3563	12591	16308	7626	4212	19798	19458
5691	18292	16130	21296	2832	830	14553	6434	18295	17956	829	476
12043	20779	1281	17745	16586	7955	12705	15449	988	20859	1768	11129
6547	22518	5552	9854	11376	6669	5359	9132	10964	1879	22087	13137
17298	3333	13752	20301	19370	2425	6946	19538	14273	15340	6427	17165
15603	12419	10809	8003	13658	4221	14064	22249	7387	13284	20981	2316
3116	8418	3386	6508	18217	3578	992	13442	3471	14855	19949	5277
19885	2816	10917	9436	18538	18659	12816	12308	15943	2515	20364	14701
8193	17579	22076	8890	2649	9329	21073	8376	15177	10882	8591	6053
5990	9814	14918	5209	3144	13848	22428	19076	5454	17056	4088	11270
5837	9604	22455	19840	1656	12234	1149	801	953	9960	21301	5581
3755	12278	22119	21098	1005	10264	13037	11702	20954	5063	1118	6454
20632	1696	19474	14911	9381	4111	13374	2932	3071	18551	22362	12923
1431	6509	19229	14012	5372	12362	17380	20272	16391	9540	13395	5132
901	19228	14568	17630	2371	4694	12396	15369	16597	3697	10741	16309
4927	13396	21621	8841	16662	11120	14081	8692	9484	15204	6565	14320
2978	9294	7482	9493	1277	4952	7813	7306	12296	12021	6645	9286
22489	13745	16653	19069	7780	15219	16969	14762	18330	10802	10479	16663
3678	16713	7751	13703	3630	4691	9472	10709	8542	7060	6112	22457
21974	20476	7333	6482	14526	7151	2644	835	10655	12264	9315	2786
16253	9488	5634	17372	788	9280	22095	18903	3706	15256	18593	5764
11115	12583	11568	13613	2331	5136	8073	15998	5630	11304	19137	5817
5580	18341	8588	12540	2454	4970	17445	2401	11869	6193	21516	10889
5190	13207	16465	9673	9771	11716	18575	9584	12794	21399	20485	9218
18691	14036	3350	18263	4846	544	19667	9933	4140	1318	20418	11128
20105	16734	2376	15699	7061	4232	15357	5339	7107	19030	7165	-21370
12103	4848	13211	22530	15360	12863	9975	6398	14067	16683	21170	1924
890	8155	15866	10131	7187	4332	1235	20330	12927	7088	5099	2302
12424	8303	17466	14322	11383	2282	15956	3414	12982	18548	15665	10961
21084	10824	18440	16819	3730	13940	188211	4864	1818	19607	7969	6546

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	Sequence IDs for homolog proteins											
	16771	5441	8459	18266	5000	15749	13014	14274	8444	47071	3097	15930
	11872	2621	7158	6942	18502	5408	10837	21928	13800	5188	19614	16117
	4719	1833	13499	3107	21492	12503	21929	7921	1429	14398	22189	6439
	12993	12307	19714	6650	18994	747	5932	18630	6683	1921	15651	5594
	6958	13597	19763	10097	19882	14124	14687	1094	5780	7770	7688	15110
	5797	7907	21169	3329	12627	4065	22067	19211	2061	7038	8909	16914
	13129	19881	16317	1551	13235	14888	1201	20264	7800	7526	2209	5887
	10798	15317	10223	11351	10105	10661	15014	2908	16412	22277	19851	12003
	19616	11003	7768	6166	4620	13850	16231	7016	20541	3458	1240	15787
	20099	9282	11480	4994	6281	18662	7992	9661	19875	11156	3619	14086
	20948	16946	3456	6143	786	6709	5954	17926	20839	22351	13277	15113
	6368	7704	18694	3644	12154	3794	21257	21638	18386	18111	21498	10731
	13776	5539	14530	20282	7762	9529	17675	15191	12380	14865	15825	2818
	16442	5901	8220	18578	13297	2495	21913	4526	16085	10965	15558	8891
	13161	15189	10152	3256	22258	1748	21271	13226	10136	22036	22190	18982
	10154	20726	17115	12652	2984	12623	1426	4475	16706	17850	21904	11245
	427	304	477	545	2132	20312	4655	16568	21093	13882	5730	7976
	7079	13035	14619	7273	2800	12728	15228	8972	19263	509	305	16894
	12545	2037	11704	9571	21379	3712	7685	4483	18456	22341	11197	13107
	22106	6203	19049	10427	16006	11733	8133		2264	12866	13782	
373:	21829	10688	1896	2695	15238	6923	13321	678	19909	6620	21886	4554
	4937	9312	12000	1954	4679	2233	18331	21411				
374:	6020	13479	5421	1087	1989	14406	16303	744	882	12075	4026	22268
	4422	9416	14897	9425	12945	10738	8798	854	13950	9451	21908	8474
	22358	10772	3605	17605	21264	20769	15607	2985	11015	4905	7656	19436
	14257	8375	8062	4389	12310	14819	10371	1341	10899	5014	18145	16619
	22100	13463	2860	1177	15365	14952	17870	14006	9642	5832	15041	1884
	15546	4286	20157	10385	20872	9791	8771	2815	22262	21484	5747	8299
	21256	22118	17091	16759	13043	22140	18776	20913	940	1270	18159	1798
	2743	20782	13248	7678	22155	12200	20855	14226	12099	17769	16419	12580
	3054	20908	14508	1936	4781	6302	8832	7652	17179	5548	11581	15473
	20439	4751	15772	5864	2710	20430	12577	14048	13591	22217	16257	11511
	9747	18047	5923	8265	7628	7942	7892	18958	3784	7603	8156	22139
	12033	735										
375:	17388	7507	6853	5756	19170	605	19514	774	18117	6385	7365	5325
	15832	13388	6982	805	9639	15679	21883					
376:	6489	1778	6165	13947	15105	6175	12001	16671	13761	6928	4769	20271
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	12548	849	3088	6774	12148	9161	12039	2189	17027	1969	2627	11841
	9768	10979	13916	11981	6032	1926	3963	5427	18199	9453	4199	2366
	9495	7328										
377:	15533	9191	10043	2753	19146	7790	4261	10984	17984	14174	13472	11804
	22074	3317	10460	14013	11181	20629	17263	5966	14272	21460	17175	8369
	11952	21759	11479	16405	2498	10527						
378:	22075	3099	19424	9211	2977	18514	18017	15584	2234	15782	4438	4584
	3716	9235	16307	16304	1846	2682	20821	956	5704	7923	18167	11822
	6140	3047	10275	21133	18224	5583	15900	13725	19275	17302	20181	18021
	3015	5962	12164	9319	20992	4622	8799	22151	20338	14742	22201	10555
	17777	10102	7163	15444	9363	21307	8269	10110	4429	6632	20691	9638
	14736	14020	10138	20244	11555	5116	14225	2312	21414	10821	2249	22550
	13699	938	20457	5430	12992	13398						
379:	2406	15415	587	9691	5895	21357	17711	19549	17251	13715		
380:	10085	21760	4289	13995	7446	9558	14863	11606	20045	17971	9039	18616
	9373	14535	4825	12951	3787	17677	5214	18052	6875	18135	21630	5232
	20890	1770	10991	8146	11813	4697	17003	7055				
381:	21131	21645	7243	20820	5674	11731	6667	10151	4817	4113	1832	17312
	4832	4163	2924	20194	9682	19740	4054	16537	8531	19852	9450	8277
	12513	18904	5869	17443	18723	22349	1228	589	14210	7986	10598	6036
	822	5873	20860	8502	1122	16499	3922	18794	17929	19216	19270	21895
	2758	12314	2468	11214	6717	21474	11827	3203	6754	13557	17019	1712
	19477	13019	5645	10923	3817	6215	7503	816	4760	3589	12238	12773
	10459	10744	9856	10749	18103	19048	3457	21457	19189	16910	16867	19415
	16265	3682	16610	16470	16356	21013	5777	8013	18006			
382:	19957	3226	10525	8530	7982	3708	16506	20265	19422	17319	17973	16769
	6887	12979	5654	18163								
383:	8694	8251	3871	9924	7519	16224	22555	14009				
384:	12702	17415	4664	4449	4325	19760	21746	3267	10368	3093	11350	3531
	16380	21838	19608	11587	8367	20351	2902	19733	18161	18210	22500	20226
	13535	5126	18613	16364	11894	11183	4057	11226	17119	9098	3211	2185
	20288	20489	21647	4103	11973	11885	10260	12393	7832	4511	20170	1928
	13833	21900	14890	1027	7922	6811	5790	14015	17065	6010	13795	9245
	9566	11876	8337	15174	2263	19217	5530	9598	9388	1659	10101	17925
	9717	14228	12740	14255	18590	12269	14674	17257	22064	8551	1059	11112
	5338	15072	18204	15279	6969	14944	11583	18391	14690	6503	2317	785

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	Sequence IDs for homolog proteins											
	6692	22080	20243	22421	4743	11968	5398	1750	12965	11391	12878	4721
	9384	20075	5074	2118	14173	6821	5012	9798	11794	9811	10818	7495
	4569	11830	12957	2497	1617	4507	10667	12465	5796	18993	12481	3573
	13319	20523	21343	19968	8041	15867	18712	11232	18921	4109	16995	2484
	14332	5833	21284	1405	18264	14069	17528	20295	17890	20822	18580	1268
	2953	21324	21132	13085	21661	13618	878	13234	5382	11592	6749	16229
	5848	4012	12378	1929	19687	9013	10182	7228	2028	14882	10560	6987
	11978	10065	16975	15791	15013	5286	17958	17087	8422	21303	2200	3761
	1089	18218	15951	21747	17124	2300	8857	8486	8383	19233	3427	1197
	12998	7171	8654	10108	13462	17054	18871	15851	8291	18960	4494	15966
	22488	18543	7773	12235	12178	22041	19129	20411	2027	19172	15806	6469
	6370	22096	4105	13426	4809	19640	4659	12156	13332	9311	588	10476
	22560	15961	14413	21548	7803	12072	17825	16719	17270	21888	3990	11256
	4092	19664	21590	20602	20735	3685	16999	11453	18129	8997	1186	3952
	7692	11037	17899	10950	13564	21682	15755	6178	12242	16297	14421	11436
	3560	21531	1486	13983	14970	9231	6305	2459	19412	13256	16829	9649
	11045	1317	16681	21053	19661	21038	7395	6841	1114	9000	14705	10494
	9108	17796	20404	8446	10945	13307	15299	1073	16289	6701	11667	17949
	18645	17044	20488	19663	20206	14400	4114	15577	20198	18423	6253	6078
	16870	15568	10782	8621	17031	19360	1692	11227	9123	16836		
385:	2321	2906	21872	10635	21078	7065	15156	1425	16772	13825	20591	13813
	12899	1192	19892	18999	8889	11465	20504	3946	12048	20666	9727	18484
	4435	1280	12630	17995	1807	1366	12411	2542	17186	15294	18206	15878
	13956	14389	4053	13057	11138	9564	13365	14654	2060	6116	1599	22293
	3117	16686	18549	738	1017	18097	20366	10906	7412	972	3303	9331
	22033	22401	5340	18297	5439	11324	19746	22005	10666	2640	21017	10814
	15503	15916	4700	10384	8762	17479	12301	18760	11416	17765		
386:	7205	16239	22108	14974	15094	21071	5878	17987	14219	8882	17848	8491
	10730	10766	11279	3262	17261							
387:	11850	8199	14384	16243	558	13030	19215	3479	17782	5827	19788	4416
	9270	4145	3077	7366	3904	3442	6662	14375	15690	11650	11821	1949
	1649	4587	11211	6236	21165	7837	18707	13824	13754	3121	9516	1966
	16645	15795	15859	18232	16579	16020	15502	22210	11865	21270	5088	2239
	6314	11933	1605	15281	22051	13665	9116	6153	21677	5334	21914	20518
	6808	1927	14427	10241	5400	1667	20796	14866	19395	5422	7965	11136
	5440	20442	14551	4855	21855	2066	15805	15888	3582	2334	3800	4016
	7072	16877	16230	17326	7806	2071	7990	18865	641	16590	21955	17280
	17308	2396	13681	3877	6148	11519						
388:	3596	7515	17959	3549	15024	13576	15991	5407	13215	8370	14374	9790
	11193	17162	12026	4861	2328	9153	3383	2598	20929	5662	2982	14262
	15841	5775	18375									
389:	1348	15757	11966	16108	15222	19104	21321	4489	18184	6470	8478	20190
	12628	857	9167	18660	16328	21136	12320	10268	9965	9361	754	20342
	17110	8283	11192	16702	18986	16654	9350	12474	2031	22089	14245	18814
	2961	13231	21209	11352	13736	3385	5559	5208	19587	21576	13363	21166
	21877	19184	16154	13751	7235	18147	10895	7829	1343	5632	11790	12936
	5995	4717	22228	14767	9074	21907	10830	11760	8348	21924	13987	8023
	20096	10747	11879	2097	22475	2738	9421	8592	11715	20682	10679	9928
390:	11664	19373	14010	12174	19349	11769	4498	2274	21231	2630	10572	10953
	8931	12005	7156	11098	17092	4856	20031	3585	18340	15441	19792	8259
	5870	21654	18857	1161	9343	17931	22246	9364				
391:	10049	13487	22261	19856	3119	7342	21599	5351	21514	16751	9423	5727
	5042	8667	12431	7989	2965	4617	5682	19205	18518	12013	6053	9576
	5713	11119	9862	16190								
392:	18732	10751	14514	17429	18757	4995	12463	17063	16460	10638	21916	17344
	6287	10622	9084	7641	13773	14486	3055	1922	8058	12612	3059	4605
	19053	5881	16145	10408	6114	13634	14741	604	18842	18868	21777	10350
	10325	1510	2222	7494	12825	2470	17446	15874	22549	13588	17843	20862
393:	14137	6491	1356	15653	9544	17800	4657	6563	18761	19273	9502	12445
	4359	12437	16199	18995	2176	8009	10587	4063	4005	20824	17620	19815
	19234	17093	19511	10545	5626	9305	16800	12265	9897	6943	20358	12184
	3707	16211	21688	10582	3368	2742	2365	10339	3898	8612	3028	11721
	15331	5828	13918	3634	19884	16538	1111	1554	14399	14371	5104	1829
	8104	17482	13063	16292	21720	7729	11408	5629	16271	21292	11860	3424
	9033	21268	21695	15296	18354	4934	13381	16156	13739	13034	4472	20876
	17313	16924	12087	18839	13963	22413	3248	944	6344	11007	8619	11418
	9828	5268	14031	21703	8516	10388	866	2809	7449	17438	17555	16805
	1636	15432	1152	10419	17275	12821	6115	15623	5603	15002	12960	
394:	3202	16855	14393	16047	12109	20443	2004	17625	4349	19221	15436	5819
	17066	19649	12670	1965	14910	21969	9893	3600	12536	3822	12850	4180
	6132	13648	21798	18884	15981	21322	10336	20424	7005	13279	15017	2477
	13011	10124	4373	14416	7377	13006	8088	4485	10568	6181	12408	4013
	2391	10416	1220	14803	9678	2564	13861	16954	3199	4561	21312	6627
	14292	4410	5823	16748	12403	14414	8669	12884	734	17278	562	6518

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	Sequence IDs for homolog proteins											
	1881	4518	21380	6494	15852	17368	13840	12084	19239	3091	7517	5984
	14268	4629	5191	19861	16641	17406	4144	18973	21415	21258	6950	14555
	7041	13342	18344	19371	17541	1834	8664	16235	11478	14116	6540	10401
	15100	22060	16196	11176	13397	19092	19747	10990	13435	9728	7131	8313
	8349	9269	11964	1483	16810	1500	2320	14402	11184	3721	1256	10000
	920	14238	8919	5685	20117	4235	9693	6412	5084	10715	7364	9817
	5924	6015	15928	18253	21113	17516	623	7726	7224	14801	7682	8966
	18692	11054	14527									
395:	15084	19366	8811	1190	6727	4321	12649	19433	12507	3995	12015	20152
	21429	17657	22463	5534	8079	16111	6899	3734	13762	19928	19272	17507
	6452	12037	16857	11523	12569	6792	18238	5763	14939	12699	21275	3930
	16987	2452	2193	21219	4796	14984	6885	7888	6130	13135	14954	1935
	2387	6161	8499	19730	6609	2287	21882	2634	15588	11487	4376	17509
	21610	2093	18802	7506	11993	4406	20544	8974	1016	16510	12662	20736
	14836	15691	17920	7734	11742	21957	21727	7743	12157			
396:	14699	6724	12500	6101								
397:	4537	6708	17900	6960	21012	6873	21604	2141	7919	10956	4205	10702
	6611	13911	7162	10797	21569	16752	6012	6869				
398:	16076	2321	4451	19562	5982	1411	2156	12558	8727	16772	14543	9800
	22191	22531	13050	12479	8829	9890	18225	2623	2538	1627	16157	3656
	21344	15134	15798	9715	5142	2700	1902	22110	11093	7017	1409	20559
	10443	9498	11500	15719								
399:	5094	13921	11673	21082	2690	17779	21361	3853	21213	10839	20373	8089
	10464	18576	8718	15705	2229	4135	17410	12062	1263	10684	4844	14376
	13578	8589	10573	17122	19674	11088	5570	7753	17311	3616	11735	4466
	20847	13877	22288	22274	8170	8179	8272	5234	21652	20395	3764	17831
	14489	8729	13018	2082	3516	719	14264	7662	13451	8424	15025	6352
	2590	8632	13053	6040	1583	16498	5182	601	17476	6142	7174	3594
	4785	18195	11021	9022	3624	8275	1685					
400:	20186	17002	688	20774	5087	2884	14965	22528	18781	1690	4912	5577
	11728	16448	16807	10976	1638	15429	8957	580	4493	5637	5091	16774
	7160	16922	15404	15627	18041	10475	11189	17861	6458	12796	2292	15539
	10144	3302	20470	15550	17536	14443	18302	11535	18222	3339	19330	20436
	12330	4213	11378	13719	1446	18705	18359	16604	7847	4055	1915	4452
	7369											
401:	8043	17358	11675	2116	16697	17985	22056	14520	11577	10169	8676	13033
	5205	2318	6687	11694	2175	13809	11141	20423	6267	21105	10537	11944
	20585	17725	18065	11722	4293	11413	1336	17250	5565	20625	13141	8797
	11621	2433	14925	19876	20907	16241	14430	8061	5447	21832	6570	13938
	7924	2863	13858	15223	21239	17416	17732					
402:	12881	6207	13353	11751	15876	1666	22177	13826	8030	20136	19068	10849
	6185	15941	3633	6034	14463	19984	9404	13322				
403:	6523	1729	4595	16330	20515	15902	19588	3043	18919	11708	20497	2327
	1441	669	18540	19877	6224	20250	22038	16853	15290	17729	14201	6522
	6639	958	6067	9352	10585	13076	22253	20296	15055	16741	856	13376
	4656	741	7600	3292	2041	12712	9536	7469	18070	17534	11560	1612
	12461	21026	10734	16245	11563	6734	14728	2065	12210	7856	6660	21451
	19555	3908	11196	7863	3537	4208	19879	1538	19512	18260	12688	20261
	4516	10861	13969	17758	753	6479	4375	12255	14160	16212	16720	16343
	8787	1275	20369	8862	14259	6209	11213	8389	15695	8160	17885	1848
	22162	17147	13696	14312	4009	8381	15581	21090	8703	15075	12930	5299
	2236	11851	22418	6073	6225	7353	12257	3365	8254	20943	7181	15879
	9322	10783	967	9671	5003	19304	21876					
	404:	20121	4845	16755	15934	12656	20703	22316	10903	1987	15141	15570
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	19322	15992	21094	9068	15986	19707	21551	8077	3154	5118	3193	22498
	2768	10551	21158	3298	8643	5107	10916	16268	21127	14373	13081	4348
	2952	5053	3842	20761	1985	10588	14743	18380	9448	6324	8451	11229
	12521	5321	13117	13654	3189	9466	973	16177	20685	18436	6742	8800
	8329	17207	10301	16839	21523	20549	8368	16906	21295	16634	14165	16440
	18858	11979	19688	11752	20704	8049	5101	12140	6150	18457	17776	10823
	1055	10714	2685	17863	16832	18771	9387	18448	11154	16274	12172	16594
	19936	10508	11531	11286	3525	16791	20273	17444	20714	13542	11356	22016
	9568	15624	2045	8938	12700	17001						
405:	15903	14278	19149	8514	3419	8145	3547	17612	11032	20571	12663	
406:	17617	22319	7205	6865	16239	9494	6282	3807	1614	20370	12460	4224
	10012	14713	14403	11097	4784	11736	5165	8086	18191	18915	19519	8491
	10730	11279	3262									
407:	2891	3958	11588	15385	3069	2735	20029	11448	11546			
408:	9532	10331	19503	14129	5699	15147	7047	5185	7604	2151	19670	9143
	1141	10189	18230	4233	9176	19023	18942	18099	5356	3212	10361	20873
	12438	9248	1233	17267	19131	21068	13009	6829	20236	14326	6208	21773
	15785	1052	14929	4869	4397	13900	6409	3254	21501	12516	1974	20560
	11275	2659	5053	9051	18988	22150	21521	17242	12835	5328	12151	12808

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	Sequence IDs for homolog proteins											
	14165	1755	10215	22220	22247	7254	20380	5061	2845	654	5018	7274
	9568	11235	6804	8938	3173	12045	19302	4028	11190	14318		
409:	17878	16387	12478	9552	20335	20588	14328	20566	9985	11470	9847	3078
	10774	13004	16036	17980	12297	19736	12682	20732	15994	18840	14761	7615
	3382	13301	14704	1253	8175	1203	14879	16511	18949	17910	4951	12305
	12551	984	5460	6545	17611	15062	3611	21636	4337	22142	17887	5729
	13561	7326	7817	4775	12683	18165	11442					
410:	19444	20278	7007	15467	10031	19083	20001	8653	7474	9943	2052	11515
	1185	15759	16848	7867	18893	18562	4415	7309	16700	646	22398	21783
	11681	20677	13180	18105	19115	9525	21934	4239	9535	3136	7961	4042
	17090	13917	13550	6807	15815	5083	14397	15406	5715	18413	1545	1181
	18323	18109	4215	21611	15464	20382	18532	10295	3243	557	7871	21405
	21910	742	17206	11102	8305	8131	8342	13021	21027	6288	21249	8657
	3604	2514	17634	15990	20228	10314	8380	7680	4394	11472	9447	8886
	14484	732	21164	5885	1582	18950	4256	13943	10878	4921	18817	9457
	13643	5491	10600	6106	7932	12303	8523	7259	15802	15381	10690	5244
	2547	9595	13530	3278	7558	787	14423	1602	7317	8244	875	22340
	2864	14957	7393	18265	8733	9103	19853	11368	18367	16756	15487	19985
	15688	15114	9775	5561	11959	3943	9409	7846	14829	11027	10403	18628
	18693	10737	1258	16202	22195	7356	22522	660	14611	1131	8690	1624
	19314	19584	2161	13946	12833	2228	22353	20610	5071	22372	14247	6017
	7666	12648	14029	21735	14114	20694	13015	18234	681	10081	11147	18808
	19321	6914	2616	12379	10311	15491	18766	3328	17588	18807	17753	12618
	11319	20579	10231	2975	15216	2793	16097	1795	18974	14473	20268	21825
	19495	18545	14979	5483	4788	9820	13325	2386	8747	14646	4173	8861
	11690	17653	8169	5892	19300	15684	9216	6651	6990	4535	11520	8301
	5772	10373	13686	13843	9665	19610	10235	17272	17334	22154	18621	865
	3789	1076	18122	12966	12081	14558	1943	10356	2299	11243	18708	10234
	14621	11538	20401	7508	14752	11476	8779	13046	15566	2029	5433	2096
	1102	12085	13461	16044	8180							
411:	9901	16263										
412:	2162	18233	20049	12022	11201	15202	8052	7238	12584	4327	7460	9562
	19525	21286	14793	5936	10320	1414	6411	4718	9260	8095	16930	16698
	18606	2323	7175	13143	20113	14775	19888	9560	2539	9038	9327	18125
	11362	1014	9813	17983	8842	7807	2893	11880	14342	9378	3540	3096
	19574	14434	16029	13644	4168	6269	3249	12029	19054	8470	14290	17635
	13553	18138	15398	9069	18935	2699	5624	1368	7752	20623	8011	16598
	2959	7392	16359	2033	13502	14870	6425	15173	5707	18089	13368	20148
	5202	12293	7625	10367	22375	9160	16642	1146	8644	18822	6890	4761
	16943	2968	15397	10530	4187	21770	6917	9741	21455	11557	12319	13100
	16735	11024	6580	16704	17268	12608	10727	17252	2824	12882	11405	20525
	6174	16284	14249	11514	4780	19770	4323	7269	18976	6189	4008	10736
	14087	19567	22011	14971	14023	17424	2305	22078	3592	16956	7560	1738
	12942	21285	20899	11460	19580	21557	17786	17161	3227	5470	5918	1584
	6167	21290	18980	5133	22328	17322	3423	15190	20764	18753	17010	16011
	3336	4391	7094	15896	7833	16618	16299	7848	21863	6217	20647	1230
	22513	18373	7471	12642	20594	15221	18254	7661	18439	4382	21156	10463
	3841	9623	18957	1044	10437	20165	17833	1374	15273	7844	19571	16820
	11643	1575	1920	1695	11209	7958	10668	13971	5416	7100	13690	4695
	12664	13185	8604	18811	916	3631	20925	6998	12127	1325	18046	17290
	2206	18785	10243	13121	8060	8498	7423	7638	19073	2589	3866	17454
	20816	16178	20033	1467	16026	8181	1941	8720	17669	4852	1609	20526
	4534	20245	18223	21627	17568	18939	13054	14168	5856	18898	11014	19510
	9810	12845	4047	20300	8236	15824	1098	16088	13424	14404	7164	14512
	21944	14356	18936	12143	10894	5086	16950	18427	2265	12701	10676	14700
	636	7556	1255	21562	20004	4018	14365	7792	21836	22515	4626	7954
	2981	3277	20156	14224	17076	11402	8579	1038	19802	8390	4147	20742
	19929	17647	3352	12885	17628	22490	3315	8629	6094	6966	14651	5256
	8279	11688	6703	11108	1457	14601	9351	8986	2075	8490	2577	15644
	14025	2586	2646	3999	9581	14960	19190	15504	18393	7405	2505	7583
	10066	9356	8520	21298	7640	20817	21774	15316	7810	6357	19520	17972
	21917	15777	13859	21642	3703	5853	1354	21366	12726	4471	1978	4480
	2810	5335	21970	14779	22384	3393	5141	2928	5815	5890	8839	5761
	19941	2036	7211	760	9097	1184	5514	15671	4895	2808	12236	11124
	11100	16580	8441	6767	10567	19813	7882	20630	8524	3825	22209	13732
	18168	5582	4896	6403	15710	3400	12466	7217	21299	649	918	4342
	3021	10027	21150	13145	6798	20339	2003	8395	18183	5409	11431	19105
	15632	1529	11293	12867	2841	12448	8092	20698	17823	17746	9681	10359
	16092	22422										
413:	22034	8322	12008	13273	812	11765	21273	20302	7255	570	20174	13723
	6666	22086	18541	9801	12646	17511	3238	4002	10019	21775	19200	1284
	18777	16126	10941	18730	16545	2655	10677	1823	3378	22507	22487	2105
	21401	16277	16134	17411	11463	10282	1387	17316	814	12211	10675	5919
	2531	8234	15950	13303	20240	15142	6343	17332	698	8256	18799	16961

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	Sequence IDs for homolog proteins											
	7465	15483	15126	11265	1248	13144	4991	910	12748	14534	20200	1113
	9537	549	10854	14460	6577	14432	1556	6735	19416	16300	21874	14903
	5716	1511	13958	10119	16522	6561	5477	12441	6266	14367	2568	7559
	19472	19810	11611	12517	13165	12364	21402	12768	9589	5941	15456	1565
	5435	14242	21793	4776	7231	1961	19032	1380	19110	4711	18525	20467
	16120	1422	22131	18435	17158	21488	4267	21287	8136	21470	13657	7855
	7462	20952	6100	21395	1091	7935	12221	4220	4275	22272	11605	1109
	6087	13735	21333	11724	18084	1628	1346	8072	15856	19515	2451	14016
	9102	7499	20103	6129	8681	14265	22363	10518	18395	20658	15572	20900
	17981	16009	11950	11074	707	8846	9190	18652	12428	10283	19835	9740
	19502											
414:	6834	6684	1593	14718	639	18288	5930	12385	11749	15764	10482	14872
	20500	17253	17922	10034	9808	1699	3559	8697	16121	8791	12687	718
	18476	13223	1062	17385	11440							
415:	13988	14945	6635	15700	20023	11536	17004	12834	5317	19374	10116	7960
	5032	17692	21336	1492	19786	6860	14502	20681	5259	9724	20051	567
	3863	6677	19709	7411	16573							
416:	5198	4396	18094	11888	17143	5694	21019	8021	21392	3175	21815	18035
	12729	6083	4640	17336	18325	1938	5227	15019	16822	2110	2441	1780
	11073	2067										
417:	4094	4249	6447	4266	21799	11386	7114	19998	8507	4118	4930	21755
	7422	470	10048	18342	16272							
418:	12195	18355	21055	18016	20402	12963	12102	17702	3106	18678	18424	22227
	19413	1979	17990	22510	17357	1360	17490	9376	2639	8398	14303	1563
	9512	20310	20534	2405	3798	12350	16708	19648	22564	959	8091	13262
	18778											
419:	8007	9185	12493	17152	21173	10594	13523	16563	10079	2431	10753	19487
	20147	9647	14147	9929	1830	1654	17021	19317	3147	1112	10779	8538
	3237	6408	13120	3049	22221	899	15039	8907	16324	4879	3957	783
	19624	12762	8261	15668	12832	19114	10457	3297	5741	17704	16175	15159
	6999	11766	8413	11239	8954	8566	11458	11367	8923	11782	3384	18544
	8298	18012	21849	14689	1883	11942	728	1701	15090	13910	20183	12952
	1872	3776	5981	21830	14524	4742	9043	15217	19665	12092	13500	7051
	5615	9310	10058	672	11082	16588	21831					
420:	11518	6542	21976	16169	2667	11216	15637	2270	12844	12784	7569	16948
	13741	15920	7877	4550	7616	14358	13182	14560	4000	4261	10693	20144
	8084	21413	5610	16074	7572	9778	1745	15641	21565	16376	10773	18848
	1071	17984	9925	22043	15210	10247	20648	3200	983	20360	6435	14763
	13495	12676	12528	8206	20705	3157	4565	9878	16048	17609	21518	13885
	7244	5309	13744	15880	19484	658	8704	16710	12907	7984	6137	22370
	19468	10410	9826	17175	20965	6796	9139	11329	17057	3353	18605	9058
	8231	2866	8504	16796	20034	12940	6134	15426	4409	917	9156	12665
	629	12908	7530									
421:	15638	19372	18500	2446	1148	7739	10757	13616	14797	4533	4130	21278
	9633	2203	20379	16812	11738	4453	7875	17989	11775	6848	21289	15564
	17637	18961	2109	17883	5751	4470	13318	19225	8496	999	19409	7694
	4874	3523	21721	18661	5643	6235	15475	4993	8534	2734	16838	841
	8087	7343	11926	5112	4748	2697	17805	22050	13444	20480	12313	19959
	1236	14235	21517	18071	19134	12869	2268	16339	6198	11473	8372	13642
	19849	19983	19150	7473	17895	14624	12838	18434	8867	10445	17390	4706
	4050	4847	16631	13356	6505	18534	1687	1794				
422:	5236	21619	6397	2990	20047	22291	6084	2760	5267	5082	12765	16136
	9918	13383	21449	6268	20961	21232	5855	7138	1995	14576	1013	12134
	10069	15073	6212	15451	8899	18412	4849	4386	4988	16988	4076	12237
	5275	16208	20027	947	6757	10538	21003	4705	12576	20998	19553	17590
	14359	11013	19927	6707	17088	18975	18429	14985	13721	17584	21718	20322
	1390	19701	8055	6576	18610	20621	22331	12128	6286	7906	19843	18623
	20065	11146	18095	21935	18101	573	11564	9180	14490	7031	11030	15407
	20068	22044	7315	18849	17381	20667	5814	8717	2914	14041	6827	11083
	22344	21424	1648	14123	11982	18740	20583	4741	19612	1957	6206	19071
	15555	14347	15150	22534	1958	16979	5465	17615	13167	9714	3221	17417
	1787	20324	4795	20150	11040	19333	5877	2311	2374	14089	20555	1581
	853	11842	5451	3675	12229	8405						
423:	7073	8473	19204	13490	15419	10302	3067	4727	8682	22082	19922	8178
	18347	11384	16646	9838								
424:	21999	10083	17047	19988	17430	10414	4089	1514	16232	9556	12818	19256
	18022	1716	9583	12552	17581	13890	9464	2246	15706	18577	15783	9368
425:	8789	9460	12638	14787	661	13830	20570	19781	2510	17126	17660	1608
	2111	19080	6968	16599	5238	20160	4150	9643	16795	2152	20203	17640
	20673	20994	13131	12812	8991	987	22355	19043	18108	15045	14625	18638
	2854	600	13108	14921	11424	11994	19459	3294	9066	11477	13026	15931
	6981	9953	20837	1046	8701	4413	3741	4408				
426:	6366	17652	5554	20635	17360	4793	14236	21110	8866	5732	11691	19410

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Sequence IDs for homolog proteins												
427:	1006	14786	20756	8495	10217	5541	16973	535	3260	11264	12854	314
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	3597	5549	20568	10778	12440	1988	13743	11485	1783	18629	526	17425
	9565	20151	9300	11185	5246	15752	2084	18185	2918	8400	3763	3837
	5746	20378	7812	13638	17369	4080	10663	17802	2070	4989	7198	21781
	14194	4437	8103	12106	16298	13285	19237	5066	19712	16970	17382	14671
	9686	5137	13854	11867	2123	3011	15148	11900	22193	17908	9773	16561
	14739	22164	2058	837	20811	16636	19327	18664	13237	18684	19318	3797
	6139	2857	17664	21589	11961	19154	21437	16338	11195	20933	21506	3533
	9255	4677	18511	4730	696	9569	17797	18687	7097	20259	4425	3003
	22502	14915	21157	1139	2541	4460	16130	21296	2832	830	14553	6434
	18295	17956	829	476	12043	3677	7659	5486	9761	5540	8443	15590
	15367	14935	4602	18472	9627	7490	20779	1281	14568	17630	2371	4694
	12396	15369	16597	3697	10741	16309	4927	13396	2277	21198	5308	21621
	8841	16662	11120	14081	7321	10424	15204	6565	14320	2978	9294	7482
	9493	1277	4952	7813	7306	12296	12021	6645	9286	22489	15165	9809
	16089	15681	13745	16653	19069	7780	12587	19236	8110	4594	14762	10802
	10479	16663	3678	16713	7751	13703	3630	4691	9472	10709	8542	7060
	6112	22457	21974	20476	7333	6482	14526	7151	2644	835	10655	12264
	9315	2786	16253	9488	5634	17372	10399	10547	16039	14345	5365	10379
	14566	788	5943	10889	5190	13207	16465	10488	17136	6257	8306	2432
	11948	16340	15326	5415	9673	15586	20108	20541	3458	1240	15787	20099
	9282	11480	4994	9189	12928	10743	7111	16707	19389	2889	19161	9422
	21510	10965	22018	15558	4315	21926	12010	3187	21634	19556	2333	13869
	18982	20495	2984	2763	5448	20219	12749	2389	7476	15067	3515	5375
	1465	12770	18281	1243	13198	9265	1763	1615	5056	11143	12570	11245
	2293	2132	20312	4655	16568	21093	13882	5730	7976	7079	13035	16007
	2800	3186	7053	15790	7591	22480	20744	22093	6055	15875	305	12545
	2037	11704	9571	21379	3712	7685	4483	18456	22341	10909	11197	13107
	16635	16006	372	18722	18324							
428:	14507	15421	14477	17494	566	7991	15716	19769	6346	11158	2783	18037
	18920	14200	1991	21228	2025	16965	22007	22121	19530	17216	16560	11719
	9318	17738	1299	21214	12334	12769	13914	10771	21809	10996	18789	3482
	8428	15625	18025	21461	4486	4864	18259	1869	18894	5076	10621	8796
	15953	1037	18120	21047	8656	2967	13154	6569	12338	19732	3033	10633
	15359	15028	16103	12423	19646	3561	2797	6835	16222	3266	19426	6571
	21319	4126	22537	6888	17781	1697	10045	1251	7003	7276	19243	14694
	15687	11467	11444	12814	7126	7580	4960	7248	3598	14355	7140	17847
	8316	17583	16488	4421	19550	8999	1180	18026	20573	8479	18820	21056
	7036	15143	13926	18737	18581	16569	13403	1142	3253	7394	4463	11832
	14382	7339	16547	15305	10604	4338	16236	16768	4138	18754	442	18246
	10039	12847	6541	21176	20831	13811	12065	10287	11127	9635	20511	19012
	13060	12724	898	4347	8702	12055	21425	20545	19336	8006	14571	5579
	15743	3704	19675	16542	16559	21229	11524	9274	11075	8804	4132	17224
	3133	3607	12684	13418	10123	13007	14891	18308	10517	2973	11620	15395
	10374	3168	3051	15872	11732	9301	740	19109	1359	17419	10051	6843
	1680	5509	10865	11707	16067	22296	1000	3406	18908	8719	9844	20469
	12031	11698	9632	4041	4022	2595	20688	6395	9511	16615	4623	22346
	2369	17333	14975	19292	12095	14281	11866	5395	16733	3840	17783	15322
	17305	10611	1428	7631	15733	5563	18432	3777	1959	18192	1274	9859
	16608	6676	5894	4159	21902	6323	6814	7759	17670	10954	17330	3090
	8154	15122	14026	9078	475	20224	15939	13183	2171	20320	12959	18620
	6196	16678	13224	21618	98701	7904	435	11481	4738	13205	11111	6886
	4385	10224	21396	16032	22294	3286	13158	7249	8239	1725	17508	13407
	19123	1165	2912	20759	22152	18157	16447	2772	12222	10847	14538	17604
	14596	20901	4797	3679	21087	19143	7452	9348	17993	21440	14394	16530
	16659	10434	15793	9088	17239	4831	6340	2684	689	15731	9528	16620
	17353	14180	11651	17070	2073	1585	8281	12298	22147	10166	22431	15463
	6601	8700	16540	2993	4260	9664	10652	15975	13842	14457	15948	11412
	5572	7389	11862	1897	19136	11526	10222	1819	9220	12697	22065	20558
	17946	2983	18633	13258	13996	5429	20450	10529	15553	3208	12002	14696
	12270	16162	9071	7594	17146	7667	11793	2416	11610	19062	19931	6868
	7221	5047	7968	10376	5672	2355	11711	4084	8726	14756	9731	18769
	5680	10960	10209	17713	4926	14217	6624	9314	3151	6850	4560	18134
	17898	12386	5636	3480	10028	2838	20595	1292	20275	12254	17594	4853
	20642	8186	16379	10383	4591	11759	11502	8591	4288	11992	17721	15333
	9201	12553	14724	3846	22481	1723	15765	17537	17720	5294	9934	3608
	16724	3395	2370	22184	6889	3455	7902	13093	4038	2297	7376	1916
	7144	16736	15894	19202	4614	10304	12063	3319	11943	21007	5703	6099
	3369	4162	18750	20614	3762	6621	7015	7304	4298	9147	11434	11341
	10440	4734	13768	14607	7695	13737	10493	7039	16005	5151	2008	20772
	4271	19954	7608	5609	5027	11303	8198	15488	16991	16228	17894	18306
	2556	6626	20616	16083	12968	22378	16437	7624	19737	2476	20184	8948
	13230	16495	6039	10274	10978	13806	5631	6912	22114	2955	21137	13954
	22400	1905	19874	16430	12918	16985	8847	4942	18505	6234	9524	15225

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	Sequence IDs for homolog proteins											
	3274	6369	1408	7297	20802	5035	20321	12454	13377	9019	4029	11248
	3758	16017	6780	2467	8343	727	18768	2737	1889	15457	2791	8559
	7622	17058	4393	1128	13953	2462	12634	4887	5138	7962	11126	15081
	22027	8042	16352	21033	8437	1952	10420	21247	20139	11118	19561	15955
	3808	17939	13239	4794	21353	13160	11932	16466	19950	18656	9789	3900
	11330	1626	21761	16275	839	16058	1199	5355	10804	10251	19141	19986
	19797	13358	5206	9701	1661	11677	2289	10875	9733	12426	10942	7723
	15784	12064	14341	5120	6223	5983	18048	8171	11041	10670	17196	16314
	20434	21075	20432	1709	8716	4904	18464	630	8403	6184	18819	13412
	17228	16302	10762	4918	9392	16256	4056	5523	9202	16022	17350	304
	477	437	537	12703	15237	17792	11159	4597	7291	15512	1072	6812
	15476	15612	4183	5466	17341	12261	10729	21044	4892	1108	1406	1630
	5617	11923	17859	18198	6967	1264	20318	12469	22123	10452	5701	13091
	15516	2225	1997	712	14602	8047	16361	6109	14712	22157	7745	16695
	22271	11050	6934	6231	7635	1574	21574	18516	4245			
429:	4085	2527	1065	15525	14455	18955	8686	14616	12315	16572	15135	18501
	11081	5251	21737	20520	691	6761	19795	13031	3691	6753	3599	17478
	19773	21114	6014	3843	12406	18706	4803	19871	5593	19334	19269	16267
	7830	3347	21925	18962	16676	22334	12165	16013	9753	7457	5446	17495
	20783	3532	19992	4641	17715	4676	10300	11655	22264	21804	2482	3288
	11375	10949	13571	5392	22506	4117	12147	9177	12485	12082	14102	16550
	8227	7887	9151	10009	2194	8035	3263	2456	10489	4324	17182	18539
	10448	18491	18289	3508	9164	17132	9114	3276	7050	5077	679	14103
	7303	20808	18812	5767	9247	20679	11242	19578	10187	6168	13518	22465
	10647	6086	8411	19641	21890	15074	12875	17324	6537	5971	5621	4007
	3671	5808	7390	2901	10617	17896	3947	21371	18983	19065	5064	8637
	18056	8308	7938	11745	19805	2000	1635	14446	18226	8264	6511	6429
	20857	18717	10669	18388	21752	2576	14131	18309	6243	2219	5023	15274
	22359	8379	1196	17230	21410	4530	10035	18136	20678	8008	3975	22206
	7027	14101	9482	8164	18390	11397	4582	20372	17760	16433	21946	13871
	7967	9095	17117	9950	6587	14695	5445	3749	17681	19020	11758	8793
	9612	10927	2881	20172	17530	3965	10328	18563	5640	17022	14773	3998
	19518	6413	13513	21860	10059	4735	8090	17595	22329	18064	11254	4553
	5196	7698	6952	13389	11495	4755	6529	14647	755	3688	17603	11692
	15799	7721	11607	1907	5972	12763	20832	5479	6622	14733	843	8870
	17397	3483	11493	19618	5858	18527	4566	20709	6716	19382	5368	13548
	7884	20519	2015	18102	11949	19869	7193	21204	8094	22071	1179	8989
	687	3082	1061	9091	4149	3083	19222	3949	20094	5822	13984	6059
	18698	5004	9193	7842	2013	15901	10055	17023	9839	17902	6839	14943
	21717	9782	8458	1749	6940	4589	14640	12339	16830	2964	18200	9685
	7385	3184	18909	12110	11069	17845	2560	4950	3891	6893	12525	5770
	4468	20897	13934	19823	2551	11904	3681	22519	2294	4619	581	12706
	20766	3718	18030	8652	13568	7092	5748	13595	21125	11323	6294	7245
	16341	18013	21906	7756	20468	12807	8952	4854	12892	20932	17233	15059
	14597	10337	3390	2083	16457	2550	6863	18213	15149	18389	13296	2910
	16845	800	9561	7305	5114	20251	14853	21958	20953	13079	4928	12827
	18923	12922	12166	4134	8385	16411	6965	15063	1198	16204	2303	10341
	9006	17038	3101	4223	12243	5951	19417	14082	8354	18716	5876	1912
	10613	2494	17074	6579	21936	20024	9076	15771	8144	18836	21381	752
	15962	2074	7618	7564	6180	14316	20422	20988	5743	1333	16210	5635
	6971	21853	13791	11654	848	13920	16054	21997	16890	8874	3252	14854
	18045	15844	1948	2167	19790	7872	15068	14737	9874	19597	19839	10412
	18454	3700	11597	3064	19734	6549	14176	16329	18535	22267	1097	4574
	8296	12640	20748	9752	18291	15724	1817	20274	2199	11298	12660	14557
	21233	19952	16014	18187	20646	4479	15036	19259	10006	11951	14208	807
	17472	22405	14906	11172	3156	4287	8159	7673	17535	1537	14931	1539
	22567	5737	13603	19699	9407	1651	6379	10581	19260	3165	14667	7864
	9195	1596	13152	16816	7742	6806	1616	17544	17707	20454	6937	3411
	18482	20603	12839	21210	2018	11104	7947	15160	8893	5218	15123	19207
	2443	10521	17888	19288	11689	13671	1060	7139	4723	16589	12750	20823
	21620	13574	8321	3982	8782	19710	7192	18007	8616	10833	19376	1910
	15804	21373	14004	10937	1232	14661	15988	3876	11632	4668	17814	12594
	19491	10832	9955	715	15438	10841	3640	9007	971	6389	21095	16446
	17276	14461	2963	15035	11615	3420	8456	9895	20407	21560	16473	17496
	7402	5937	16861	18408	18177	14755	15184	9227	12946	18987	11729	4477
	14072	12541	20612	4203	11063	18943	22467	12279	17726	13181	1130	19124
	12801	22244	16404	4962	17046	2469	2626	10801	569	7725	2704	8430
	18169	17621	14239	22342	20154	12018	6110	3490	20465	12047	553	5605
	2628	16250	2059	9087	3888	731	1827	21528	6858	5758	9971	9055
	19121	12596	9582	4484	11624	14798	6138	15283	7826	6756	11874	17055
	9759	17852	4798	22395	20864	12972	13464	710	16153	11807	13928	12179
	4667	18624	20452	2395	16837	8335	12798	16367	2473	10503	15101	11372
	17828	16195	20015	2994	16716	1892	19350	3636	17068	17570	11645	1327
	7475	20149	10068	20414	14198	6292	22295	12872	21980	3940	12542	18299

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Sequence IDs for homolog proteins												
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	10785	4319	20931	20293	12868	20904	13240	9080	5315	18550	5568	3790
	19960	18123	4607	21807	11927	7809	10838	3410	7219	3828	9117	4802
	17766	7596	18685	14850	2868	2410	17525	18227	5587	748	9922	6817
	13414	4122	14886	6795	20797	1302	13981	13919	12280	20227	13694	3432
	3581	17689	19868	22144	2368	4292	15152	803	7632	8409	12829	22148
	18235	17947	2085	4436	22035	19521	12094	1279	20990	7209	22178	9906
	5312	962	12098	7610	20672	14380	1096	4197	11149	11974	5660	10939
	21240	21535	6515	17591	13604	20996	6136	21870	19319	4234	6030	1908
	3858	15291	7352	15060	2897	10563	1195	7862	18600	13786	13041	4898
	2026	19040	19171	16313	14963	5034	1080	22252	3765	15468	11773	5638
	12937	5393	13796	9419	21859	15071	8173	759	8785	10233	12251	10936
	13190	19896	6977	14271	14981	14593	7058	1904	16109	1104	9497	9142
	17439	2429	3251	1743	15595	776	11599	957	18835	15453	11273	11954
	11554	9554	14263	13171	11110	17426	11221	20644	11573	20653	13888	8606
	21124	21083	881	7084	6656	7589	1372	21363	12603	1875	14364	12080
	923	17921	6852	4045	16278	13047	5535	17042	3118	9872	3494	11980
	20390	19044	13195	11777	10230	14014	9456	5040	5358	12359	10174	7896
	15061	19132	17294	9949	7651	19331	16609	5096	11833	5926	12692	793
	7709	17994	10740	21923	4044	18803	7948	12708	4621	7049	15789	3183
	19757	20773	18237	13118	11870	7824	12271	20914	19595	2904	7799	5575
	11905	17160	7767	15836	1947	9981	9284	16661	19158	10592	7940	12764
	14604	1540	8753	2822	16765	15532	1631	9675	17723	5039	9590	12994
	21045											
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	17842	9521	21420	10703	799	9651	7127	11809	20361	1641	6056	19650
	2134	9375	17502	21016	902	22224	8402	19626	7011	22503	19144	15490
	2388	16766	6922	16601	9905							
431:	10556	12984	17708	9241	19697	1495	14030	9734	14027	5836	7290	3964
	13438	20803	17948	4643	8743	19246	8822	22019	15937	17296	18828	14438
	21756	1588	19060	15098	4646	10462						
432:	9532	10331	15934	2046	6293	19503	15147	5699	7047	14129	17105	9079
	5185	13130	2151	9143	1141	10189	18230	19023	8431	18942	18099	5356
	3212	10361	22388	21551	20873	5482	17963	7910	21068	13009	6829	14326
	20236	6208	21773	15785	14929	1052	4869	16502	3926	4567	14892	13401
	6433	9709	18261	6409	22223	21368	11301	6931	15940	17666	21501	12516
	3358	6554	1974	4835	20560	11275	2659	5053	16358	7498	14297	15569
	19582	20331	6857	8522	22493	2638	19738	13482	13654	7414	12151	12808
	14165	1755	10215	8018	22220	22247	7254	20380	2845	654	7274	5061
	5018	9568	9818	1494	3725	11235	10859	8938	12700	17001	19302	11190
	4028	12045	3173	14318								
433:	540	20745	4392	9539	7190	4968	12434	2894	9916	18824	15969	2549
	13484	14142	5455	8922	14475	9503	12306	9461	18965	943	1591	20055
	3802	8501	6629	7934	6828	21142						
434:	18584	20810	16027	15628	21406	7354	15327	14802	20743	2149	9585	6022
	1273	9506	9718	22409	3023							
435:	20813	11290	7991	15677	22007	11719	11530	9318	1246	18259	1869	18894
	5076	8796	1194	21241	4280	6152	3266	19426	6888	17781	10045	1251
	15687	11467	7270	18820	4999	20923	20417	3253	11348	11482	14368	12055
	19675	16542	16559	11524	9274	4132	12684	10517	11459	11732	9301	1359
	17419	6843	11707	16067	9844	20469	16615	1849	2369	12095	14281	7631
	725	21902	14026	3032	7802	1337	3062	21087	17626	17682	15601	15731
	689	16620	17353	12317	12298	15292	10166	14717	13048	9220	15209	1054
	10376	2355	11711	10028	2838	4853	11759	11502	9201	22481	15765	5294
	9934	19837	18485	1903	16398	7376	3319	11943	7304	11341	13768	5151
	2008	20772	16083	22378	12968	19737	8948	3528	5985	21137	7297	17939
	4794	21353	18048	8171	10670	8716	12196	630	6184	9202	16022	537
	15237	12703	1072	5466	12261	21044	4892	1108	11923	17859	5617	712
	6109	7745	16695	11050								
436:	16500	8982	2601	9214	5987	9273	2383	3132	16871	4889	1471	
437:	14507	14477	15421	18062	17494	2654	566	7991	19769	6346	18037	2783
	11158	1991	2025	16965	22007	22121	19530	17738	1299	10771	4864	1869
	18259	5076	18894	10621	8796	1194	21241	4280	16103	3266	19426	6888
	1697	10045	1251	7276	7003	19243	7580	12814	7126	16291	7248	3598
	18820	18737	12671	18581	16569	13403	4999	20923	1142	14188	5501	20417
	21625	3253	10604	7339	7394	4463	10287	9635	12724	898	4347	12691
	8702	12055	20545	15743	3704	10510	16542	16559	21229	11524	9274	11075
	8804	17224	3133	3607	10123	13418	15872	11732	740	19109	1359	17419
	10051	6843	5509	1680	11707	10865	22296	16067	1000	18908	3406	9844
	20469	8719	4041	6395	20688	22346	4623	17333	14975	11866	3840	16733
	5395	17783	17305	10611	7631	1274	3777	16608	21902	3032	10224	13407
	20759	22152	18157	1337	16447	12222	2772	10847	17604	4797	20901	21087
	19143	7452	8263	17993	16659	22147	10166	2993	14457	11862	9220	12697

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	Sequence IDs for homolog proteins											
	16162	17146	7667	9071	7594	19062	11610	5047	11793	10376	5672	2355
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	11502	8591	4288	15333	9201	12553	3846	15765	17537	5294	9934	16724
	3395	2370	4038	2297	1916	7144	12063	3319	11943	4162	7304	4298
	9147	11434	11341	10440	4734	13768	5151	2008	20772	4271	19954	22378
	12968	22114	2955	21137	20802	5035	10180	17939	4794	16466	19950	18656
	13358	19797	9733	18048	8171	11041	10670	17196	16314	21075	20434	20432
	4222	8716	4904	18464	630	8403	6184	18819	5523	6647	14751	16022
	17350	12703	4597	17792	11159	7291	15512	1072	15476	6812	15612	4183
	17341	12261	10729	21044	9980	1108	4892	1406	22046	17859	11923	5617
	18198	6967	5043	1264	22123	20318	12469	10452	12218	13091	15516	5701
	8047	16361	6109	14712	21918	22157	7745	16695	22271	11050	6934	7635
	6231											
438:	3768	9465	20939	10052	11543	2583	2455	10554	14401	2398	18197	15151
	12975	22406	10665	9509	15663	5927	13360	6164	16012	7099	21660	8046
	5207	4255	5194	15420	1613	12275	14710	16908	3629	20166	7194	4457
	5992	7677	13929	12101	15458	11274	20283	7521	14721			
439:	14966	4405	7118	6146	8600	7777	22037	13873	8489	21468	8655	19547
	10433	17970	9362	20687	16031	887	7010	20077	4253	21851	14561	6562
	15040	11590	1611	13370	21623	10658	13700	6147	16428	6376	14491	7527
	12266	22380	14286	8408	4247	10369	7295	19540	12488	11421	18418	20410
	4446	3422	5527	5306	1906	20728	7396	20941	2529	6606	4873	7218
	19654	13098	12189	18969	15325	4309	13598	20706	9719	8328	20122	16518
	4685	8609	21086	1946	9979	2746	15560	7370	17671	15455	6005	3018
	4686	4101	22066	4236	21839	3651	4990	11914	15738	6771	3325	20546
	14826	19572	9615	13650	13899	13584	8742	3543	17869	19591	17545	22430
	2960	4200	2077	8177	7719	2622	6263	9849	1470	5989	1311	21426
	17824	7804	768	15927	14310	9131	19750	19247	21469	14334	14266	14771
	6820	17114	15394	15812	13253	2599	12929	5170	19859	15229	15346	19250
	1984	14570	11409	5996	20660	21736	20018	22326	19741	21896	19744	14409
	13692	3399	3194	17618	14100	18368	2518	690	20346	14843	6521	4745
	19127	22103	15018	18736	20115	1684	21656	3590	20651	2319	16368	7672
	3740	21690	1173	6846	5212	19894	8599	13173	8940	12978	16135	15091
	18853	20615	1491	18437	15682	13879	16777	19476	17619	1577	7748	13631
	13915	10365	12457	15298	8901	8625	5241	7358	14305	18568	18524	14410
	11871	21891	15823	20498	6200	9264	16240	19297	18458	2821	14785	3126
	14169	5798	9737	21776	19585	3198	14858	22300	7338	8554	11016	18990
	9617	18528	8024	16993	22122	4137	8570	22146	12226	9200	11674	21612
	14895	9476	16664	3321	16193	18447	16049	5313	18953	8533	11938	13683
	5508	2740	18932	19696	7262	8603	9275	18376	10691	20818	7714	1458
	12356	7720	7819	17020	17844	13115	5156	10998	6550	16814	12176	777
	14663	18952	3941	6256	10163	1231	14652	12351	20934	5346	3674	3417
	3413	20689	13348	3105	5424	8660	8772	19183	22278	21459	16873	20072
	17128	16743	19690	4218	3991	11096	10955	5602	886	19026	21015	19125
	13706	10726	19356	12958	17574	18510	16516	22357	8610	3240	7095	3522
	21988	5616	7937	3174	1747	3775	10024	6702	4908	6372	2579	18940
	21345	5519	15356	13540	14244	5795	14821	14518	20309	12120	2485	17587
	14150	15819	9978	12910	11595	16932	1960	694	14412	11488	18681	8778
	12679	17521	8810	5092	21175	2974	13020	10931	21585	2789	4153	18786
	18329	1083	19178	2493	21206	9256	15592	13324	16856	12883	15416	22022
	685	13962	7186	2183	1824	7815	9340	13838	4490	22377	18686	9359
	16226	1355	9864	4384	15337	14450	4671	8942	10589	3962	9323	19836
	12509	15215	5193	8404	6144	21817	7541	10871	1525	21274	13622	9110
	8628	2177	7874	14877	8824	18554	3163	18907	15713	2835	16426	3153
	20949	2770	7004	14833	12848	4690	18093	18783	15352	8130	7593	18583
	3501	4178	14120	14899	3694	21340	1642	6921	16503	11048	5058	2817
	9969	13347	19955	11925	20475	21679	16040	21148	2936	11490	9879	3668
	15510	9259	5266	11317	15129	15828	17404	18074	18271	12632	22568	6154
	19613	4529	14306	9441	17517	20968	2859	19635	2252	15293	3989	7716
	16280	13326	11344	11586	14234	9625	5215	13361	1156	16246	444	20628
	5316	13449	3080	16715	10685	19801	5171	1815	3509	16084	17427	995
	9018	10526	18574	10099	13402	17849	6159	17431	3824	555	9659	14148
	9887	22551	16739	20950	2267	11455	5169	15137	17589	4048	18400	8026
	1816	14675	4107	22512	7319	16725	20176	1188	3250	10266	3394	15649
	6275	16233	11157	7931	10836	20212	6842	21580	18201	18602	7675	17976
	14515	12856	12375	20806	1835	10204	928	877	18843	14059	6197	22517
	12239	14250	21061	548	2492	19311	18449	5757	16595	21416	19162	10349
	18182	5204	19779	22446	2313	11619	20729	18442	6595	12083	6350	
440:	13290	13287	12491	9089	17221	9777	9141	4749	6525	10696	2418	
441:	5159	5787	3587	20298	1786	13310	1389	10380	15437	20220	15554	14498
	1082	9121	21871	18718	1610	17142	16098	20306	17432	20695	8310	15692
	2042	20770	15746	11972	20448	7362	5959	17865	8865	4630	3037	6655
	4037	16478	11125	6160	10003	14982	9652	7150	5560	21884	7298	3602
	9622	20738	13828	4091	21632	1885	10098	5784	19579	11915	1619	4973

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	Sequence IDs for homolog proteins											
	4953	15722	18588	9009	3874	3245	15203	22499	1147	19826	15124	8880
	21552	2999	14657	21323	6418	1393	5831	1681	17953	9370	9708	13283
	7660	9230	20542	6634	21649	6803	7555	12376	14548	16219	9559	21885
	10474	5522	13930	9391	12268	15620	22031	14151	12757	13437	1509	3933
	21317	8728	11995	13090	16778	17402	11699	16105	1278	2276	10571	834
	14094	1564	4767	5915	1665	19312	9166	2756	14136	20976	11340	16028
	13738	1229										
442:	12225	16626	7991	19769	20707	21228	18920	15677	22007	1246	1299	4864
	1869	18259	5076	18894	8796	1194	21241	3266	19426	6888	17781	10045
	1251	11444	7126	7580	7248	17460	18820	16569	4999	20923	5501	20417
	12724	12691	8702	12055	8006	14571	19675	16542	11524	14891	11459	15395
	15872	9301	740	19109	15861	1359	17419	10051	6843	5509	16067	22296
	18908	12031	4041	3840	17305	10611	1428	10769	7631	21902	14896	20759
	22152	18157	1337	10847	14596	3679	21087	17626	10092	3743	21220	22333
	4831	12317	17353	2073	22147	9664	11526	9220	2983	5429	13258	10529
	12270	3138	6868	10376	2355	11711	9314	6624	17713	17898	12386	10028
	20595	10383	4591	11502	11759	11992	15333	9201	12553	15765	5294	4038
	7144	1916	10304	3319	11943	7304	9147	4298	11434	11341	9677	12289
	5151	20772	19954	22175	19748	3020	16083	19737	21137	3274	6780	14060
	10848	7124	17939	21761	1661	9701	6223	5983	18048	10670	1709	8716
	12196	630	8582	9202	16022	17350	7291	21223	15476	12261	21044	1108
	4892	1406	22046	11923	18198	6967	22123	20318	12469	10452	8047	6109
	14712	7745	11374									
443:	620	12442	20304	1418	14021	9656	19898	1753	11261	6048	9339	20785
	14195	2548	20087	4601	12996	2180	21054	8933	8763	20471	14140	10491
	10186	6478	12177	17437	1521	8613	20482	15739	2169	12190	15573	15908
	1717	6770	16901	15379	7349	10141	17028	12150	9400	11457	15837	15021
	17531	12650	16974	10219	14993							
444:	7118	14966	4405	6146	8600	7777	13873	22037	8489	21468	8655	10433
	19547	9362	20687	16031	20077	4253	21851	14561	6562	15040	11590	1611
	13370	21623	10658	6147	16428	19540	10369	13700	14491	7527	4247	14286
	12266	12488	6376	22380	18418	8408	11421	7295	20410	4446	3422	5527
	5306	1906	20728	7396	2529	20941	4873	7218	19654	13098	12189	18969
	15325	4309	13598	20706	8328	9719	20122	2746	15560	1946	9979	21086
	17671	6005	7370	15455	3018	4101	4686	22066	4236	21839	3651	4990
	11914	15738	3325	6771	20546	14826	19572	13650	9615	13899	13584	3543
	17869	19591	17545	22430	2960	2077	4200	8177	7719	2622	6263	9849
	1470	5989	1311	17824	21426	7804	768	15927	14310	9131	19750	19247
	21469	14771	14334	14266	15812	15394	17114	6820	2599	19859	12929	5170
	15229	15346	19250	1984	14570	11409	5996	21736	20018	22326	20660	19741
	21896	19744	14409	13692	3194	17618	3399	17236	14100	18368	2518	690
	20346	14843	15018	1684	18736	20115	21656	3590	20651	1173	5212	6846
	8599	19894	13173	12978	8940	16135	15091	18853	20615	1491	15682	13879
	16777	19476	17619	1577	7748	13631	13915	10365	15298	12457	8901	8625
	14305	18568	18524	14410	11871	21891	6326	13311	6747	13835	5310	2038
	11820	1116	18682	439	21539	20042	6396	15465	17351	4069	12600	18504
	4527	20683	15823	12851	18338	6200	20498	9264	16240	12538	14814	15115
	18458	19297	9737	21776	14169	5798	3126	14785	19585	3198	14858	22300
	21664	7338	8554	18990	21738	9617	20013	11016	8024	16993	22122	4137
	8570	22146	12226	9200	11674	21612	9476	3321	16049	16193	18447	11938
	8533	5508	13683	2740	18932	19696	7262	8603	10691	18376	20818	7714
	1970	8639	12180	20962	1458	12356	17844	7720	17020	7819	13115	5156
	10998	6550	16814	12176	14663	777	18952	6256	3941	3417	3413	3105
	5424	8660	20689	13348	8772	19183	11096	16873	22278	886	21459	3991
	19690	4218	5602	3174	1747	6702	4908	10024	2579	6372	18940	5795
	3775	14821	5519	15356	13540	14518	21345	14244	20309	12120	2485	9978
	17587	11595	12910	15819	14150	694	16932	8778	1960	5092	17521	2770
	2183	685	22022	12883	15416	13962	6144	1824	7815	19836	4384	4671
	16226	8942	1355	9864	10589	14450	7186	13838	9359	9340	18686	9323
	3962	4490	22377	15337	15215	7874	5193	8404	21817	7541	12509	3501
	10871	1525	9110	13622	8628	14833	3163	18554	15713	21274	8824	16426
	20949	2177	14877	7004	3153	18907	12848	18783	14120	4690	11925	18093
	14899	15352	6921	18583	19635	16503	3694	21340	9969	7593	11048	11344
	11586	14234	13449	3080	16715	19801	3509	17427	16084	10099	17849	13402
	6159	17431	14148	3824	555	9659	22551	9887	2267	16739	20950	11455
	5169	15137	16725	1188	20176	3250	10266	3394	15649	6275	16233	11157
	7931	10836	20212	6842	17976	21580	18201	7675	18602	14515	12856	12375
	20806	1835	928	877	14059	18843	6197	22517	12239	14250	21061	548
	2492	19311	18449	5757	16595	10349	18182	5204	19779	22446	2313	11619
	20729	18442	6595	12083	6350							
445:	21014	8217	3568	15315	16602	22197	20633	10719	22273	7927	12557	3214
	5391	17035	16717	18176	3239	21949	541	17286	20722	21074	17292	19789
	4688	6904	4467	1219	19816	19041	17181	21332	18859	22211	8218	2257
	6585	7606	16882	11061	6736	15760	18569	22238	10997	3586	4444	11325

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	Sequence IDs for homolog proteins											
	16288	5712	12397	13355	14617	8607	12841	4510	17747	8828	10495	7078
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	11389	3370	20781	7301	10605	20844	14047	14130	22186	16977	10134	11180
	19900	10713	1464	7899	2349	6473	6149	17373	2862	15797	14327	10299
	17623	20126	6074	2179	9070	18653	19230	14764	18671	15774	11854	9254
	7597	9029	4935	1891	7776	14288	7040	20201	10153	16227	4268	19425
	11328	17458	2842	14940	6228	15942	6091	22429	723	13304	7975	9105
	16127	19403	11783	823	6252	21376	13980	4302	22514	6008	19617	15008
	5641	9634	543	14573	2873	11280	18674	12111	5653	8223	7146	12775
	12377	16801	7816	4017	16666	19793	7002					
446:	10867	18970	4967	22194	5235	18316	19541	18967	16679	12435	17897	14632
	9836	7200	3244	4931	6155	724	767	11956	2291	15034	1158	4627
	22468	2941	13822	6431	20840	3978	3058	2820	4352	17463	13357	17354
	2351	1025	3451	8214	2208							
447:	3349	11861	16061	20185	18887	5336	6597	12949	13433	7265	3983	19704
	21765	4512	9383	17441	11806	19145	7957	1660	16578	8361	12877	12285
	6745	14055	16201	22143	8158	1754	1561	9710	18005	11717	18079	2243
	21572	10276	6672	1451	5576	13128	10885	6027	6068	15496	10454	833
	15308	2899	11018	20697	14627	3974	7859	15270	16400	15938	15725	15423
	5811	19619	2698	19513	5502	3862	14005	6242	14353	16413	5739	5131
	1844	15747	8386	4651	22360	19139	7085	13831	22094	8195	21288	3065
	16776	4822	18118	19091	5553	12572	14834	21349	16815	8955	13075	12733
	4648	21653	22049	5403	1029	1877	1485	22486	14277	19152	7372	4606
	21858	17690	9703	12831	6467	10808	13527	19173	11175	11657	2942	16325
	1265	17141	11133	17532	18407	20507	14912	8705	18889	792	12024	4746
	6954	5377	14106	3811	9106	7669	17506	18207	11911	10409	20449	9181
	18488	21792	22305	9003	12668	7458	11471	11697	19342	10966	5324	17192
	9173	21172	21538	9379	8949	22434	3555	19594	13734	5195	4504	5963
	14256	6939	6345	1162	18406	2357	17784	1442	4331	6935	5879	18326
	2240	20428	19414	11272	3444	14731	8631	1809	21833	14869	9442	3632
	12121	8845	20490	19745	13155	12792	12563	14861	14746	14813	4528	17811
	1567	2911	10316	11855	21730	13905	22042	3872	20386	9570	6304	9122
	6011	10819	2612	733	11892	20852	15230	16137	13985	13024	11612	8752
	1512	3948	22301	14196	1070	2951	8433	842	12944	19948	22053	9341
	9353	1718	16198	8546	15048	9919	20674	21812	3909	10843	16432	15654
	4043	6714	14847	8707	9886	20997	22088	13038	8037	9178	2878	21388
	5352	3851	6484	13259	20733	16180	20444	5834	17651	21480	13792	22149
	13049	13689	6933	5650	21822	22010	13935	7093	15175	21104	21571	13059
	14166	1320	14676	19388	12387	10615	2572	18647	16738	21225	7210	15278
	11859	4902	21097	13308	18378	12809	17277	1707	10671	4638	13485	7397
	2352	5048	7941	13275	5252	11316	3053	9127	6631	5081	2879	17029
	14783	12504	3446	5574	11878	2839	3228	16798	6179	1088	1402	19752
	22525	21445	16859	10813	2895	8708	2051	20050	10689	13359	6382	9920
	16804	3557	13937	22048	15372	19186	2356	21850	10645	17724	7740	18043
	18443	14254	8080	7679	18267	13583	7611	8668	2471	7128	21146	15408
	1163	8078	5556	13897	17262	5961	22314	15730	18968	650	8513	11528
	7068	3085	14046	13243	11222	15011	3976	1105	15891	1507	6229	10269
	17937	9774	5505	5939	7480	1497	3041	15132	9987	18054	121992	1835
	22529	20727	7448	2979	5186	13110	17553	15284	15066	21091	12304	13927
	2253	22173	14128	9863	4969	20557	7177	21588	7134	20606	17839	15095
	4399	2214	21594	19310	3008	2570	8102	16155	4099	18252	20237	9891
	20458	14831	9119	9194	7573	11856	2558	21715	10855	5766	15158	3389
	1154	11165	21797	3985	15097	8881	12231	16104	647	19765	22387	4155
	2561	4615	21305	15139	4964	16030	20281	8285	15689	12785	2196	1531
	12335	20138	9927	1132	4098	6925	14275	10776	22136	15697	16176	15977
	2664	9816	17562	11028	11930	10157	8670	12353	12574	2954	21428	12735
	2392	5226	8680	17177	8835	7167	15667	18591	21341	2172	3869	15589
	20343	19825	5210	7091	22444	3844	717	18902	14808	11659	1785	13405
	22226	8233	21693	10456	13156	14660	12659	6461	10253	7132	5280	16881
	15728	12322	846	14049	12744	8140	20493	15683	11033	12989	5866	18113
	1964	14109	15020	20584	17016	18813	5845	7915	21617	20412	1643	20533
	8020	9158	19107	2930	21064	15660	21586	18572	10523	4610	13545	7585
	1761	2480	16383	16486	1541	8462	2592	3201	11077	14726	20135	9411
	9402	12669	15995	15348	7755	8168	551	8916	3112	13876	21933	12219
	14513	6877	8898	8597	18116	8268	9085	9769	11890	21961	11709	10758
	12800	8640	1212	10509	21023	21751	11267	1557	18735	18051	21254	15200
	5771	17912	3381	18702	19564	12819	15172	17593	8712	8128	1909	6496
	14338	16091	948	17565	16614	18595	11540	18075	9306	10608	12167	9268
	17453	12880	21522	13525	10162	5843	7885	18002	13496	9474	11489	13260
	14139	10989	5078	5480	16165	3428	2826	5882	20175	15811	16116	7879
	5318	8325	1069	22306	21302	6156	22394	14294	5702	4766	568	15271
	1077	16409	17778	9726	14452	21497	5648	10532	3647	15330	8350	18444
	19227	19834	3890	21780	12302	13191	21151	13104	12185	20101	10857	11960
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TABLE 17-continued

Sequence IDs for homolog proteins												
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	19872	21481	5282	5245	2363	9283	17848	10766	892	11279	3262	
449:	13633	5900	8539	14672	20311	964	12233	10478	5805	8760	4906	10137
	3902	1838	13999	21067	4596	12781	4010	10761	8601	11786	6187	19637
	20291	12933	1404	16680	16262	4172	11107	2757	4381	11802	14386	6750
	3881	20169	3124	11582	4779	14837	16691	21558	16323	14350	7275	16234
	10634	8984	12657	3036	20253	12586	15643	8362	20529	4086	15778	15634
	10975	7311	15107	8618	8213	4431	2716	12985	488	2869	18696	12025
	7468	6477	4900	14759	645	8641	3783	17104	16899	21903	9293	2872
	7277	12282	7350	15064	2602	14650	13112	15517	7433	889	15267	21911
	19806	10064	15339	1645	20835	16525	12947	16705	22317	19397	18277	11661
	16082	8992	9337	17911	12718	11845	12581	12948	1001	4151	15609	5506
	19445	5163	11501	20741	15240	10944	3217	5255	11017	20435	15575	13834
	12427	2375	8287	6080	20581	16884	20690	12613	4380	15312	5145	10145
	1126	13494	15530	15431	22255	22276	19919	8963	4880	20168	20601	7009
	15363	10724	8126	7044	20981	3898	22554	17967				
450:	1006	429	10217	535	507	533	306	478	314	12870	18461	5240
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	2857	17664	21589	11961	19154	21437	11195	20933	21506	3533	4677	18511
	4730	696	9569	17797	18687	7097	20259	15252	13221	22502	14915	21157
	22126	18059	20371	3563	12591	16308	7626	4212	20262	19798	19458	5691
	18292	11428	18877	16130	21296	2832	830	14553	6434	18295	17956	829
	476	12043	9077	20779	1281	17745	16586	7955	12705	15449	988	20859
	1768	11129	6547	22518	5552	9854	11376	6669	5359	9132	10964	1879
	22087	13137	17298	3333	13752	20301	19370	2425	6946	19538	14273	15340
	6427	17165	15603	12419	10809	8003	13658	18296	14064	4221	14568	17630
	2371	4694	12396	15369	16597	3697	10741	16309	4927	13396	9785	21621
	8841	16662	11120	14081	15204	6565	14320	2978	9294	7482	9493	1277
	4952	7813	7306	12296	12021	6645	9286	22489	13745	16653	19069	7780
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	4691	9472	10709	8542	7060	6112	22457	21974	20476	7333	6482	14526
	7151	2644	835	10655	12264	9315	2786	16253	9488	5634	17372	16548
	13727	19096	10973	788	10889	5190	13207	16465	13178	9673	5374	9771
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	6281	18662	7992	9661	19875	11156	3619	14086	20948	16946	3456	6143
	786	6709	5954	17926	20839	22351	13277	10965	15558	18982	2984	11245
	2132	20312	4655	16568	21093	13882	5730	7976	7079	13035	2800	305
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	3094	11197	13107	16006	532							
451:	3345	751	19630	15890	21334	2502	16406	10364	15556	10330	10995	14378
	13458	16021	7590	20173	3502	572	19897	3673	12693	3848	6462	21994
	20804	17582	4276	16244	8615	17497	11060	9796	2390	21178	7166	2759
	19905	12817	14186	14243	5490	6784	5792	13470	1101	12561	6617	11241
	6402	9027	20751	1813	16709	11278	10008	3046	7793	13443	5592	8736
	3403	14205	19027	2511	14794	10004	16347	3927	13109	8732	21235	10480
	19155	2047	21601	2804	11826	19016	20937	21978	13295	3255	17452	6272
	19822	8274	14395	20792	19448	1967	4644	19536	3230	8051	21408	16552
	17526	4434	6675	10332	16527	11695	11834	4106	21315	20826	18978	17269
	22168	21255	19151	14377	2774	19782	12983	9784	9962	16564	850	18492
	20740	21582	7445	1779	10977	17687	11634	18743	18450	11001	19140	11439
	11743	13008	6064	17602	13592	13552	15418	11134	16033	20106	17363	12458
	12874	6513	15906	16223	1784	874	1125	9165	17183	4284	8998	583
	17287	963	5591	19466	4320	9188	20258	21605	17648	19691	3335	6816
	19609	22222	3733	6330	8114	19196	6605	22558	3373	5980	4992	10542
	21937	2186	4838	2923	20053	20960	4335	13352	2747	5898	8059	18499
	19914	7292	2255	21251	19565	10896	14138	1474	1803	22420	2054	18604
	4980	12543	19544	7953	17754	18426	21889	21464	7125	21785	14725	10578
	7357	2460	2281	4747	13666	6881	21446	19660	14216	1004	17442	21195
	9433	21820	7213	8549	21471	8344	17607	6026	13716	12371	18944	19208
	20867	13887	15334	8749	16682	14433	12986	7761	12475	15833	15505	8725
	627	20270	7644	15253	15959	13593	13483	12343	18196	3966	1640	20730
	3351	10803	1315	1603	19482	6421	12053	1137	8850	12068	12197	8734
	19465	2535	2409	22297	7627	19726	1553	13474	15450	3620	5719	11963
	3815	19768	758	13039	16269	11639	7621	5670	7361	8209	17309	14298
	22309	19799	6584	3893	10041	3814	2858	7122	20012	8232	12230	820
	11268	7920	3024	942	16980	14141	2812	19328	19907	16962	16151	12559
	3658	994	16669	2146	14691	14451	2080	3146	18837	7883	935	4402
	21465	15552	7472	6823	18275	16984	17026	7620	5223	8813	21417	1708
	22055	15118	13508	19764	22214	16335	1874	6227	19122	5567	20812	16276
	19961	11837	11145	14544	15166	9889	16056	20845	14946	6840	722	13349
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Sequence IDs for homolog proteins												
452:	21725	4108	17790	10816	10072	11215	7845	21938	14000	12290	9072	2188
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	2880	22230	1218	9626	19047	3040	17741	3001	15767	17052	3724	7152
	16952	20547	5794	17379	9932	18642	18433	2347	8182	3667	10010	9258
	4330	16872	13931	10125	15345	15750	14295	6095	14904	11788	22535	2662
	5270	2833	2917	19197	11031	8241	18241	12357	932	9546	3545	5011
	5922	15762	21458	11169	19093	2950	4496	8786	17325	12345	8819	14838
	11101	7574	21973	11052	5177	10577	9162	18537	19268	11571	9690	8586
	17826	10897	21454	12803	2767	20158	11415	6066	16018	13857	10790	8706
	12567	13232	21790	2221	16327	22364	9930	11940	14381	12027	5625	20421
	6213	18883	15885	991	14231	1117	8576	18603	5865	1558	1668	7347
	20793	5291	16647	5611								
454:	10637	2260	13315	5883	11574	14796	9991	4552	7533	6653	8525	1420
	15386	21880	6261	12607	8500	22030	1956					
455:	7653	1606	10840	3715	10418	14035	4843	2101	19615	10922	3554	1735
	3155	13503	6907	7784	20054	21733	1169	1452	5818	22385		
456:	0											
457:	3034	22132	9120	13729	6791	11897	5149	22382	7782	1951		
458:	21696	15323	6711	794	10202	21441	6649	17320	15012	6988	16064	7702
	2108	7337	13972	18351	2384	18596	11446	5769	20712	818	9873	11398
	20352	19777	18363	16843	5030	6560	11056	12761	9908	4279	12906	8596
	16833	6392	2335	20071	16868	4580	21828	17448	14949	21452	5673	10050
	5093	22411	1705	11285	10329	5612						
459:	655	11975	8069	20491	17684	1394	19340	17701	5908	684	14348	21852
	5434	14730	2715	13227	21854	8282	16106	10308	21982	7567	4049	15967
	16174	14809	13372	20868	798	20016	19024	1342	3575	14227		
460:	19142	17102	15893	22335	12299	15442	11496	10074	5733	14018	4497	12860
	17771	17375	8161	11868	317	11262	6451	9249	12173	13520	2381	4681
	6996	6490	9579	1276	5404	8032	6363	10026	7316	14084	8908	17837
	8863	19169	750	18053	13467	9093	12920	8746	301	4625	12849	8975
	1460	8614	20285	11049	15351	15199	22494	14045	10173	6414	13682	21841
	1623	17211	18365	4519	21203	2011	22000	10060	950	10516	18657	11078
	6908	20626	18762	9992	11321	16068	13071	20575	9335	10629	4241	17420
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	20317	6124	1526	12392	16093	22474	21550	2099	15300	14848	1309	13170
	19435	2632	6374	14407	14649	12249	8309	550	7797	3769	17901	16142
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	9064	5045	14968	9551	2414	1646	4753	1805	18175	18991	9750	1618
	17712	22081	22029	14969	2458	1011	14504	3779	21507	6619	4824	5015
	20098	2353	13906	16938	1847	13819	11957	12498	17391	1983	2927	13991
	20531	20599	1625	606	8646	7497	11561	11796	8562	3676	16567	11565
	15599	13705	12415	13948	1711	2922	7520	21985	563	3562	1939	5754
	19800	6341	9042	15748	16577	12974	4827	4371	1092	14881	16895	20528
	1513	6790	19711	13821	5656	6520	2463	9526	17821	1888	18587	10549
	18855	4858	7028	14908	22205	5964	4933	4340	5271	927	8374	3316
	20014	21527	5008	9914	10822	13989	15266	13163	17347	7197	21212	6338
	1401	3445	561	14444	20426	12281	9349	20565	7453	19524	4093	17235
	8735	14800	9217	16762	10080	19195	11057	11977	8958	21372	19693	20196
	6610	14503	22133	19181								
461:	21226	10722	9090	9917	17608	3307	17248	19659	12888	16315	15869	13541
	11628	14989	5547	13844	21236	9910	11202	10862	3786	7783	20043	16159
	21123	21149	1353	5976	20875	12245	2040	1496	18804	8260	2945	3653
	21684	4427	20639	22232	20700	626	868	17999	20858	2479	14206	10988
	22292	12471	7299	12462	21503	15092	2732	4462	16160	13957	17698	19014
462:	10915	15022	4450	11366	20814	8548	7447	2554	10246	14947	16967	18188
	8578	3396	12439	21412	21085	10559	15980	13299	6199	5121	3610	8985
	5265	4663	6420	19456	9646	7090	9324	14666	21020	13611	3580	3309
	3503	10431	15493	1658	4414	10484	19347	18475	3196	10873	7062	5347
	14932	697	8959	9970	13746	17123	19066	3791	6974	21237	4075	21728
	13369	5804	15214	3905	7104	15534	15425	15645	14841	13863	17523	14583
	13266	16008	19678	809	17661							
463:	15610	19505	3188	13558	22207	789	18180	4508	22145	6608	12144	14753
	3301	17632	6183	18032	8172	21197	9377	13065	15119	10305	14673	12954
	12468	8469										
464:	7246	2525	8937	1249	20791	2442	13757	2102	8484	20391	22436	8284
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	10624	18917	21915	21121	18416	17053	8529	2009	1335	2989	17827	5789
	7577	14095	21524	13803	19598	11276	12421	21337	2916	21144	20276	15766
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	Sequence IDs for homolog proteins											
	4509	3285	1871	22443	9056	14293	11451	17137	11684	5432	21943	5119
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	14155	18379	19003	4754	6752	7557	21304	14324	2929	15268	11094	6025
	8713	14222	2187	1975	2856	8286	16534	8056	9369	15871	22373	5414
	5457	8512	14839	13626	13511	18521	18560	2002	4104	11038	15162	19653
	9129											
465:	6459	6394	20221	2332	21782	13055	10580	2279	21367	19818	15567	13294
	11815	16237	17819	16570	1622	15858	19159	18654	9082	10360	8884	
466:	17835	13628	20663									
467:	20037	7346	1314	12511	16115	17491	18854	2329				
468:	17297	12034	9186	19531	5960	3320	6107	989	17365	1448	5740	10535
	13789	18153	3130	2668	16090	6274	11423	19113	19718			
469:	8693	16592	5005	19306	6604	16732	9754	13116	8230	21139	4079	5166
	18517	6465	2795	16685	16688	21959	6043	13767	6173	22310	3259	13685
	20252	7455	5044	3534	9389	10900	11649	8773	10993	11006	9330	11087
	5753	19387	21478	15236	21689	1435	21991	913	7484	14285	18519	20798
	16122	2721	770	15723	20967	12158	21702	18984	12751	12455	5999	11116
	11824	9843	12418	7936	7869	5363	4568	3972	16205	22566	18031	20763
	17285	18882	7781	5471	19353	4312	4716	18663	9603	15043	11217	14246
	16326	9289	1155	13216	13122	13400	3648	8238	13201	897	19164	9520
	12035	8212	12560	22169	3281	12562	11339	17667	12309	8806	22280	18666
	22125	9307	6640	20092	2145	19241	15914	1213	13453	5332	61332	1968
	9060	20524	10171	20916	20091	19282	10648	21566	4242	19533	11739	14917
	21058	17627	7451	13855	20246	872	19965	10868	11173	2843	8856	6802
	6353	5160	6251	13175	12961	12248	21646	18733	1820	15077	6061	2722
	19163	13367	10128	22117	17264	16640	22485	19560	8034	1100	17788	13010
	7758	19682	1515	12783	21145	7575	3152	16168	2508	13380	8293	1473
	9684	17719	8565	4032	17866	18951	14592	14121	19857	5090	19600	22439
	21996	16150	952	14805	7722	18382	14204	12365	18343	18356	17329	19831
	6021	4198	17799	3839	721	9477	11433	18772	8387	1287	8906	17051
	17649	19824	20739	20085	3542	5975	20850	9850	9401	8873	15065	7512
	19446	6993	10543	8853	18552	12124	18137	16070	1895	21102	9226	7191
	4365	12533	4665	5929	15384	20652	15768	3859				
470:	4094	4249	6447	417	9699	4266	21799	19998	8507	4118	4930	21755
	7422	16272										
471:	5778	13042	20693	6337	16080	1704	20548	2346	20737	5152	6633	17650
	2524	19716	3465	3548	16517	9459	12501	10090	1759	3273	12472	21412
	14456	8135	18797	3137	17061	3402	9770	1269	2404	4759	7648	8568
	8662	21076	11318	18004	13312	14804	6000	10393	14666	21987	3309	18931
	14379	6524	14185	6945	8382	7629	16509	1933	4728	21025	17218	17638
	1752	16078	3430	16885	19841	13228	577	3035	15647	12625	14586	21237
	4075	7439	13720	15834	12529	21705	3905	17339	10133	5868	20567	18269
	22275	13814	5994	10239	18618	20112	19325	13266	2962	2905	3571	
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	19280	10142	3469	11718	8642	15847	3638	2801	9326	3742	10221	13816
	4884	3280	9923	15873	20214	10492	13528	8475	3713	15933	21666	11740
	1633	11990	9134	17965	1788	6764	20492	17131	19212	13533	16793	11371
	8594	20347	3728	17461	13823	8134	22260	7419	19185	22026	3272	1884
	8730	8990	19977	1859	10999	4586	16348	19281	19991	11567	1008	20028
	7658	20830	19756	20878	3207	20070	2980	18632	2087	6612	5122	7489
	19025	20408	5867	8896	19056	19348	18818	3699	779	22456	11541	15161
	11135	20058	2201	6739	16612	14992	19392	15341	8872	4204	21922	22540
	19457	14075	4186	15353	17073	5661	13025	14487	6849	20671	6103	10343
	4142	17366	14159	18164	2380	8153	15839	19958	6670	2506	8947	15249
	9712	1377	18798	8620	19625	10515	9429	5493	7939	18930	8714	19761
	3572	20073	19642	9602	11161	7180	10987	2971	8438	4675	8709	2938
	4636	3485	9435	18162	15411	20078	14563	15262	14349	19829	9555	8928
	16342	19361	1362	12060	11259	1940	18358	7454	21475	16972	20517	14458
	5311	4246	3026	9206	21394	17932	5647	18756	632	3100	13204	18856
	14390	13351	12707	15711	10265	18751	14958	5221	17138	17198	808	10940
	11642	19473	3009	13298	15678	3551	14990	9133	19864	6205	1024	9670
	22172	21447	19672	2996	6377	6123	21676	2672	19700	21984	15674	9974
	14920	2725	11780	7537	15508	9998	18115	3670	16824	20178	4972	18635
	8472	13466	21265	2831	8951	14511	7701	18486	7554	17622	11381	6309
	22198	20143	15854	21658	12398	12681	11609	16625	12161	6162	3022	5109
	7314	14439	8366	13945	12198	11746	13801	5301	15197	3210	11365	15206
	17546	19669	2720	10926	1742	6963	11828	6972	1267	14550	8450	11591
	19644	11212	14447	15125	18385	14497	17159	5903	832	17245	7432	3663
	3061	9406	7511	4860	10188	13056	4196	11132	3684	3623	8675	8119
	10193	16296	17100	11852	16004	17566	10552					
473:	2421	20836	18507	17807	18922	14668	9172	2056	648	16255	7978	2322
	11200											
474:	17916	15231	15741	4645	21977	15829	10291	21573	1806	2663	8036	9618
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Sequence IDs for homolog proteins												
	1986	19706	22092	8766	6813	17830	10853	21281	13394	5285	8139	21004
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	9957	13288	6516	22526	16496	14873	10471	18290	3086	11953	18592	3185
	9418	17135	8081	9593	19180	4673	7979	1300	13933	16544	16782	15551
	8460	15960	13997	3405	1566	21046	8636	17134	6596	6512	13346	15639
	21591	15042	12093	14396	9252	18637	22523	6953	16784	6262	16933	22448
	4612	19863	6076	19303	12192	16828	17089	4133	19601	6118	3344	15088
	14986	21070	2153	771	3291	10644	20638	4377	21183	9519	21234	11970
	21215	18173	18301	17764	13810	10948	3781	21029	11162	16613	18091	22003
	3801	21866	22213	6526	5846	20765	21771	14860	5007	861	6743	5529
	14267	14880	21391	10210	5693	5970	3793	15855	1007	13001	6878	9875
	16912	19329	13614	10333	13714	8204	21112	6903	1133	21262	21547	15703
	21338	6248	15242	13567	16788	11020	18655	19496	10528	22414	8142	17440
	20388	7760	17480	18357	14595	12914	2829	16249	2569	7096	6689	12534
	6105	16041	9145	9242	1552	1379	10313	9596	10872	11771	3268	15445
	593	5820	18410	6984	14744	9713	10053	1383	8837	676	4305	10421
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	18640	4083	1527	285	19285	5385	17557	20851	15693	17304	1683	14391
	15965	19854	8425	14916								
475:	17494	14507	18062	7991	15677	2025	16965	15154	22007	1299	4864	1869
	18259	5076	18894	10621	1194	21241	4280	3561	13154	8656	12338	18120
	3266	19426	6888	17781	1697	1251	15687	7276	7126	4960	7248	3598
	8316	21056	7036	15143	13926	18581	16569	4999	20923	5501	4338	10604
	10287	9635	11127	8702	12055	20545	19675	16542	11075	17224	15872	11732
	6843	1680	5509	10865	16067	3406	18908	8719	4022	6395	4623	22346
	12095	17333	5395	17305	10611	7631	18432	21902	7759	3032	10224	17508
	1337	3062	10847	4797	20901	3679	21087	9348	17993	3743	10092	14394
	9088	16620	9528	17353	12317	17070	22147	22431	10652	9220	12697	20558
	11610	11793	17146	2355	4084	3480	10028	2838	20595	20642	8186	16379
	10383	4591	4288	8591	15333	9201	15765	5294	3608	4038	2297	7144
	1916	16736	3319	11341	10440	4734	20772	4271	19954	7624	2955	17939
	21353	11932	19797	2289	9733	10875	12426	18048	20434	18464	630	8403
	6184	18819	5523	17228	16302	10762	9202	16022	17350	11159	4597	17792
	15612	4183	5466	17341	10729	21044	9980	4892	1108	1406	18198	1264
	712	13091	8047	14712	22157	7745	6934	7635				
476:	3284	22524	15910	13589	1006	11575	20349	10911	18523	22545	13067	2372
	10217	9609	535	306	507	533	5233	478	4966	9015	21390	314
	1764	12941	18461	9866	21665	7323	5049	9997	7294	5240	7571	6367
	19001	13429	2814	21443	20459	1880	1396	3615	13867	7787	22538	13411
	13344	8482	1205	18398	13083	12473	14941	17485	1550	757	11281	11029
	21967	827	1873	21174	14091	5281	885	7332	8229	10933	12672	21103
	4400	1012	15883	7812	7121	22179	16424	1339	1866	3474	11617	19918
	16996	14296	1352	17699	9135	12367	19265	15111	3388	20896	20167	6697
	6564	10047	19989	9358	22350	21749	15375	4618	531	16283	300	534
	286	6575	7081	11468	2641	13543	15224	3097	15540	19380	19031	14287
	6260	5051	12104	13901	11086	12459	12824	919	13271	15196	6303	4194
	14638	1182	15803	1842	19299	7287	2857	17664	21589	11961	19154	12506
	21814	4986	5343	21106	6334	21437	20936	11195	21506	2582	22069	5476
	3533	7949	19583	22113	4677	18511	4730	696	9569	17797	18687	7097
	20259	15252	13221	13305	450	22502	14915	21157	19855	11089	1744	10324
	19917	6730	2195	2037	13563	12591	16308	7626	4212	19798	19458	5691
	18292	8005	20912	21422	6721	10358	13601	6637	1272	17775	16130	21296
	2832	830	14553	6434	18295	17956	829	12043	2457	5731	4395	10908
	3209	13959	12384	5220	21843	19341	16539	19751	20779	1281	13763	17745
	16586	7955	12705	15449	988	20859	1768	11129	6547	22518	5552	9854
	11376	6669	5359	9132	10964	14922	1879	22087	13137	17298	3333	13752
	20301	19370	2425	14659	6946	19538	14273	15340	6427	17165	15603	7257
	12419	10809	8003	13658	14064	4221	7387	13284	20981	2316	3116	8418
	3386	6508	18217	3578	22249	992	13442	3471	14855	19949	5277	19885
	2816	10917	9436	18538	18659	12816	12308	15943	2515	20364	14701	8193
	17579	22076	8890	2649	9329	21073	8376	15177	10882	859	5990	9814
	16053	5209	7718	3144	13848	22428	19076	5454	17056	14918	4088	11270
	5837	9604	22455	19840	12234	1149	801	953	9960	21301	1656	3755
	12278	22119	13793	21098	1005	10264	13037	11702	20954	5581	5063	1118
	6454	20632	1696	6301	9792	5396	19474	14911	20315	9381	4111	11600
	7691	13374	2932	3071	18551	22362	1431	8710	12923	6509	19229	14012
	5372	12362	17380	14108	20272	16391	19694	13395	5132	901	14568	17630
	2371	4694	12396	15369	13051	16597	3697	10741	16309	4927	13396	21621
	8841	16662	11120	14081	21259	19449	8692	9484	15204	6565	18317	14304
	2769	14320	2978	9294	7482	9493	1277	4952	7813	7306	12296	21386
	12021	6645	16505	9286	22489	3622	13745	16653	19069	7780	15219	16969
	14762	10802	10479	16663	3678	16713	7751	13703	3630	4691	9472	10709
	8542	7060	6112	22457	21974	20476	7333	6482	14526	7151	2644	835
	10655	12264	9315	2786	16253	9488	5634	17372	3836	18362	11559	7637

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	Sequence IDs for homolog proteins											
	4946	18143	12059	6995	17942	3772	3625	788	20809	16318	18862	7143
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	2331	5136	8073	15998	5630	11304	19137	5817	5580	18341	8588	12540
	2454	4970	17445	2401	11869	6193	2434	3951	10889	5190	13207	16465
	5825	17346	3323	13177	5354	2210	9333	13864	21502	19147	15973	9673
	11863	9771	9608	11716	16811	18575	9584	12794	21399	20485	9218	18691
	3350	18263	4846	544	19667	9933	4140	1318	20418	11128	20105	16734
	2376	15699	7061	4232	15357	14036	5339	7107	19030	7165	21370	12103
	4848	13211	22530	15360	12863	9975	6398	14067	16683	21170	1924	890
	8155	15866	10131	7187	4332	1235	20330	12927	7088	5099	2302	12424
	8303	17466	14322	11383	2282	15956	3414	12982	18548	15665	10961	21084
	10824	18440	16819	3730	13940	18821	14864	1818	19607	7969	6546	16771
	5441	8459	18266	5000	15749	13014	14274	8444	4707	13097	15930	11872
	2621	7158	6942	18502	5408	10837	21928	13800	5188	19614	16117	4719
	1833	13499	3107	21492	12503	21929	7921	1429	14398	22189	6439	12993
	12307	19714	6650	21398	18994	747	5932	18630	6683	1921	15651	5594
	6958	13597	19763	10097	14124	14687	1094	5780	7770	7688	15110	5797
	7907	21169	3329	12627	4065	19882	22067	19211	2061	7038	8909	16914
	13129	19881	16317	1551	13235	14888	1201	20264	7800	7526	2209	7384
	5887	10798	15317	10223	11351	10105	10661	15014	2908	16412	22277	19851
	12003	19616	11003	7768	6166	4620	8674	20541	3458	1240	15787	20099
	9282	11480	4994	19545	802	17144	13420	13439	14301	1357	14011	7026
	1145	6281	5258	6013	2805	18662	7992	9661	19875	11156	3619	14086
	20948	16946	3456	6143	786	6709	5954	17926	20839	22351	21072	13277
	15307	11701	15113	22057	6368	7704	18694	3644	12154	3794	21257	21638
	18386	18111	21498	10731	13776	5539	14530	20282	7762	9529	17675	15191
	12380	14865	15825	2818	5956	16442	6255	5901	8220	6918	18578	17465
	13297	2495	21913	4526	16085	10965	15558	22565	22251	810	14127	7570
	2692	13168	10912	15666	20574	4894	2526	10115	18982	19796	4020	2984
	11522	11245	21570	8695	427	16749	17392	7325	10184	2132	20312	4655
	16568	21093	13882	5730	7976	7079	13035	2800	16658	18348	16408	4157
	5264	8112	509	307	305	12545	2037	11704	9571	21379	3712	7685
	4483	18456	22341	3397	11197	13107	675	16006	532	20604	18536	
477:	14477	7991	15716	18037	2783	11158	22007	11719	9318	11530	1246	21214
	10621	8796	4280	19646	1037	3266	19426	6571	6888	17781	1697	10045
	1251	14694	7276	7126	12814	14355	17583	1180	17847	8316	20573	7140
	18820	7036	21056	15143	13926	18581	4999	20923	5501	1142	3253	7339
	4338	16547	15305	10287	11127	20511	19012	13060	4347	12691	12055	3704
	15743	19675	16542	21229	11524	9274	11075	8804	17224	3133	3607	10123
	11459	11620	2973	15872	11732	19109	740	1359	17419	10051	6843	1680
	16067	3406	4041	4022	9511	2595	4623	2369	19292	17333	5395	17305
	10611	1428	7631	15733	18432	1959	21902	6814	13183	20320	12959	3032
	4738	13205	22294	3286	19123	13158	20759	22152	18157	16447	10847	14538
	4797	21087	7452	19143	16659	16620	11651	17070	10166	6601	15463	22431
	10652	13842	11862	19136	1897	9220	12697	22065	20558	17946	13996	16162
	7667	10376	2355	4084	14756	8726	10960	18769	3480	2838	20595	20275
	1292	4853	20642	11502	11759	11992	9201	12553	14724	15765	17537	5294
	9934	3608	15894	19202	4614	3319	11943	7304	4298	9147	11434	11341
	10440	4734	13768	7695	7039	10493	13737	14607	16005	5151	2008	20772
	4271	19954	4883	11303	15488	5027	17894	16991	7608	5609	16228	8198
	18306	2556	6626	5829	13676	20616	12968	22378	16437	7624	20184	6039
	10274	13230	16495	10978	13806	5631	6912	2955	21137	12918	16985	16430
	8847	22400	13954	1905	19874	18505	9524	7297	20802	5035	20321	12454
	9019	13953	2462	4887	16352	1889	17058	15457	8559	7962	11126	15081
	22027	2791	7622	8042	4393	8437	1128	12634	21033	21247	5138	1952
	10420	4794	21353	11932	13160	19797	13358	2289	10875	9733	12426	14341
	7723	5120	12064	10942	15784	8171	17196	20434	21075	20432	4222	8716
	18464	12196	630	8403	8582	6184	18819	9392	16256	4056	17228	16302
	10762	13412	17350	12703	17792	4597	11159	7291	1072	4183	5466	17341
	4892	1108	22046	1630	17859	11923	5617	18198	20318	1264	22123	2225
	1997	13091	5701	8047	6109	22157	7745	16695	6934	1574	18516	
478:	19887	10135	21002	14580	12123	15919	12579	5844	2744	4525	1601	15195
	13066	547	20326	18377	314	8202	4733	7841	16690	17977	2012	6367
	10918	3637	18964	16866	17780	7398	19262	8152	16337	16385	15522	10127
	11277	18934	3901	22130	7812	16808	7324	19680	2408	19428	11882	19522
	16434	9215	10784	19210	9199	9487	12925	15096	6578	16140	12862	976
	11288	12658	20505	12973	11420	19873	8358	17414	300	8602	17310	6259
	15328	15736	16123	1022	4666	6077	8815	10323	18236	1980	4532	17009
	7605	19668	1127	2857	17664	21589	11961	19154	6093	3017	11359	3533
	21439	16651	4677	18511	4730	696	9569	17797	18687	7097	20259	450
	9399	14915	21157	20002	20371	3563	12591	16308	15626	7639	2807	13480
	8017	8740	16746	716	21161	1662	7626	4212	19798	19458	5691	18292
	16130	21296	2832	830	14553	6434	18295	22345	20848	19451	4148	6755
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	Sequence IDs for homolog proteins											
	22518	5552	9854	11376	6669	5359	9132	10964	1879	22087	13137	17298
	3333	13752	20301	19370	2425	6946	14568	4694	21621	8841	16662	11120
	14081	7280	15204	6565	1345	14320	2978	9294	7482	9493	1277	7813
	7306	12296	12021	6645	9286	22489	13745	16653	19069	7780	16663	20476
	7333	6482	14526	7151	14429	6992	788	4653	2925	17755	9673	7253
	9771	3362	11716	21088	4458	18575	9584	12794	21399	14605	15265	10699
	6281	18662	7992	9661	19875	11156	3619	14086	20948	16946	3456	6143
	16455	786	6709	5954	17926	20839	22351	19605	13277	16667	9507	1392
	9772	15558	21992	22438	5600	18371	10363	19255	11144	11875	3318	21951
	4300	19052	16019	10566	17447	7523	21878	18982	5589	4804	15183	17109
	19009	17084	20892	22180	11635	13124	4102	12865	2079	3506	509	6351
	4815	532	372	6844	9299	5904	14428					
479:	21743	1760	3495	6194	14521	17761	15144	21403	16214	6891	10614	7713
	1057	3816	17150	12489	10225	5157	8783					
480:	21754	6794	12450	9614	4412	5824	9276	21813	1463	11059	4808	13206
	9578	13428	3072	15596	4328	3690	8876	7086	15462	6444	12263	8993
	5420	6407	12246	1242	4404	4259	22020	4611	9408	14680	3680	10238
	9797	6568	8934	7500								
481:	17081	17400	17733	17377	12323	9631	5203	18639	16889	16035	17467	19493
	3726	14585	14637									
482:	6638	7562	10477	1852	4661	1068	13778	18473	9233	12209	5474	831
	3220	16416	19485	21657	17736	2773	6559	19274	11791	2362	1290	
483:	15521	9926	9372	3535	14815	17378	15342	16992	22270	6694	8651	10442
	9501	20248	14291	19051	3324	8926	19254	5893	16393	10149	19420	11920
	8831	8248	4517	12007	9386	15721	21801	17774	10932	11965	11946	
484:	3750	6233	2713	11380	12023	5512	8397	9963	4401	17914	21042	20938
	15212	2563	21028	4455	18141	21707	15335	2976	12163			
485:	12915	8353	10649	15559	21532	1766	2706	8964	20052	20655	17361	14417
	5510	14469	5001	8855	14600	20649	14614	15591	20286	2606	9471	1305
	12051	13261	12077	17015	15608	2231	9209	13625	14471	16566	18336	20911
	10270	15117	22496	11939	2250	12212	10593	15979	5988			
486:	21080	8598	20902	564	3747	14584	4202	15248	1415	21487	2776	8440
	6441	6856	4639	13249	14411	6300	7237	7568	8497	20720	5330	2288
	3218	10413	16585	19827	2466	13415	19277	19479	4274	5139	8341	13715
487:	6455	20477	1176	8864	15945	3915	15571	16266	6450	1211	18350	6737
	21409	1653	14641	22433	16158	5655	11725					
488:	13633	11464	17818	4487	22079	19811	14672	20311	5875	1804	5805	8760
	3617	12276	17631	6644	1838	1416	13999	2846	1536	21067	951	9346
	9547	21436	4596	13884	12781	4010	10761	12933	16680	14715	12582	16262
	4172	17700	6985	11107	17731	21246	3488	4816	11798	4381	9680	2173
	8661	11802	13722	4211	7971	6750	14655	2765	2588	17564	9533	14335
	13862	22447	12417	16557	9483	20169	6497	2050	3881	20747	3124	21130
	11454	11582	14837	2614	4779	6358	16323	14350	7275	16234	10634	8984
	18673	3036	12657	921	5211	10884	8362	20529	8627	7103	8149	15778
	6773	11819	1672	12073	7102	20447	2872	7433	19593	19806	21911	5516
	15286	11661	8992	14562	3219	17911	15808	5506	20741	21530	15240	20344
	18214	15575	12427	3217	20435	7796	2375	11017	10944	13834	12971	20581
	6080	16884	1900	7505	3937	11188	811	9207	2830	20690	12613	5666
	4380	15312	18349	17639	10145	13494	664	6567	13052	6979	13432	17364
	2224	22187	6961	13798	7944	4112	9995	15431	15530	10764	1676	8678
	7407	22255	22276	8963	4880	11857	15344	7420	20168	20601	21712	7009
	15363	8126	3045	7044	2098	12067	13898	7690				
489:	21080	8598	20111	19932	20211	6441	6856	13249	4639	14411	6300	15103
	8497	20720	5330	2288	19827	16585	13715					
490:	18170	1316	6082	19848	9272	9871	15911	5917	19405	7429	21327	20596
	8045	10178	4720	16346	7401	11417	5176	9427	22532	19611	6616	10826
	2235	7529	22399	668	22163	10888	10947	17345	20889	1019	13964	12858
	12745	21803	19731	15370	19455							
491:	14629											
492:	9026	18203	9034	17176	19316	18425	10191	3057	4291	19993	19117	633
	19344	14181	6581	17129	12690	10130	10179	8823	14022	7424	4363	
493:	11676	10500	20010	22061	13770	5046	17871	10828	15052	1942	11251	10057
	14213											
494:	2867	20983	17787	12926	13702	2680	4336	1898	7033	4692	1931	11547
	4004	17355	7966	21453	6141	17522	20009	20155	3861	20641	13805	9004
	5518	9100	6706	6460	9101	19945	14203	18615	8818	2078	21644	13350
	9869	8593										
495:	10049	5921	9432	4046	3753	21873	9833	14362	8333	13672	19390	1216
	3131	18992	9486	11253								
496:	3127	1607	15003	2751	9086	18256	7201	3526	20063	8184	14575	14132
	3886	15754	11997	10334	8002	19176	6325	12719	15443	14454	10921	14581
	14745	9990	9911	1762	10972	16402	1520	16638	1856	10874	3967	20026
	4426	20686	9163	20462	20942	17529	11988	17803	8476	6783	21168	19191
	2426	12096	15664	7561	11891	12826	17289	3387	19858	12743	9853	19481

TABLE 17-continued

	Sequence IDs for homolog proteins											
	615	8569	14610	1310	14283	3903	16792	22556	12950	6759	5113	5803
	20040	13866	7531	12876	9534	7024	13251	663	2377	20537	22479	20413
	17045	11984	22225	3341	1812	7226	19298	20768	6766	10544	12090	22407
	18361	8222	5162	22240	11887	8295	15781	14468	2137	9880	12861	16260
	21244	21191	22495									
497:	4536	12720	13909	16764	14068	5500	2174	17809	20213			
498:	7246	13566	4922	7189	11908	21432	19713	9021	8001	4169	9591	18319
	12836	14209	15108	20572	4881	2021	2629	13362	21200	14093	18917	5199
	21121	8529	17053	2009	2989	6906	19492	5789	6127	7577	22482	6916
	4185	8063	10716	15947	17616	22376	714	9711	8995	19804	16484	10432
	16415	18397	17120	5711	20348	11410	22426	5459	17025	20374	5057	3996
	1399	16384	8557	3401	18399	9470	18719	2158	3928	19925	15780	1172
	19003	4754	6752	7557	15694	2929	15268	8286	16534	8056	2719	1955
	18895	5457	22161	17041	8512	21678	7854	18098	13647	15831	11038	15162
	8205											
499:	14500	1413	1282	1702	21840	19911	17917	16929	17820	4161	16375	12532
	18092	1532	5902	19438	13718	6024	19735	13044	2787	19276	8082	9213
	13875	2729	19946	19636	13441	11906	5009	21052	8166	12467	5788	10596
	21948	8953	11461	18890	14782	22256	22200	7502	22419	22028	9688	19279
	20234	20394	3662	13624	5037	17822	19294					
500:	17384	19962	11922	12514	975	11652	22218	7145	9489	16374	595	10439
	11174	6276	2673	2273	5345	20790	14336	21369	16362	13555	12890	20920
	16827	21155	6409	16703	4160	18249	5053	1371	16010	3265	21504	10158
	7203	22449	12631	15261	19335	9198	7318	16504	7195	4503	21207	10641
	8201	15388	10167	17571	2611	3434	12571	13501	9308	8098	13986	4294
	6690	17338	11438	16124	14788	9510	20668	22077	11494	16723	5320	3714
	18672	19620	11228	1183	17223	1503	20710	7345	17503	10327	18402	18415
	3756	1040	19384	13970	1810	20021	12766	10244	7980	16489	3481	1266
	2213	5652	5230	6678	19037	22307	5389	18546	3014	22259		
501:	16649	18243	16414	4207	20589	9444	16449					
502:	22464	13448	15971	16611	16582	2337	16931	10640	13818	19924	15868	13017
	5333	7271	18106	6613	20999	5327	19529	19566	15187	19703	13925	6927
	17013	11388	20074	15701	3553	10267	14357					
503:	10199	16886	2241	18245	1886	9716	7985	8744	20562	11084	13088	19819
	22302	17049	990	2306	15235	2417	1433	2115	19923	19064	1002	16264
	8492	2272	709	13399	12601	4956	19182	6191	7426	9434	14994	11105
	6247	10698	8645									
504:	8253	556	21865	11532	13731	17389	13431	10078	1271	12610	10733	21490
	10485	18060	14669	11177	20124	7109	12716	1462	14936	5986	8097	5080
	6289	3372	19867	2939	10924	773	11608	16138	4495	6375	38291	0354
	13565	9492	7772	17813	19072	19386	6691	804	12615	3475	9031	16143
	1291	12201	12820	1857	14937	19224	20789	10619	4585	1580	8663	12262
	20460	1321	17853	6723	5237	11503	749	5651	8384	14280	17145	5419
	15332	13013	5297	12732	19655	7901	7020	16059	19539	4387	1475	21505
	2671	5714	1191	2608	21672	3296	15495	21919	1209	12295	15820	14193
	14631	6254	7207	20109	13220	15146						
505:	15140	1261	13853	2474	14749	2848	6699	13353	5174	10742	4290	12981
	5167	19956	3782	14080	3433							
506:	4704	7409	3027	1782	17403	2728	12116	22243	18039	19464	20608	21816
	20161	9586	9832	1168	20257	8215	2055	2915	21159	8994	19097	4800
	10831	3258	3511	5759	8010	5683	18509	3517	13649	8892	8848	13892
	15978	11205	19106	17806	10914	8163	22263	5036	9958	17199	17195	12100
	14343	7851	2637	16675	11823							
507:	1698	1006	429	10217	7363	6232	18461	5240	6367	19001	18925	7778
	526	3438	7812	20057	286	2857	17664	21589	11961	19154	21437	11195
	20933	21506	3533	4677	18511	4730	696	9569	17797	18687	7097	20259
	15252	13221	450	11335	20777	12713	22502	14915	21157	20371	3563	12591
	16308	7626	4212	19798	19458	5691	18292	17864	4456	16130	21296	2832
	830	14553	6434	18295	17956	829	476	12043	20779	1281	17745	16586
	7955	12705	15449	988	20859	1768	11129	6547	22518	5552	9854	11376
	6669	5359	9132	10964	1879	22087	13137	884	17298	3333	13752	20301
	19370	2425	6946	19538	14273	15340	6427	17165	15603	12419	10809	8003
	13658	14064	4221	7387	13284	20981	2316	3116	8418	3386	6508	18217
	3578	22249	992	13442	3471	14855	19949	5277	19885	2816	10917	9436
	18538	18659	12816	12308	15943	2515	20364	14701	8193	17579	22076	8890
	2649	9329	21073	8376	15177	10882	859	5990	9814	16053	5209	3144
	13848	22428	19076	5454	17056	14918	4088	11270	5837	9604	22455	19840
	12234	1149	801	953	9960	21301	1656	3755	12278	22119	21098	1005
	10264	13037	11702	20954	5581	5063	1118	6454	20632	1696	19474	14911
	9381	4111	13374	2932	3071	18551	22362	1431	12923	6509	19229	14012
	5372	12362	17380	20272	16391	13395	5132	901	9540	19228	14568	17630
	2371	4694	12396	15369	16597	3697	10741	16309	4927	13396	21621	8841
	16662	11120	14081	21135	8692	9484	15204	6565	14320	2978	9294	7482
	9493	1277	4952	7813	7306	12296	12021	6645	9286	22489	13745	16653

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	Sequence IDs for homolog proteins											
	19069	7780	15219	16969	14762	18330	10802	10479	16663	3678	16713	7751
	13703	3630	4691	9472	10709	8542	7060	6112	22457	21974	20476	7333
	6482	14526	7151	2644	835	10655	12264	9315	2786	16253	9488	5634
	17372	788	11307	11198	9280	22095	18903	3706	15256	18593	5764	11115
	12583	11568	13613	2331	5136	8073	15998	5630	11304	19137	5817	5580
	14145	18341	8588	12540	2454	4970	17445	2401	11869	6193	21516	10889
	5190	13207	16465	9673	9771	11716	22279	18575	9584	12794	21399	20485
	9218	18691	3350	18263	4846	544	19667	9933	4140	1318	20418	11128
	20105	16734	2376	15699	7061	4232	15357	14036	5339	7107	19030	7165
	21370	12103	4848	13211	22530	15360	12863	9975	6398	14067	16683	21170
	1924	890	8155	15866	10131	7187	4332	1235	20330	12927	7088	5099
	2302	12424	8303	17466	14322	11383	2282	15956	3414	12982	18548	15665
	10961	21084	10824	18440	16819	3730	13940	18821	14864	1818	19607	7969
	6546	16771	5441	8459	18266	5000	15749	13014	14274	8444	4707	13097
	15930	11872	2621	7158	6942	18502	5408	10837	21928	13800	5188	19614
	16117	4719	1833	13499	3107	21492	12503	21929	7921	1429	14398	22189
	6439	12993	12307	19714	6650	18994	747	5932	18630	6683	1921	15651
	5594	6958	13597	19763	10097	14124	14687	1094	5780	7770	7688	15110
	5797	7907	21169	3329	4065	19882	12627	22067	19211	2061	7038	8909
	16914	13129	19881	16317	1551	13235	14888	1201	20264	7800	7526	2209
	5887	10798	15317	10223	11351	10105	10661	15014	2908	16412	22277	19851
	12003	19616	11003	7768	6166	4620	13850	16231	7016	2717	20541	3458
	1240	15787	20099	9282	11480	4994	6281	18662	7992	9661	19875	11156
	3619	14086	20948	16946	3456	6143	786	6709	5954	17926	20839	22351
	13277	21057	15113	6368	7704	18694	3644	12154	3794	21257	21638	18386
	18111	21498	10731	13776	5539	14530	20282	7762	9529	17675	15191	12380
	14865	15825	2818	16442	5901	8220	18578	13297	2495	21913	4526	16085
	10965	15558	18982	2984	11245	20659	477	304	427	12456	2132	20312
	4655	16568	21093	13882	5730	7976	7079	13035	2800	19890	12545	2037
	11704	9571	21379	3712	7685	4483	18456	22341	11197	13107	12449	16006
	532											
508:	19543	4932	20425	19108	19812	10140	21350	7766	14738	13289	13966	559
	10501	18670	21326	12614	16425	9945	1996	21651	12806	13430	17362	21330
509:	5942	14707	1006	429	20069	10217	6051	533	535	478	10352	18305
	21211	21561	20755	17549	15547	13386	8817	2523	18461	15773	19497	5240
	22508	3614	6367	19001	3539	12446	15801	15469	13944	13012	20409	13620
	15377	4732	4983	11962	10129	873	20622	7812	18242	8809	14606	18228
	2931	3322	9023	6902	3558	3304	13684	21120	3950	12291	4958	21675
	7657	4473	17017	4318	22410	19999	2415	22330	534	6329	4819	10093
	8054	966	16945	14639	6901	14032	21397	2354	2669	10194	5075	2367
	11025	6751	20059	21308	14038	2857	17664	21589	11961	19154	2340	7408
	6244	17569	13074	21437	14633	11195	20933	21506	4167	3533	18759	4677
	18511	4730	696	9569	17797	18687	7097	20259	15252	13221	450	10725
	22502	14915	21157	18816	20371	3563	12591	16308	7626	4212	19798	19458
	5691	18292	16130	21296	2832	830	14553	6434	18295	17956	829	476
	12043	2658	7437	19427	14568	17630	2371	4694	12396	15369	16597	3697
	10741	16309	4927	13396	21621	8841	16662	11120	14081	8692	9484	15204
	6565	14320	2978	9294	7482	9493	1277	4952	7813	7306	12296	12021
	6645	9286	22489	13745	16653	19069	7780	15219	16969	14762	18330	10802
	10479	16663	3678	16713	7751	13703	3630	4691	9472	10709	8542	7060
	6112	22457	21974	20476	7333	6482	14526	7151	2644	835	10655	12264
	9315	2786	16253	9488	5634	17372	21009	788	5630	10889	5190	13207
	16465	3748	4100	8138	14088	9673	20541	3458	1240	15787	20099	9282
	11480	4994	5496	4783	20946	10965	15558	12797	4801	18251	14926	14677
	6310	18248	15246	7925	15740	18982	2984	5765	4060	11245	20786	4379
	2132	20312	4655	16568	21093	13882	5730	7976	7079	13035	2360	2800
	16617	17577	19315	17164	15726	12545	2037	11704	9571	21379	3712	7685
	4483	18456	22341	11197	13107	2227	16006	17470	10632	372	16331	4975
	18567	13264										
510:	2585	13077	1296	15698	1085	3129	8567	7012	16480	1063	15389	13708
	17974	17451	15792	19280	10142	3469	4227	11718	15847	3638	2801	9326
	10221	3742	13816	3280	4884	9923	11360	17722	15873	1490	20214	10492
	13528	3713	8475	15933	21666	11740	9134	1633	11990	17965	20492	19212
	13533	17131	16793	11371	3728	8594	17461	20347	8134	13823	22260	9279
	7419	22025	5521	19185	8730	10999	4586	16348	19281	11567	19991	17098
	20028	1067	6210	7658	19756	20830	10712	16037	2865	20878	3207	18632
	20070	2980	6612	2087	5122	7489	19025	20408	5867	9692	13244	17130
	19056	19348	18818	779	3699	15218	22456	11541	11135	2201	20058	15161
	16612	6739	10651	14992	19392	15341	4204	21922	22540	19457	14075	17880
	4186	15353	17073	5661	13025	14487	20671	6849	10343	6103	4142	17366
	14159	2380	18164	13366	8153	19958	15839	6670	8947	2506	15249	9712
	22234	1377	18798	8620	19625	10515	15887	9429	5493	7939	18930	19761
	8714	3572	20073	19642	9602	11161	19552	7180	10987	2971	8438	4675
	2938	8709	9900	4636	9435	3485	18162	15411	20078	15262	14563	3415

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Sequence IDs for homolog proteins												
	19829	9555	8928	16342	19361	1362	1940	12060	11259	18358	21475	7454
	16972	20517	14458	5311	9206	3026	4246	21394	11663	5647	21680	18756
	632	3100	18856	13204	14390	13351	12707	15711	10265	5221	14958	18751
	17138	17198	2504	8197	10940	11642	7410	19473	13298	3551	3009	15678
	14990	9133	18124	6205	1024	9670	14097	21447	2996	6377	19672	22172
	21975	4551	21676	6123	2672	21984	2725	19700	14920	15674	7537	9974
	11780	5242	13895	9998	3670	18115	16824	20178	18010	7493	13466	21265
	8951	14511	18486	7701	6098	7554	17622	11381	6309	22198	19059	21658
	15854	16625	12681	12161	11609	12398	6162	3022	5109	7314	14439	8366
	13945	12198	11746	19463	8918	13801	5301	15197	3210	11365	15206	19669
	17546	2720	10926	1742	6963	11828	6972	8450	14550	1267	11591	19644
	11212	14447	15125	21242	13309	14497	17159	832	17245	5903	7432	18321
	3663	3061	4860	9406	7511	10188	13056	4196	11132	3684	3623	8675
	14569	21430	19252	10739	16443	8119	10193	17100	16296	16004	11852	17566
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	12394	6016	4944	12546	7522	2423	2681	8552	10982	7116	5314	12119
	21099	18607	12329	4674	13459	21805	3969	14769	20266	22203	3114	336
	12480	7283	9746	8207	7204	14337	11300	20397	20746	1530	5147	14828
	21034	3906	2359	21177	8537	10139	16166	2594	13784	16485	20871	14720
	1825	16147	17234	8065	17167	16501	11902	18924	5861	14539	14230	2788
	2072	18571	2501	4192	13524	4842	3095	7769	10089	16575	6956	16293
	11570	10846	19759	20187	21448	19904	10891	15038	1868	12675	6957	653
	16915	12203	12409	8067	4947	19061	2619	13364	4888	5566	10650	17254
	18049	16316	7313	11076	14440	1765	10770	13783	5839	16261	12061	9852
	10237	10732	19814	4893	6882	6805	4262	4557	3971	6381	1527	13153
	22347	12730	10796	30841	8028	9061	7136	21153	925	8750	18082	12774
	8584	13536	12518	6788	979	8900	18133	5696	15970	16063	14470	16701
	5862	12183	3705	6658	16350	9557	8971	3717	1724	22354	16718	3854
	3536	4599	16869	11895	16555	16258	4214	20552	21819	7135	16259	15280
	4762	13775	4531	3367	13517	21549	8105	18643	4066	13282	14115	5130
	10429	5920	4306	3192	5443	21499	6557	11929	20598	20903	4176	9050
	15849	2723	15314	5993	12041	21869	14163	7930	9081	20569	9795	20396
	11150	12443	4358	9475	10811	2552	11877	17685	21729	20974	12598	14790
	20989	15004	17240	6237	17208	21930	8580	11818	5442	17259	20256	16046
	5065	2308	2128	12182	17118	2251	7155	2892	13229	9845	20431	4311
	16583	21037	18490	9763	6826	11713	15211	21554	16813	7056	18009	3039
	19296	6673	11484	17841	21732	6456	2378	9054	19996	15355	21362	7381
512:	11789	20550	12924	14464	4011	19063	17858	14825	17933	18215	18506	8574
	11311	14714	10870	5173	18503	12871	11792	6319	5991	16072	5679	7664
	7997	7724	13724	15843	5179	21486	13257	20843	5253	15239	8745	4317
	11829	5762	17201									
513:	5799	17656	10980	3449	13335	20959	11238	9736	21154	8759	1349	18282
	16665	17907	1107	9170	6492	20516	7727	5847	9065	19902	9931	8677
	21320	19055	9044	19475	21629	4209	3873	10407	3831	21694	7261	11569
	1480	1407	5128	14542	607	2784	18463	12009	8535	4917	22501	18918
	12152	19362	6874	3988	10827	20140	18080	14167	1710	4124	3650	20877
	6031	11044	12822	11665	16321	4669	19156	10011	15957	10312	16955	17469
	9415	12205	21650	12324	10985	4763	17086	19498	18609	9205	19889	13760
	11234	3128	3060	17868	7045	10721	18775	8340	16607	22199	8687	3652
	8147	19720	4090	22058	13973	15250	5813	3005	6442	5423	4181	11396
	20254	11686	18648	22257	3514	5054	17718	19944	22383	13148	10185	9304
	9674	13580	20000	5106	14024	15026	15535	16386	22442	21036	12653	8647
	894	4170	18619	16370	14161	13064	13337	2689				
514:	19430	2217	13653	7909	3447	18614	2248	3672	3914	9037	2661	14057
515:	21829	10688	1896	2695	15238	6923	13321	678	19909	21886	6620	4554
	4937	9312	1954	4679	2233	18331	21411					
516:	12014	16420	2750	15538	18414	1466	5013	18876	17795	12046	9951	6600
	5934	11750	5835	2034	4693	13740	10307	909	4231	1436	13779	16112
	13219	4984	13214	18231	18179	2811	4814	18531	554	6050	18257	2903
	3484	19943	17271	7129	1721	20263	20319	16055	20881	9942	13994	18838
	11636	7029	16119	5257	1043	19478	20619	13417	11422	10160	20613	5029
	8196	19429	9805	1861	17540	5288	14683	10272	7443	2656	16627	2315
	772	9104	9410	4096	4548	9824	8485	17962	16475	22107	21011	15087
	8840	15594	20392	9440	6125	9757	11164	17673	20924	4254	8176	16401
	14437	18646	12057	12830	10159	17174	8040					
517:	13062	19774	2825	8829	8332	18558	21964	19050	1627	16157	11534	19742
	19647	13280	1517	9695	19320	10835	10293	13202	9174	14643	15719	
518:	3195	21607	10760	14223	22323	21616	11305	21976	16169	8132	2667	11216
	15637	4652	2270	8808	10309	18374	9291	7790	12784	7569	1295	5525
	20767	17464	15920	7877	6705	4550	14008	15544	7616	1791	14358	15686
	13182	14560	16722	8357	1472	4000	4261	10693	20144	4624	13338	17893
	7464	11142	13491	15676	17655	17116	17984	9925	18333	10247	16818	4579
	2385	20648	983	3200	6435	14763	13495	12036	16066	6740	14948	2307

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	Sequence IDs for homolog proteins											
	14063	6851	10240	1728	16533	12629	10196	17078	16048	17609	11181	20629
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	15176	815	7329	1175	20218	8827	7588	658	8704	16710	12907	17705
	21364	16998	4945	15440	14372	12879	20119	17194	19468	10410	10451	11618
	12006	12191	17175	20965	12916	6796	9139	17057	11008	18605	3353	4650
	12741	1237	7988	20088	8231	4522	18497	11952	2866	15466	10449	5850
	8504	22473	14806	5364	12620	20699	20034	4409	917	9156	629	12665
	12908	7530										
519:	11427	19017	6602	1864	10522	13385	3923	15070	3821	6415	1572	5050
	15882	10935	5721	20535	12645	22402	8448	1350	7112	8649	5148	21245
	11236	6476	14907	12714	20807	15311	9469	4739	13575	9732	8564	14799
	12721	13373	4868	12893	19038	13333	8973	17817	15414	18146	11390	22248
	13609	10100	15109	10007	5125	12633	6880	5388	20060	21032	8509	17168
	19622	20280	21442	12066	17299	20123	12902	2062	656	6457	19453	20032
	10850	8420	3813	21339	19516	16171	21635	2450	21079	19226	22202	17856
	19847	1215	16964	11846	9253	18683	16927	3145	2877	4684	8416	4696
	4925	14172	18178	10122	20134	11437	19509	20038	17265	10957	11114	11985
	13382	4424	21277	6642	11395	19354	3216	17000	10584	4383	608	11099
	3606	4061	6926	11774	3799	5172	3696	17840	9961	17641	22548	13507
	6182	1731	2207	5353	5367	13860	8912	20922	11967	3241	16963	17734
	10073	13903	22521	12149	4120	617	13506	13612	8031	6763	7546	6218
	16311	10707	1223	21269	9414	8360	4885	3852	955	17284	19833	11354
	2803	14827	1301	19175	10717	10910	12224	11516	13340	5262	5684	2178
	13200	5913	9157	7959	17542	20440	18229	4805	8038	13587	16238	15602
	18860	3544	7650	12674	17624	7074	576	17060	7413	22374	15047	21681
	651	17560	6085	12160	12805	10775	4709	11401	6838	18364	17014	10752
	17012	8980	17510	10711	8219	16107	16692	19401	17191	18405	15984	5384
	19201	4362	883	6527	6410	867	12321	17889	17964	11941	14152	6591
	4578	7461	4633	14845	14113	9478	16306	10792	5394	8423	16472	5538
	5726	15272	22541	13274	19969	1344	17982	3299	6241	17488	6970	16632
	2724	14874	2212	22392	12804	12135	15618	11858	552	17686	5585	19912
	21050	1222	14554	13068	15732	8905	5854					
520:	12932	18316	8070	15251	8216	15182	21583	18345	17227	19404	5489	17421
	19679	6636	1134	14441	20247	13276	19767	5072				
521:	14618	7172	4577	10111	4971	9921	11310	2304	19058	4919	2407	21318
	6019	13841	12405	6079	22166	21222	11447	3834	2957	2876	3847	10030
	3657	8737	2532	19313	13162	19695	11283	21477	13270	11090	20277	5569
	11224	1524	7689	5785	1443	1174	5378	3463	7893	2512	20456	11012
	5357	17062	17203	17936	14894	10285	19219	19980	15015	19783	22068	1918
	19153	5369	14302	9654	16742	15180	4073	14772	14901	3954	13470	8012
	15898	12241	11155	18311	11712	3109	18530	17791	1700	6065	18830	8838
	7741	20399	7063	8515	13562	2024	8969	7647	12054	19078	2184	16655
	8540	7852	16491	13169	20514	20202	7535	18320	11710	7747	15987	17730
	7302	1993	2766	4031	5562	21493	10046	1799	4731	18131	8100	10005
	7123	2520	10396	22156	9867	7052	11207	4505	21049	11504	21868	11614
	5889	12118	13000	22505	2411	10176	6296	9619	18566	20017	11928	3767
	11046	7551	2528	11302	21596	6991	7083	2350	736	10023	5402	21313
	14934	14110	14248	11521	15498	3429	17829	15576	19218	22393	10506	19723
	20354	6720	17694	8466	4273	4916	22208	20427	9107	15921	4439	10197
	2338	16397	13942	15715	20725	18142	3311	2926	10795	3889	17244	10288
	19160	8477	12011	3565	21062	9658	16357	6172	2617	1734	15245	22324
	7974	4678	3698	3992	10876	20303	19258	17048	4272	20359	11598	8412
	6693	19116	5690	8276	912	4024	10472	12647	6733	5738	15800	21800
	3295	8590	20011	17717	4177	7227	20102	5504	13132	11762	15477	18479
	9793	17968	11404	21844	17913	17281	14938	1225	7663	13582	11349	16247
	19951	3778	8781	7268	10618	18594	14849	15471	22337	22454	4787	4244
	12088	1992	9332	15917	17106	13790	19542	19573	2089	1592	7878	12361
	19383	14253	17356	4238	9481	1439						
522:	14431	6239	11377	22466	13606	11763	4871	19242	19036	9779	970	4882
	15417	18050	2958	13661	18314	19970	8044	8672	8262	4077	12369	12815
	15194	7431	19112	585	5289	17307	6089	5537	5935	21766	1304	15168
	4356	6485	15400	19439	706	14453	1031	5411	11160	12131	10020	11249
	8415	21643	14449	14017	1963	10261	1703	1878	4023	12040	9720	17260
	21578	15343	11117	16514	14299	20222	12107	18114	13664	4184	14261	16823
	13551	22313	3921	1998	666	4628	20928	18508	9588	8794	5200	619
	4115	20171	1555	3070	5376	7843	10040	19791	19447	20093	16957	19231
523:	5718	10805	6298	2166	20556	21748	9437	8027	3472	10338	7212	20501
	11491	4341	11669	9303	16917	8868	14506	2160	21476	17596	18688	9966
	15557	11767	2124	18956	7553	18747	18697	17873	7757	16320	22134	13292
	7913	9948	6980	17735	634	12444	16435	5350	17955	19423	15565	11353
	20128	13016	5239	860	22552	2379	6033	16520	21986	17573	5222	14074
	2603	19569	20484	2875	1313	5161	7288	21179	5370	19621	980	10087
	20381	3366	6986	21533	16164	20883	3426	1157	16729	6898	20593	17576
	9698	12169	10986	8048	17173	5809	21767	582	9317	13750	3110	18945

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	Sequence IDs for homolog proteins											
	19532	13594	14859	19926	14149	16203	18916	2694	2259	3885	16893	6833
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	1851	20107	18714									
524:	5146	21711	9443	19434	17798	8271	15157	6680	1121	22072	17654	19028
	13218	6405	9244	5217	7137	8194	21221	12019	13471	17578	11153	9140
	11727	17633	3462	17166	6295	21753	828	13617	9059	2402	16458	7601
	13675	21744	12228	3556	9011	10297	8699	1058	17727	3732	888	19098
	19007	20328	22435	9743	8151	9884	5912	13874	1793	20963	14276	11662
	13913	18489	16461	9898	8731	15745	3973	880	2296	9092	18765	17370
	18888	13547	17231	13680	4367	14754	17832	2159	8925	6054	4836	21950
	16483	17585	20898	15188	9783	19045	2088	7805	5781	7540	21423	10626
	3232	3412	16951	12593	7133	7230	17422	10172	19629	20061	15226	16396
	13106	16858	12395	8064	18608	10913	18148	14559	11640	22231	949	3806
	922	6047	14424	20294	21512	2844	21750	10411	1285	598	9413	13278
	5979	15078	9781	11382	15932	16934	17171	3994	21427	3887	3113	10974
	15635	18526	5503	9904	16377	17644	12020	15507	18396	5802	16207	16206
	6951	13409	14980	12042	9197	20762	11969	14942	19111	1373	9467	797
	8518	2947	13489	6590	10901	7185	7646	6204	6548	8825	7264	13425
	13837	10201	11983	19803	21421	11553	9049	3356	19634	16334	3944	7749
	20163	662	8190	6651	20724	22285	8240	12389	5598	11233	14315	15485
	11282	20624	12145	12327	13242	17891	1217	8203	12727	22111	8826	9668
	20863	11483	21587									
525:	6387	20127	15922	6468	22478	5164	14961	7042	16305	2182	16677	7733
	8221	13250	4225	10787	11039	2823	13281	6380	6824	6360	20082	1398
	14175	14977	21194	5933	9986	10799	2049	7444	4924	15193	2703	12215
	13851	836	5401	12967	18193	18801	1103	3308	20749	18446	18404	15606
	19308	7496	14462	10044	21187	16900	8754	16101	22544	1746	5089	13111
	9288	15179	4423	14999	11584	15673	5028	18076	21294	12622	21553	14776
	12325	6837	10013	20597	20543	11805	18067	18468	4428	3795	8921	3661
	8624	4476	13323	11313	7963	22062	20636	18513	1030	8805	22083	5807
	3830	19568	5055	4025	10497	21824	10898	19772	590	10473	8226	20982
	6273	21435	16209	9607	18881	10143	5700	11596	10735	19808	17961	19021
	1837	21662	20927	1365	7598	21243	15848	17757	8577	12564	9707	7488
	9892	1675	13967	1620	3282	2358	18278	15275	15531	18220	21540	22120
	14812	13263	6574	14679	2574	16215	1945	10259	15499	11627	12347	2605
	6895	7286	10483	2487	10289	3346	7293	9601	10220	7996	4547	4237
	7808	7341	5250	14483								
526:	8075	16099	8242	429	13036	10217	18174	535	533	507	306	11062
	15313	16399	14594	314	3820	5717	20464	15374	18461	18690	9504	8137
	11945	3327	4030	1064	15390	4708	6367	19001	8581	6859	18172	3305
	18107	12112	13896	2465	12130	19906	4949	17359	16220	13607	10705	15889
	16978	8246	16554	18467	9002	9780	17882	21655	20242	9063	5705	9204
	9915	11991	16148	15840	14589	6171	20389	6007	14898	1840	4491	7812
	8977	13027	6371	15170	21310	12535	9755	2819	3052	12267	8377	3804
	7983	22167	21674	22450	891	13549	7113	14532	9354	7858	8394	2044
	9345	2341	6836	19148	17763	286	18665	2645	14240	13516	9032	15489
	8304	7822	9993	17083	7310	5481	11010	1093	7789	21306	21699	11113
	8956	18128	7880	3416	6279	2857	11961	19154	10481	11542	21609	21506
	3533	6663	3391	4677	18511	4730	696	9569	17797	18687	7097	20259
	15252	13221	3261	14692	22502	14915	21157	20371	3563	12591	16308	7626
	16130	21296	2832	830	14553	6434	18295	17956	20230	10392	12043	21065
	20779	1281	17745	3289	3754	5487	8587	11548	12578	2882	5552	16586
	7955	1768	22518	12705	15449	988	20859	11129	6547	9854	11376	6669
	5359	9132	10964	19776	1879	22087	13137	13752	17298	3333	20301	19370
	15830	2425	6946	19538	14273	15340	6427	17165	15603	12419	10809	8003
	13658	14568	12544	17630	2371	4694	12396	15369	16597	3697	10741	13396
	21621	16662	8841	11120	14081	13456	21472	7487	12898	12787	8692	9484
	15204	6565	11203	14320	2978	9294	7482	9493	1277	4952	7813	7306
	12296	12021	6645	9286	22489	13745	16653	19069	7780	15219	16969	19357
	14762	10802	10479	16663	3678	16713	7751	13703	3630	4691	9472	10709
	8542	7060	6112	22457	21974	20476	7333	6482	14526	7151	2644	835
	10655	12264	17372	10889	6281	10965	15558	5973	1482	22476	19408	9637
	5773	5016	20819	18982	19997	4572	640	19168	8691	17905	2970	2132
	20312	4655	16568	21093	13882	5730	7976	7079	13035	3505	2800	12522
	8939	2155	3206	2017	15587	6277	1297	1423	18728	305	509	12545
	2037	11704	9571	21379	13089	11197	13107	22367	17943	2420	7599	5997
	372	1801	21374	16528	8722	16672						
527:	3642	15482	8461	18796	11646	4433	18911	12512	19895	14727	7891	5229
	8941	8192	671	3621	19293	20133	7775	16444	5601	9047	7456	1332
	15241	20870	3570	13126	6335	14830	17816	4052	1048	11934	7415	16817
	11466	15006	17149	16740	13546	20225	18675	12360	11085	4464	12955	7636
	18831	17524	21731	2244	8988	9012	18649	8617	6285	18612	1053	1455
	4829	16779	15889	18827	14953	12980	10447	1034	15656	2581	22412	4354
	10756	21138	3468	6872	6990	15371	16865	14170	14485	16553	7703	21199

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	Sequence IDs for homolog proteins											
	6847	729	14001	18779	7182	2836	8312	3038	18069	16737	4357	10422
	3567	6722	22039	3264	5085	20829	6719	2934	10564	14973	13027	2205
	9393	19576	7148	2665	6959	16605	4997	17039	7857	4310	11556	19590
	12715	6725	8377	3489	3770	22024	3546	20586	5189	20926	2245	1604
	7700	18947	5485	22116	21537	11706	18715	21536	17691	17398	2949	3079
	6290	961	6042	4750	8302	20882	5852	13136	16392	2643	14077	9240
	11996	3702	14090	19402	7233	5546	10148	20680	8638	3269	15282	9663
	15009	15604	8648	14392	18782	10570	6318	19862	13514	13217	3980	5231
	11578	4812	18337	3004	3073	8249	18941	9036	3233	864	15080	19930
	6746	1476	10866	20483	19942	7450	762	21276	3235	15320	22462	11955
	1562	13099	7710	9136	7251	16129	19467	10892	10630	13600	12857	14732
	4581	18096	3518	12368	1009	17283	4039	6864	5773	6063	15842	16851
	18149	7977	14608	4572	10553	4514	11848	18068	17157	12223	18597	15178
	10550	11835	16242	11778	20884	16907	14445	5068	7404	1516	6277	17663
	17662	21513	5526	14789	7565	21347	1238	10660	18496	16381	20827	19639
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	19677	20195	3911	3945	21129	6446						
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	19074	13384	7518	15985	8336	5383	3907	13379	12855	14509	12217	3398
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	9052	1023	10386	2348	6364	14482	15814	7746	9263	3529	9935	10786
	20919	12407	11705	8493	5095	8481	6104	3104	14770	19267	1032	17399
	8085	17728	7344	673	15714	3361	5103	21218	15350	7539	761	19758
	16925	17515	8371	9594	13769	16744	17772	4420	8605	6819	6628	9541
	19100	13982	7360	20665	9903	5639	8487	13488	9666	5511	11106	17709
	5021	19088	20007	12811	14758	15329	7823	21543	20508	1178	5558	16935
	1252	7312	20192	18963	5305	19575	17193	1262	3577	20951	2711	18829
	9159	6009	6176	17751	9694	17992	12429	15448	4598	18452	7077	10597
	16197	705	8820	11971	19192	1370	996	1578	21971	6312	17349	2736
	3936	10254	10398	22265	20083	15853	14066	5564	9113	3087	1078	7435
	14028	16372	9321	18704	8983	21564	9660	11558	17282	12695	19057	13847
	17094	11400	7613	2232	17213	17103	19378	6072	14868	8879	6825	12193
	1427	3275	9458	15007	6271	4411	4190	12430	16366	20438	15680	10929
	4035	20030	4556	17229	4660	597	1587	15707	4334	22484	21035	8211
	16251	13133	11295	2966	14058	5665	6592	8738	6102	13087	3436	12074
	14546	13772	20692	10970	19345	13509	5329	19187	16282	9968	21671	9048
	8976	7492	21462	19662	8457	8317	18846	12864	10746	4141	8673	21010
	10417	4329	7895	998	10132	8852	14795	5620	6695	13781	19165	7258
	20895	4154	7359	12259	11737	12704	21606	3865	5520	6932	12901	20940
	15027	3236	4907	20734	15492	10607	2472	15046	8506	18724	11671	15259
	15936	7889	5596	2053	6905	8323	16351	10263	15826	21160	19461	17456
	3953	3584	4314	64281	4221	4758	5800	22365	17678	16252	14893	17154
	19437	16453	21224	9572	16225	9367	1899	8751	8426	12483	4441	20592
	6867	2168	16928	13225	22460	20208	12970	2591	5304	13498	21581	4699
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	21739	19681	11533	3338	3956	11364	17988					
531:	15910	22524	13589	1006	11575	20349	18523	10911	13067	10217	9609	5233
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	2814	21443	1880	1396	3615	13867	7787	22538	13411	13344	1205	18398
	13083	17485	1550	757	11281	11029	21967	827	1873	21174	14091	5281
	885	7332	8229	21103	4400	1012	15883	7812	7121	16424	1339	1866
	3474	11617	19918	14296	1352	17699	12367	3388	20896	20167	6697	19989
	9358	15375	4618	11468	13543	3097	15540	19380	14287	5051	11086	12824
	13271	15196	6303	4194	1182	15803	1842	19299	2857	17664	21589	11961
	19154	12506	21814	6334	21437	20936	11195	20933	21506	22069	5476	3533
	19583	7949	4677	18511	4730	696	9569	17797	18687	7097	20259	15252
	13221	13305	450	22502	14915	21157	6730	2195	19855	10324	11089	1744
	19917	16130	21296	2832	830	14553	6434	18295	17956	829	476	12043
	2457	13959	12384	5220	3209	19341	5731	10908	4395	21843	14568	17630
	2371	4694	12396	15369	13051	16597	3697	10741	16309	4927	13396	21621
	8841	16662	11120	14081	19449	21259	15204	6565	18317	14304	4952	7813
	7306	12296	12021	6645	21386	16505	9286	22489	3622	14762	18330	10802
	10479	16663	3678	16713	7751	13703	3630	4691	9472	10709	8542	7060
	6112	22457	21974	20476	7333	6482	14526	7151	2644	835	10655	12264
	9315	2786	16253	9488	5634	17372	3836	7637	4946	18143	11559	18362
	12059	10889	5190	13207	16465	17346	3323	5354	5825	2210	19147	9333
	13177	20541	3458	1240	15787	20099	9282	11480	4994	14011	1145	19545
	802	17144	13420	13439	14301	1357	10965	15558	22251	22565	810	7570
	2692	15666	13168	10912	20574	4894	2526	18982	4020	19796	2984	11522
	11245	21570	8695	16749	17392	2132	20312	4655	16568	21093	13882	5730
	7976	7079	13035	2800	16658	18348	16408	4157	8112	5264	305	12545
	2037	11704	9571	21379	3712	7685	4483	18456	22341	3397	11197	13107
	675	16006	20604	18536								

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Sequence IDs for homolog proteins												
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	14319	21808	15520	1498	14212	14282	19450	526	3987	18034	12939	14517
	22533	14740	7812	18725	15422	12515	6665	8294	20640	9749	7933	18742
	10601	1528	14184	8297	11430	21253	7897	4901	7308	16574	19527	9882
	8330	6186	16730	3076	15579	16073	19400	17335	2857	17664	21589	11961
	19154	6997	3197	21437	4440	11195	20933	21506	3533	4677	18511	4730
	696	9569	17797	18687	7097	20259	2920	15252	13221	3452	14930	450
	11335	20777	12713	22502	14915	21157	14054	10864	5059	21184	8816	9146
	14653	14579	20371	3563	12591	16308	7626	4212	19798	19458	5691	18292
	7706	5100	4540	16130	21296	2832	830	14553	6434	18295	17956	829
	476	12043	13241	11023	4301	9298	2269	1306	13291	17064	20779	5613
	1281	17745	11486	9723	16586	7955	12705	15449	988	20859	1768	11129
	6547	22518	5552	9854	11376	6669	5359	9132	10964	1879	22087	13137
	17298	3333	13752	20301	19370	2425	20461	6946	19538	14273	15340	6427
	17165	15603	12419	10809	8003	13658	14064	14568	17630	2371	4694	12396
	15369	16597	3697	10741	12482	16309	4927	13396	21621	8841	16662	11120
	14081	15751	4903	21508	18755	14599	6384	8692	9484	15204	6565	14320
	2978	9294	7482	9493	1277	4952	7813	7306	12296	12021	6645	9286
	22489	13745	16653	19069	7780	15219	16969	14762	18330	10802	10479	16663
	3678	16713	7751	13703	3630	4691	9472	10709	8542	7060	6112	22457
	21974	20476	7333	6482	14526	7151	2644	835	10655	12264	9315	2786
	16253	9488	5634	17372	1733	20453	21787	16624	7001	20828	13302	10357
	4549	788	10490	19133	12318	5515	9280	22095	18903	3706	15256	18593
	5764	11115	12583	11568	13613	2331	5136	8073	15998	5630	11304	19137
	5817	5580	3044	18341	8588	5857	12540	2454	4970	16919	17445	2401
	11869	6193	21516	10889	5190	13207	16465	9673	11625	9771	2283	11716
	19554	905	7481	12401	19686	13656	22135	9553	18575	9584	12794	5644
	21399	20485	9218	18691	3350	18263	4846	544	19667	9933	4140	1318
	20418	11128	20105	16734	2376	15699	7061	4232	15357	14036	5339	7107
	19030	7165	21370	12103	4848	13211	22530	15360	12863	9975	6398	14067
	16683	21170	1924	890	8155	15866	10131	7187	4332	1235	20330	12927
	7088	5099	2302	12424	8303	17466	14322	11383	2282	15956	3414	12982
	18548	15665	10961	21084	10824	18440	16819	3730	13940	18821	14864	1818
	19607	7969	6546	16771	5441	8459	18266	5000	15749	13014	14274	8444
	4707	13097	15930	11872	2621	7158	6942	18502	5408	10837	21928	13800
	5188	19614	16117	4719	1833	13499	3107	21492	12503	21929	7921	1429
	14398	22189	6439	12993	12307	19714	6650	18994	747	5932	18630	6683
	1921	15651	5594	6958	13597	19763	10097	14124	14687	1094	5780	7770
	7688	15110	5797	7907	21169	3329	12627	4065	19882	22067	19211	2061
	7038	8909	16914	13129	19881	11720	16317	1551	13235	14888	1201	20264
	7800	7526	2209	5887	15285	10798	15317	10223	11351	10105	10661	15014
	2908	16412	22277	19851	12003	19616	11003	7768	6166	21613	4620	13850
	16231	7016	2717	20541	3458	1240	15787	20099	9282	11480	4994	937
	16775	18459	14476	9221	17450	6281	18662	7992	9661	19875	11156	3619
	14086	20948	16946	3456	6143	786	6709	5954	17926	20839	22351	13277
	11255	5140	4283	9455	4818	14459	5187	16668	10965	15558	17215	14289
	11685	4388	14119	18982	2984	11245	304	477	427	18112	965	2900
	2132	20312	4655	16568	21093	13882	5730	7976	7079	13035	5498	2800
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	11961	19154	21437	11195	20933	21506	3533	4677	18511	4730	696	9569
	17797	18687	7097	20259	15252	13221	450	11335	20777	12713	22502	14915
	21157	20371	3563	12591	16308	7626	4212	19798	19458	5691	18292	16130
	21296	2832	830	14553	6434	18295	17956	829	476	12043	20779	1281
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	9854	11376	6669	5359	9132	10964	1879	22087	13137	17298	3333	13752
	20301	19370	2425	6946	19538	14273	15603	15340	6427	17165	12419	10809
	8003	13658	14064	4221	7387	13284	20981	2316	3116	8418	3386	6508
	18217	3578	22249	992	13442	3471	14855	19949	5277	19885	2816	10917
	9436	18538	18659	12816	12308	15943	2515	20364	14701	8193	17579	22076
	8890	2649	9329	21073	8376	15177	10882	859	5990	9814	16053	5209
	3144	13848	22428	19076	5454	17056	14918	4088	11270	5837	9604	22455
	19840	12234	1149	801	953	9960	21301	1656	3755	12278	22119	21098
	1005	10264	13037	11702	20954	5581	5063	1118	6454	20632	1696	19474
	14911	9381	4111	13374	2932	3071	18551	22362	1431	12923	6509	19229
	14012	5372	12362	17380	20272	16391	13395	5132	901	9540	19228	11589
	13306	3179	14568	17630	2371	4694	12396	15369	11784	16597	3697	10741
	16309	4927	13396	21621	8841	16662	11120	14081	8692	9484	15204	6565
	14320	2978	9294	7482	9493	1277	4952	7813	7306	12296	12021	6645
	9286	22489	13745	16653	19069	7780	15219	16969	14762	18330	10280	10802
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	Sequence IDs for homolog proteins											
	6112	22457	21974	20476	7333	6482	14526	7151	2644	835	10655	12264
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	18593	5764	11115	12583	11568	13613	2331	5136	8073	15998	5630	11304
	19137	5817	5580	18341	8588	12540	2454	4970	17445	2401	11869	6193
	21516	2447	10889	5190	13207	16465	9673	9771	11716	18575	9584	12794
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	20418	11128	20105	16734	2376	15699	7061	4232	15357	14036	5339	7107
	19030	7165	21370	12103	4848	13211	22530	15360	12863	9975	6398	14067
	16683	21170	1924	890	8155	15866	10131	7187	4332	1235	20330	12927
	7088	5099	2302	12424	8303	17466	14322	11383	2282	15956	3414	12982
	18548	15665	10961	21084	10824	18440	16819	3730	13940	18821	14864	1818
	19607	7969	6546	16771	5441	8459	18266	5000	15749	13014	14274	8444
	4707	13097	15930	11872	2621	7158	6942	18502	5408	10837	21928	13800
	5188	19614	16117	4719	1833	13499	3107	21492	12503	21929	7921	1429
	14398	22189	747	6439	12993	12307	19714	6650	18994	5932	18630	6683
	1921	15651	5594	6958	13597	19763	10097	4065	14124	14687	1094	5780
	7770	7688	15110	5797	7907	21169	3329	12627	19882	22067	19211	2061
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	22277	19851	12003	19616	11003	7768	6166	4620	16231	13850	7016	2717
	20886	14522	5254	15519	20541	3458	1240	15787	20099	9282	11480	4994
	6281	18662	7992	9661	19875	11156	3619	14086	20948	16946	3456	6143
	786	6709	5954	17926	20839	22351	13277	15113	6368	7704	18694	3644
	12154	3794	21257	21638	18386	18111	21498	10731	13776	5539	14530	20282
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	10192	13836	5240	2653	20833	3564	1870	11250	6367	19001	20137	15672
	13176	20207	8314	4015	1887	8795	21466	7023	18171	6876	8560	16477
	13630	10793	4136	5249	17099	9152	2730	4724	8684	5821	3710	16562
	22562	9500	21952	12129	1151	5863	2635	13579	5947	9543	6219	4851
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	9067	2618	1308	1202	16045	2887	3970	22176	2992	14189	2020	3687
	18669	17082	7279	10946	10754	10583	4481	915	16903	18701	14442	11182
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	3441	9629	4034	4019	17401	1207	22219	1481	5143	2857	17664	21589
	11961	19154	12425	21437	17489	11195	20933	21506	3533	12843	4677	18511
	4730	696	9569	17797	18687	7097	20259	20966	15252	13221	11335	20777
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	6645	9286	22489	19908	893	14762	18330	10802	10479	16663	3678	16713
	7751	13703	3630	4691	9472	10709	8542	7060	6112	22457	21974	20476
	7333	6482	14526	7151	2644	835	10655	12264	9315	2786	16253	9488
	5634	17372	2081	12643	15099	7425	15838	10094	788	3348	9280	22095
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	8073	15998	11304	19137	5817	4430	5580	8588	18341	12540	2454	4970
	17445	2401	10889	5190	13207	16465	11291	16479	21467	4263	2705	9673
	20541	3458	1240	15787	20099	9282	11480	4994	2798	5475	1814	2683
	8435	4345	3627	15897	9366	6281	20716	18662	7992	9661	19875	11156
	21818	3619	14086	20948	16946	3456	6143	786	6709	5954	17926	20839
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	21704	8464										
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	20933	21506	3533	4677	18511	4730	696	9569	17797	18687	7097	20259
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	16308	7626	4212	19798	19458	5691	18292	16130	21296	2832	830	14553
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	15449	988	20859	1768	11129	6547	22518	5552	9854	11376	6669	5359
	9132	10964	1879	22087	13137	17298	3333	13752	20301	19370	2425	6946
	19538	14273	15340	6427	17165	15603	12419	10809	8003	13658	14064	4221
	7387	13284	20981	2316	3116	8418	3386	6508	18217	3578	22249	992

TABLE 17-continued

	Sequence IDs for homolog proteins											
	14855	13442	3471	19949	5277	19885	2816	10917	9436	18538	18659	12816
	12308	15943	2515	20364	14701	8193	17579	22076	8890	2649	9329	21073
	8376	15177	10882	859	5990	9814	16053	5209	3144	13848	22428	19076
	5454	17056	14918	4088	11270	5837	9604	22455	19840	12234	1149	801
	953	9960	21301	1656	3755	12278	22119	21098	1005	10264	13037	11702
	20954	5581	5063	1118	6454	20632	1696	19474	14911	9381	4111	13374
	2932	3071	18551	22362	1431	12923	6509	19229	14012	5372	12362	17380
	20272	16391	13395	5132	901	9540	19228	14568	17630	2371	4694	12396
	15369	16597	3697	10741	16309	4927	13396	21621	8841	16662	11120	14081
	8692	9484	15204	6565	14320	2978	9294	7482	9493	1277	4952	7813
	7306	12296	12021	6645	9286	22489	13745	16653	19069	7780	15219	16969
	14762	18330	10802	10479	16663	3678	16713	7751	13703	3630	4691	9472
	10709	8542	7060	6112	22457	21974	20476	7333	6482	14526	7151	2644
	835	10655	12264	9315	2786	16253	9488	5634	17372	788	9280	22095
	18903	3706	15256	18593	5764	11115	12583	11568	13613	2331	5136	8073
	15998	5630	11304	19137	5817	5580	8588	18341	12540	2454	4970	17445
	2401	11869	6193	21516	10889	5190	13207	16465	9673	9771	11716	18575
	9584	12794	21399	20485	9218	18691	3350	18263	4846	544	19667	9933
	4140	1318	20418	11128	20105	16734	2376	15699	7061	4232	15357	14036
	5339	7107	19030	7165	21370	12103	4848	13211	22530	15360	12863	9975
	6398	14067	16683	21170	1924	890	8155	15866	10131	7187	4332	1235
	20330	12927	7088	5099	2302	12424	8303	17466	14322	11383	2282	15956
	3414	12982	18548	15665	10961	21084	10824	18440	16819	3730	13940	18821
	14864	1818	19607	7969	6546	16771	5441	8459	18266	5000	15749	13014
	14274	8444	4707	13097	15930	11872	2621	7158	6942	18502	5408	10837
	21928	13800	5188	19614	16117	4719	1833	13499	3107	21492	12503	21929
	7921	1429	14398	22189	6439	12993	12307	19714	6650	18994	747	5932
	18630	6683	1921	15651	5594	6958	13597	19763	10097	14124	14687	1094
	5780	7770	7688	15110	5797	7907	21169	3329	19882	12627	4065	22067
	19211	2061	7038	8909	16914	13129	19881	16317	1551	13235	14888	1201
	20264	7800	7526	2209	5887	10798	15317	10223	11351	10105	10661	15014
	2908	16412	22277	19851	12003	19616	11003	7768	6166	4620	13850	16231
	7016	2717	20541	3458	1240	15787	20099	9282	11480	4994	6281	18662
	7992	9661	19875	11156	3619	14086	20948	16946	3456	6143	786	6709
	5954	17926	20839	22351	13277	15113	6368	7704	18694	3644	12154	3794
	21257	21638	18386	18111	21498	10731	13776	5539	14530	20282	7762	9529
	17675	15191	12380	14865	15825	2818	16442	5901	8220	18578	13297	2495
	21913	4526	16085	10965	15558	18982	2984	11245	16474	304	477	427
	5067	2132	20312	4655	16568	21093	13882	5730	7976	7079	13035	2800
	20416	509	307	305	12545	2037	11704	9571	21379	3712	7685	4483
	18456	22341	11197	13107	13268	16006	428					
536:	8250	5293	17519	10969	8775	16532	10286	11811	5689	2871	680	20415
	14104	16888	17043	10273	6777	22396	602	4866	12333	9909	22327	4344
	9005	16476	2573	10616	19638	15657	8950	4378	2657	3364	21708	985
	6316	8776	2238	13856	1099	10466	19656	6879	9313	19604	12069	8122
	21385	16087	20487	1424	14078	2427	4175	7418	9385	16892	15809	3499
	16714	5768	6322	13627	19469	8252	19551	14976	12742	10499	11322	9597
	3569	9336	20132	5283	22127	10381	3149	7067	13886	7478	3897	20869
	19398	13086	4191	3669	20800	6799	8453	17539	21956	5724	13878	16687
	1797											
537:	12225	7991	19769	20707	6346	21228	18920	15677	22007	17216	1246	1299
	3482	8428	4864	1869	18259	5076	18894	10621	1194	21241	4280	10372
	9939	3461	22101	14388	9687	1934	3266	19426	6888	17781	1697	1251
	15687	11467	11444	7248	4960	3598	18026	17460	7270	18737	20522	18581
	16569	13403	4999	20923	3253	12847	6541	12065	13811	442	18246	10039
	21176	20831	13532	19077	10287	9635	12724	898	43471	1482	12691	8702
	12055	8006	14571	19675	16542	21229	14891	11459	15395	15872	9301	10051
	6843	5509	11707	10865	18908	12031	9844	20469	4041	4623	22346	1849
	12095	14281	3840	16733	15322	21786	17305	10611	1428	7631	22045	6676
	5894	8015	21902	14896	17330	3090	15122	7759	6196	16678	475	20224
	3032	21119	21396	1165	20759	22152	18157	1337	3062	12222	10847	14596
	3679	21087	17626	3743	10092	21220	22333	4831	6340	2684	14394	17353
	12317	2073	22147	10166	9664	11412	21185	7389	11862	11526	9220	2983
	5429	13258	10529	12270	6868	5672	2355	11711	9314	17713	6624	12386
	17898	3480	10028	20275	1292	12254	17594	20642	4853	10383	4591	8186
	16379	15333	9201	15765	17720	5294	9934	7376	4038	2297	1916	7144
	16736	10304	3319	3762	20614	11341	10440	4734	9677	12289	20772	4271
	19954	22175	3020	19748	16083	8948	19737	22114	2955	21137	3274	1408
	6780	10848	7124	14060	11449	17939	4794	16058	21761	10251	4961	19141
	1661	9701	6223	5983	18048	10670	17196	1709	4904	12196	630	8403
	8582	6184	18819	3380	9202	16022	17350	12703	15237	17792	4597	11159
	1072	20441	15476	15612	17341	12261	21044	4892	1108	1406	22046	18198
	6967	20318	12469	22123	7645	10452	1264	712	14602	6109	14712	22157
	7745	16695	11050	22271	21574							

TABLE 17-continued

Sequence IDs for homolog proteins												
538:	8633	21066	20486	15659	19893	20341	18625	7202	9210	15561	8243	19452
	10486	9599	20104	5911	17836	3744	3313	22371	13393	8083	14598	8878
	4121	11696	16024	6949	9760	18073	21021	1691	3955	13639	14076	5677
	2739	10860	20215	14300	10639	13585	11393	3392	7331	2940	4631	3646
	14037	5709	8396	7169	3234	9515	13640	21141	9848	13213	16854	10018
	17683	4171	20607	15041	2557	19483	17558	19443	20760	13774	16065	5097
	13747	713	8505	18788	18352	817	5302	8167	10335	22171	13497	18845
	11474	8093	22332	17185	18392	15387	7019	17613	13932	22281	9232	21810
	19046	14214	6221	10362	21188	12117	2909	9179	16519	21842	14950	5628
	5467	18729	7240	8434	11000	2806	17205	1863	9645	18886	6782	20838
	7708	6070	7788	22286	19842	16891	9527	18008	7791	11889	5849	2006
	3823	12758	17857	15410	11552	11047	5550	18384	903	18870	12346	18758
	1298	11723	11231	13187	11334	10943	11898	11754	4492	6688	19935	13184
	13651	1487	20841	6884	6464	8803	16050	6362	1430	1363	10992	6297
	3031	2620	18570	22021	21438	13674	22415	1440	6599	17348	16403	2064
	5725	621	12956	13371	3689	813	8410	17547	5880	7069	7272	13965
	9296	18273	16456	7801	2112	17834	8758	7378	19838	6388	10579	19671
	16279	806	14835	2530	4277	795	12076	5622	13454	3935	4559	18529
	18155	19209	15646	5247	6539	16369	5499	21300	14158	12126	17163	16184
	993	21342	16623	17172	10687	11363	1456	21186	21282	21603	10623	6475
	17459	18745	21602	9996	3042	16551	1505	5224	5300	3833	4119	10925
	11838	21509	15409	13868	11753	16835	13881	7206	18880	6510	4201	3942
	968	5155	13073	10765	5458	12673	3180	3108	15770	908	21482	5413
	18381	14279	4351	15582	22158	16937	12412	13635	14711	5969	9888	21962
	11801	16194	10513	4703	11781	15593	17383	18258	9184	7699	9109	1971
	18780	3171	11419	10405	631	15583	21710	7483	5744	22254	12810	13894
	20089	6909	5948	3120	15669	17412	19244	2016	16850	22002	7260	14202
	3293	4461	2271	14582	18598	17872	1569	18470	5671	8965	4082	7327
	22511	15167	1160	15734	5450	19432	14387	14587	3176	8359	18160	11357
	15085	6948	5337	2567	10321	22182	10881	10168	18477	12537	19015	20260
	2170	18422	2440	3225	5484	1260	1822	7532	19248	7693	4353	10441
	2660	5734	10038	19976	3453	19019	1674	12312	16581	10232	3727	1523
	2140	22432	20580	9947	19324	20180	1384	2325	18901	10198	20110	9744
	9208	3182	14144	18875	14329	929	22054	2752	4524	986	977	21117
	9567	9679	12352	20957	4772	12912	19652	11510	5608	21827	13765	8183
	14331	13670	20503	12206	21116	22320	844	2226	21795	13733	11051	20995
	2615	7715	4478	2290	12549	15082	2491	2301	14182	15076	1227	10071
	3792	13186	4722	1595	10880	11269	8528	3213	14537	4257	8761	17108
	4834	2651	19705	3355	7552	6681						

Example 3

Consensus Sequence Build

[0171] ClustalW program was selected for multiple sequence alignments of the amino acid sequence of SEQ ID NO: 379 and 10 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. Attached are the sequences of SEQ ID NO: 379, its homologs and the consensus sequence SEQ ID NO: 22569 at the end. The symbols for consensus sequence are (1) uppercase letters for 100% identity in all positions of multiple sequence alignment output; (2) lowercase letters for >=70% identity; symbol; (3) "X" indicated <70% identity; (4) dashes "-" meaning that gaps were in >=70% sequences.

```
SEQ ID NO
2406      -------------------------MGSNGGSSNNNNNKVLEKPGQDQLVQQQQQQQE-
15414     -------------------------MGSNGGSSNNNNNKVLEKPGQDQLVQQQQHPQE-
587       ------------------------------------MMGRVMEKPSQDLLQQQQQ-----
9696      ------------------------------------MMGRVMEKPSQDLLQQQQQ-----
5895      ------------------------------------MMGRVMEKPSQDLLQQQQQ-----
17251     MFGNGNCDVDNEKTIITSSKWTQSEIDDHKVSMASSTGNRVMEKPGQELLQQQQQ-----
19549     ----------------------------------------MEKQGQELLQQHHQQQQQQ
379       -----------------------------------MQSKNMIVASSHQQQQQQQPQQPQP
21357     --------MGLSSKQVSSSGLDWKQTLLEAQNLELPKPNLMRKQQQQQQQQQQQTQPNSE
17711     --------MGLSSKQVSSSGLDWKQTLLEAQNLELPKPNLMRKQQQQQQQQQQQTQPNSE
13715     ----------------------------------LTLTKCCMQRGSHFRSRSGSQEARS
consensus -------------------------xxxxxxxxxxxxxxxxxxxxqxxxqqqqxxxxxx
22569
```

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APKCPRCDSSNTKFCYYNNYSLSQPRHECKACKRYWTRGGTLRNVPVGGGCRRNKRVKRP
APKCPRCDSSNTKFCYYNNYSLSQPRHFCKACKRYWTRGGTLRNVPVGGGCRRNKRVERP
ALKCPRCESSNTKFCYYNNYSLSQPRHFCKACKRYWTRGGTLRNVPVGGGCRKNKRVKRP
ALKCPRCESSNTKFCYYNNYSLSQPRHFCKACKRYWTRGGTLRNVPVGGGCRKNKRVKRP
ALKCPRCESSNTKFCYYNNYSLSQPRHFCKACKRYWTRGGTLRNVPVGGGCRKNKRVKRP
ALRCPRCDSSNTKFCYYNNYSLTQPRHFCKACKRYWTRGGTLRNVPVGGGCRKNKRLKRP
ALKCPRCDSSNTKFCYYNNYSLSQPRHFCKACKRYWTRGGTLRNVPVGGGYRRNNKRSTS
QLKCPRCDSSNTKFCYYNNYSLSQPRHFCKACKRYWTRGGTLRNVPVGGSYRKNKRVKRP
SLKCPRCDSTNTKFCYYNNYNKSQPRHFCRACKRHWTKGGTLRNVPVGG-GRKNKRVKKS
SLKCPRCDSTNTKFCYYNNYNKSQPRHFCRACKRHWTKGGTLRNVPVGG-GRKNKRVRKS
GSSMSRCNSMDTKFCYYNNYNVNQPRHFCKNCQRYWTAGGSMRNVPVGAGRRKNKHTGSV
xlkcpRCxSsnTKFCYYNNYslsQPRHFCkaCkRyWTrGGtlRNVPVGggXRkNkrvxxx

LITTNPSSAAIDTAASNNSSN-SSSAPLQPPIDTASTS--------------NHINPLFY
TTSPCSAAIDTASNSSNSSSAPTAAASLQPQIDTASTS--------------NHTNPLFY
TNHGDSSSSAANSPSSSNSNPPSQPHLDNIIASSSTTN------------HINNISPFFY
TNHGDSSSSAANSPSSSNSNPPSQPHTDNIIASSSTTN------------HINNTSPFFY
TNHGDSSSSAANSPSSSNSNPPSQPHIDNIIASSSTTN------------HINNISPFFY
TYPCSNNNNIDFSASPSSSTPSSVVANPNPPSQSQQQQQQQQHHSFDIAATSNHINTMLY
SSNGPTSTTTLIKRPISTIETATTSNSSSPSSTHSSTS--------------NHMNPMEY
------STATTTTASTVSTTNSSSPNNPHQISHFSSMN----------------HHPLFY
TTPTTTSSTTTTPITTATSTCTATVTTSIGNNNNNMDAMLG----------CYSHMTIQT
ITTPITTSSTTTHQSQPPLQLALPQSQPQLATTTTTWMLCW----------VVTAT----
YRHTVITPDSLASLQVDGPDLVDHKPLSPEKVNGTILKFG--------------PDAPLC
xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx----------xxxxxxxxxy

GLPSSS-SDVNLPLFSRFGSRISSS----GFDLQLNNALGLGFSSGVLSNEASDNNGYR-
GLPSSS-SDVNLPLFSRFGSRISSS----GFDLQLNNALGLGFSSRVLSNEASDNNRYR-
GG-----DVMSSVPFPRFNLHSQLN------------ALGLGFSTGVSENGFSTSNNN--
GG-----DVMSSVPFPRFNLHSQLN------------ALGLGFSTGVSENGFSTSNNN--
GG-----DVMSSVPFPRFNLHSQLN------------ALGLGFSTGVSENGFSTSNNN--
GGNSCH-DVMNFPFSTRFNSTTRVSNPASGYDNLPQNGLGLGFSSGILMSAAGGEVNLNH
GLSSTNNPCDPNLPFSRENITSRLSTSSGYDLQPQMNFFGLGFSSGFENNGYTNGFNTS-
GLSDHMSSCNNNLPMIPSRFSDSSK------------TCSSSGLESEFLSSGFSSLSALG
PLADDQKNMSSSLYQALIRPPPLLLQQQNLLNTRELEGKDFGIGIGNGNNGTFPSSTLAL
------------------------------------------------------------
ESMASILNLGEQNLSSQLDFTAGAE-----------NREETSCSSACKPVKKKDITQHN-
gxxxxxxxxxxxxxxxxxxxxxxx----xxxxxxxxxxxgxsxxxxxxxxxxxxxxx-

-------------NWFGSNNTLLSSYTSTTSTTTPAMSSLLSSSLLQQKFMTDGVD----
-------------SGEGSNNMLLSSYTSTT-TTTPAMSSLLLQQKFISGGLKNDAD----
------------SFFSAYNSMFGSSSSSTCAPSTPVMASLLSSTLLQQNLMGGGG---GG
------------SFFSAYNSMFGSSSSSTCAPSTPVMASLLSCTLLQQNFMGGGG---GG
------------SFFSAYNSMFGSSSSSTCAPSTPVMASLLSSTLLQQKLMSGGG---GG
HHHHHHDEGSYRNGFSTSNNNNYSSIFGSSSTTTPVMASLLSSTLLQQKFMGTGGGIKGG
----------------NNNYDSIFSSSTSASNNTSVMPSVLSSTLLQHKFFDDGLK----
--------LGLPHQMSHDHTINGSFINNSTTNKPFLLSGLFGSSMSSSSTLLQHP-----
P-------------IPHQSQSLLFPFSASSRSFDTNPCSVVSTSLRSSNVYNYGED----
------------------------------------------------------------
------------------------------------------------------------
------------xxxxxxxxxxxxxxxxxxxxxxxxxxsxxxxxxxxxxxxxxxx--xx

--------STNTFQHGLGLTPLEQLQMASDHSSEAGMVALKDVKVELGQNNRLEWNNGAA
--------SSNTPQHGLSLTSLEQLQIASDHSSEAGMVALKDVKVELGQNNNRLEWNGGA
VKGRDHDQGDNTFHGLAPLQGLRVEGDSNNNIGSKEVKGEGQNRPEWSNNNNNNNNNGGG
VKGRDHDQGDNTFHGLAPLQGLRVEGDSNNNIGSKEVKGEGQNRFEWSNNNNNNNNNGGG
EGEEVVIMIKVATLSMAWHRYKGCKWKGTIIIVTILAQKK--------------------
GGGGGGDDDPFHHHQEMDSKEVKLGEGLQNRLDQWNMNNLNGNGGAVFQNQMENMGLSDN
----------YGSDAGSNGAFQDLQFGSKMQNQMEHIGGFYDPASSIYLNATSSSAIGVW
----------HKPMNNGGDMLGQSHLQTLASLQDLHVGGNNEDMKYKEGKLDQISGNING
---------QFKAIEEPTTNSTTATIVPSTGGTNNTHHPWEIAAATSGVGLGTSSNSNYW
------------------------------------------------------------
------------------------------------------------------------
xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

CQSQIQHVGLYDPSLYWNNSAATALGVWNDQAANIGSSVTSLI
FQSQIQHVGLYDPLLYWNN-SATALGVWNDQAANIGSSVTSLI
GQNQMEHVGLSDPNSLYWN-TATGLGAWSDQPNNIGPSVTSLI
GQNQMEHVGLSDPNSLYWN-TATGLGAWSDQPN-IGPSVTSLI
--------------------------------------------
NASLYWNNNHNNSNNNTSA-TATGLSSVWSTDQPGSNSVSSLI
NDQGANNTGSSVTSLI---------------------------
FMSSSSSLDPSNYNNMWNNASVVNGAWLDPTNNNVGSSLTSLI
NWEDFDSLVSTDLKDPWDDSDIKP-------------------
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Example 4

Corn Transformation Construct

[0172] GATEWAY™ destination vectors (available from Invitrogen Life Technologies, Carlsbad, Calif.) are constructed for insertion of trait-improving DNA for corn transformation. The elements of each destination vector are summarized in Table 18 below and include a selectable marker transcription region and a DNA insertion transcription region. The selectable marker transcription region comprises a Cauliflower Mosaic Virus 35S promoter operably linked to a gene encoding neomycin phosphotransferase II (nptII) followed by both the 3' region of the *Agrobacterium tumefaciens* nopaline synthase gene (nos) and the 3' region of the potato proteinase inhibitor II (pinII) gene. The DNA insertion transcription region comprises a rice actin 1 promoter, a rice actin 1 exon 1 intron1 enhancer, an att-flanked insertion site and the 3' region of the potato pinII gene. Following standard procedures provided by Invitrogen the att-flanked insertion region is replaced by recombination with trait-improving DNA, in a sense orientation for expression of a trait-improving protein and in a gene suppression orientation (i.e., either anti-sense orientation or in a sense- and anti-sense orientation) for a trait-improving suppression of a protein. Although the vector with trait-improving DNA inserted at the att-flanked insertion region is useful for plant transformation by direct DNA delivery, such as microprojectile bombardment, it is preferable to bombard target plant tissue with tandem transcription units that have been cut from the vector. For *Agrobacterium*-mediated transformation of plants the vector also comprises T-DNA borders from *Agrobacterium* flanking the transcription units.

[0173] Vectors for *Agrobacterium*-mediated transformation are prepared with each of the trait-improving genes having a sequence of SEQ ID NO:1 through SEQ ID NO:269 with the DNA solely in sense orientation for expression of the encoded, cognate trait-improving protein and in a gene suppression orientation for suppression of the cognate protein. Each vector is transformed into corn callus which is propagated into a plant that is grown to produce transgenic seed for each transgenic event. Progeny plants are self-pollinated to produce seed which is selected for homozygous seed. Homozygous seed is used for producing inbred plants, for introgressing the trait into elite lines, and for crossing to make hybrid seed. The progeny transgenic plants comprising the trait-improving DNA with a sequence of SEQ ID NO: 1 through SEQ ID NO: 269 have one or more improved traits identified by agronomic trait screening including, but not limited to, enhanced nitrogen use efficiency, increased yield, enhanced water use efficiency, growth under cold stress and enhanced oil, starch and protein levels. Transgenic corn including inbred and hybrids are also produced with DNA from each of the identified homologs of DNA of SEQ ID NO: 1 through SEQ ID NO: 269 to provide transgenic seeds and plants which are identified from total transgenic events by screening for the improved agronomic trait. Transgenic corn plants are also produced where the trait-improving DNA is transcribed by each of the promoters from the group selected from, a maize globulin 1 promoter, a maize oleosin promoter, a glutelin 1 promoter, an aldolase promoter, a zein Z27 promoter, a pyruvate orthophosphate dikinase (PPDK) promoter, a soybean 7S alpha promoter, a peroxiredoxin antioxidant (Perl) promoter and a CaMV 35S promoter.

[0174] Seed produced by the plants is provided to growers to enable production of corn crops with improved traits associated with the trait-improving DNA.

TABLE 18

FUNCTION	ELEMENT	REFERENCE
DNA insertion transcription region	Rice actin 1 promoter	U.S. Pat. No. 5,641,876
	Rice actin 1 exon 1, intron 1 enhancer	U.S. Pat. No. 5,641,876
DNA insertion transcription region (att -flanked insertin region)	AttR1	GATEWAY ™ Cloning Technology Instruction Manual
	CmR gene	GATEWAY ™ Cloning Technology Instruction Manual
	ccdA, ccdB genes	GATEWAY ™ Cloning Technology Instruction Manual
	attR2	GATEWAY ™ Cloning Technology Instruction Manual
DNA insertion transcription region	Potato pinII 3' region	An et al., (1989) Plant Cell 1: 115–122
selectable marker transcription region	CaMV 35S promoter	U.S. Pat. No. 5,858,742
	nptII selectable marker	U.S. Pat. No. 5,858,742
	nos 3region	U.S. Pat. No. 5,858,742
	PinII 3' region	An et al., (1989) Plant Cell 1: 115–122
E. coli maintenance region	ColE1 origin of replication	
	F1 origin of replication	
	Bla ampicillin resistance	

Example 5

Soybean Transformation Construct

[0175] Constructs for use in transformation of soybean are prepared by restriction enzyme based cloning into a common expression vector. Elements of an exemplary common expression vector are shown in Table 19 below and include a selectable marker expression cassette and a gene of interest expression cassette. The selectable marker expression cassette comprises *Arabidopsis* act 7 gene (AtAct7) promoter with intron and 5'UTR, the transit peptide of *Arabidopsis* EPSPS, the synthetic CP4 coding region with dicot preferred codon usage and a 3' UTR of the nopaline synthase gene.

[0176] The gene of interest expression cassette comprises a Cauliflower Mosaic Virus 35S promoter operably linked to a trait-improving gene in a sense orientation for expression of a trait-improving protein and in a gene suppression orientation (i.e., either anti-sense orientation or in a sense- and anti-sense orientation for a trait-improving suppression of a protein.

[0177] Vectors similar to that described above are constructed for use in *Agrobacterium* mediated soybean transformation systems, with each of the trait-improving DNA having a sequence of SEQ ID NO:1 though SEQ ID NO:269 and the respective identified homologs with the DNA in sense orientation for expression of the encoded, cognate protein and in a gene suppression arrangement for suppression of the cognate protein. Each vector is transformed into soybean embryo tissue to produce transgenic events which are grown into plants that produce progeny transgenic plants and seed for screening to identify the transgenic soybean plants of this invention that exhibit the enhanced agronomic trait imparted by DNA with a sequence of SEQ ID NO:1 through SEQ ID NO:269 or a respective homolog. The transgenic soybean plants of this invention are identified by agronomic trait screening including, but not limited to, enhanced nitrogen use efficiency, increased yield, enhanced water use efficiency, growth under cold stress and enhanced oil, starch and protein levels. Transgenic soybean plants are also produced where the trait-improving DNA is transcribed by a napin promoter and *Arabidopsis* SSU promoter.

[0178] Seed produced by the plants is provided to growers to enable production of soybean crops with improved traits associated with the trait-improving DNA.

TABLE 19

Function	Element	Reference
Agro transformation	B-ARGtu.right border	Depicker, A. et al (1982) Mol Appl Genet 1: 561–573
Antibiotic resistance	CR-Ec.aadA-SPC/STR	
Repressor of primers from the ColE1 plasmid	CR-Ec.rop	
Origin of replication	OR-Ec.oriV-RK2	
Agro transformation	B-ARGtu.left border	Barker, R. F. et al (1983) Plant Mol Biol 2: 335–350
Plant selectable marker expression cassette	*Arabidopsis* act 7 gene (AtAct7) promoter with intron and 5'UTR	McDowell et al., (1996) Plant Physiol. 111: 699–711.
	5' UTR of *Arabidopsis* act 7 gene	
	Intron in 5'UTR of AtAct7	
	Transit peptide region of *Arabidopsis* EPSPS	Klee, H. J. et at (1987) MGG 210: 437–442
	Synthetic CP4 coding region with dicot preferred codon usage	
	A 3' UTR of the nopaline synthase gene of Agrobacterium tumefaciens Ti plasmid	U.S. Pat. No. 5,858,742
Plant gene of interest expression cassette	Promoter for 35S RNA from CaMV containing a duplication of the −90 to −350 region	U.S. Pat. No. 5,322,938
	Gene of interest insertion site	
	Cotton E6 3' end	GenBank accession U30508

Example 6

Cotton Transformation

[0179] Vectors similar to that described above for soybean transformation are constructed for use in *Agrobacterium* mediated cotton transformation systems, with each of the trait-improving DNA having a sequence of SEQ ID NO:1 though SEQ ID NO:269 and the respective identified homologs with the DNA in sense orientation for expression of the encoded, cognate protein and in a gene suppression arrangement for suppression of the cognate protein. Each vector is transformed into cotton embryo tissue to produce transgenic events which are grown into plants that produce progeny transgenic plants and seed for screening to identify the transgenic soybean plants of this invention that exhibit the enhanced agronomic trait imparted by DNA with a sequence of SEQ ID NO:1 through SEQ ID NO:269 or a respective homolog. The transgenic cotton plants of this invention are identified by agronomic trait screening including, but not limited to, enhanced nitrogen use efficiency, increased yield, enhanced water use efficiency, growth under cold stress and enhanced oil, starch and protein levels. Transgenic cotton plants are also produced where the trait-improving DNA is transcribed by a napin promoter and *Arabidopsis* SSU promoter.

[0180] Seed produced by the plants is provided to growers to enable production of cotton crops with improved traits associated with the trait-improving DNA.

SEQUENCE LISTING

The patent application contains a lengthy "Sequence Listing" section. A copy of the "Sequence Listing" is available in electronic form from the USPTO web site (http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US20060075522A1). An electronic copy of the "Sequence Listing" will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

We claim:

1. Transgenic seed for a crop plant having in its genome trait-improving recombinant DNA which expresses a succinate semialdehyde dehydrogenase.

2. Transgenic seed according to claim 1 wherein transgenic plants grown from said seed exhibit increased yield as compared to control plants.

3. Transgenic seed according to claim 1 wherein expression of said recombinant DNA provides improved tolerance to water deficit stress as compared to control plants.

4. Transgenic seed according to claim 1 wherein expression of said recombinant DNA provides improved tolerance to salinity stress as compared to control plants.

5. Transgenic seed according to claim 1 wherein expression of said recombinant DNA provides improved tolerance to heat stress as compared to control plants.

6. Transgenic seed of claim wherein said DNA is derived from *Agrobacterium tumefaciens*.

7. Transgenic seed according to claim 1, wherein,

(a) said crop is susceptible to a yield-limiting environment; and

(b) transgenic plants grown from said transgenic seed thrive in said yield-limiting environment.

8. Transgenic seed according to claim 7, wherein said yield-limiting environment is water deficit stress, heat stress, or high salinity stress.

9. Transgenic seed of claim 1 wherein said succinate semialdehyde dehydrogenase has an amino acid sequence that is at least 90% identical to a consensus amino acid sequence determined from an alignment of sequences for the succinate semialdehyde dehydrogenase of SEQ ID NO: 442 and the homologs disclosed in Table 17.

10. A method of facilitating production of a crop comprising providing to a grower of said crop transgenic seed of claim 1.

11. A method according to claim 10, wherein transgenic plants grown from said seed exhibit increased yield as compared to control plants.

12. A method according to claim 10, wherein

(a) said crop is susceptible to a yield-limiting environment; and

(b) transgenic plants grown from said transgenic seed thrive in said yield-limiting environment.

13. A method of claim 10, wherein said yield-limiting environment is heat stress, water deficit stress or high salinity stress.

14. Transgenic seed for a crop plant, wherein the genome of said transgenic seed comprises trait-improving recombinant DNA from a gene which expresses a protein having an amino acid sequence with at least 90% identity to a consensus amino acid sequence in the group consisting of a consensus amino acid sequence for SEQ ID NO: 270 and homologs thereof disclosed in Table 17 through a consensus amino acid sequence for SEQ ID NO:538 and homologs thereof disclosed in Table 17.

15. Transgenic seed according to claim 14 wherein transgenic plants grown from said seed exhibit increased yield as compared to control plants.

16. Transgenic seed according to claim 14, wherein

(a) transgenic plants grown from said seed exhibit increased yield as compared to control plants when said plants are grown in a yield-limiting environment of water deficit stress and said protein has the function of the protein with an amino acid sequence selected from the group consisting of SEQ ID NO: 270, 273, 300, 302, 306, 310, 313, 315 through 374, 382, 388, 390 through 392, 397, 402 through 431, 434, 436 through 450, 454, 466, 469, 472, 476, 478, 479, 491, 504 through 538, and homologs thereof disclosed in Table 17;

(b) transgenic plants grown from said seed exhibit increased yield as compared to control plants when said plants are grown in a yield-limiting environment of heat stress and said protein has the function of the protein with an amino acid sequence selected from the group consisting of SEQ ID NO: 273, 306, 310, 313, 352 through 372, 407 through 412, 419, 434, 436, 437, 442, 444, 445, 466, 479, 491, 504, 505, 508, 509, 512, 533, and homologs thereof disclosed in Table 17;

(c) transgenic plants grown from said seed exhibit increased yield as compared to control plants when said plants are grown in a yield-limiting environment of high salinity stress and said protein has the function of the protein with an amino acid sequence selected from the group consisting of SEQ ID NO: 270, 347, 358, 363, 392, 407, 411, 436, 440, 442-450, 476, 478, 504-538, and homologs thereof disclosed in Table 17;

(d) transgenic plants grown from said seed exhibit increased yield as compared to control plants when said plants are grown in a yield-limiting environment of cold stress and said protein has the function of the protein with an amino acid sequence selected from the group consisting of SEQ ID NO: 270 through 316, 352, 353, 360, 361, 363, 368, 373, 382, 383, 389, 398, 402 through 407, 409, 413, 414, 416, 431 through 435, 438, 439, 443, 444, 459, 461, 477, 504 through 508, 510, 514, 521, and homologs thereof disclosed in Table 17;

(e) transgenic plants grown from said seed exhibit increased yield as compared to control plants when said plants are grown in a yield-limiting environment of reduced nitrogen availability stress and said protein has the function of the protein with amino acid sequence of SEQ ID NO: 316, 351, 375, 389 through 401, 505, and homologs thereof disclosed in Table 17;

(f) transgenic plants grown from said seed exhibit increased yield as compared to control plants when said plants are grown in a yield-limiting environment of shade stress and said protein has the function of the protein with an amino acid sequence selected from the group consisting of SEQ ID NO: 293, 300, 307, 316, 370, 373 through 388, 397, 400, 444, 468, 511, 535, and homologs thereof disclosed in Table 17.

17. A recombinant DNA construct comprising a promoter functional in a plant cell operably linked to trait-improving recombinant DNA from gene for a protein having an amino acid sequence with at least 90% identity to a consensus amino acid sequence in the group consisting of a consensus amino acid sequence for SEQ ID NO: 270 and homologs thereof disclosed in Table 17 through a consensus amino acid sequence for SEQ ID NO: 538 and homologs thereof disclosed in Table 17.

18. A method of facilitating production of a crop comprising providing to a grower of said crop transgenic seed of claim 14.

19. A method according to claim 18, wherein transgenic plants grown from said seed exhibit increased yield as compared to control plants.

20. A method according to claim 18, wherein

(a) transgenic plants grown from said seed exhibit increased yield as compared to control plants when said plants are grown in a yield-limiting environment of water deficit stress and said protein has the function of the protein with an amino acid sequence selected from the group consisting of SEQ ID NO: 270, 273, 300, 302, 306, 310, 313, 315 through 374, 382, 388, 390 through 392, 397, 402 through 431, 434, 436 through 450, 454, 466, 469, 472, 476, 478, 479, 491, 504 through 538, and homologs thereof disclosed in Table 17;

(b) transgenic plants grown from said seed exhibit increased yield as compared to control plants when said plants are grown in a yield-limiting environment of heat stress and said protein has the function of the protein with an amino acid sequence selected from the group consisting of SEQ ID NO: 273, 306, 310, 313, 352 through 372, 407 through 412, 419, 434, 436, 437, 442, 444, 445, 466, 479, 491, 504, 505, 508, 509, 512, 533, and homologs thereof;

(c) transgenic plants grown from said seed exhibit increased yield as compared to control plants when said plants are grown in a yield-limiting environment of high salinity stress and said protein has the function of the protein with an amino acid sequence selected from the group consisting of SEQ ID NO: 270, 347, 358, 363, 392, 407, 411, 436, 440, 442-450, 476, 478, 504-538, and homologs thereof disclosed in Table 17;

(d) transgenic plants grown from said seed exhibit increased yield as compared to control plants when said plants are grown in a yield-limiting environment of cold stress and said protein has the function of the protein with an amino acid sequence selected from the group consisting of SEQ ID NO: 270 through 316, 352, 353, 360, 361, 363, 368, 373, 382, 383, 389, 398, 402 through 407, 409, 413, 414, 416, 431 through 435, 438, 439, 443, 444, 459, 461, 477, 504 through 508, 510, 514, 521, and homologs thereof disclosed in Table 17;

(e) transgenic plants grown from said seed exhibit increased yield as compared to control plants when said plants are grown in a yield-limiting environment of reduced nitrogen availability stress and said protein has the function of the protein with amino acid sequence of SEQ ID NO: 316, 351, 375, 389 through 401, 505, and homologs thereof disclosed in Table 17;

(f) transgenic plants grown from said seed exhibit increased yield as compared to control plants when said plants are grown in a yield-limiting environment of shade stress and said protein has the function of the protein with an amino acid sequence selected from the group consisting of SEQ ID NO: 293, 300, 307, 316, 370, 373 through 388, 397, 400, 444, 468, 511, 535, and homologs thereof disclosed in Table 17.

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