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(54) **Title**: NUCLEOTIDE SEQUENCES AND CORRESPONDING POLYPEPTIDES CONFERRING IMPROVED NITROGEN USE EFFICIENCY CHARACTERISTICS IN PLANTS

(57) **Abstract**: Methods and materials for modulating low-nitrogen tolerance levels in plants are disclosed. For example, nucleic acids encoding low nitrogen tolerance-modulating polypeptides are disclosed as well as methods for using such nucleic acids to transform plant cells. Also disclosed are plants having increased low-nitrogen tolerance levels and plant products produced from plants having increased low-nitrogen tolerance levels.

NUCLEOTIDE SEQUENCES AND CORRESPONDING POLYPEPTIDES CONFERRING IMPROVED NITROGEN USE EFFICIENCY CHARACTERISTICS IN PLANTS

INCORPORATION-BY-REFERENCE OF SEQUENCE LISTING OR TABLE

[0001] The material in the accompanying sequence listing is hereby incorporated by reference in its entirety into this application. The accompanying file, named 2009_02_12_SequenceListing_2750_1699WO1.txt was created on February 12, 2009 and is 6.27 MB. The file can be accessed using Microsoft Word on a computer that uses Windows OS.

TECHNICAL FIELD

[0002] the present invention relates to methods and materials involved in tolerance of a plant to limiting exogenous nitrogen sources. For example, this document provides plants having increased low-nitrogen tolerance levels as well as materials and methods for making plants and plant products having increased low-nitrogen tolerance levels.

BACKGROUND

[0003] Nitrogen is often the rate-limiting element in plant growth, and all field crops have a fundamental dependence on exogenous nitrogen sources.

[0004] According to a recent study published in Field Crops Research (Volume 100, Issues 2-3, 1 February 2007, Pages 210-217), Nitrogenous fertilizer, which is usually supplied as ammonium nitrate, potassium nitrate, or urea, typically accounts for 40% of the costs associated with crops, such as corn and wheat in intensive agriculture.

[0005] Improving nitrogen use efficiency of crop plants is an important goal towards reducing input costs and reducing the environmental consequences of intensive nitrogen fertilization on the environment. Increased efficiency of nitrogen use by plants should enable the production of higher yields with existing fertilizer inputs and/or enable existing yields of crops to be obtained with lower fertilizer input, or better yields on soils of poorer quality. Also, higher amounts of proteins in the crops could also be produced more cost-effectively.

[0006] Plants have a number of means to cope with nutrient deficiencies, such as poor nitrogen availability. One important mechanism senses nitrogen availability in the soil and

respond accordingly by modulating gene expression while a second mechanism is to sequester or store nitrogen in times of abundance to be used later. The nitrogen sensing mechanism relies on regulated gene expression and enables rapid physiological and metabolic responses to changes in the supply of inorganic nitrogen in the soil by adjusting nitrogen uptake, reduction, partitioning, remobilization and transport in response to changing environmental conditions. Nitrate acts as a signal to initiate a number of responses that serve to reprogram plant metabolism, physiology and development (Redinbaugh et al. (1991) *Physiol. Plant.* 82, 640–650.; Forde (2002) *Annual Review of Plant Biology* 53, 203-224). Nitrogen-inducible gene expression has been characterized for a number of genes in some detail. These include nitrate reductase, nitrite reductase, 6-phosphoglucante dehydrogenase, and nitrate and ammonium transporters (Redinbaugh et al. (1991) *Physiol. Plant.* 82, 640–650; Huber et al. (1994) Plant Physiol 106, 1667-1674; Hwang et al. (1997) *Plant Physiol.* 113, 853-862; Redinbaugh et al. (1998) *Plant Science* 134, 129-140; Gazzarrini et al. (1999) *Plant Cell* 11, 937-948; Glass et al. (2002) *J. Exp. Bot.* 53, 855-864; Okamoto et al. (2003) *Plant Cell Physiol.* 44, 304-317).

[0007] In the fields of agriculture and forestry, efforts are constantly being made to produce plants with an increased growth potential in order to feed the ever-increasing world population and to guarantee the supply of reproducible raw materials. There is a need for methods of increasing nitrogen use efficiency in plants, which leads to better growth potential and more biomass. This is done conventionally through plant breeding. The breeding process is, however, both time-consuming and labor-intensive. Furthermore, appropriate breeding programs must be performed for each relevant plant species. In addition, although great progresses that have been made about nitrogen utilization and the components involved in nitrogen use efficiency, such as nitrogen uptake, nitrogen assimilation and nitrogen partitioning or remobilization, much is still unknown about many of these complex interactions. Therefore, there is a continuing need for generally applicable processes that improve forest or agricultural plant growth to suit particular needs depending on specific environmental conditions. For example, genes that confer tolerance to growth on low nitrogen supply are valuable product prototypes for manipulating nitrogen use efficiency in plants (Good et al., 2004). One strategy to achieve such desirable traits involves genetic manipulation of plant characteristics through the introduction of exogenous nucleic acids conferring increased efficiency of nitrogen use by plants, which in turn should enable the production of higher yields with existing fertilizer inputs and/or enable existing yields of crops to be obtained with lower fertilizer input, or better yields on soils of poorer quality.

Such approaches have the advantage of not usually being limited to one plant species, but instead being transferable among plant species. The present invention relates to a method for increasing growth potential, and/or increasing levels of nitrogen use efficiency in plants, characterized by expression of recombinant DNA molecules stably integrated into the plant genome

SUMMARY

[0008] The present invention provides methods and materials related to plants having modulated levels of low-nitrogen tolerance. For example, the present invention provides transgenic plants and plant cells having increased levels of low-nitrogen tolerance, nucleic acids (*i.e.* isolated polynucleotides), polypeptides encoded thereby used to generate transgenic plants and plant cells having increased levels of low-nitrogen tolerance, and methods for making plants and plant cells having increased levels of low-nitrogen tolerance. Such plants and plant cells can be grown under limiting exogenous nitrogen without stunted growth and diminished yields. Plants having increased low-nitrogen tolerance levels may be useful to produce biomass which may be converted to a liquid fuel or other chemicals and/or to produce food and feed on land that is currently marginally productive, resulting in an overall expansion of arable land.

[0009] Methods of producing a plant tissue are provided herein. In one aspect, a method comprises growing a plant cell comprising an exogenous nucleic acid. The exogenous nucleic acid comprises a regulatory region operably linked to a nucleotide sequence encoding a polypeptide. The Hidden Markov Model (HMM) bit score of the amino acid sequence of the polypeptide is greater than about 20, using an HMM generated from the amino acid sequences depicted in one of Figures 1-57. The tissue has a difference in the level of low-nitrogen tolerance as compared to the corresponding level in tissue of a control plant that does not comprise the exogenous nucleic acid.

[0010] In another aspect, a method comprises growing a plant cell comprising an exogenous nucleic acid. The exogenous nucleic acid comprises a regulatory region operably linked to a nucleotide sequence encoding a polypeptide having 80 percent or greater sequence identity to an amino acid sequence set forth in SEQ ID NO:3, SEQ ID NO:49, SEQ ID NO:77, SEQ ID NO:97, SEQ ID NO:100, SEQ ID NO:152, SEQ ID NO:166, SEQ ID NO:186, SEQ ID NO:208, SEQ ID NO:218, SEQ ID NO:234, SEQ ID NO:246, SEQ ID NO:300, SEQ ID NO:332, SEQ ID NO:368, SEQ ID NO:510, SEQ ID NO:533, SEQ ID NO:556, SEQ ID NO:558, SEQ ID NO:593, SEQ ID NO:613, SEQ ID NO:646, SEQ ID

NO:687, SEQ ID NO:730, SEQ ID NO:746, SEQ ID NO:769, SEQ ID NO:792, SEQ ID NO:824, SEQ ID NO:828, SEQ ID NO:853, SEQ ID NO:855, SEQ ID NO:891, SEQ ID NO:917, SEQ ID NO:944, SEQ ID NO:976, SEQ ID NO:982, SEQ ID NO:1054, SEQ ID NO:1099, SEQ ID NO:1112, SEQ ID NO:1116, SEQ ID NO:1157, SEQ ID NO:1159, SEQ ID NO:1166, SEQ ID NO:1185, SEQ ID NO:1194, SEQ ID NO:1210, SEQ ID NO:1274, SEQ ID NO:1302, SEQ ID NO:1342, SEQ ID NO:1385, SEQ ID NO:1409, SEQ ID NO:1428, SEQ ID NO:1437, SEQ ID NO:1463, SEQ ID NO:1491, SEQ ID NO:1510, SEQ ID NO:1525, SEQ ID NO:1537, SEQ ID NO:1554, or SEQ ID NO:1577. A plant and/or plant tissues produced from the plant cell has a difference in the level of low-nitrogen tolerance as compared to the corresponding level of low-nitrogen tolerance of a control plant that does not comprise the exogenous nucleic acid.

[0011] In another aspect, a method comprises growing a plant cell comprising an exogenous nucleic acid. The exogenous nucleic acid comprises a regulatory region operably linked to a nucleotide sequence having 80 percent or greater sequence identity to a nucleotide sequence, or a fragment thereof, set forth in SEQ ID NO:1, SEQ ID NO:48, SEQ ID NO:76, SEQ ID NO:96, SEQ ID NO:99, SEQ ID NO:151, SEQ ID NO:165, SEQ ID NO:175, SEQ ID NO:185, SEQ ID NO:207, SEQ ID NO:217, SEQ ID NO:233, SEQ ID NO:245, SEQ ID NO:299, SEQ ID NO:331, SEQ ID NO:367, SEQ ID NO:509, SEQ ID NO:532, SEQ ID NO:555, SEQ ID NO:557, SEQ ID NO:592, SEQ ID NO:612, SEQ ID NO:645, SEQ ID NO:686, SEQ ID NO:729, SEQ ID NO:745, SEQ ID NO:768, SEQ ID NO:791, SEQ ID NO:823, SEQ ID NO:827, SEQ ID NO:852, SEQ ID NO:854, SEQ ID NO:890, SEQ ID NO:916, SEQ ID NO:943, SEQ ID NO:975, SEQ ID NO:981, SEQ ID NO:1053, SEQ ID NO:1098, SEQ ID NO:1111, SEQ ID NO:1115, SEQ ID NO:1156, SEQ ID NO:1158, SEQ ID NO:1165, SEQ ID NO:1184, SEQ ID NO:1193, SEQ ID NO:1209, SEQ ID NO:1273, SEQ ID NO:1301, SEQ ID NO:1341, SEQ ID NO:1384, SEQ ID NO:1408, SEQ ID NO:1427, SEQ ID NO:1462, SEQ ID NO:1490, SEQ ID NO:1509, SEQ ID NO:1524, SEQ ID NO:1536, SEQ ID NO:1553, or SEQ ID NO:1576. A plant and/or plant tissues produced from the plant cell has a difference in the level of low-nitrogen tolerance as compared to the corresponding level low-nitrogen tolerance of a control plant that does not comprise the exogenous nucleic acid.

[0012] In another aspect, the invention provides a method of producing a plant, the method comprising growing a plant cell comprising an exogenous nucleic acid that is effective for downregulating an endogenous nucleic acid in the plant cell, wherein the endogenous nucleic acid encodes a polypeptide, and wherein the HMM bit score of the amino

acid sequence of the polypeptide is greater than about 20, said HMM based on the amino acid sequences depicted in one of Figures 1-57

[0013] Methods of modulating the level of low-nitrogen tolerance in a plant are provided herein. In one aspect, a method comprises introducing into a plant cell an exogenous nucleic acid, that comprises a regulatory region operably linked to a nucleotide sequence encoding a polypeptide. The HMM bit score of the amino acid sequence of the polypeptide is greater than about 20, using an HMM generated from the amino acid sequences depicted in one of Figures 1-57. A plant and/or plant tissue produced from the plant cell has a difference in the level of low-nitrogen tolerance as compared to the corresponding level of low-nitrogen tolerance of a control plant that does not comprise the exogenous nucleic acid.

[0014] In certain embodiments, the HMM bit score of the amino acid sequence of the polypeptide is greater than about 40, using an HMM generated from the amino acid sequences depicted in one of Figures 1-57, wherein the polypeptide comprises a Pfam domain having 70 percent or greater sequence identity to a Pfam domain of any one of the polypeptides in the sequence listing.

[0015] In another aspect, a method comprises modulating the level of low-nitrogen tolerance in a plant by introducing into a plant cell an exogenous nucleic acid that comprises a regulatory region operably linked to a nucleotide sequence encoding a polypeptide having 80 percent or greater sequence identity to an amino acid sequence set forth in SEQ ID NO:3, SEQ ID NO:49, SEQ ID NO:77, SEQ ID NO:97, SEQ ID NO:100, SEQ ID NO:152, SEQ ID NO:166, SEQ ID NO:186, SEQ ID NO:208, SEQ ID NO:218, SEQ ID NO:234, SEQ ID NO:246, SEQ ID NO:300, SEQ ID NO:332, SEQ ID NO:368, SEQ ID NO:510, SEQ ID NO:533, SEQ ID NO:556, SEQ ID NO:558, SEQ ID NO:593, SEQ ID NO:613, SEQ ID NO:646, SEQ ID NO:687, SEQ ID NO:730, SEQ ID NO:746, SEQ ID NO:769, SEQ ID NO:792, SEQ ID NO:824, SEQ ID NO:828, SEQ ID NO:853, SEQ ID NO:855, SEQ ID NO:891, SEQ ID NO:917, SEQ ID NO:944, SEQ ID NO:976, SEQ ID NO:982, SEQ ID NO:1054, SEQ ID NO:1099, SEQ ID NO:1112, SEQ ID NO:1116, SEQ ID NO:1157, SEQ ID NO:1159, SEQ ID NO:1166, SEQ ID NO:1185, SEQ ID NO:1194, SEQ ID NO:1210, SEQ ID NO:1274, SEQ ID NO:1302, SEQ ID NO:1342, SEQ ID NO:1385, SEQ ID NO:1409, SEQ ID NO:1428, SEQ ID NO:1437, SEQ ID NO:1463, SEQ ID NO:1491, SEQ ID NO:1510, SEQ ID NO:1525, SEQ ID NO:1537, SEQ ID NO:1554, or SEQ ID NO:1577, or a fragment thereof. A plant and/or plant tissue produced from the plant cell has a difference in the level of low-nitrogen tolerance as compared to the corresponding level of

low-nitrogen tolerance of a control plant that does not comprise the exogenous nucleic acid.

[0016] In another aspect, a method comprises modulating the level of low-nitrogen tolerance in a plant by introducing into a plant cell an exogenous nucleic acid, that comprises a regulatory region operably linked to a nucleotide sequence having 80 percent or greater sequence identity to a nucleotide sequence set forth in SEQ ID NO:1, SEQ ID NO:48, SEQ ID NO:76, SEQ ID NO:96, SEQ ID NO:99, SEQ ID NO:151, SEQ ID NO:165, SEQ ID NO:175, SEQ ID NO:185, SEQ ID NO:207, SEQ ID NO:217, SEQ ID NO:233, SEQ ID NO:245, SEQ ID NO:299, SEQ ID NO:331, SEQ ID NO:367, SEQ ID NO:509, SEQ ID NO:532, SEQ ID NO:555, SEQ ID NO:557, SEQ ID NO:592, SEQ ID NO:612, SEQ ID NO:645, SEQ ID NO:686, SEQ ID NO:729, SEQ ID NO:745, SEQ ID NO:768, SEQ ID NO:791, SEQ ID NO:823, SEQ ID NO:827, SEQ ID NO:852, SEQ ID NO:854, SEQ ID NO:890, SEQ ID NO:916, SEQ ID NO:943, SEQ ID NO:975, SEQ ID NO:981, SEQ ID NO:1053, SEQ ID NO:1098, SEQ ID NO:1111, SEQ ID NO:1115, SEQ ID NO:1156, SEQ ID NO:1158, SEQ ID NO:1165, SEQ ID NO:1184, SEQ ID NO:1193, SEQ ID NO:1209, SEQ ID NO:1273, SEQ ID NO:1301, SEQ ID NO:1341, SEQ ID NO:1384, SEQ ID NO:1408, SEQ ID NO:1427, SEQ ID NO:1462, SEQ ID NO:1490, SEQ ID NO:1509, SEQ ID NO:1524, SEQ ID NO:1536, SEQ ID NO:1553, or SEQ ID NO:1576, or a fragment thereof. A plant and/or plant tissue produced from the plant cell has a difference in the level of low-nitrogen tolerance as compared to the corresponding level of low-nitrogen tolerance of a control plant that does not comprise the exogenous nucleic acid.

[0017] Plant cells comprising an exogenous nucleic acid are provided herein. In one aspect, the exogenous nucleic acid comprises a regulatory region operably linked to a nucleotide sequence encoding a polypeptide. The HMM bit score of the amino acid sequence of the polypeptide is greater than about 20, using an HMM based on the amino acid sequences depicted in one of Figures 1-57. The plant has a difference in the level of low-nitrogen tolerance as compared to the corresponding level of low-nitrogen tolerance of a control plant that does not comprise the exogenous nucleic acid. In another aspect, the exogenous nucleic acid comprises a regulatory region operably linked to a nucleotide sequence encoding a polypeptide having 80 percent or greater sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:49, SEQ ID NO:77, SEQ ID NO:97, SEQ ID NO:100, SEQ ID NO:152, SEQ ID NO:166, SEQ ID NO:186, SEQ ID NO:208, SEQ ID NO:218, SEQ ID NO:234, SEQ ID NO:246, SEQ ID NO:300, SEQ ID NO:332, SEQ ID NO:368, SEQ ID NO:510, SEQ ID NO:533, SEQ ID NO:556, SEQ ID NO:558, SEQ ID NO:593, SEQ ID NO:613, SEQ ID NO:646, SEQ ID

NO:687, SEQ ID NO:730, SEQ ID NO:746, SEQ ID NO:769, SEQ ID NO:792, SEQ ID NO:824, SEQ ID NO:828, SEQ ID NO:853, SEQ ID NO:855, SEQ ID NO:891, SEQ ID NO:917, SEQ ID NO:944, SEQ ID NO:976, SEQ ID NO:982, SEQ ID NO:1054, SEQ ID NO:1099, SEQ ID NO:1112, SEQ ID NO:1116, SEQ ID NO:1157, SEQ ID NO:1159, SEQ ID NO:1166, SEQ ID NO:1185, SEQ ID NO:1194, SEQ ID NO:1210, SEQ ID NO:1274, SEQ ID NO:1302, SEQ ID NO:1342, SEQ ID NO:1385, SEQ ID NO:1409, SEQ ID NO:1428, SEQ ID NO:1437, SEQ ID NO:1463, SEQ ID NO:1491, SEQ ID NO:1510, SEQ ID NO:1525, SEQ ID NO:1537, SEQ ID NO:1554, and SEQ ID NO:1577. A plant and/or plant tissue produced from the plant cell has a difference in the level of low-nitrogen tolerance as compared to the corresponding level of low-nitrogen tolerance of a control plant that does not comprise the exogenous nucleic acid. In another aspect, the exogenous nucleic acid comprises a regulatory region operably linked to a nucleotide sequence having 80 percent or greater sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:48, SEQ ID NO:76, SEQ ID NO:96, SEQ ID NO:99, SEQ ID NO:151, SEQ ID NO:165, SEQ ID NO:175, SEQ ID NO:185, SEQ ID NO:207, SEQ ID NO:217, SEQ ID NO:233, SEQ ID NO:245, SEQ ID NO:299, SEQ ID NO:331, SEQ ID NO:367, SEQ ID NO:509, SEQ ID NO:532, SEQ ID NO:555, SEQ ID NO:557, SEQ ID NO:592, SEQ ID NO:612, SEQ ID NO:645, SEQ ID NO:686, SEQ ID NO:729, SEQ ID NO:745, SEQ ID NO:768, SEQ ID NO:791, SEQ ID NO:823, SEQ ID NO:827, SEQ ID NO:852, SEQ ID NO:854, SEQ ID NO:890, SEQ ID NO:916, SEQ ID NO:943, SEQ ID NO:975, SEQ ID NO:981, SEQ ID NO:1053, SEQ ID NO:1098, SEQ ID NO:1111, SEQ ID NO:1115, SEQ ID NO:1156, SEQ ID NO:1158, SEQ ID NO:1165, SEQ ID NO:1184, SEQ ID NO:1193, SEQ ID NO:1209, SEQ ID NO:1273, SEQ ID NO:1301, SEQ ID NO:1341, SEQ ID NO:1384, SEQ ID NO:1408, SEQ ID NO:1427, SEQ ID NO:1462, SEQ ID NO:1490, SEQ ID NO:1509, SEQ ID NO:1524, SEQ ID NO:1536, SEQ ID NO:1553, and SEQ ID NO:1576, or a fragment thereof. A plant and/or plant tissue of a plant produced from the plant cell has a difference in the level of low-nitrogen tolerance as compared to the corresponding level of low-nitrogen tolerance of a control plant that does not comprise the exogenous nucleic acid. A transgenic plant comprising such a plant cell is also provided.

[0018] Isolated nucleic acids are also provided. In one aspect, an isolated nucleic acid comprises a nucleotide sequence having 80% or greater sequence identity to the nucleotide sequence set forth in SEQ ID NO:1, SEQ ID NO:48, SEQ ID NO:76, SEQ ID NO:96, SEQ ID NO:99, SEQ ID NO:151, SEQ ID NO:165, SEQ ID NO:175, SEQ ID

NO:185, SEQ ID NO:207, SEQ ID NO:217, SEQ ID NO:233, SEQ ID NO:245, SEQ ID NO:299, SEQ ID NO:331, SEQ ID NO:367, SEQ ID NO:509, SEQ ID NO:532, SEQ ID NO:555, SEQ ID NO:557, SEQ ID NO:592, SEQ ID NO:612, SEQ ID NO:645, SEQ ID NO:686, SEQ ID NO:729, SEQ ID NO:745, SEQ ID NO:768, SEQ ID NO:791, SEQ ID NO:823, SEQ ID NO:827, SEQ ID NO:852, SEQ ID NO:854, SEQ ID NO:890, SEQ ID NO:916, SEQ ID NO:943, SEQ ID NO:975, SEQ ID NO:981, SEQ ID NO:1053, SEQ ID NO:1098, SEQ ID NO:1111, SEQ ID NO:1115, SEQ ID NO:1156, SEQ ID NO:1158, SEQ ID NO:1165, SEQ ID NO:1184, SEQ ID NO:1193, SEQ ID NO:1209, SEQ ID NO:1273, SEQ ID NO:1301, SEQ ID NO:1341, SEQ ID NO:1384, SEQ ID NO:1408, SEQ ID NO:1427, SEQ ID NO:1462, SEQ ID NO:1490, SEQ ID NO:1509, SEQ ID NO:1524, SEQ ID NO:1536, SEQ ID NO:1553, or SEQ ID NO:1576. In another aspect, an isolated nucleic acid comprises a nucleotide sequence encoding a polypeptide having 80% or greater sequence identity to the amino acid sequence set forth in SEQ ID NO:3, SEQ ID NO:49, SEQ ID NO:77, SEQ ID NO:97, SEQ ID NO:100, SEQ ID NO:152, SEQ ID NO:166, SEQ ID NO:186, SEQ ID NO:208, SEQ ID NO:218, SEQ ID NO:234, SEQ ID NO:246, SEQ ID NO:300, SEQ ID NO:332, SEQ ID NO:368, SEQ ID NO:510, SEQ ID NO:533, SEQ ID NO:556, SEQ ID NO:558, SEQ ID NO:593, SEQ ID NO:613, SEQ ID NO:646, SEQ ID NO:687, SEQ ID NO:730, SEQ ID NO:746, SEQ ID NO:769, SEQ ID NO:792, SEQ ID NO:824, SEQ ID NO:828, SEQ ID NO:853, SEQ ID NO:855, SEQ ID NO:891, SEQ ID NO:917, SEQ ID NO:944, SEQ ID NO:976, SEQ ID NO:982, SEQ ID NO:1054, SEQ ID NO:1099, SEQ ID NO:1112, SEQ ID NO:1116, SEQ ID NO:1157, SEQ ID NO:1159, SEQ ID NO:1166, SEQ ID NO:1185, SEQ ID NO:1194, SEQ ID NO:1210, SEQ ID NO:1274, SEQ ID NO:1302, SEQ ID NO:1342, SEQ ID NO:1385, SEQ ID NO:1409, SEQ ID NO:1428, SEQ ID NO:1437, SEQ ID NO:1463, SEQ ID NO:1491, SEQ ID NO:1510, SEQ ID NO:1525, SEQ ID NO:1537, SEQ ID NO:1554, or SEQ ID NO:1577.

[0019] In another aspect, methods of identifying a genetic polymorphism associated with variation in the level of low-nitrogen tolerance are provided. The methods include providing a population of plants, and determining whether one or more genetic polymorphisms in the population are genetically linked to the locus for a polypeptide selected from the group consisting of the polypeptides depicted in Figures 1-57, SEQ ID NO:556, SEQ ID NO:853, SEQ ID NO:1157, and functional homologs thereof, such as those in the Sequence Listing. The correlation between variation in the level of low-nitrogen tolerance in a tissue in plants of the population and the presence of the one or more genetic polymorphisms in plants of the population is measured, thereby permitting identification of

whether or not the one or more genetic polymorphisms are associated with such variation.

[0020] In another aspect, the invention provides a method of making a plant line, said method comprising:

a) determining whether one or more genetic polymorphisms in a population of plants is associated with the locus for a polypeptide selected from the group consisting of the polypeptides depicted in Figures 1-57, SEQ ID NO: 556, SEQ ID NO: 853, and SEQ ID NO: 1157 and functional homologs thereof;

b) identifying one or more plants in said population in which the presence of at least one allele at said one or more genetic polymorphisms is associated with variation in a trait;

c) crossing each said one or more identified plants with itself or a different plant to produce seed;

d) crossing at least one progeny plant grown from said seed with itself or a different plant; and

e) repeating steps c) and d) for an additional 0-5 generations to make said plant line, wherein said at least one allele is present in said plant line.

[0021] Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention pertains. Although methods and materials similar or equivalent to those described herein can be used to practice the invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

[0022] The details of one or more embodiments of the invention are set forth in the accompanying drawings and the description below. Other features, objects, and advantages of the invention will be apparent from the description and drawings, and from the claims.

DESCRIPTION OF THE DRAWINGS

[0023] Figure 1 is an alignment of Ceres SEEDLINE No.ME00919 (SEQ ID NO:3) with homologous and/or orthologous amino acid sequences GI No.5921925 (SEQ ID NO:4), CeresClone:1929222 (SEQ ID NO:6), CeresAnnot:1471370 (SEQ ID NO:10), GI No.84380741 (SEQ ID NO:21), GI No.5921926 (SEQ ID NO:22), GI No.84514161 (SEQ ID NO:25), CeresClone:779234 (SEQ ID NO:27), CeresClone:1600726 (SEQ ID NO:29), GI No.78183420 (SEQ ID NO:36), CeresClone:1877346 (SEQ ID NO:38), GI No.125562440

(SEQ ID NO:39), GI No.115477665 (SEQ ID NO:40), GI No.1173624 (SEQ ID NO:46), and GI No.84468276 (SEQ ID NO:47). In all the alignment figures shown herein, a dash in an aligned sequence represents a gap, *i.e.*, a lack of an amino acid at that position. Identical amino acids or conserved amino acid substitutions among aligned sequences are identified by boxes. Figure 1 and the other alignment figures provided herein were generated using the program MUSCLE version 3.52.

[0024] Figure 2 is an alignment of ME01312 (SEQ ID NO:49) with homologous and/or orthologous amino acid sequences CeresClone:1869410 (SEQ ID NO:51), CeresAnnot:1540549 (SEQ ID NO:53), CeresClone:978708 (SEQ ID NO:58), CeresClone:1623097 (SEQ ID NO:60), GI No.92873064 (SEQ ID NO:63), GI No.37051131 (SEQ ID NO:64), GI No.3341468 (SEQ ID NO:65), CeresClone:937560 (SEQ ID NO:67), CeresClone:456844 (SEQ ID NO:69), GI No.125564100 (SEQ ID NO:70), GI No.52077334 (SEQ ID NO:71), GI No.113205234 (SEQ ID NO:73), and CeresAnnot:6100272 (SEQ ID NO:75).

[0025] Figure 3 is an alignment of ME01463 (SEQ ID NO:77) with homologous and/or orthologous amino acid sequences GI No.2811029 (SEQ ID NO:78), CeresClone:1853284 (SEQ ID NO:80), CeresAnnot:1476446 (SEQ ID NO:82), CeresClone:527024 (SEQ ID NO:87), GI No.27527063 (SEQ ID NO:88), CeresClone:913632 (SEQ ID NO:90), CeresClone:1386710 (SEQ ID NO:92), GI No.115461885 (SEQ ID NO:93), and CeresAnnot:6054519 (SEQ ID NO:95)

[0026] Figure 4 is an alignment of ME01910 (SEQ ID NO:100) with homologous and/or orthologous amino acid sequences GI No.585238 (SEQ ID NO:101), GI No.90704789 (SEQ ID NO:102), CeresClone:1895729 (SEQ ID NO:104), CeresAnnot:1442808 (SEQ ID NO:108), CeresClone:1104700 (SEQ ID NO:113), GI No.32966575 (SEQ ID NO:116), GI No.4996567 (SEQ ID NO:117), GI No.62286644 (SEQ ID NO:118), GI No.2623960 (SEQ ID NO:119), GI No.585241 (SEQ ID NO:120), GI No.790929 (SEQ ID NO:122), CeresClone:579112 (SEQ ID NO:125), CeresClone:244199 (SEQ ID NO:137), CeresClone:1725848 (SEQ ID NO:144), GI No.6474950 (SEQ ID NO:145), GI No.125546057 (SEQ ID NO:146), GI No.115455945 (SEQ ID NO:147), GI No.2641211 (SEQ ID NO:149), and GI No.30024108 (SEQ ID NO:150).

[0027] Figure 5 is an alignment of ME02538 (SEQ ID NO:152) with homologous and/or orthologous amino acid sequences CeresClone:1843642 (SEQ ID NO:154), CeresAnnot:1459112 (SEQ ID NO:158), CeresClone:953633 (SEQ ID NO:162), and CeresClone:587957 (SEQ ID NO:164).

[0028] Figure 6 is an alignment of ME02603 (SEQ ID NO:166) with homologous and/or orthologous amino acid sequences CeresClone:1857256 (SEQ ID NO:168), CeresAnnot:1442042 (SEQ ID NO:170), GI No.89257469 (SEQ ID NO:174), CeresClone:389818 (SEQ ID NO:177), CeresClone:2019147 (SEQ ID NO:181), GI No.125537720 (SEQ ID NO:182), GI No.115443697 (SEQ ID NO:183), and GI No.20340241 (SEQ ID NO:184).

[0029] Figure 7 is an alignment of ME02613 (SEQ ID NO:186) with homologous and/or orthologous amino acid sequences CeresAnnot:1490274 (SEQ ID NO:188), CeresClone:873093 (SEQ ID NO:193), GI No.6635384 (SEQ ID NO:194), CeresClone:663726 (SEQ ID NO:196), GI No.92881411 (SEQ ID NO:197), CeresClone:686525 (SEQ ID NO:199), CeresClone:1524364 (SEQ ID NO:201), CeresClone:1742159 (SEQ ID NO:203), and GI No.125543535 (SEQ ID NO:204).

[0030] Figure 8 is an alignment of ME02801 (SEQ ID NO:208) with homologous and/or orthologous amino acid sequences CeresClone:981621 (SEQ ID NO:214) and CeresClone:564714 (SEQ ID NO:216).

[0031] Figure 9 is an alignment of ME03123 (SEQ ID NO:218) with homologous and/or orthologous amino acid sequences CeresClone:1899168 (SEQ ID NO:220), CeresAnnot:1494669 (SEQ ID NO:222), CeresClone:1017441 (SEQ ID NO:225), CeresClone:1065937 (SEQ ID NO:227), CeresClone:1822919 (SEQ ID NO:229), GI No.125553329 (SEQ ID NO:230), GI No.115439053 (SEQ ID NO:231), and CeresAnnot:6040744 (SEQ ID NO:1052).

[0032] Figure 10 is an alignment of ME04204 (SEQ ID NO:234) with homologous and/or orthologous amino acid sequences CeresAnnot:1519952 (SEQ ID NO:236), CeresClone:234768 (SEQ ID NO:241), GI No.108707052 (SEQ ID NO:242), and GI No.55978030 (SEQ ID NO:244).

[0033] Figure 11 s an alignment of ME04477 (SEQ ID NO:246) with homologous and/or orthologous amino acid sequences CeresClone:1620215 (SEQ ID NO:248), GI No.38016527 (SEQ ID NO:249), CeresClone:1798756 (SEQ ID NO:251), CeresAnnot:1460527 (SEQ ID NO:255), GI No.119720772 (SEQ ID NO:260), CeresClone:708446 (SEQ ID NO:262), GI No.92896423 (SEQ ID NO:265), GI No.113196593 (SEQ ID NO:267), GI No.75133829 (SEQ ID NO:268), CeresClone:1030374 (SEQ ID NO:270), CeresClone:1387149 (SEQ ID NO:274), GI No.5031281 (SEQ ID NO:277), CeresClone:1775820 (SEQ ID NO:279), GI No.35187687 (SEQ ID NO:286), GI No.115468934 (SEQ ID NO:290), GI No.118424243 (SEQ ID NO:296), and

CeresAnnot:6063957 (SEQ ID NO:298).

[0034] Figure 12 is an alignment of ME04507 (SEQ ID NO:300) with homologous and/or orthologous amino acid sequences CeresAnnot:1513514 (SEQ ID NO:302), CeresClone:923483 (SEQ ID NO:310), CeresClone:304357 (SEQ ID NO:312), CeresClone:1902716 (SEQ ID NO:316), GI No.116309713 (SEQ ID NO:319), GI No.38345408 (SEQ ID NO:321), and CeresAnnot:6017635 (SEQ ID NO:325).

[0035] Figure 13 is an alignment of ME04587 (SEQ ID NO:332) with homologous and/or orthologous amino acid sequences Ceres ANNOT ID no.1474882 (SEQ ID NO:334), Ceres ANNOT ID no.553243 (SEQ ID NO:338), Public GI ID no.5514645 (SEQ ID NO:339), Ceres CLONE ID no.464376 (SEQ ID NO:341), Public GI ID no.1345643 (SEQ ID NO:346), Public GI ID no.5832707 (SEQ ID NO:347), Public GI ID no.81157968 (SEQ ID NO:348), Public GI ID no.6118407 (SEQ ID NO:349), Public GI ID no.5081817 (SEQ ID NO:351), Public GI ID no.125556057 (SEQ ID NO:353), Public GI ID no.115468946 (SEQ ID NO:354), Public GI ID no.5915860 (SEQ ID NO:356), Public GI ID no.6979544 (SEQ ID NO:358), Public GI ID no.5832709 (SEQ ID NO:359), Public GI ID no.6979542 (SEQ ID NO:360), Public GI ID no.14278923 (SEQ ID NO:364), Public GI ID no.81157970 (SEQ ID NO:365), Public GI ID no.81157972 (SEQ ID NO:366), Public GI ID no.169793907 (SEQ ID NO:2541), Public GI ID no.84514153 (SEQ ID NO:2543), Public GI ID no.184202209 (SEQ ID NO:2544), Ceres ANNOT ID no.8459850 (SEQ ID NO:2546), Ceres ANNOT ID no.8743452 (SEQ ID NO:2548), Public GI ID no.157327290 (SEQ ID NO:2549), Public GI ID no.148839039 (SEQ ID NO:2550), Public GI ID no.197209782 (SEQ ID NO:2551), Public GI ID no.171906244 (SEQ ID NO:2553).

[0036] Figure 14 is an alignment of ME04753 (SEQ ID NO:368) with homologous and/or orthologous amino acid sequences GI No.21388658 (SEQ ID NO:369), GI No.4704605 (SEQ ID NO:371), GI No.90704785 (SEQ ID NO:372), GI No.115529229 (SEQ ID NO:373), GI No.20152613 (SEQ ID NO:374), CeresClone:1916226 (SEQ ID NO:376), CeresAnnot:1460836 (SEQ ID NO:392), GI No.83032218 (SEQ ID NO:420), GI No.1346180 (SEQ ID NO:422), CeresClone:621487 (SEQ ID NO:425), GI No.6273331 (SEQ ID NO:433), GI No.92874469 (SEQ ID NO:434), GI No.1778374 (SEQ ID NO:436), GI No.18076086 (SEQ ID NO:437), GI No.2674201 (SEQ ID NO:438), GI No.2267567 (SEQ ID NO:440), GI No.544426 (SEQ ID NO:441), GI No.6911144 (SEQ ID NO:444), GI No.469071 (SEQ ID NO:447), GI No.1934994 (SEQ ID NO:450), GI No.82623423 (SEQ ID NO:451), GI No.90265701 (SEQ ID NO:454), GI No.544423 (SEQ ID NO:455), CeresClone:1320097 (SEQ ID NO:458), CeresClone:1469740 (SEQ ID NO:465),

CeresClone:1740834 (SEQ ID NO:473), GI No.2226370 (SEQ ID NO:474), GI No.27527723 (SEQ ID NO:475), CeresClone:1762613 (SEQ ID NO:477), GI No.125545195 (SEQ ID NO:488), GI No.108710322 (SEQ ID NO:494), GI No.34851124 (SEQ ID NO:504), GI No.111162637 (SEQ ID NO:505), GI No.7024451 (SEQ ID NO:506), and GI No.1229138 (SEQ ID NO:507).

[0037] Figure 15 is an alignment of ME04772 (SEQ ID NO:510) with homologous and/or orthologous amino acid sequences GI No.38016521 (SEQ ID NO:511), CeresClone:1895044 (SEQ ID NO:513), CeresAnnot:1512198 (SEQ ID NO:517), CeresClone:682503 (SEQ ID NO:521), CeresClone:685324 (SEQ ID NO:523), CeresClone:1384414 (SEQ ID NO:525), CeresClone:1739919 (SEQ ID NO:527), CeresClone:2002832 (SEQ ID NO:529), GI No.125531563 (SEQ ID NO:530), and GI No.115478344 (SEQ ID NO:531).

[0038] Figure 16 is an alignment of ME04909 (SEQ ID NO:533) with homologous and/or orthologous amino acid sequences CeresClone:1839156 (SEQ ID NO:535), GI No.56605378 (SEQ ID NO:536), CeresAnnot:1467946 (SEQ ID NO:538), GI No.110931704 (SEQ ID NO:539), GI No.92869601 (SEQ ID NO:542), GI No.12005328 (SEQ ID NO:543), GI No.119331596 (SEQ ID NO:546), GI No.7705206 (SEQ ID NO:547), GI No.18874263 (SEQ ID NO:548), CeresClone:753605 (SEQ ID NO:550), CeresClone:291733 (SEQ ID NO:552), and GI No.21902114 (SEQ ID NO:553).

[0039] Figure 17 is an alignment of ME05194 (SEQ ID NO:558) with homologous and/or orthologous amino acid sequences GI No.400972 (SEQ ID NO:559), GI No.81158002 (SEQ ID NO:560), CeresClone:1834135 (SEQ ID NO:569), CeresAnnot:1467218 (SEQ ID NO:571), CeresClone:1104143 (SEQ ID NO:575), GI No.87240745 (SEQ ID NO:576), GI No.13161397 (SEQ ID NO:577), GI No.18652400 (SEQ ID NO:578), GI No.18652398 (SEQ ID NO:579), CeresClone:778892 (SEQ ID NO:581), CeresClone:222523 (SEQ ID NO:583), GI No.82492267 (SEQ ID NO:584), GI No.41393750 (SEQ ID NO:585), GI No.4335857 (SEQ ID NO:586), CeresClone:1776394 (SEQ ID NO:588), GI No.125555681 (SEQ ID NO:589), GI No.115468460 (SEQ ID NO:590), and GI No.51980210 (SEQ ID NO:591).

[0040] Figure 18 is an alignment of ME05267 (SEQ ID NO:593) with homologous and/or orthologous amino acid sequences CeresAnnot:1511954 (SEQ ID NO:595), CeresClone:560687 (SEQ ID NO:599), CeresClone:579724 (SEQ ID NO:603), CeresClone:286197 (SEQ ID NO:605), and GI No.115489090 (SEQ ID NO:610).

[0041] Figure 19 is an alignment of ME05300 (SEQ ID NO:613) with homologous

and/or orthologous amino acid sequences CeresAnnot:6431448 (SEQ ID NO:615), CeresClone:969084 (SEQ ID NO:620), CeresClone:471052 (SEQ ID NO:622), CeresClone:733048 (SEQ ID NO:624), CeresClone:1062332 (SEQ ID NO:626), CeresClone:1743166 (SEQ ID NO:634), CeresClone:1778589 (SEQ ID NO:638), GI No.125548354 (SEQ ID NO:643), and GI No.115458464 (SEQ ID NO:644).

[0042] Figure 20 is an alignment of ME05341 (SEQ ID NO:646) with homologous and/or orthologous amino acid sequences CeresClone:1808421 (SEQ ID NO:648), CeresAnnot:1452653 (SEQ ID NO:656), CeresClone:1660955 (SEQ ID NO:660), CeresClone:1287179 (SEQ ID NO:668), CeresClone:1770929 (SEQ ID NO:676), GI No.125542421 (SEQ ID NO:679), GI No.115450741 (SEQ ID NO:681), and CeresAnnot:6063505 (SEQ ID NO:685).

[0043] Figure 21 is an alignment of ME05392 (SEQ ID NO:687) with homologous and/or orthologous amino acid sequences CeresClone:1841531 (SEQ ID NO:689), CeresAnnot:1507382 (SEQ ID NO:691), CeresClone:978410 (SEQ ID NO:699), CeresClone:527314 (SEQ ID NO:703), GI No.92893019 (SEQ ID NO:706), CeresClone:638935 (SEQ ID NO:708), CeresClone:1437744 (SEQ ID NO:712), CeresClone:1728293 (SEQ ID NO:718), GI No.125526460 (SEQ ID NO:721), GI No.115463325 (SEQ ID NO:724), and GI No.40642817 (SEQ ID NO:728).

[0044] Figure 22 is an alignment of ME05429 (SEQ ID NO:730) with homologous and/or orthologous amino acid sequences CeresAnnot:1539629 (SEQ ID NO:732), CeresClone:682471 (SEQ ID NO:735), CeresClone:729869 (SEQ ID NO:737), GI No.115459766 (SEQ ID NO:738), and CeresAnnot: 6026765 (SEQ ID NO:742).

[0045] Figure 23 is an alignment of ME05493 (SEQ ID NO:746) with homologous and/or orthologous amino acid sequences CeresAnnot:1455092 (SEQ ID NO:748), GI No.15229284 (SEQ ID NO:751), CeresClone:961796 (SEQ ID NO:753), CeresClone:706956 (SEQ ID NO:755), GI No.87162911 (SEQ ID NO:758), CeresClone:1061446 (SEQ ID NO:760), GI No.125540686 (SEQ ID NO:761), GI No.115447931 (SEQ ID NO:762), GI No.20152976 (SEQ ID NO:763), and CeresAnnot:6007280 (SEQ ID NO:765).

[0046] Figure 24 is an alignment of ME05885 (SEQ ID NO:769) with homologous and/or orthologous amino acid sequences CeresClone:1808741 (SEQ ID NO:771), CeresAnnot:1437729 (SEQ ID NO:773), CeresClone:952789 (SEQ ID NO:777), CeresClone:724313 (SEQ ID NO:779), CeresClone:791239 (SEQ ID NO:783), CeresClone:208975 (SEQ ID NO:785), CeresClone:1727075 (SEQ ID NO:789), and GI No.115475611 (SEQ ID NO:790).

[0047] Figure 25 is an alignment of ME07344 (SEQ ID NO:792) with homologous and/or orthologous amino acid sequences CeresClone:1843695 (SEQ ID NO:794), GI No.56605376 (SEQ ID NO:799), CeresAnnot:1508502 (SEQ ID NO:801), CeresClone:1239229 (SEQ ID NO:805), GI No.92893962 (SEQ ID NO:808), CeresClone:327364 (SEQ ID NO:810), CeresClone:1820378 (SEQ ID NO:816), GI No.125524748 (SEQ ID NO:819), and GI No.115435036 (SEQ ID NO:821).

[0048] Figure 26 is an alignment of ME07859 (SEQ ID NO:824) with homologous amino acid sequence Fragment_of_Ceres ANNOT ID no.6007357 (SEQ ID NO:826), Fragment_of_Ceres CLONE ID no.771707 (SEQ ID NO:1708), and Fragment_of_Ceres CLONE ID no.1790436 (SEQ ID NO:1713).

[0049] Figure 27 is an alignment of ME08464 (SEQ ID NO:828) with homologous and/or orthologous amino acid sequences CeresAnnot:1499777 (SEQ ID NO:832), GI No.22328730 (SEQ ID NO:837), GI No.92886131 (SEQ ID NO:839), GI No.559921 (SEQ ID NO:840), CeresClone:910787 (SEQ ID NO:842), CeresClone:1797432 (SEQ ID NO:844), GI No.116310135 (SEQ ID NO:845), GI No.38345464 (SEQ ID NO:847), and GI No.90657544 (SEQ ID NO:850).

[0050] Figure 28 is an alignment of ME11735 (SEQ ID NO:855) with homologous and/or orthologous amino acid sequences GI No.35187445 (SEQ ID NO:856), CeresClone:1798230 (SEQ ID NO:858), CeresAnnot:1500963 (SEQ ID NO:862), CeresClone:567542 (SEQ ID NO:868), CeresClone:702251 (SEQ ID NO:870), CeresClone:1606777 (SEQ ID NO:876), CeresClone:1789146 (SEQ ID NO:878), GI No.116309500 (SEQ ID NO:885), and GI No.115446281 (SEQ ID NO:886).

[0051] Figure 29 is an alignment of ME12910 (SEQ ID NO:891) with homologous and/or orthologous amino acid sequences CeresAnnot:1466353 (SEQ ID NO:893), CeresClone:519143 (SEQ ID NO:898), GI No.2501497 (SEQ ID NO:901), GI No.119394507 (SEQ ID NO:904), GI No.62857206 (SEQ ID NO:905), CeresClone:766529 (SEQ ID NO:907), GI No.62857204 (SEQ ID NO:908), GI No.125534279 (SEQ ID NO:911), GI No.115485437 (SEQ ID NO:912), GI No.23955910 (SEQ ID NO:913), and GI No.22759895 (SEQ ID NO:915).

[0052] Figure 30 is an alignment of ME12927 (SEQ ID NO:917) with homologous and/or orthologous amino acid sequences CeresAnnot:1503548 (SEQ ID NO:919), CeresClone:37778 (SEQ ID NO:921), CeresClone:681297 (SEQ ID NO:923), CeresClone:575835 (SEQ ID NO:925), CeresClone:1714750 (SEQ ID NO:935), CeresClone:1721907 (SEQ ID NO:937), and GI No.115451923 (SEQ ID NO:940).

[0053] Figure 31 is an alignment of ME12929 (SEQ ID NO:944) with homologous and/or orthologous amino acid sequences CeresAnnot:1447562 (SEQ ID NO:946), GI No.98962139 (SEQ ID NO:947), CeresClone:641607 (SEQ ID NO:950), CeresClone:1715150 (SEQ ID NO:962), CeresClone:1873767 (SEQ ID NO:964), GI No.115468306 (SEQ ID NO:967), and CeresAnnot:6059980 (SEQ ID NO:972).

[0054] Figure 32 is an alignment of ME12954 (SEQ ID NO:976) with homologous and/or orthologous amino acid sequences CeresClone:957229 (SEQ ID NO:978) and CeresAnnot:1496202 (SEQ ID NO:980).

[0055] Figure 33 is an alignment of ME12970 (SEQ ID NO:982) with homologous and/or orthologous amino acid sequences CeresClone:1935438 (SEQ ID NO:984), GI No.117573664 (SEQ ID NO:985), GI No.68349002 (SEQ ID NO:991), GI No.68348998 (SEQ ID NO:992), CeresAnnot:1497170 (SEQ ID NO:995), GI No.15221718 (SEQ ID NO:996), GI No.3860331 (SEQ ID NO:1001), CeresClone:1075911 (SEQ ID NO:1003), GI No.2920839 (SEQ ID NO:1008), CeresClone:698452 (SEQ ID NO:1011), CeresClone:2019456 (SEQ ID NO:1023), GI No.90399071 (SEQ ID NO:1026), GI No.115459588 (SEQ ID NO:1028), and GI No.68349016 (SEQ ID NO:1032).

[0056] Figure 34 is an alignment of ME13021 (SEQ ID NO:1054) with homologous and/or orthologous amino acid sequences GI No.2493647 (SEQ ID NO:1055), CeresClone:1924252 (SEQ ID NO:1057), GI No.461736 (SEQ ID NO:1058), CeresAnnot:1542060 (SEQ ID NO:1061), GI No.15226314 (SEQ ID NO:1068), GI No.464727 (SEQ ID NO:1072), CeresClone:480644 (SEQ ID NO:1074), GI No.124301264 (SEQ ID NO:1075), GI No.1710807 (SEQ ID NO:1076), GI No.110349923 (SEQ ID NO:1077), GI No.1762130 (SEQ ID NO:1078), CeresClone:706098 (SEQ ID NO:1080), GI No.3790441 (SEQ ID NO:1083), CeresClone:1795282 (SEQ ID NO:1085), GI No.125546535 (SEQ ID NO:1086), GI No.115488160 (SEQ ID NO:1088), GI No.84468456 (SEQ ID NO:1092), GI No.116060917 (SEQ ID NO:1095), and CeresAnnot:6039555 (SEQ ID NO:1097).

[0057] Figure 35 is an alignment of ME13064 (SEQ ID NO:1099) with homologous and/or orthologous amino acid sequences CeresAnnot:1528508 (SEQ ID NO:1101), CeresClone:9248 (SEQ ID NO:1103), GI No.87240560 (SEQ ID NO:1105), GI No.19453 (SEQ ID NO:1106), CeresClone:1795329 (SEQ ID NO:1108), and GI No.108862979 (SEQ ID NO:1109).

[0058] Figure 36 is an alignment of ME13071 (SEQ ID NO:1112) with homologous and/or orthologous amino acid sequences GI No.125541485 (SEQ ID NO:1113), and GI

No.115449245 (SEQ ID NO:1114).

[0059] Figure 37 is an alignment of ME13087 (SEQ ID NO:1116) with homologous and/or orthologous amino acid sequences CeresClone:100062822 (SEQ ID NO:1118), CeresAnnot:1440025 (SEQ ID NO:1120), GI No.15238538 (SEQ ID NO:1123), GI No.69111473 (SEQ ID NO:1129), GI No.92873711 (SEQ ID NO:1132), GI No.55734106 (SEQ ID NO:1133), GI No.2346974 (SEQ ID NO:1134), CeresClone:569852 (SEQ ID NO:1136), CeresClone:1715326 (SEQ ID NO:1138), CeresClone:1608104 (SEQ ID NO:1140), GI No.115456237 (SEQ ID NO:1141), GI No.68655289 (SEQ ID NO:1143), GI No.81022807 (SEQ ID NO:1144), GI No.75706704 (SEQ ID NO:1145), and CeresAnnot:6016055 (SEQ ID NO:1147).

[0060] Figure 38 is an alignment of ME13107 (SEQ ID NO:1159) with homologous and/or orthologous amino acid sequences CeresClone:1371824 (SEQ ID NO:1161), GI No.22585 (SEQ ID NO:1162), GI No.22208482 (SEQ ID NO:1163), and GI No.16073 (SEQ ID NO:1164).

[0061] Figure 39 is an alignment of ME13108 (SEQ ID NO:1166) with homologous and/or orthologous amino acid sequences GI No.99109436 (SEQ ID NO:1167), CeresClone:1627939 (SEQ ID NO:1169), CeresClone:1840433 (SEQ ID NO:1171), CeresAnnot:1524198 (SEQ ID NO:1173), CeresClone:1650 (SEQ ID NO:1175), CeresClone:691979 (SEQ ID NO:1177), GI No.92876897 (SEQ ID NO:1180), CeresClone:1774130 (SEQ ID NO:1182), and GI No.115450018 (SEQ ID NO:1183).

[0062] Figure 40 is an alignment of ME13110 (SEQ ID NO:1185) with homologous and/or orthologous amino acid sequences CeresClone:737317 (SEQ ID NO:1187), CeresClone:1880853 (SEQ ID NO:1189), GI No.125558381 (SEQ ID NO:1190), and GI No.115472157 (SEQ ID NO:1191).

[0063] Figure 41 is an alignment of ME13125 (SEQ ID NO:1194) with homologous and/or orthologous amino acid sequences CeresClone:1938817 (SEQ ID NO:1196), CeresAnnot:1457245 (SEQ ID NO:1200), CeresClone:577910 (SEQ ID NO:1202), Public PUBLICCLONE ID no.100736184 (SEQ ID NO:1203), GI No.125553355 (SEQ ID NO:1204), and GI No.5091600 (SEQ ID NO:1205).

[0064] Figure 42 is an alignment of ME13149 (SEQ ID NO:1210) with homologous and/or orthologous amino acid sequences GI No.1703374 (SEQ ID NO:1211), CeresClone:1846330 (SEQ ID NO:1213), GI No.29124979 (SEQ ID NO:1216), CeresAnnot:1531725 (SEQ ID NO:1218), GI No.3334321 (SEQ ID NO:1229), CeresClone:571410 (SEQ ID NO:1232), GI No.39653273 (SEQ ID NO:1233), GI

No.92875403 (SEQ ID NO:1234), GI No.11131026 (SEQ ID NO:1235), GI No.77812440 (SEQ ID NO:1236), GI No.89475524 (SEQ ID NO:1238), GI No.3182919 (SEQ ID NO:1239), GI No.7643794 (SEQ ID NO:1240), GI No.1710851 (SEQ ID NO:1241), GI No.115501471 (SEQ ID NO:1242), GI No.77999251 (SEQ ID NO:1243), GI No.3450893 (SEQ ID NO:1249), CeresClone:704589 (SEQ ID NO:1251), CeresClone:1384151 (SEQ ID NO:1253), CeresClone:1713894 (SEQ ID NO:1259), GI No.125560752 (SEQ ID NO:1264), GI No.115475543 (SEQ ID NO:1265), GI No.3182922 (SEQ ID NO:1267), GI No.145353078 (SEQ ID NO:1268), GI No.11131023 (SEQ ID NO:1269), GI No.47026845 (SEQ ID NO:1270), and GI No.38353642 (SEQ ID NO:1272).

[0065] Figure 43 is an alignment of ME13151 (SEQ ID NO:1274) with homologous and/or orthologous amino acid sequences CeresClone:1884601 (SEQ ID NO:1276), CeresAnnot:1445717 (SEQ ID NO:1280), CeresClone:527903 (SEQ ID NO:1284), GI No.92891722 (SEQ ID NO:1285), CeresClone:790881 (SEQ ID NO:1287), CeresClone:299417 (SEQ ID NO:1289), CeresClone:1993894 (SEQ ID NO:1291), GI No.125539547 (SEQ ID NO:1294), GI No.48716424 (SEQ ID NO:1295), GI No.84468278 (SEQ ID NO:1297), and CeresAnnot:6036303 (SEQ ID NO:1300).

[0066] Figure 44 is an alignment of ME13153 (SEQ ID NO:1302) with homologous and/or orthologous amino acid sequences GI No.70609690 (SEQ ID NO:1303), CeresClone:1927524 (SEQ ID NO:1305), CeresAnnot:1467310 (SEQ ID NO:1311), GI No.45935270 (SEQ ID NO:1313), CeresClone:718446 (SEQ ID NO:1317), GI No.92875133 (SEQ ID NO:1318), GI No.1706318 (SEQ ID NO:1319), GI No.3252856 (SEQ ID NO:1320), GI No.1169238 (SEQ ID NO:1326), GI No.31296711 (SEQ ID NO:1327), CeresClone:1468893 (SEQ ID NO:1330), GI No.51587340 (SEQ ID NO:1331), CeresClone:1796201 (SEQ ID NO:1333), GI No.125543034 (SEQ ID NO:1334), GI No.115476804 (SEQ ID NO:1336), GI No.75268060 (SEQ ID NO:1339), and GI No.75268007 (SEQ ID NO:1340).

[0067] Figure 45 is an alignment of ME13177 (SEQ ID NO:1342) with homologous and/or orthologous amino acid sequences CeresAnnot:1443786 (SEQ ID NO:1346), GI No.15239172 (SEQ ID NO:1355), GI No.562190 (SEQ ID NO:1363), GI No.83032266 (SEQ ID NO:1364), CeresClone:602910 (SEQ ID NO:1366), GI No.7242793 (SEQ ID NO:1370), GI No.116167 (SEQ ID NO:1371), GI No.2190259 (SEQ ID NO:1372), GI No.5420278 (SEQ ID NO:1373), GI No.1064931 (SEQ ID NO:1374), GI No.6093215 (SEQ ID NO:1377), GI No.461726 (SEQ ID NO:1378), GI No.89111295 (SEQ ID NO:1379), GI No.82949283 (SEQ ID NO:1380), GI No.125537180 (SEQ ID NO:1381), GI No.115489300

(SEQ ID NO:1382), and GI No.55978000 (SEQ ID NO:1383).

[0068] Figure 46 is an alignment of ME13200 (SEQ ID NO:1385) with homologous and/or orthologous amino acid sequences CeresAnnot:1503394 (SEQ ID NO:1387), GI No.4914437 (SEQ ID NO:1390), CeresClone:638126 (SEQ ID NO:1393), GI No.124360540 (SEQ ID NO:1394), GI No.7981380 (SEQ ID NO:1395), GI No.118137433 (SEQ ID NO:1396), CeresClone:1723374 (SEQ ID NO:1398), CeresClone:1785379 (SEQ ID NO:1400), GI No.125553354 (SEQ ID NO:1401), GI No.115471859 (SEQ ID NO:1404), and CeresAnnot:6040771 (SEQ ID NO:1407).

[0069] Figure 47 is an alignment of ME13204 (SEQ ID NO:1409) with homologous and/or orthologous amino acid sequences CeresClone:1939206 (SEQ ID NO:1413), CeresAnnot:1453316 (SEQ ID NO:1415), GI No.79319075 (SEQ ID NO:1418), GI No.124359953 (SEQ ID NO:1419), CeresClone:891431 (SEQ ID NO:1421), GI No.125536578 (SEQ ID NO:1424), and GI No.20270065 (SEQ ID NO:1425).

[0070] Figure 48 is an alignment of ME14649 (SEQ ID NO:1428) with homologous and/or orthologous amino acid sequences CeresClone:1978733 (SEQ ID NO:1430), CeresAnnot:1476165 (SEQ ID NO:1432), CeresClone:871529 (SEQ ID NO:1436), CeresClone:1043344 (SEQ ID NO:1439), CeresClone:786542 (SEQ ID NO:1442), CeresClone:346115 (SEQ ID NO:1444), CeresClone:1821683 (SEQ ID NO:1452), GI No.125533171 (SEQ ID NO:1453), and GI No.77553492 (SEQ ID NO:1457)

[0071] Figure 49 is an alignment of ME16546 (SEQ ID NO:1463) with homologous and/or orthologous amino acid sequences CeresAnnot:1444102 (SEQ ID NO:1465), CeresClone:582439 (SEQ ID NO:1471), CeresClone:579953 (SEQ ID NO:1473), GI No.125539335 (SEQ ID NO:1474), and GI No.115445987 (SEQ ID NO:1476).

[0072] Figure 50 is an alignment of ME17567 (SEQ ID NO:1491) with homologous and/or orthologous amino acid sequences CeresClone:1895876 (SEQ ID NO:1493), CeresAnnot:1464522 (SEQ ID NO:1495), CeresClone:968434 (SEQ ID NO:1499), CeresClone:686479 (SEQ ID NO:1501), CeresClone:1564962 (SEQ ID NO:1503), GI No.125549699 (SEQ ID NO:1504), GI No.125591612 (SEQ ID NO:1505), and CeresAnnot:6006969 (SEQ ID NO:1508).

[0073] Figure 51 is an alignment of ME17932 (SEQ ID NO:1510) with homologous and/or orthologous amino acid sequences CeresClone:1842178 (SEQ ID NO:1512), CeresAnnot:1475265 (SEQ ID NO:1516) and CeresClone:1044646 (SEQ ID NO:1520).

[0074] Figure 52 is an alignment of ME17936 (SEQ ID NO:1525) with homologous and/or orthologous amino acid sequences CeresAnnot:1454324 (SEQ ID NO:1527),

CeresClone:1652842 (SEQ ID NO:1534), and GI No.75214620 (SEQ ID NO:1535).

[0075] Figure 53 is an alignment of ME18275 (SEQ ID NO:1537) with homologous and/or orthologous amino acid sequences CeresAnnot:1514086 (SEQ ID NO:1539), CeresClone:1087909 (SEQ ID NO:1543), CeresClone:1359070 (SEQ ID NO:1545), GI No.92880913 (SEQ ID NO:1548), CeresClone:932449 (SEQ ID NO:1550), and CeresClone:1788695 (SEQ ID NO:1552).

[0076] Figure 54 is an alignment of ME18924 (SEQ ID NO:1554) with homologous and/or orthologous amino acid sequences GI No.82469976 (SEQ ID NO:1555), CeresAnnot:1533704 (SEQ ID NO:1563), CeresClone:524404 (SEQ ID NO:1565), CeresClone:846541 (SEQ ID NO:1567), CeresClone:1769321 (SEQ ID NO:1571), GI No.125528559 (SEQ ID NO:1572), GI No.125572823 (SEQ ID NO:1574), and GI No.84453208 (SEQ ID NO:1575).

[0077] Figure 55 is an alignment of ME19182 (SEQ ID NO:1577) with homologous and/or orthologous amino acid sequences GI No.4033417 (SEQ ID NO:1040), GI No.5669924 (SEQ ID NO:1041), GI No.40642617 (SEQ ID NO:1440), GI No.90399018 (SEQ ID NO:1485), GI No.115464117 (SEQ ID NO:1487), GI No.75164812 (SEQ ID NO:1578), CeresClone:1794223 (SEQ ID NO:1580), CeresAnnot:1471422 (SEQ ID NO:1590), CeresClone:968096 (SEQ ID NO:1607), GI No.6752884 (SEQ ID NO:1608), GI No.47775656 (SEQ ID NO:1609), CeresClone:1020799 (SEQ ID NO:1611), GI No.87240865 (SEQ ID NO:1622), GI No.2500047 (SEQ ID NO:1623), CeresClone:705340 (SEQ ID NO:1627), CeresClone:1430456 (SEQ ID NO:1637), GI No.84619270 (SEQ ID NO:1648), and CeresClone:1821143 (SEQ ID NO:1651).

[0078] Figure 56 is an alignment of ME20628 (SEQ ID NO:1437) with homologous and/or orthologous amino acid sequences GI No.113367236 (SEQ ID NO:173), GI No.115477615 (SEQ ID NO:212), GI No.125542223 (SEQ ID NO:361), GI No.1838976 (SEQ ID NO:421), CeresClone:1547185 (SEQ ID NO:443), CeresAnnot:1450452 (SEQ ID NO:740), and GI No.92870675 (SEQ ID NO:1461).

[0079] Figure 57 is an alignment of ME01821 (SEQ ID NO:97) with homologous and/or orthologous amino acid sequences Public GI ID no.167480754 (SEQ ID NO:2013) and Public GI ID no.83830869 (SEQ ID NO:2015).

DETAILED DESCRIPTION

[0080] The invention provides methods and materials related to modulating low-nitrogen tolerance levels in plants. In some embodiments, the plants may also have

modulated levels of low-nitrogen tolerance. The methods can include transforming a plant cell with a nucleic acid encoding a low nitrogen tolerance-modulating polypeptide, wherein expression of the polypeptide results in a modulated level of low-nitrogen tolerance. Plant cells produced using such methods can be grown to produce plants having an increased tolerance to conditions with limiting exogenous nitrogen sources. Such plants can be used for the production of higher yields and biomasses with existing fertilizer inputs, and/or enable existing yields and biomass of crops to be obtained with lower fertilizer input, or better yields and biomasses on soils of poorer quality.

I. Definitions:

[0081] "Amino acid" refers to one of the twenty biologically occurring amino acids and to synthetic amino acids, including D/L optical isomers.

[0082] "Cell type-preferential promoter" or "tissue-preferential promoter" refers to a promoter that drives expression preferentially in a target cell type or tissue, respectively, but may also lead to some transcription in other cell types or tissues as well.

[0083] "Control plant" refers to a plant that does not contain the exogenous nucleic acid present in a transgenic plant of interest, but otherwise has the same or similar genetic background as such a transgenic plant. A suitable control plant can be a non-transgenic wild type plant, a non-transgenic segregant from a transformation experiment, or a transgenic plant that contains an exogenous nucleic acid other than the exogenous nucleic acid of interest.

[0084] "Domains" are groups of substantially contiguous amino acids in a polypeptide that can be used to characterize protein families and/or parts of proteins. Such domains have a "fingerprint" or "signature" that can comprise conserved primary sequence, secondary structure, and/or three-dimensional conformation. Generally, domains are correlated with specific in vitro and/or in vivo activities. A domain can have a length of from 10 amino acids to 400 amino acids, *e.g.*, 10 to 50 amino acids, or 25 to 100 amino acids, or 35 to 65 amino acids, or 35 to 55 amino acids, or 45 to 60 amino acids, or 200 to 300 amino acids, or 300 to 400 amino acids.

[0085] "Down-regulation" refers to regulation that decreases production of expression products (mRNA, polypeptide, or both) relative to basal or native states.

[0086] "Exogenous" with respect to a nucleic acid indicates that the nucleic acid is part of a recombinant nucleic acid construct, or is not in its natural environment. For example, an exogenous nucleic acid can be a sequence from one species introduced into another species, *i.e.*, a heterologous nucleic acid. Typically, such an exogenous nucleic acid

is introduced into the other species via a recombinant nucleic acid construct. An exogenous nucleic acid can also be a sequence that is native to an organism and that has been reintroduced into cells of that organism. An exogenous nucleic acid that includes a native sequence can often be distinguished from the naturally occurring sequence by the presence of non-natural sequences linked to the exogenous nucleic acid, *e.g.*, non-native regulatory sequences flanking a native sequence in a recombinant nucleic acid construct. In addition, stably transformed exogenous nucleic acids typically are integrated at positions other than the position where the native sequence is found. It will be appreciated that an exogenous nucleic acid may have been introduced into a progenitor and not into the cell under consideration. For example, a transgenic plant containing an exogenous nucleic acid can be the progeny of a cross between a stably transformed plant and a non-transgenic plant. Such progeny are considered to contain the exogenous nucleic acid.

[0087] "Expression" refers to the process of converting genetic information of a polynucleotide into RNA through transcription, which is catalyzed by an enzyme, RNA polymerase, and into protein, through translation of mRNA on ribosomes.

[0088] "Heterologous polypeptide" as used herein refers to a polypeptide that is not a naturally occurring polypeptide in a plant cell, *e.g.*, a transgenic *Panicum virgatum* plant transformed with and expressing the coding sequence for a nitrogen transporter polypeptide from a *Zea mays* plant.

[0089] "Isolated nucleic acid" as used herein includes a naturally-occurring nucleic acid, provided one or both of the sequences immediately flanking that nucleic acid in its naturally-occurring genome is removed or absent. Thus, an isolated nucleic acid includes, without limitation, a nucleic acid that exists as a purified molecule or a nucleic acid molecule that is incorporated into a vector or a virus. A nucleic acid existing among hundreds to millions of other nucleic acids within, for example, cDNA libraries, genomic libraries, or gel slices containing a genomic DNA restriction digest, is not to be considered an isolated nucleic acid.

[0090] "Low Nitrogen Conditions" as used herein refers to nitrogen concentrations which lead to nitrogen deficiency symptoms such as pale green leaf color, chlorosis and reduced growth and vigor. Typically, low nitrogen conditions lead to a reduction of at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 60%, 70%, 80% or 90% in growth and/or vigor.

[0091] "Modulation" of the level of low-nitrogen tolerance refers to the change in the level of tolerance of a plant to limiting exogenous nitrogen sources that is observed as a result of expression of, or transcription from, an exogenous nucleic acid in a plant cell. The change

in low-nitrogen tolerance level is measured by changes in plant size and greenness as well as greater photosynthesis efficiency, relative to the corresponding level in control plants in an environment with limiting nitrogen supply.

[0092] "Nucleic acid" and "polynucleotide" are used interchangeably herein, and refer to both RNA and DNA, including cDNA, genomic DNA, synthetic DNA, and DNA or RNA containing nucleic acid analogs. Polynucleotides can have any three-dimensional structure. A nucleic acid can be double-stranded or single-stranded (*i.e.*, a sense strand or an antisense strand). Non-limiting examples of polynucleotides include genes, gene fragments, exons, introns, messenger RNA (mRNA), transfer RNA, ribosomal RNA, siRNA, micro-RNA, ribozymes, cDNA, recombinant polynucleotides, branched polynucleotides, nucleic acid probes and nucleic acid primers. A polynucleotide may contain unconventional or modified nucleotides.

[0093] "Operably linked" refers to the positioning of a regulatory region and a sequence to be transcribed in a nucleic acid so that the regulatory region is effective for regulating transcription or translation of the sequence. For example, to operably link a coding sequence and a regulatory region, the translation initiation site of the translational reading frame of the coding sequence is typically positioned between one and about fifty nucleotides downstream of the regulatory region. A regulatory region can, however, be positioned as much as about 5,000 nucleotides upstream of the translation initiation site, or about 2,000 nucleotides upstream of the transcription start site.

[0094] "Polypeptide" as used herein refers to a compound of two or more subunit amino acids, amino acid analogs, or other peptidomimetics, regardless of post-translational modification, *e.g.*, phosphorylation or glycosylation. The subunits may be linked by peptide bonds or other bonds such as, for example, ester or ether bonds. Full-length polypeptides, truncated polypeptides, point mutants, insertion mutants, splice variants, chimeric proteins, and fragments thereof are encompassed by this definition.

[0095] "Progeny" includes descendants of a particular plant or plant line. Progeny of an instant plant include seeds formed on F_1, F_2, F_3, F_4, F_5, F_6 and subsequent generation plants, or seeds formed on BC_1, BC_2, BC_3, and subsequent generation plants, or seeds formed on F_1BC_1, F_1BC_2, F_1BC_3, and subsequent generation plants. The designation F_1 refers to the progeny of a cross between two parents that are genetically distinct. The designations F_2, F_3, F_4, F_5 and F_6 refer to subsequent generations of self- or sib-pollinated progeny of an F_1 plant.

[0096] "Regulatory region" refers to a nucleic acid having nucleotide sequences that influence transcription or translation initiation and rate, and stability and/or mobility of a

transcription or translation product. Regulatory regions include, without limitation, promoter sequences, enhancer sequences, response elements, protein recognition sites, inducible elements, protein binding sequences, 5′ and 3′ untranslated regions (UTRs), transcriptional start sites, termination sequences, polyadenylation sequences, introns, and combinations thereof. A regulatory region typically comprises at least a core (basal) promoter. A regulatory region also may include at least one control element, such as an enhancer sequence, an upstream element or an upstream activation region (UAR). For example, a suitable enhancer is a cis-regulatory element (-212 to -154) from the upstream region of the octopine synthase (ocs) gene. Fromm et al. (1989) *The Plant Cell*, 1:977-984.

[0097] "Up-regulation" refers to regulation that increases the level of an expression product (mRNA, polypeptide, or both) relative to basal or native states.

[0098] "Vector" refers to a replicon, such as a plasmid, phage, or cosmid, into which another DNA segment may be inserted so as to bring about the replication of the inserted segment. Generally, a vector is capable of replication when associated with the proper control elements. The term "vector" includes cloning and expression vectors, as well as viral vectors and integrating vectors. An "expression vector" is a vector that includes a regulatory region.

II. Polypeptides

[0099] Polypeptides described herein include low nitrogen tolerance-modulating polypeptides. Low nitrogen tolerance-modulating polypeptides can be effective to modulate low-nitrogen tolerance levels when expressed in a plant or plant cell. Such polypeptides typically contain at least one domain indicative of low nitrogen tolerance-modulating polypeptides, as described in more detail herein. Low nitrogen tolerance-modulating polypeptides typically have an HMM bit score that is greater than 20, as described in more detail herein. In some embodiments, low nitrogen tolerance-modulating polypeptides have greater than 80 % identity to SEQ ID NO:3, SEQ ID NO:49, SEQ ID NO:77, SEQ ID NO:97, SEQ ID NO:100, SEQ ID NO:152, SEQ ID NO:166, SEQ ID NO:186, SEQ ID NO:208, SEQ ID NO:218, SEQ ID NO:234, SEQ ID NO:246, SEQ ID NO:300, SEQ ID NO:332, SEQ ID NO:368, SEQ ID NO:510, SEQ ID NO:533, SEQ ID NO:556, SEQ ID NO:558, SEQ ID NO:593, SEQ ID NO:613, SEQ ID NO:646, SEQ ID NO:687, SEQ ID NO:730, SEQ ID NO:746, SEQ ID NO:769, SEQ ID NO:792, SEQ ID NO:824, SEQ ID NO:828, SEQ ID NO:853, SEQ ID NO:855, SEQ ID NO:891, SEQ ID NO:917, SEQ ID NO:944, SEQ ID NO:976, SEQ ID NO:982, SEQ ID NO:1054, SEQ ID NO:1099, SEQ ID NO:1112,

SEQ ID NO:1116, SEQ ID NO:1157, SEQ ID NO:1159, SEQ ID NO:1166, SEQ ID NO:1185, SEQ ID NO:1194, SEQ ID NO:1210, SEQ ID NO:1274, SEQ ID NO:1302, SEQ ID NO:1342, SEQ ID NO:1385, SEQ ID NO:1409, SEQ ID NO:1428, SEQ ID NO:1437, SEQ ID NO:1463, SEQ ID NO:1491, SEQ ID NO:1510, SEQ ID NO:1525, SEQ ID NO:1537, SEQ ID NO:1554, or SEQ ID NO:1577, as described in more detail herein.

A. Domains Indicative of Low Nitrogen Tolerance-Modulating Polypeptides

[0100] A low nitrogen tolerance-modulating polypeptide can contain a P450 domain, which is characteristic of polypeptides belonging to the Cytochrome P450 superfamily. Cytochrome P450s are haem-thiolate proteins involved in the oxidative degradation of various compounds. They are particularly well known for their role in the degradation of environmental toxins and mutagens. In plants, these proteins are important for the biosynthesis of several compounds such as hormones, defensive compounds and fatty acids. Sequence conservation is relatively low within the family - there are only 3 absolutely conserved residues - but their general topography and structural fold are highly conserved. The conserved core is composed of a coil termed the 'meander', a four-helix bundle, helices J and K, and two sets of beta-sheets. These constitute the haem-binding loop, the proton-transfer groove and the conserved EXXR motif in helix K. While prokaryotic P450s are soluble proteins, most eukaryotic P450s are associated with microsomal membranes. Their general enzymatic function is to catalyse regiospecific and stereospecific oxidation of non-activated hydrocarbons at physiological temperatures. SEQ ID NO:3 and SEQ ID NO:332 set forth the amino acid sequence of *Arabidopsis* clones, identified herein as ME00919 (SEQ ID NO:3) and ME04587 (SEQ ID NO:332) respectively, that are predicted to encode polypeptides containing a Cytochrome P450 domain.

[0101] A low nitrogen tolerance-modulating polypeptide can contain a zf-Dof domain, which is conserved in several DNA-binding proteins of higher plants. Dof domain is a zinc finger DNA-binding domain that shows resemblance to the Cys2 zinc finger, although it has a longer putative loop where an extra Cys residue is typically conserved. The motif is also present in SEQ ID NO:49, which sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME01312 (SEQ ID NO:49), that is predicted to encode a polypeptide containing a zf-Dof domain.

[0102] A low nitrogen tolerance-modulating polypeptide can contain an Aminotran_3 domain characteristic of polypeptides belonging to the aminotransferase Class-III family. Aminotransferases share certain mechanistic features with other pyridoxalphosphate-

dependent enzymes, such as the covalent binding of the pyridoxalphosphate group to a lysine residue. Class-III aminotransferases include acetylornithine aminotransferase , which catalyzes the transfer of an amino group from acetylornithine to alpha-ketoglutarate, yielding N-acetyl-glutamic-5-semi-aldehyde and glutamic acid; ornithine aminotransferase , which catalyzes the transfer of an amino group from ornithine to alpha-ketoglutarate, yielding glutamic-5-semi-aldehyde and glutamic acid; omega-amino acid--pyruvate aminotransferase, which catalyzes transamination between a variety of omega-amino acids, mono- and diamines, and pyruvate; 4-aminobutyrate aminotransferase; GABA transaminase, which catalyzes the transfer of an amino group from GABA to alpha-ketoglutarate, yielding succinate semialdehyde and glutamic acid; DAPA aminotransferase, a bacterial enzyme (bioA), which catalyzes an intermediate step in the biosynthesis of biotin, the transamination of 7-keto-8-aminopelargonic acid to form 7,8-diaminopelargonic acid; 2,2-dialkylglycine decarboxylase, a Burkholderia cepacia (Pseudomonas cepacia) enzyme (dgdA) that catalyzes the decarboxylating amino transfer of 2,2-dialkylglycine and pyruvate to dialkyl ketone, alanine and carbon dioxide; glutamate-1-semialdehyde aminotransferase (GSA); *Bacillus subtilis* aminotransferases yhxA and yodT; *Haemophilus influenzae* aminotransferase HI0949; and *Caenorhabditis elegans* aminotransferase. On the basis of sequence similarity, these various enzymes can be grouped into subfamilies. The aminotran_3 domain is also present in SEQ ID NO:77, which set forth the amino acid sequences of *Arabidopsis* clone, identified herein as Ceres ME01463 (SEQ ID NO:77), that is predicted to encode polypeptides containing an aminotran_3 domain.

[0103] A low nitrogen tolerance-modulating polypeptide can contain a linker histone domain characteristic of polypeptides belonging to the linker histone H1 and H5 family. Linker histone H1 is an essential component of chromatin structure. H1 links nucleosomes into higher order structures. Histone H5 performs the same function as histone H1, and replaces H1 in certain cells. The structure of GH5, the globular domain of the linker histone H5 fold is similar to the DNA-binding domain of the catabolite gene activator protein, CAP, thus providing a possible model for the binding of GH5 to DNA. The domain is also present in SEQ ID NO:100, which sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME01910 (SEQ ID NO:100), that is predicted to encode a polypeptide containing a linker histone domain.

[0104] A low nitrogen tolerance-modulating polypeptide can contain a zf-C3HC4 domain, which is predicted to be characteristic of proteins belonging to the C3HC4 type zinc-finger (RING finger) protein family. The C3HC4 type zinc-finger (RING finger) is a

cysteine-rich domain of approximately 40 to 60 residues that coordinates two zinc ions, and is probably involved in mediating protein-protein interactions. Members of the C3HC4 type zinc-finger (RING finger) protein family contain the loosely conserved sequence: C-X2-C-X(9-39)-C-X(1-3)-H-X(2-3)-C-X2-C-X(4-48)-C-X2-C where X is any amino acid. The domain is also present in SEQ ID NOs:166, 746, 976, 1428, which set forth the amino acid sequences of *Arabidopsis* clones, identified herein as Ceres ME02603 (SEQ ID NO:166), ME05493 (SEQ ID NO:746), ME12954 (SEQ ID NO:976), ME14649 (SEQ ID NO:1428) respectively, that are predicted to encode polypeptides containing a zf-C3HC4 domain.

[0105] A low nitrogen tolerance-modulating polypeptide can contain a Gal_Lectin domain characteristic of a galactose binding lectin domain protein. SEQ ID NO:208 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME02801 (SEQ ID NO:208), that is predicted to encode a polypeptide containing a galactose binding lectin domain.

[0106] A low nitrogen tolerance-modulating polypeptide can contain a TRP_1 domain characteristic of tetratricopeptide repeat (TPR) domain protein. The tetratricopeptide repeat is a structural motif present in a wide range of proteins identified in various different organisms, ranging from bacteria to humans. It mediates protein-protein interactions and the assembly of multiprotein complexes. Sequence alignment of the TPR domains reveals a consensus sequence defined by a pattern of small and large amino acids. Proteins containing TPRs are involved in a variety of biological processes, such as cell cycle regulation, transcriptional control, mitochondrial and peroxisomal protein transport, neurogenesis and protein folding. The X-ray structure of a domain containing three TPRs from protein phosphatase 5 revealed that TPR adopts a helixturnhelix arrangement, with adjacent TPR motifs packing in a parallel fashion, resulting in a spiral of repeating anti-parallel alpha-helices. The two helices are denoted helix A and helix B. The packing angle between helix A and helix B is ~24° within a single TPR and generates a right-handed superhelical shape. Helix A interacts with helix B and with helix A' of the next TPR. Two protein surfaces are generated: the inner concave surface is contributed to mainly by residue on helices A, and the other surface presents residues from both helices A and B.

[0107] A low nitrogen tolerance-modulating polypeptide can contain a TRP_2 tetratricopeptide repeat domain, which is predicted to be characteristic of scaffold-proteins in multiprotein complexes. The TPR_2 domain consists of approximately 34-amino-acid motif with a loose consensus and is present, usually as multiple tandem repeats, in proteins with many cellular functions, including mitosis, transcription, protein transport, and development.

Structural analysis of the TPR-2 domain demonstrates that it forms two α-helical regions separated by a turn, such that apposed bulky and small side chains form a "knob and hole" structure. In general, the hydrophobic surface of this structure mediates protein-protein interactions between TPR- and non-TPR-containing proteins.

[0108] SEQ ID NO:234 sets forth the amino acid sequence of *Arabidopsis* clone, identified herein as Ceres ME04204 (SEQ ID NO:234), that is predicted to encode a polypeptide containing a TRP_1 tetratricopeptide repeat domain and a TRP_2 tetratricopeptide repeat domain. SEQ ID NO:1510 sets forth the amino acid sequence of *Arabidopsis* clone, identified herein as Ceres ME17932 (SEQ ID NO:1510), that is predicted to encode a polypeptide containing a TRP_2 tetratricopeptide repeat domain.

[0109] A low nitrogen tolerance-modulating polypeptide can contain a zf-AN1 domain characteristic of polypeptides belonging to the AN1-like Zinc finger domain protein family. The AN1-like Zinc finger domain was first identified as a zinc finger at the C-terminus of An1 a ubiquitin-like protein in *Xenopus laevis*. The following pattern describes the zinc finger: C-X2-C-X(9-12)-C-X(1-2)-C-X4-C-X2-H-X5-H-X-C, where X can be any amino acid, and numbers in brackets indicate the number of residues.

[0110] A low nitrogen tolerance-modulating polypeptide can contain a zf-A20 domain, which is characteristic of A20- (an inhibitor of cell death)-like zinc fingers. In animals, A20-like zinc fingers are believed to mediate self-association in A20. These fingers also mediate IL-1-induced NF-kappa B activation. SEQ ID NO: 246 sets forth the amino acid sequence of *Arabidopsis* clone, identified herein as Ceres ME04477 (SEQ ID NO:246), that is predicted to encode a polypeptide containing an AN1-like Zinc finger domain and zf-A20 domain.

[0111] A low nitrogen tolerance-modulating polypeptide can contain an Aa_trans domain, or transmembrane amino acid transporter domain, which is predicted to be characteristic of amino acid transporters and amino acid permeases. The domain is also present in SEQ ID NO:300, which sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME04507 (SEQ ID NO:300), that is predicted to encode a polypeptide containing an transmembrane amino acid transporter domain.

[0112] A low nitrogen tolerance-modulating polypeptide can contain an RNA recognition motif (as known as RRM_1, RRM, RBD, or RNP domain), which is characteristic of polypeptides belonging to the single strand RNA-binding protein superfamily. RRM proteins have a variety of RNA binding preferences and functions, and include heterogeneous nuclear ribonucleoproteins (hnRNPs), proteins implicated in

regulation of alternative splicing, protein components of small nuclear ribonucleoproteins, and proteins that regulate RNA stability and translation. The RRM in heterodimeric splicing factor U2 snRNP auxiliary factor (U2AF) appears to have two RRM-like domains with specialized features for protein recognition. The motif also appears in a few single stranded DNA binding proteins. The typical RRM consists of four anti-parallel beta-strands and two alpha-helices arranged in a beta-alpha-beta-beta-alpha-beta fold with side chains that stack with RNA bases. Specificity of RNA binding is determined by multiple contacts with surrounding amino acids. A third helix is present during RNA binding in some cases. The motif is also present in SEQ ID NO:368 and SEQ ID NO:1274, which set forth the amino acid sequences of *Arabidopsis* clones, identified herein as Ceres ME04753 (SEQ ID NO:368) and ME13151 (SEQ ID NO:1274) respectively, that are predicted to encode polypeptides containing an RNA recognition motif.

[0113] A low nitrogen tolerance-modulating polypeptide can contain an NTF2 domain characteristic of a nuclear transport factor 2 (NTF2) polypeptide. NTF2 is a homodimer of approximately 14kDa subunits which stimulates efficient nuclear import of a cargo protein. NTF2 binds to both RanGDP and FxFG repeat-containing nucleoporins. NTF2 binds to RanGDP sufficiently strongly for the complex to remain intact during transport through nucleopore complexes (NPCs), but the interaction between NTF2 and FxFG nucleoporins is much more transient, which would enable NTF2 to move through the NPC by hopping from one repeat to another. NTF2 folds into a cone with a deep hydrophobic cavity, the opening of which is surrounded by several negatively charged residues. RanGDP binds to NTF2 by inserting a conserved phenylalanine residue into the hydrophobic pocket of NTF2 and making electrostatic interactions with the conserved negatively charged residues that surround the cavity. A structurally similar domain appears in other nuclear import proteins. SEQ ID NO:1274, which sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME13151 (SEQ ID NO:1274), that is predicted to encode a polypeptide containing a NTF2 domain.

[0114] A low nitrogen tolerance-modulating polypeptide can contain a DUF1218 domain. SEQ ID NO:1274, which sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME04772 (SEQ ID NO:510), that is predicted to encode a polypeptide containing a DUF1218 domain.

[0115] A low nitrogen tolerance-modulating polypeptide can contain a Myb-like DNA-binding domain characteristic of polypeptides belonging to a protein family whose members contain the DNA binding domains from Myb proteins, as well as the SANT domain

family. SEQ ID NO:533, which sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME04909 (SEQ ID NO:533), that is predicted to encode a polypeptide containing a Myb-like DNA-binding domain.

[0116] A low nitrogen tolerance-modulating polypeptide can contain a FAD_binding_4 domain. This domain is predicted to be characteristic of polypeptides belonging to a family of enzymes that use FAD (flavin adenine dinucleotide) as a co-factor, most of the enzymes are similar to oxygen oxidoreductase, containing a covalently bound FAD group which is attached to a histidine via an 8-alpha-(N3-histidyl)-riboflavin linkage.

[0117] A low nitrogen tolerance-modulating polypeptide can contain a BBE domain, which is predicted to be characteristic of a berberine bridge and berberine bridge-like enzyme. BBE enzymes are typically involved in the biosynthesis of numerous isoquinoline alkaloids. They catalyse the transformation of the N-methyl group of (S)-reticuline into the C-8 berberine bridge carbon of (S)-scoulerine. SEQ ID NO:558 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME05194 (SEQ ID NO:558), that is predicted to encode a polypeptide containing an FAD_binding_4 domain and a BBE domain.

[0118] A low nitrogen tolerance-modulating polypeptide can contain a prefoldin (PFD) domain characteristic of polypeptides belonging to the prefoldin subunit family. Prefoldin (PFD) is a chaperone that typically interacts with type II chaperonins, hetero-oligomers lacking an obligate co-chaperonin that are found in eukaryotes (chaperonin-containing T-complex polypeptide-1 (CCT)) and archaea. Eukaryotic PFD can typically bind both actin and tubulin co-translationally. The chaperone can then delivers the target protein to CCT, interacting with the chaperonin through the tips of the coiled coils. SEQ ID NO:593 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME05267 (SEQ ID NO:593), that is predicted to encode a polypeptide containing a prefoldin domain.

[0119] A low nitrogen tolerance-modulating polypeptide can contain an HR-lesion domain characteristic of polypeptides belonging to a family of plant proteins can be associated with the hypersensitive response (HR) pathway of defense against plant pathogens. The domain is also present in SEQ ID NO: 646, which sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME05341 (SEQ ID NO: 646), that is predicted to encode a polypeptide containing an HR-lesion domain.

[0120] A low nitrogen tolerance-modulating polypeptide can contain a DUF538 domain. SEQ ID NO:687 sets forth the amino acid sequence of an *Arabidopsis* clone,

identified herein as Ceres ME05392 (SEQ ID NO:687), that is predicted to encode a polypeptide containing a DUF538 domain.

[0121] A low nitrogen tolerance-modulating polypeptide can contain a zinc finger C-x8-C-x5-C-x3-H type domain (zf-CCCH), which is characteristic of polypeptides belonging to the zinc finger protein superfamily. Members of zinc finger domains proteins are thought to be involved in DNA-binding, and exist as different types. Proteins containing zinc finger domains of the C-x8-C-x5-C-x3-H type include zinc finger proteins from eukaryotes involved in cell cycle or growth phase-related regulation. It has been shown that different CCCH zinc finger proteins interact with the 3' untranslated region of various mRNA. SEQ ID NO:792 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME07344 (SEQ ID NO:792), that is predicted to encode a polypeptide containing a zf-CCCH domain.

[0122] A low nitrogen tolerance-modulating polypeptide can contain a DUF246 domain. SEQ ID NO:828 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME08464 (SEQ ID NO:828), that is predicted to encode a polypeptide containing a DUF246 domain.

[0123] A low nitrogen tolerance-modulating polypeptide can contain a C2 domain. The C2 domain is a Ca2+-dependent membrane-targeting module found in many cellular proteins involved in signal transduction or membrane trafficking. C2 domains are unique among membrane targeting domains in that they typically show wide range of lipid selectivity for the major components of cell membranes, including phosphatidylserine and phosphatidylcholine. SEQ ID NO:982 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME12970 (SEQ ID NO:982), that is predicted to encode a polypeptide containing an C2 domain.

[0124] A low nitrogen tolerance-modulating polypeptide can contain a Cpn60_TCP1 domain characteristic of polypeptides belonging to the TCP-1/cpn60 chaperonin family. This family includes members from the HSP60 chaperone family and the TCP-1 (T-complex protein) family. Chaperonins, a subfamily of molecular chaperones, are typically essential for the correct folding and assembly of polypeptides into oligomeric structures. Chaperonins are typically found in abundance in prokaryotes, chloroplasts and mitochondria. They are typically required for normal cell growth, and are stress-induced, acting to stabilize or protect disassembled polypeptides under heat-shock conditions. SEQ ID NO: 1054 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME13021 (SEQ ID NO: 1054), that is predicted to encode a polypeptide containing a Cpn60_TCP1 domain.

[0125] A low nitrogen tolerance-modulating polypeptide can contain a zf-C2H2 domain characteristic of a C2H2 zinc finger domain polypeptide. Zinc finger domains are nucleic acid-binding protein structures composed of 25 to 30 amino-acid residues including 2 conserved Cys and 2 conserved His residues in a C-2-C-12-H-3-H type motif. The 12 residues separating the second Cys and the first His are mainly polar and basic, implicating this region in particular in nucleic acid binding. They have the ability to bind to both RNA and DNA, and it has been suggested that the zinc finger may thus represent the original nucleic acid binding protein. It has also been suggested that a Zn-centered domain could be used in a protein interaction, *e.g.* in protein kinase C. Many classes of zinc fingers are characterized according to the number and positions of the histidine and cysteine residues involved in the zinc atom coordination. In C2H2 zinc finger class, the first pair of zinc coordinating residues are cysteines, while the second pair are histidines. The motif is also present in SEQ ID NO:1116, which sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME13087 (SEQ ID NO:1116), that is predicted to encode a polypeptide containing a zf-C2H2 domain.

[0126] A low nitrogen tolerance-modulating polypeptide can contain a zein domain characteristic of polypeptides belonging to the zein family of seed storage proteins. SEQ ID NO:1159, which sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME13107 (SEQ ID NO: 1159), that is predicted to encode a polypeptide containing a zein domain.

[0127] A low nitrogen tolerance-modulating polypeptide can contain a snf7 domain characteristic of polypeptides belonging to a family of eukaryotic proteins related to yeast SNF7. SEQ ID NO:1185 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME13110 (SEQ ID NO:1185), that is predicted to encode a polypeptide containing a snf7 domain.

[0128] A low nitrogen tolerance-modulating polypeptide can contain an HhH-GPD domain characteristic of polypeptides belonging to the HhH-GPD base excision DNA repair protein superfamily. Members of the HhH-GPD base excision DNA repair protein superfamily contain helix-hairpin-helix and Gly/Pro rich loop followed by a conserved aspartate. This domain is found in a diverse range of structurally related DNA repair proteins. The domain is also present in SEQ ID NO:1194 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME13125 (SEQ ID NO:1194), that is predicted to encode a polypeptide containing an HhH-GPD domain.

[0129] A low nitrogen tolerance-modulating polypeptide can contain an Arf domain characteristic of polypeptides belonging to the ADP-ribosylation factor family. The small ADP ribosylation factor (Arf) GTP-binding proteins are major regulators of vesicle biogenesis in intracellular traffic. They are the founding members of a growing family that includes Arl (Arf-like), Arp (Arf-related proteins) and the remotely related Sar (Secretion-associated and Ras-related) proteins. Arf proteins cycle between inactive GDP-bound and active GTP-bound forms that bind selectively to effectors. The classical structural GDP/GTP switch is characterized by conformational changes at the so-called switch 1 and switch 2 regions, which bind tightly to the gamma-phosphate of GTP but poorly or not at all to the GDP nucleotide. Structural studies of Arf1 and Arf6 have revealed that although these proteins feature the switch 1 and 2 conformational changes, they depart from other small GTP-binding proteins in that they use an additional, unique switch to propagate structural information from one side of the protein to the other. The GDP/GTP structural cycles of human Arf1 and Arf6 feature a unique conformational change that affects the beta2beta3 strands connecting switch 1 and switch 2 (interswitch) and also the amphipathic helical N-terminus. SEQ ID NO: 1210 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME13149 (SEQ ID NO:1210), that is predicted to encode a polypeptide containing an Arf domain.

[0130] A low nitrogen tolerance-modulating polypeptide can contain a Pyridoxal_deC domain characteristic of pyridoxal-dependent decarboxylase polypeptide. Pyridoxal-dependent decarboxylases typically share regions of sequence similarity, particularly in the vicinity of a conserved lysine residue, which provides the attachment site for the pyridoxal-phosphate (PLP) group. Pyridoxal phosphate is the active form of vitamin B6 (pyridoxine or pyridoxal). PLP is a versatile catalyst, acting as a coenzyme in a multitude of reactions, including decarboxylation, deamination and transamination. PLP-dependent enzymes, including pyridoxal-dependent decarboxylases, are involved in the biosynthesis of amino acids and amino acid-derived metabolites, but they are also found in the biosynthetic pathways of amino sugars and in the synthesis or catabolism of neurotransmitter. SEQ ID NO:1302 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME13153 (SEQ ID NO:1302), that is predicted to encode a polypeptide containing a Pyridoxal_deC domain.

[0131] A low nitrogen tolerance-modulating polypeptide can contain a Cyclin_C domain, which is characteristic to the C-terminal domain of polypeptides belonging to the Cyclin family. Cyclins are eukaryotic proteins that play an active role in controlling nuclear

cell division cycles, and regulate cyclin dependent kinases (CDKs). Cyclins, together with the p34 (cdc2) or cdk2 kinases, form the Maturation Promoting Factor (MPF). There are two main groups of cyclins, G1/S cyclins, which play a role in the control of the cell cycle at the G1/S (start) transition, and G2/M cyclins, which play a role in the control of the cell cycle at the G2/M (mitosis) transition. G2/M cyclins accumulate steadily during G2 and are abruptly destroyed as cells exit from mitosis (at the end of the M-phase). Cyclins typically contain two domains of similar all-alpha fold, of which this family corresponds with the C-terminal domain.

[0132] A low nitrogen tolerance-modulating polypeptide can contain a Cyclin_N domain, which defines the N-terminal domain of polypeptides belonging to the Cyclin family. SEQ ID NO: 1342 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME13177 (SEQ ID NO: 1342), that is predicted to encode a polypeptide containing a Cyclin_C domain and a Cyclin_N domain

[0133] A low nitrogen tolerance-modulating polypeptide can contain a DUF1442 domain. SEQ ID NO:1463, which sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME16546 (SEQ ID NO:1463), that is predicted to encode a polypeptide containing a DUF1442 domain.

[0134] A low nitrogen tolerance-modulating polypeptide can contain an HLH domain characteristic of polypeptides belonging to the Helix-loop-helix DNA-binding domain superfamily. Basic helix-loop-helix proteins (bHLH) are a group of eukaryotic transcription factors that can exert a determinative influence in a variety of developmental pathways. These transcription factors are characterized by a conserved bHLH domain that mediates specific dimerization. They can facilitate the conversion of inactive monomers to trans-activating dimers at appropriate stages of development. Members of this superfamily can be classified into discrete categories according to dimerization, DNA binding and expression characteristics. SEQ ID NO:1537 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME18275 (SEQ ID NO:1537), that is predicted to encode a polypeptide containing an HLH domain.

[0135] A low nitrogen tolerance-modulating polypeptide can contain a CRAL_TRIO domain characteristic of the C-terminal of retinaldehyde/retinal-binding protein family. In animals, retinaldehyde/retinal-binding proteins may be functional components of the visual cycle. Cellular retinaldehyde-binding protein (CRALBP) may function as a substrate carrier protein that modulates interaction of these retinoids with visual cycle enzymes. The multidomain protein Trio can bind the LAR transmembrane tyrosine phosphatase, contains a

protein kinase domain, and has separate rac-specific and rho-specific guanine nucleotide exchange factor domains. Trio is a multifunctional protein that can integrate and amplify signals involved in coordinating actin remodeling, which is necessary for cell migration and growth. Other members of the family are transfer proteins that include, guanine nucleotide exchange factor that may function as an effector of RAC1, phosphatidylinositol/phosphatidylcholine transfer protein that is required for the transport of secretory proteins from the Golgi complex and alpha-tocopherol transfer protein that enhances the transfer of the ligand between separate membranes.

[0136] A low nitrogen tolerance-modulating polypeptide can contain a CRAL_TRIO_N which defines the N-terminal of retinaldehyde/retinal-binding protein family.

[0137] A low nitrogen tolerance-modulating polypeptide can contain an EMP24_GP25L domain characteristic of polypeptides belonging to the emp24/gp25L/p24 family/GOLD gene family. Members of this family are implicated in bringing cargo forward from the ER and binding to coat proteins by their cytoplasmic domains. This domain corresponds closely to the beta-strand rich GOLD domain. The GOLD domain is often found combined with lipid- or membrane-association domains. p24 proteins are major membrane components of COPI- and COPII-coated vesicles and are implicated in cargo selectivity of ER to Golgi transport. Multiple members of the p24 family are found in all eukaryotes, from yeast to mammals. Members of the p24 family are type I membrane proteins with a signal peptide at the amino terminus, a lumenal coiled-coil (extracytosolic) domain, a single transmembrane domain with conserved amino acids, and a short cytoplasmic tail. They may be grouped into at least three subfamilies based on primary sequence. One subfamily comprises yeast Emp24p and mammalian p24A. Another subfamily comprises yeast Erv25p and mammalian Tmp21, and the third subfamily comprises mammalian gp25L proteins. SEQ ID NO:1554 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME18924 (SEQ ID NO:1554), that is predicted to encode a polypeptide containing a CRAL_TRIO domain, a CRAL_TRIO_N domain, and a EMP24_GP25L domain.

[0138] A low nitrogen tolerance-modulating polypeptide can contain a Pyrophosphatase domain, which is predicted to be characteristic of an inorganic pyrophosphatase (PPase). PPase is the enzyme responsible for the hydrolysis of pyrophosphate (PPi) which is formed principally as the product of the many biosynthetic reactions that utilize ATP. PPases may require the presence of divalent metal cations, with magnesium conferring the highest activity. Among other residues, a lysine has been

postulated to be part of or close to the active site. The sequences of PPases share some regions of similarities, among which is a region that contains three conserved aspartates that are involved in the binding of cations. SEQ ID NO:1577 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME19182 (SEQ ID NO:1577), that is predicted to encode a polypeptide containing a Pyrophosphatase domain.

[0139] A low nitrogen tolerance-modulating polypeptide can contain a bZIP_1 domain characteristic of polypeptides belonging to the superfamily of basic ZIP transcription factors. Members of the eukaryotic bZIP transcription factor superfamily contain a basic region mediating sequence-specific DNA-binding followed by a leucine zipper region required for dimerization. SEQ ID NO: 1437 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres ME20628 (SEQ ID NO: 1437), that is predicted to encode a polypeptide containing a bZIP_1 domain.

B. Functional Homologs Identified by Reciprocal BLAST

[0140] In some embodiments, one or more functional homologs of a reference low nitrogen tolerance-modulating polypeptide defined by one or more of the Pfam descriptions indicated above are suitable for use as low nitrogen tolerance-modulating polypeptides. A functional homolog is a polypeptide that has sequence similarity to a reference polypeptide, and that carries out one or more of the biochemical or physiological function(s) of the reference polypeptide. A functional homolog and the reference polypeptide may be natural occurring polypeptides, and the sequence similarity may be due to convergent or divergent evolutionary events. As such, functional homologs are sometimes designated in the literature as homologs, or orthologs, or paralogs. Variants of a naturally occurring functional homolog, such as polypeptides encoded by mutants of a wild type coding sequence, may themselves be functional homologs. Functional homologs can also be created via site-directed mutagenesis of the coding sequence for a low nitrogen tolerance-modulating polypeptide, or by combining domains from the coding sequences for different naturally-occurring low nitrogen tolerance-modulating polypeptides ("domain swapping"). The term "functional homolog" is sometimes applied to the nucleic acid that encodes a functionally homologous polypeptide.

[0141] Functional homologs can be identified by analysis of nucleotide and polypeptide sequence alignments. For example, performing a query on a database of nucleotide or polypeptide sequences can identify homologs of low nitrogen tolerance-modulating polypeptides. Sequence analysis can involve BLAST, Reciprocal BLAST, or PSI-BLAST analysis of nonredundant databases using a low nitrogen tolerance-modulating

polypeptide amino acid sequence as the reference sequence. Amino acid sequence is, in some instances, deduced from the nucleotide sequence. Those polypeptides in the database that have greater than 20% sequence identity are candidates for further evaluation for suitability as a low nitrogen tolerance-modulating polypeptide. Amino acid sequence similarity allows for conservative amino acid substitutions, such as substitution of one hydrophobic residue for another or substitution of one polar residue for another. If desired, manual inspection of such candidates can be carried out in order to narrow the number of candidates to be further evaluated. Manual inspection can be performed by selecting those candidates that appear to have domains present in low nitrogen tolerance-modulating polypeptides, *e.g.*, conserved functional domains.

[0142] Conserved regions can be identified by locating a region within the primary amino acid sequence of a low nitrogen tolerance-modulating polypeptide that is a repeated sequence, forms some secondary structure (*e.g.*, helices and beta sheets), establishes positively or negatively charged domains, or represents a protein motif or domain. *See*, *e.g.*, the Pfam web site describing consensus sequences for a variety of protein motifs and domains on the World Wide Web at sanger.ac.uk/Software/Pfam/ and pfam.janelia.org/. A description of the information included at the Pfam database is described in Sonnhammer *et al.* (1998) *Nucl. Acids Res.*, 26:320-322; Sonnhammer *et al.* (1997) *Proteins*, 28:405-420; and Bateman *et al.* (1999) *Nucl. Acids Res.*, 27:260-262. Conserved regions also can be determined by aligning sequences of the same or related polypeptides from closely related species. Closely related species preferably are from the same family. In some embodiments, alignment of sequences from two different species is adequate.

[0143] Typically, polypeptides that exhibit at least about 40% amino acid sequence identity are useful to identify conserved regions. Conserved regions of related polypeptides exhibit at least 20% amino acid sequence identity (*e.g.*, at least 50%, at least 60%, at least 70%, at least 80%, or at least 90% amino acid sequence identity). In some embodiments, a conserved region exhibits at least 92%, 94%, 96%, 98%, or 99% amino acid sequence identity.

[0144] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:3 are provided in Figure 1 and in the Sequence Listing. Such functional homologs include SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:36, SEQ ID

NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, and SEQ ID NO:47. In some cases, a functional homolog of SEQ ID NO:3 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:3.

[0145] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:49 are provided in Figure 2 and in the Sequence Listing. Such functional homologs include SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, and SEQ ID NO:75. In some cases, a functional homolog of SEQ ID NO:49 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:49.

[0146] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:77 are provided in Figure 3 and in the Sequence Listing. Such functional homologs include SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:95, and CeresAnnot: 839064 (SEQ ID NO:1479). In some cases, a functional homolog of SEQ ID NO:77 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:77.

[0147] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:100 are provided in Figure 4 and in the Sequence Listing. Such functional homologs include SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, and SEQ ID NO:150. In some cases, a functional homolog of SEQ ID NO:100 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%,

95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:100.

[0148] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:152 are provided in Figure 5 and in the Sequence Listing. Such functional homologs include SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, and SEQ ID NO:164. In some cases, a functional homolog of SEQ ID NO:152 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:152.

[0149] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:166 are provided in Figure 6 and in the Sequence Listing. Such functional homologs include SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, and SEQ ID NO:184. In some cases, a functional homolog of SEQ ID NO:166 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:166.

[0150] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:186 are provided in Figure 7 and in the Sequence Listing. Such functional homologs include SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, and SEQ ID NO:206. In some cases, a functional homolog of SEQ ID NO:186 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:186.

[0151] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:208 are provided in Figure 8 and in the Sequence Listing. Such functional homologs include SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:214, and SEQ ID NO:216. In some cases, a functional homolog of SEQ ID NO:208 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:208.

[0152] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:218 are provided in Figure 9 and in the Sequence Listing. Such functional homologs include SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:1039, SEQ ID NO:1049, and SEQ ID NO:1052. In some cases, a functional homolog of SEQ ID NO:218 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:218.

[0153] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:234 are provided in Figure 10 and in the Sequence Listing. Such functional homologs include SEQ ID NO:236, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, and SEQ ID NO:244. In some cases, a functional homolog of SEQ ID NO:234 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:234.

[0154] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:246 are provided in Figure 11 and in the Sequence Listing. Such functional homologs include SEQ ID NO:248, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:262, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:268, SEQ ID NO:270, SEQ ID NO:272, SEQ ID NO:274, SEQ ID NO:276, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID NO:296, and SEQ ID NO:298. In some cases, a functional homolog of SEQ ID NO:246 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:246.

[0155] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:300 are provided in Figure 12 and in the Sequence Listing. Such functional homologs include SEQ ID NO:302, SEQ ID NO:304, SEQ ID NO:306, SEQ ID NO:308, SEQ ID NO:310, SEQ ID NO:312, SEQ ID NO:314, SEQ ID NO:316, SEQ ID NO:318, SEQ ID NO:319, SEQ ID NO:320, SEQ ID NO:321, SEQ ID NO:322, SEQ ID

NO:323, SEQ ID NO:325, SEQ ID NO:327, and SEQ ID NO:329. In some cases, a functional homolog of SEQ ID NO:300 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:300.

[0156] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:332 are provided in Figure 13 and in the Sequence Listing. Such functional homologs include SEQ ID NO:332, SEQ ID NO:334, SEQ ID NO:335, SEQ ID NO:336, SEQ ID NO:338, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:342, SEQ ID NO:343, SEQ ID NO:344, SEQ ID NO:345, SEQ ID NO:346, SEQ ID NO:347, SEQ ID NO:348, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:352, SEQ ID NO:353, SEQ ID NO:354, SEQ ID NO:355, SEQ ID NO:356, SEQ ID NO:357, SEQ ID NO:358, SEQ ID NO:359, SEQ ID NO:360, SEQ ID NO:362, SEQ ID NO:363, SEQ ID NO:364, SEQ ID NO:365, SEQ ID NO:366, SEQ ID NO:2541, SEQ ID NO:2542, SEQ ID NO:2543, SEQ ID NO:2544, SEQ ID NO:2546, SEQ ID NO:2548, SEQ ID NO:2549, SEQ ID NO:2550, SEQ ID NO:2551, SEQ ID NO:2552, and SEQ ID NO:2553. In some cases, a functional homolog of SEQ ID NO:332 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:332.

[0157] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:368 are provided in Figure 14 and in the Sequence Listing. Such functional homologs include SEQ ID NO:369, SEQ ID NO:370, SEQ ID NO:371, SEQ ID NO:372, SEQ ID NO:373, SEQ ID NO:374, SEQ ID NO:376, SEQ ID NO:378, SEQ ID NO:380, SEQ ID NO:382, SEQ ID NO:384, SEQ ID NO:386, SEQ ID NO:388, SEQ ID NO:390, SEQ ID NO:392, SEQ ID NO:394, SEQ ID NO:396, SEQ ID NO:398, SEQ ID NO:399, SEQ ID NO:401, SEQ ID NO:403, SEQ ID NO:404, SEQ ID NO:406, SEQ ID NO:408, SEQ ID NO:410, SEQ ID NO:412, SEQ ID NO:414, SEQ ID NO:416, SEQ ID NO:418, SEQ ID NO:419, SEQ ID NO:420, SEQ ID NO:422, SEQ ID NO:423, SEQ ID NO:425, SEQ ID NO:427, SEQ ID NO:428, SEQ ID NO:430, SEQ ID NO:432, SEQ ID NO:433, SEQ ID NO:434, SEQ ID NO:435, SEQ ID NO:436, SEQ ID NO:437, SEQ ID NO:438, SEQ ID NO:439, SEQ ID NO:440, SEQ ID NO:441, SEQ ID NO:444, SEQ ID NO:445, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:449, SEQ ID NO:450, SEQ ID NO:451, SEQ ID NO:452, SEQ ID NO:453, SEQ ID NO:454, SEQ ID NO:455, SEQ ID NO:456, SEQ ID NO:458, SEQ ID NO:459, SEQ ID NO:461, SEQ ID

NO:463, SEQ ID NO:465, SEQ ID NO:467, SEQ ID NO:469, SEQ ID NO:471, SEQ ID NO:473, SEQ ID NO:474, SEQ ID NO:475, SEQ ID NO:477, SEQ ID NO:479, SEQ ID NO:481, SEQ ID NO:483, SEQ ID NO:485, SEQ ID NO:487, SEQ ID NO:488, SEQ ID NO:489, SEQ ID NO:490, SEQ ID NO:491, SEQ ID NO:492, SEQ ID NO:494, SEQ ID NO:495, SEQ ID NO:496, SEQ ID NO:497, SEQ ID NO:498, SEQ ID NO:499, SEQ ID NO:500, SEQ ID NO:501, SEQ ID NO:502, SEQ ID NO:504, SEQ ID NO:505, SEQ ID NO:506, SEQ ID NO:507, and SEQ ID NO:508. In some cases, a functional homolog of SEQ ID NO:368 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:368.

[0158] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:510 are provided in Figure 15 and in the Sequence Listing. Such functional homologs include SEQ ID NO:511, SEQ ID NO:513, SEQ ID NO:515, SEQ ID NO:517, SEQ ID NO:521, SEQ ID NO:523, SEQ ID NO:525, SEQ ID NO:527, SEQ ID NO:529, SEQ ID NO:530, and SEQ ID NO:531. In some cases, a functional homolog of SEQ ID NO:510 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:510.

[0159] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:533 are provided in Figure 16 and in the Sequence Listing. Such functional homologs include SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:541, SEQ ID NO:542, SEQ ID NO:543, SEQ ID NO:544, SEQ ID NO:545, SEQ ID NO:546, SEQ ID NO:547, SEQ ID NO:548, SEQ ID NO:550, SEQ ID NO:552, SEQ ID NO:553, and SEQ ID NO:554. In some cases, a functional homolog of SEQ ID NO:533 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:533.

[0160] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:558 are provided in Figure 17 and in the Sequence Listing. Such functional homologs include SEQ ID NO:559, SEQ ID NO:560, SEQ ID NO:561, SEQ ID NO:562, SEQ ID NO:563, SEQ ID NO:564, SEQ ID NO:565, SEQ ID NO:566, SEQ ID NO:567, SEQ ID NO:569, SEQ ID NO:571, SEQ ID NO:572, SEQ ID NO:573, SEQ ID NO:575, SEQ ID NO:576, SEQ ID NO:577, SEQ ID NO:578, SEQ ID NO:579, SEQ ID NO:581, SEQ ID NO:583, SEQ ID NO:584, SEQ ID NO:585, SEQ ID NO:586, SEQ ID

NO:588, SEQ ID NO:589, SEQ ID NO:590, and SEQ ID NO:591. In some cases, a functional homolog of SEQ ID NO:558 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:558.

[0161] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:593 are provided in Figure 18 and in the Sequence Listing. Such functional homologs include SEQ ID NO:595, SEQ ID NO:597, SEQ ID NO:599, SEQ ID NO:601, SEQ ID NO:603, SEQ ID NO:605, SEQ ID NO:607, SEQ ID NO:609, SEQ ID NO:610, and SEQ ID NO:611. In some cases, a functional homolog of SEQ ID NO:593 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:593.

[0162] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:613 are provided in Figure 19 and in the Sequence Listing. Such functional homologs include SEQ ID NO:615, SEQ ID NO:617, SEQ ID NO:618, SEQ ID NO:620, SEQ ID NO:622, SEQ ID NO:624, SEQ ID NO:626, SEQ ID NO:628, SEQ ID NO:630, SEQ ID NO:632, SEQ ID NO:634, SEQ ID NO:636, SEQ ID NO:638, SEQ ID NO:640, SEQ ID NO:642, SEQ ID NO:643, and SEQ ID NO:644. In some cases, a functional homolog of SEQ ID NO:613 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:613.

[0163] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:646 are provided in Figure 20 and in the Sequence Listing. Such functional homologs include SEQ ID NO:648, SEQ ID NO:650, SEQ ID NO:652, SEQ ID NO:654, SEQ ID NO:656, SEQ ID NO:658, SEQ ID NO:660, SEQ ID NO:662, SEQ ID NO:664, SEQ ID NO:666, SEQ ID NO:668, SEQ ID NO:670, SEQ ID NO:672, SEQ ID NO:674, SEQ ID NO:676, SEQ ID NO:678, SEQ ID NO:679, SEQ ID NO:680, SEQ ID NO:681, SEQ ID NO:682, SEQ ID NO:683, and SEQ ID NO:685. In some cases, a functional homolog of SEQ ID NO:646 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:646.

[0164] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:687 are provided in Figure 21 and in the Sequence Listing. Such functional homologs include SEQ ID NO:689, SEQ ID NO:691, SEQ ID NO:693, SEQ ID NO:694, SEQ ID NO:696, SEQ ID NO:697, SEQ ID NO:699, SEQ ID NO:701, SEQ ID NO:703, SEQ ID NO:705, SEQ ID NO:706, SEQ ID NO:708, SEQ ID NO:710, SEQ ID NO:712, SEQ ID NO:714, SEQ ID NO:716, SEQ ID NO:718, SEQ ID NO:720, SEQ ID NO:721, SEQ ID NO:722, SEQ ID NO:723, SEQ ID NO:724, SEQ ID NO:725, SEQ ID NO:726, SEQ ID NO:727, and SEQ ID NO:728. In some cases, a functional homolog of SEQ ID NO:687 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:687.

[0165] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:730 are provided in Figure 22 and in the Sequence Listing. Such functional homologs include SEQ ID NO:732, SEQ ID NO:733, SEQ ID NO:735, SEQ ID NO:737, SEQ ID NO:738, and SEQ ID NO:742. In some cases, a functional homolog of SEQ ID NO:730 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:730.

[0166] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:746 are provided in Figure 23 and in the Sequence Listing. Such functional homologs include SEQ ID NO:748, SEQ ID NO:750, SEQ ID NO:751, SEQ ID NO:753, SEQ ID NO:755, SEQ ID NO:757, SEQ ID NO:758, SEQ ID NO:760, SEQ ID NO:761, SEQ ID NO:762, SEQ ID NO:763, SEQ ID NO:765, and SEQ ID NO:767. In some cases, a functional homolog of SEQ ID NO:746 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:746.

[0167] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:769 are provided in Figure 24 and in the Sequence Listing. Such functional homologs include SEQ ID NO:771, SEQ ID NO:773, SEQ ID NO:775, SEQ ID NO:777, SEQ ID NO:779, SEQ ID NO:781, SEQ ID NO:783, SEQ ID NO:785, SEQ ID NO:787, SEQ ID NO:789, and SEQ ID NO:790. In some cases, a functional homolog of SEQ ID NO:769 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%,

52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:769.

[0168] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:792 are provided in Figure 25 and in the Sequence Listing. Such functional homologs include SEQ ID NO:794, SEQ ID NO:796, SEQ ID NO:798, SEQ ID NO:799, SEQ ID NO:801, SEQ ID NO:803, SEQ ID NO:805, SEQ ID NO:807, SEQ ID NO:808, SEQ ID NO:810, SEQ ID NO:812, SEQ ID NO:814, SEQ ID NO:816, SEQ ID NO:818, SEQ ID NO:819, SEQ ID NO:820, SEQ ID NO:821, and SEQ ID NO:822. In some cases, a functional homolog of SEQ ID NO:792 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:792.

[0169] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:824 are provided in Figure 26 and in the Sequence Listing. Such functional homologs include, but not limited to, SEQ ID NO:826, SEQ ID NO:1696, SEQ ID NO:1698, SEQ ID NO:1700, SEQ ID NO:1702, SEQ ID NO:1704, SEQ ID NO:1706, SEQ ID NO:1708, SEQ ID NO:1710, SEQ ID NO:1711, SEQ ID NO:1713, SEQ ID NO:1714, SEQ ID NO:1715, and SEQ ID NO:1716. In some cases, a functional homolog of SEQ ID NO:824 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:824.

[0170] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:828 are provided in Figure 27 and in the Sequence Listing. Such functional homologs include SEQ ID NO:830, SEQ ID NO:832, SEQ ID NO:834, SEQ ID NO:836, SEQ ID NO:837, SEQ ID NO:838, SEQ ID NO:839, SEQ ID NO:840, SEQ ID NO:842, SEQ ID NO:844, SEQ ID NO:845, SEQ ID NO:846, SEQ ID NO:847, SEQ ID NO:848, SEQ ID NO:849, SEQ ID NO:850, and SEQ ID NO:851. In some cases, a functional homolog of SEQ ID NO:828 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:828.

[0171] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:855 are provided in Figure 28 and in the Sequence Listing. Such functional homologs include SEQ ID NO:856, SEQ ID NO:858, SEQ ID NO:860, SEQ ID

NO:862, SEQ ID NO:864, SEQ ID NO:866, SEQ ID NO:868, SEQ ID NO:870, SEQ ID NO:872, SEQ ID NO:874, SEQ ID NO:876, SEQ ID NO:878, SEQ ID NO:880, SEQ ID NO:882, SEQ ID NO:884, SEQ ID NO:885, SEQ ID NO:886, SEQ ID NO:887, SEQ ID NO:888, and SEQ ID NO:889. In some cases, a functional homolog of SEQ ID NO:855 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:855.

[0172] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:891 are provided in Figure 29 and in the Sequence Listing. Such functional homologs include SEQ ID NO:893, SEQ ID NO:894, SEQ ID NO:895, SEQ ID NO:896, SEQ ID NO:898, SEQ ID NO:900, SEQ ID NO:901, SEQ ID NO:902, SEQ ID NO:903, SEQ ID NO:904, SEQ ID NO:905, SEQ ID NO:907, SEQ ID NO:908, SEQ ID NO:909, SEQ ID NO:910, SEQ ID NO:911, SEQ ID NO:912, SEQ ID NO:913, SEQ ID NO:914, and SEQ ID NO:915. In some cases, a functional homolog of SEQ ID NO:891 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:891.

[0173] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:917 are provided in Figure 30 and in the Sequence Listing. Such functional homologs include SEQ ID NO:919, SEQ ID NO:921, SEQ ID NO:923, SEQ ID NO:925, SEQ ID NO:927, SEQ ID NO:929, SEQ ID NO:931, SEQ ID NO:933, SEQ ID NO:935, SEQ ID NO:937, SEQ ID NO:939, and SEQ ID NO:940. In some cases, a functional homolog of SEQ ID NO:917 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:917.

[0174] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:944 are provided in Figure 31 and in the Sequence Listing. Such functional homologs include SEQ ID NO:946, SEQ ID NO:947, SEQ ID NO:948, SEQ ID NO:950, SEQ ID NO:952, SEQ ID NO:954, SEQ ID NO:956, SEQ ID NO:958, SEQ ID NO:960, SEQ ID NO:962, SEQ ID NO:964, SEQ ID NO:966, SEQ ID NO:967, SEQ ID NO:968, SEQ ID NO:969, SEQ ID NO:970, SEQ ID NO:972, and SEQ ID NO:974. In some cases, a functional homolog of SEQ ID NO:944 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%,

95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:944.

[0175] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:976 are provided in Figure 32 and in the Sequence Listing. Such functional homologs include, but not limited to, SEQ ID NO:978 and SEQ ID NO:980. In some cases, a functional homolog of SEQ ID NO:976 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:976.

[0176] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:982 are provided in Figure 33 and in the Sequence Listing. Such functional homologs include SEQ ID NO:984, SEQ ID NO:985, SEQ ID NO:986, SEQ ID NO:987, SEQ ID NO:988, SEQ ID NO:989, SEQ ID NO:990, SEQ ID NO:991, SEQ ID NO:992, SEQ ID NO:993, SEQ ID NO:995, SEQ ID NO:996, SEQ ID NO:998, SEQ ID NO:1000, SEQ ID NO:1001, SEQ ID NO:1003, SEQ ID NO:1005, SEQ ID NO:1007, SEQ ID NO:1008, SEQ ID NO:1009, SEQ ID NO:1011, SEQ ID NO:1013, SEQ ID NO:1015, SEQ ID NO:1016, SEQ ID NO:1018, SEQ ID NO:1019, SEQ ID NO:1021, SEQ ID NO:1023, SEQ ID NO:1025, SEQ ID NO:1026, SEQ ID NO:1027, SEQ ID NO:1028, SEQ ID NO:1029, SEQ ID NO:1030, SEQ ID NO:1031, SEQ ID NO:1032, and SEQ ID NO:1033. In some cases, a functional homolog of SEQ ID NO:982 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:982.

[0177] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1054 are provided in Figure 34 and in the Sequence Listing. Such functional homologs include SEQ ID NO:1055, SEQ ID NO:1057, SEQ ID NO:1058, SEQ ID NO:1059, SEQ ID NO:1061, SEQ ID NO:1063, SEQ ID NO:1065, SEQ ID NO:1067, SEQ ID NO:1068, SEQ ID NO:1070, SEQ ID NO:1071, SEQ ID NO:1072, SEQ ID NO:1074, SEQ ID NO:1075, SEQ ID NO:1076, SEQ ID NO:1077, SEQ ID NO:1078, SEQ ID NO:1080, SEQ ID NO:1082, SEQ ID NO:1083, SEQ ID NO:1085, SEQ ID NO:1086, SEQ ID NO:1087, SEQ ID NO:1088, SEQ ID NO:1089, SEQ ID NO:1090, SEQ ID NO:1091, SEQ ID NO:1092, SEQ ID NO:1093, SEQ ID NO:1094, SEQ ID NO:1095, and SEQ ID NO:1097. In some cases, a functional homolog of SEQ ID NO:1054 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%,

70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1054.

[0178] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1099 are provided in Figure 35 and in the Sequence Listing. Such functional homologs include SEQ ID NO:1101, SEQ ID NO:1103, SEQ ID NO:1104, SEQ ID NO:1105, SEQ ID NO:1106, SEQ ID NO:1108, SEQ ID NO:1109, and SEQ ID NO:1110. In some cases, a functional homolog of SEQ ID NO:1099 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1099.

[0179] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1112 are provided in Figure 36 and in the Sequence Listing. Such functional homologs include SEQ ID NO:1113 and SEQ ID NO:1114. In some cases, a functional homolog of SEQ ID NO:1112 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1112.

[0180] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1116 are provided in Figure 37 and in the Sequence Listing. Such functional homologs include SEQ ID NO:1118, SEQ ID NO:1120, SEQ ID NO:1122, SEQ ID NO:1123, SEQ ID NO:1125, SEQ ID NO:1126, SEQ ID NO:1128, SEQ ID NO:1129, SEQ ID NO:1131, SEQ ID NO:1132, SEQ ID NO:1133, SEQ ID NO:1134, SEQ ID NO:1136, SEQ ID NO:1138, SEQ ID NO:1140, SEQ ID NO:1141, SEQ ID NO:1142, SEQ ID NO:1143, SEQ ID NO:1144, SEQ ID NO:1145, SEQ ID NO:1147, SEQ ID NO:1149, SEQ ID NO:1151, SEQ ID NO:1153, and SEQ ID NO:1155. In some cases, a functional homolog of SEQ ID NO:1116 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1116.

[0181] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1159 are provided in Figure 38 and in the Sequence Listing. Such functional homologs include SEQ ID NO:1161, SEQ ID NO:1162, SEQ ID NO:1163, and SEQ ID NO:1164. In some cases, a functional homolog of SEQ ID NO:1159 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%,

70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1159.

[0182] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1166 are provided in Figure 39 and in the Sequence Listing. Such functional homologs include SEQ ID NO:1167, SEQ ID NO:1169, SEQ ID NO:1171, SEQ ID NO:1173, SEQ ID NO:1175, SEQ ID NO:1177, SEQ ID NO:1179, SEQ ID NO:1180, SEQ ID NO:1182, and SEQ ID NO:1183. In some cases, a functional homolog of SEQ ID NO:1166 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1166.

[0183] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1185 are provided in Figure 40 and in the Sequence Listing. Such functional homologs include SEQ ID NO:1187, SEQ ID NO:1189, SEQ ID NO:1190, SEQ ID NO:1191, and SEQ ID NO:1192. In some cases, a functional homolog of SEQ ID NO:1185 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1185.

[0184] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1194 are provided in Figure 41 and in the Sequence Listing. Such functional homologs include SEQ ID NO:1196, SEQ ID NO:1198, SEQ ID NO:1200, SEQ ID NO:1202, SEQ ID NO:1203, SEQ ID NO:1204, SEQ ID NO:1205, SEQ ID NO:1206, SEQ ID NO:1207, and SEQ ID NO:1208. In some cases, a functional homolog of SEQ ID NO:1194 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1194.

[0185] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1210 are provided in Figure 42 and in the Sequence Listing. Such functional homologs include SEQ ID NO:1211, SEQ ID NO:1213, SEQ ID NO:1215, SEQ ID NO:1216, SEQ ID NO:1218, SEQ ID NO:1220, SEQ ID NO:1222, SEQ ID NO:1224, SEQ ID NO:1226, SEQ ID NO:1228, SEQ ID NO:1229, SEQ ID NO:1230, SEQ ID NO:1232, SEQ ID NO:1233, SEQ ID NO:1234, SEQ ID NO:1235, SEQ ID NO:1236, SEQ ID NO:1237, SEQ ID NO:1238, SEQ ID NO:1239, SEQ ID NO:1240, SEQ ID NO:1241, SEQ ID NO:1242, SEQ ID NO:1243, SEQ ID NO:1244, SEQ ID NO:1245, SEQ ID NO:1246, SEQ ID NO:1247, SEQ ID NO:1248, SEQ ID NO:1249, SEQ ID NO:1251, SEQ

ID NO:1253, SEQ ID NO:1255, SEQ ID NO:1257, SEQ ID NO:1259, SEQ ID NO:1261, SEQ ID NO:1263, SEQ ID NO:1264, SEQ ID NO:1265, SEQ ID NO:1266, SEQ ID NO:1267, SEQ ID NO:1268, SEQ ID NO:1269, SEQ ID NO:1270, SEQ ID NO:1271, and SEQ ID NO:1272. In some cases, a functional homolog of SEQ ID NO:1210 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1210.

[0186] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1274 are provided in Figure 43 and in the Sequence Listing. Such functional homologs include SEQ ID NO:1276, SEQ ID NO:1278, SEQ ID NO:1280, SEQ ID NO:1281, SEQ ID NO:1282, SEQ ID NO:1284, SEQ ID NO:1285, SEQ ID NO:1287, SEQ ID NO:1289, SEQ ID NO:1291, SEQ ID NO:1293, SEQ ID NO:1294, SEQ ID NO:1295, SEQ ID NO:1296, SEQ ID NO:1297, SEQ ID NO:1298, and SEQ ID NO:1300. In some cases, a functional homolog of SEQ ID NO:1274 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1274.

[0187] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1302 are provided in Figure 44 and in the Sequence Listing. Such functional homologs include SEQ ID NO:1303, SEQ ID NO:1305, SEQ ID NO:1307, SEQ ID NO:1309, SEQ ID NO:1311, SEQ ID NO:1312, SEQ ID NO:1313, SEQ ID NO:1314, SEQ ID NO:1315, SEQ ID NO:1317, SEQ ID NO:1318, SEQ ID NO:1319, SEQ ID NO:1320, SEQ ID NO:1321, SEQ ID NO:1322, SEQ ID NO:1323, SEQ ID NO:1324, SEQ ID NO:1325, SEQ ID NO:1326, SEQ ID NO:1327, SEQ ID NO:1328, SEQ ID NO:1330, SEQ ID NO:1331, SEQ ID NO:1333, SEQ ID NO:1334, SEQ ID NO:1335, SEQ ID NO:1336, SEQ ID NO:1337, SEQ ID NO:1338, SEQ ID NO:1339, and SEQ ID NO:1340. In some cases, a functional homolog of SEQ ID NO:1302 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1302.

[0188] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1342 are provided in Figure 45 and in the Sequence Listing. Such functional homologs include SEQ ID NO:1344, SEQ ID NO:1346, SEQ ID NO:1348, SEQ ID NO:1350, SEQ ID NO:1352, SEQ ID NO:1354, SEQ ID NO:1355, SEQ ID NO:1357,

SEQ ID NO:1358, SEQ ID NO:1360, SEQ ID NO:1361, SEQ ID NO:1362, SEQ ID NO:1363, SEQ ID NO:1364, SEQ ID NO:1366, SEQ ID NO:1367, SEQ ID NO:1369, SEQ ID NO:1370, SEQ ID NO:1371, SEQ ID NO:1372, SEQ ID NO:1373, SEQ ID NO:1374, SEQ ID NO:1375, SEQ ID NO:1376, SEQ ID NO:1377, SEQ ID NO:1378, SEQ ID NO:1379, SEQ ID NO:1380, SEQ ID NO:1381, SEQ ID NO:1382, and SEQ ID NO:1383. In some cases, a functional homolog of SEQ ID NO:1342 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1342.

[0189] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1385 are provided in Figure 46 and in the Sequence Listing. Such functional homologs include SEQ ID NO:1387, SEQ ID NO:1389, SEQ ID NO:1390, SEQ ID NO:1391, SEQ ID NO:1393, SEQ ID NO:1394, SEQ ID NO:1395, SEQ ID NO:1396, SEQ ID NO:1398, SEQ ID NO:1400, SEQ ID NO:1401, SEQ ID NO:1402, SEQ ID NO:1403, SEQ ID NO:1404, SEQ ID NO:1405, and SEQ ID NO:1407. In some cases, a functional homolog of SEQ ID NO:1385 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1385.

[0190] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1409 are provided in Figure 47 and in the Sequence Listing. Such functional homologs include SEQ ID NO:1411, SEQ ID NO:1413, SEQ ID NO:1415, SEQ ID NO:1417, SEQ ID NO:1418, SEQ ID NO:1419, SEQ ID NO:1421, SEQ ID NO:1423, SEQ ID NO:1424, SEQ ID NO:1425, and SEQ ID NO:1426. In some cases, a functional homolog of SEQ ID NO:1409 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1409.

[0191] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1428 are provided in Figure 48 and in the Sequence Listing. Such functional homologs include SEQ ID NO:1430, SEQ ID NO:1432, SEQ ID NO:1434, SEQ ID NO:1436, SEQ ID NO:1439, SEQ ID NO:1442, SEQ ID NO:1444, SEQ ID NO:1446, SEQ ID NO:1448, SEQ ID NO:1450, SEQ ID NO:1452, SEQ ID NO:1453, SEQ ID NO:1454, SEQ ID NO:1455, SEQ ID NO:1456, SEQ ID NO:1457, SEQ ID NO:1458, and SEQ ID NO:1459. In some cases, a functional homolog of SEQ ID NO:1428 has an amino

acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1428.

[0192] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1463 are provided in Figure 49 and in the Sequence Listing. Such functional homologs include SEQ ID NO:1465, SEQ ID NO:1467, SEQ ID NO:1469, SEQ ID NO:1471, SEQ ID NO:1473, SEQ ID NO:1474, SEQ ID NO:1475, SEQ ID NO:1476, and SEQ ID NO:1477. In some cases, a functional homolog of SEQ ID NO:1463 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1463.

[0193] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1491 are provided in Figure 50 and in the Sequence Listing. Such functional homologs include SEQ ID NO:1493, SEQ ID NO:1495, SEQ ID NO:1497, SEQ ID NO:1499, SEQ ID NO:1501, SEQ ID NO:1503, SEQ ID NO:1504, SEQ ID NO:1505, SEQ ID NO:1506, and SEQ ID NO:1508. In some cases, a functional homolog of SEQ ID NO:1491 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1491.

[0194] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1510 are provided in Figure 51 and in the Sequence Listing. Such functional homologs include SEQ ID NO:1512, SEQ ID NO:1514, SEQ ID NO:1516, SEQ ID NO:1518, SEQ ID NO:1520, SEQ ID NO:1522, and SEQ ID NO:1523. In some cases, a functional homolog of SEQ ID NO:1510 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1510.

[0195] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1525 are provided in Figure 52 and in the Sequence Listing. Such functional homologs include SEQ ID NO:1527, SEQ ID NO:1529, SEQ ID NO:1530, SEQ ID NO:1532, SEQ ID NO:1534, and SEQ ID NO:1535. In some cases, a functional homolog of SEQ ID NO:1525 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1525.

[0196] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1537 are provided in Figure 53 and in the Sequence Listing. Such functional homologs include SEQ ID NO:1539, SEQ ID NO:1540, SEQ ID NO:1541, SEQ ID NO:1543, SEQ ID NO:1545, SEQ ID NO:1547, SEQ ID NO:1548, SEQ ID NO:1550, SEQ ID NO:1552, SEQ ID NO:2386, SEQ ID NO:2388, SEQ ID NO:2390, SEQ ID NO:2391, and SEQ ID NO:2392. In some cases, a functional homolog of SEQ ID NO:1537 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1537.

[0197] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1554 are provided in Figure 54 and in the Sequence Listing. Such functional homologs include SEQ ID NO:1555, SEQ ID NO:1557, SEQ ID NO:1559, SEQ ID NO:1561, SEQ ID NO:1563, SEQ ID NO:1565, SEQ ID NO:1567, SEQ ID NO:1569, SEQ ID NO:1571, SEQ ID NO:1572, SEQ ID NO:1573, SEQ ID NO:1574, and SEQ ID NO:1575. In some cases, a functional homolog of SEQ ID NO:1554 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1554.

[0198] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1577 are provided in Figure 55 and in the Sequence Listing. Such functional homologs include SEQ ID NO:1035, SEQ ID NO:1036, SEQ ID NO:1037, SEQ ID NO:1040, SEQ ID NO:1041, SEQ ID NO:1043, SEQ ID NO:1044, SEQ ID NO:1046, SEQ ID NO:1047, SEQ ID NO:1048, SEQ ID NO:1050, SEQ ID NO:1440, SEQ ID NO:1480, SEQ ID NO:1481, SEQ ID NO:1482, SEQ ID NO:1483, SEQ ID NO:1484, SEQ ID NO:1485, SEQ ID NO:1486, SEQ ID NO:1487, SEQ ID NO:1488, SEQ ID NO:1578, SEQ ID NO:1580, SEQ ID NO:1582, SEQ ID NO:1584, SEQ ID NO:1586, SEQ ID NO:1588, SEQ ID NO:1590, SEQ ID NO:1592, SEQ ID NO:1594, SEQ ID NO:1596, SEQ ID NO:1598, SEQ ID NO:1599, SEQ ID NO:1601, SEQ ID NO:1602, SEQ ID NO:1605, SEQ ID NO:1607, SEQ ID NO:1608, SEQ ID NO:1609, SEQ ID NO:1611, SEQ ID NO:1613, SEQ ID NO:1615, SEQ ID NO:1617, SEQ ID NO:1619, SEQ ID NO:1621, SEQ ID NO:1622, SEQ ID NO:1623, SEQ ID NO:1624, SEQ ID NO:1625, SEQ ID NO:1627, SEQ ID NO:1629, SEQ ID NO:1631, SEQ ID NO:1633, SEQ ID NO:1635, SEQ ID NO:1637, SEQ ID NO:1639, SEQ ID NO:1643, SEQ ID NO:1645, SEQ ID NO:1648, SEQ ID NO:1649, SEQ ID NO:1651, and SEQ ID NO:1653. In some cases, a functional homolog

of SEQ ID NO:1577 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1577.

[0199] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1437 are provided in Figure 56 and in the Sequence Listing. Such functional homologs include SEQ ID NO:173, SEQ ID NO:212, SEQ ID NO:361, SEQ ID NO:421, SEQ ID NO:443, SEQ ID NO:740, SEQ ID NO:744, SEQ ID NO:942, and SEQ ID NO:1461. In some cases, a functional homolog of SEQ ID NO:1437 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1437.

[0200] Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:97 are provided in Figure 57 and in the Sequence Listing. Such functional homologs include SEQ ID NO:2010, SEQ ID NO:2011, SEQ ID NO:2013, SEQ ID NO:2015, SEQ ID NO:2017. In some cases, a functional homolog of SEQ ID NO:97 has an amino acid sequence with at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:97.

[0201] The identification of conserved regions in a low nitrogen tolerance-modulating polypeptide facilitates production of variants of low nitrogen tolerance-modulating polypeptides. Variants of low nitrogen tolerance-modulating polypeptides typically have 10 or fewer conservative amino acid substitutions within the primary amino acid sequence, *e.g.*, 7 or fewer conservative amino acid substitutions, 5 or fewer conservative amino acid substitutions, or between 1 and 5 conservative substitutions. A useful variant polypeptide can be constructed based on one of the alignments set forth in Figure 1-57 and/or homologs identified in the Sequence Listing. Such a polypeptide includes the conserved regions, arranged in the order depicted in the Figure from amino-terminal end to carboxy-terminal end. Such a polypeptide may also include zero, one, or more than one amino acid in positions marked by dashes. When no amino acids are present at positions marked by dashes, the length of such a polypeptide is the sum of the amino acid residues in all conserved regions. When amino acids are present at all positions marked by dashes, such a polypeptide has a length that is the sum of the amino acid residues in all conserved regions and all dashes.

C. Functional Homologs Identified by HMMER

[0202] In some embodiments, useful low nitrogen tolerance-modulating polypeptides include those that fit a Hidden Markov Model based on the polypeptides set forth in any one of Figures 1-57. A Hidden Markov Model (HMM) is a statistical model of a consensus sequence for a group of functional homologs. See, Durbin et al. (1998) *Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids*, Cambridge University Press, Cambridge, UK. An HMM is generated by the program HMMER 2.3.2 with default program parameters, using the sequences of the group of functional homologs as input. The multiple sequence alignment is generated by ProbCons (Do et al. (2005) Genome Res., 15(2):330-40) version 1.11 using a set of default parameters: -c, --consistency REPS of 2; -ir, --iterative-refinement REPS of 100; -pre, --pre-training REPS of 0. ProbCons is a public domain software program provided by Stanford University.

[0203] The default parameters for building an HMM (hmmbuild) are as follows: the default "architecture prior" (archpri) used by MAP architecture construction is 0.85, and the default cutoff threshold (idlevel) used to determine the effective sequence number is 0.62. HMMER 2.3.2 was released October 3, 2003 under a GNU general public license, and is available from various sources on the World Wide Web such as hmmer.janelia.org; hmmer.wustl.edu; and fr.com/hmmer232/. Hmmbuild outputs the model as a text file.

[0204] The HMM for a group of functional homologs can be used to determine the likelihood that a candidate low nitrogen tolerance-modulating polypeptide sequence is a better fit to that particular HMM than to a null HMM generated using a group of sequences that are not structurally or functionally related. The likelihood that a candidate polypeptide sequence is a better fit to an HMM than to a null HMM is indicated by the HMM bit score, a number generated when the candidate sequence is fitted to the HMM profile using the HMMER hmmsearch program. The following default parameters are used when running hmmsearch: the default E-value cutoff (E) is 10.0, the default bit score cutoff (T) is negative infinity, the default number of sequences in a database (Z) is the real number of sequences in the database, the default E-value cutoff for the per-domain ranked hit list (domE) is infinity, and the default bit score cutoff for the per-domain ranked hit list (domT) is negative infinity. A high HMM bit score indicates a greater likelihood that the candidate sequence carries out one or more of the biochemical or physiological function(s) of the polypeptides used to generate the HMM. A high HMM bit score is at least 20, and often is higher. Slight variations in the HMM bit score of a particular sequence can occur due to factors such as the order in which sequences are processed for alignment by multiple sequence alignment

algorithms such as the ProbCons program. Nevertheless, such HMM bit score variation is minor.

[0205] The low nitrogen tolerance-modulating polypeptides discussed below fit the indicated HMM with an HMM bit score greater than 20 (*e.g.*, greater than 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, or 500). In some embodiments, the HMM bit score of a low nitrogen tolerance-modulating polypeptide discussed below is about 50%, 60%, 70%, 80%, 90%, or 95% of the HMM bit score of a functional homolog provided the Sequence Listing of this application. In some embodiments, a low nitrogen tolerance-modulating polypeptide discussed below fits the indicated HMM with an HMM bit score greater than 20, and has a domain indicative of a low nitrogen tolerance-modulating polypeptide. In some embodiments, a low nitrogen tolerance-modulating polypeptide discussed below fits the indicated HMM with an HMM bit score greater than 20, and has 70% or greater sequence identity (*e.g.*, 75%, 80%, 85%, 90%, 95%, or 100% sequence identity) to an amino acid sequence shown in any one of Figures 1-57.

[0206] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 800 when fitted to an HMM generated from the amino acid sequences set forth in Figure 1 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, and SEQ ID NO:47.

[0207] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 150 when fitted to an HMM generated from the amino acid sequences set forth in Figure 2 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, and SEQ ID NO:75.

[0208] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 540 when fitted to an HMM generated from the amino acid sequences set forth in Figure 3 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ

ID NO:84, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:95, and SEQ ID NO:1479.

[0209] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 210 when fitted to an HMM generated from the amino acid sequences set forth in Figure 4 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, and SEQ ID NO:150.

[0210] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 90 when fitted to an HMM generated from the amino acid sequences set forth in Figure 5 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, and SEQ ID NO:164.

[0211] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 230 when fitted to an HMM generated from the amino acid sequences set forth in Figure 6 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, and SEQ ID NO:184.

[0212] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 90 when fitted to an HMM generated from the amino acid sequences set forth in Figure 7 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, and SEQ ID NO:206.

[0213] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 380 when fitted to an HMM generated from the amino acid sequences set forth in Figure 8 are identified in the Sequence Listing of this application. Such

polypeptides include SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:214, and SEQ ID NO:216.

[0214] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 110 when fitted to an HMM generated from the amino acid sequences set forth in Figure 9 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:1039, SEQ ID NO:1049, and SEQ ID NO:1052.

[0215] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 220 when fitted to an HMM generated from the amino acid sequences set forth in Figure 10 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:234, SEQ ID NO:236, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, and SEQ ID NO:244.

[0216] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 150 when fitted to an HMM generated from the amino acid sequences set forth in Figure 11 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:246, SEQ ID NO:248, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:262, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:268, SEQ ID NO:270, SEQ ID NO:272, SEQ ID NO:274, SEQ ID NO:276, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID NO:296, and SEQ ID NO:298.

[0217] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 950 when fitted to an HMM generated from the amino acid sequences set forth in Figure 12 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:300, SEQ ID NO:302, SEQ ID NO:304, SEQ ID NO:306, SEQ ID NO:308, SEQ ID NO:310, SEQ ID NO:312, SEQ ID NO:314, SEQ ID NO:316, SEQ ID NO:318, SEQ ID NO:319, SEQ ID NO:320, SEQ ID NO:321, SEQ ID NO:322, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, and SEQ ID NO:329.

[0218] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 460 when fitted to an HMM generated from the amino acid sequences set forth in Figure 13 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:332, SEQ ID NO:334, SEQ ID NO:335, SEQ ID NO:336,

SEQ ID NO:338, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:342, SEQ ID NO:343, SEQ ID NO:344, SEQ ID NO:345, SEQ ID NO:346, SEQ ID NO:347, SEQ ID NO:348, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:352, SEQ ID NO:353, SEQ ID NO:354, SEQ ID NO:355, SEQ ID NO:356, SEQ ID NO:357, SEQ ID NO:358, SEQ ID NO:359, SEQ ID NO:360, SEQ ID NO:362, SEQ ID NO:363, SEQ ID NO:364, SEQ ID NO:365, SEQ ID NO:366, SEQ ID NO:2541, SEQ ID NO:2542, SEQ ID NO:2543, SEQ ID NO:2544, SEQ ID NO:2546, SEQ ID NO:2548, SEQ ID NO:2549, SEQ ID NO:2550, SEQ ID NO:2551, SEQ ID NO:2552, and SEQ ID NO:2553.

[0219] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 150 when fitted to an HMM generated from the amino acid sequences set forth in Figure 14 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:368, SEQ ID NO:369, SEQ ID NO:370, SEQ ID NO:371, SEQ ID NO:372, SEQ ID NO:373, SEQ ID NO:374, SEQ ID NO:376, SEQ ID NO:378, SEQ ID NO:380, SEQ ID NO:382, SEQ ID NO:384, SEQ ID NO:386, SEQ ID NO:388, SEQ ID NO:390, SEQ ID NO:392, SEQ ID NO:394, SEQ ID NO:396, SEQ ID NO:398, SEQ ID NO:399, SEQ ID NO:401, SEQ ID NO:403, SEQ ID NO:404, SEQ ID NO:406, SEQ ID NO:408, SEQ ID NO:410, SEQ ID NO:412, SEQ ID NO:414, SEQ ID NO:416, SEQ ID NO:418, SEQ ID NO:419, SEQ ID NO:420, SEQ ID NO:422, SEQ ID NO:423, SEQ ID NO:425, SEQ ID NO:427, SEQ ID NO:428, SEQ ID NO:430, SEQ ID NO:432, SEQ ID NO:433, SEQ ID NO:434, SEQ ID NO:435, SEQ ID NO:436, SEQ ID NO:437, SEQ ID NO:438, SEQ ID NO:439, SEQ ID NO:440, SEQ ID NO:441, SEQ ID NO:444, SEQ ID NO:445, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:449, SEQ ID NO:450, SEQ ID NO:451, SEQ ID NO:452, SEQ ID NO:453, SEQ ID NO:454, SEQ ID NO:455, SEQ ID NO:456, SEQ ID NO:458, SEQ ID NO:459, SEQ ID NO:461, SEQ ID NO:463, SEQ ID NO:465, SEQ ID NO:467, SEQ ID NO:469, SEQ ID NO:471, SEQ ID NO:473, SEQ ID NO:474, SEQ ID NO:475, SEQ ID NO:477, SEQ ID NO:479, SEQ ID NO:481, SEQ ID NO:483, SEQ ID NO:485, SEQ ID NO:487, SEQ ID NO:488, SEQ ID NO:489, SEQ ID NO:490, SEQ ID NO:491, SEQ ID NO:492, SEQ ID NO:494, SEQ ID NO:495, SEQ ID NO:496, SEQ ID NO:497, SEQ ID NO:498, SEQ ID NO:499, SEQ ID NO:500, SEQ ID NO:501, SEQ ID NO:502, SEQ ID NO:504, SEQ ID NO:505, SEQ ID NO:506, SEQ ID NO:507, and SEQ ID NO:508.

[0220] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 410 when fitted to an HMM generated from the amino acid sequences set forth in Figure 15 are identified in the Sequence Listing of this application. Such

polypeptides include SEQ ID NO:510, SEQ ID NO:511, SEQ ID NO:513, SEQ ID NO:515, SEQ ID NO:517, SEQ ID NO:521, SEQ ID NO:523, SEQ ID NO:525, SEQ ID NO:527, SEQ ID NO:529, SEQ ID NO:530, and SEQ ID NO:531.

[0221] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 520 when fitted to an HMM generated from the amino acid sequences set forth in Figure 16 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:533, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:541, SEQ ID NO:542, SEQ ID NO:543, SEQ ID NO:544, SEQ ID NO:545, SEQ ID NO:546, SEQ ID NO:547, SEQ ID NO:548, SEQ ID NO:550, SEQ ID NO:552, SEQ ID NO:553, and SEQ ID NO:554.

[0222] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 1150 when fitted to an HMM generated from the amino acid sequences set forth in Figure 17 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:558, SEQ ID NO:559, SEQ ID NO:560, SEQ ID NO:561, SEQ ID NO:562, SEQ ID NO:563, SEQ ID NO:564, SEQ ID NO:565, SEQ ID NO:566, SEQ ID NO:567, SEQ ID NO:569, SEQ ID NO:571, SEQ ID NO:572, SEQ ID NO:573, SEQ ID NO:575, SEQ ID NO:576, SEQ ID NO:577, SEQ ID NO:578, SEQ ID NO:579, SEQ ID NO:581, SEQ ID NO:583, SEQ ID NO:584, SEQ ID NO:585, SEQ ID NO:586, SEQ ID NO:588, SEQ ID NO:589, SEQ ID NO:590, and SEQ ID NO:591.

[0223] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 340 when fitted to an HMM generated from the amino acid sequences set forth in Figure 18 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:593, SEQ ID NO:595, SEQ ID NO:597, SEQ ID NO:599, SEQ ID NO:601, SEQ ID NO:603, SEQ ID NO:605, SEQ ID NO:607, SEQ ID NO:609, SEQ ID NO:610, and SEQ ID NO:611.

[0224] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 140 when fitted to an HMM generated from the amino acid sequences set forth in Figure 19 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:613, SEQ ID NO:615, SEQ ID NO:617, SEQ ID NO:618, SEQ ID NO:620, SEQ ID NO:622, SEQ ID NO:624, SEQ ID NO:626, SEQ ID NO:628, SEQ ID NO:630, SEQ ID NO:632, SEQ ID NO:634, SEQ ID NO:636, SEQ ID NO:638, SEQ ID NO:640, SEQ ID NO:642, SEQ ID NO:643, and SEQ ID NO:644.

[0225] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 250 when fitted to an HMM generated from the amino acid sequences

set forth in Figure 20 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:646, SEQ ID NO:648, SEQ ID NO:650, SEQ ID NO:652, SEQ ID NO:654, SEQ ID NO:656, SEQ ID NO:658, SEQ ID NO:660, SEQ ID NO:662, SEQ ID NO:664, SEQ ID NO:666, SEQ ID NO:668, SEQ ID NO:670, SEQ ID NO:672, SEQ ID NO:674, SEQ ID NO:676, SEQ ID NO:678, SEQ ID NO:679, SEQ ID NO:680, SEQ ID NO:681, SEQ ID NO:682, SEQ ID NO:683, and SEQ ID NO:685.

[0226] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 170 when fitted to an HMM generated from the amino acid sequences set forth in Figure 21 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:687, SEQ ID NO:689, SEQ ID NO:691, SEQ ID NO:693, SEQ ID NO:694, SEQ ID NO:696, SEQ ID NO:697, SEQ ID NO:699, SEQ ID NO:701, SEQ ID NO:703, SEQ ID NO:705, SEQ ID NO:706, SEQ ID NO:708, SEQ ID NO:710, SEQ ID NO:712, SEQ ID NO:714, SEQ ID NO:716, SEQ ID NO:718, SEQ ID NO:720, SEQ ID NO:721, SEQ ID NO:722, SEQ ID NO:723, SEQ ID NO:724, SEQ ID NO:725, SEQ ID NO:726, SEQ ID NO:727, and SEQ ID NO:728.

[0227] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 210 when fitted to an HMM generated from the amino acid sequences set forth in Figure 22 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:730, SEQ ID NO:732, SEQ ID NO:733, SEQ ID NO:735, SEQ ID NO:737, SEQ ID NO:738, and SEQ ID NO:742.

[0228] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 230 when fitted to an HMM generated from the amino acid sequences set forth in Figure 23 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:746, SEQ ID NO:748, SEQ ID NO:750, SEQ ID NO:751, SEQ ID NO:753, SEQ ID NO:755, SEQ ID NO:757, SEQ ID NO:758, SEQ ID NO:760, SEQ ID NO:761, SEQ ID NO:762, SEQ ID NO:763, SEQ ID NO:765, and SEQ ID NO:767.

[0229] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 180 when fitted to an HMM generated from the amino acid sequences set forth in Figure 24 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:769, SEQ ID NO:771, SEQ ID NO:773, SEQ ID NO:775, SEQ ID NO:777, SEQ ID NO:779, SEQ ID NO:781, SEQ ID NO:783, SEQ ID NO:785, SEQ ID NO:787, SEQ ID NO:789, and SEQ ID NO:790.

[0230] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 300 when fitted to an HMM generated from the amino acid sequences

set forth in Figure 25 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:792, SEQ ID NO:794, SEQ ID NO:796, SEQ ID NO:798, SEQ ID NO:799, SEQ ID NO:801, SEQ ID NO:803, SEQ ID NO:805, SEQ ID NO:807, SEQ ID NO:808, SEQ ID NO:810, SEQ ID NO:812, SEQ ID NO:814, SEQ ID NO:816, SEQ ID NO:818, SEQ ID NO:819, SEQ ID NO:820, SEQ ID NO:821, and SEQ ID NO:822.

[0231] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 190 when fitted to an HMM generated from the amino acid sequences set forth in Figure 26 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:824, SEQ ID NO:826, SEQ ID NO:1696, SEQ ID NO:1698, SEQ ID NO:1700, SEQ ID NO:1702, SEQ ID NO:1704, SEQ ID NO:1706, SEQ ID NO:1708, SEQ ID NO:1710, SEQ ID NO:1711, SEQ ID NO:1713, SEQ ID NO:1714, SEQ ID NO:1715, and SEQ ID NO:1716..

[0232] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 630 when fitted to an HMM generated from the amino acid sequences set forth in Figure 27 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:828, SEQ ID NO:830, SEQ ID NO:832, SEQ ID NO:834, SEQ ID NO:836, SEQ ID NO:837, SEQ ID NO:838, SEQ ID NO:839, SEQ ID NO:840, SEQ ID NO:842, SEQ ID NO:844, SEQ ID NO:845, SEQ ID NO:846, SEQ ID NO:847, SEQ ID NO:848, SEQ ID NO:849, SEQ ID NO:850, and SEQ ID NO:851.

[0233] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 95 when fitted to an HMM generated from the amino acid sequences set forth in Figure 28 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:855, SEQ ID NO:856, SEQ ID NO:858, SEQ ID NO:860, SEQ ID NO:862, SEQ ID NO:864, SEQ ID NO:866, SEQ ID NO:868, SEQ ID NO:870, SEQ ID NO:872, SEQ ID NO:874, SEQ ID NO:876, SEQ ID NO:878, SEQ ID NO:880, SEQ ID NO:882, SEQ ID NO:884, SEQ ID NO:885, SEQ ID NO:886, SEQ ID NO:887, SEQ ID NO:888, and SEQ ID NO:889.

[0234] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 850 when fitted to an HMM generated from the amino acid sequences set forth in Figure 29 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:891, SEQ ID NO:893, SEQ ID NO:894, SEQ ID NO:895, SEQ ID NO:896, SEQ ID NO:898, SEQ ID NO:900, SEQ ID NO:901, SEQ ID NO:902, SEQ ID NO:903, SEQ ID NO:904, SEQ ID NO:905, SEQ ID NO:907, SEQ ID NO:908,

SEQ ID NO:909, SEQ ID NO:910, SEQ ID NO:911, SEQ ID NO:912, SEQ ID NO:913, SEQ ID NO:914, and SEQ ID NO:915.

[0235] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 300 when fitted to an HMM generated from the amino acid sequences set forth in Figure 30 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:917, SEQ ID NO:919, SEQ ID NO:921, SEQ ID NO:923, SEQ ID NO:925, SEQ ID NO:927, SEQ ID NO:929, SEQ ID NO:931, SEQ ID NO:933, SEQ ID NO:935, SEQ ID NO:937, SEQ ID NO:939, and SEQ ID NO:940.

[0236] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 60 when fitted to an HMM generated from the amino acid sequences set forth in Figure 31 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:944, SEQ ID NO:946, SEQ ID NO:947, SEQ ID NO:948, SEQ ID NO:950, SEQ ID NO:952, SEQ ID NO:954, SEQ ID NO:956, SEQ ID NO:958, SEQ ID NO:960, SEQ ID NO:962, SEQ ID NO:964, SEQ ID NO:966, SEQ ID NO:967, SEQ ID NO:968, SEQ ID NO:969, SEQ ID NO:970, SEQ ID NO:972, and SEQ ID NO:974.

[0237] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 340 when fitted to an HMM generated from the amino acid sequences set forth in Figure 32 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:976, SEQ ID NO:978, and SEQ ID NO:980.

[0238] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 180 when fitted to an HMM generated from the amino acid sequences set forth in Figure 33 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:982, SEQ ID NO:984, SEQ ID NO:985, SEQ ID NO:986, SEQ ID NO:987, SEQ ID NO:988, SEQ ID NO:989, SEQ ID NO:990, SEQ ID NO:991, SEQ ID NO:992, SEQ ID NO:993, SEQ ID NO:995, SEQ ID NO:996, SEQ ID NO:998, SEQ ID NO:1000, SEQ ID NO:1001, SEQ ID NO:1003, SEQ ID NO:1005, SEQ ID NO:1007, SEQ ID NO:1008, SEQ ID NO:1009, SEQ ID NO:1011, SEQ ID NO:1013, SEQ ID NO:1015, SEQ ID NO:1016, SEQ ID NO:1018, SEQ ID NO:1019, SEQ ID NO:1021, SEQ ID NO:1023, SEQ ID NO:1025, SEQ ID NO:1026, SEQ ID NO:1027, SEQ ID NO:1028, SEQ ID NO:1029, SEQ ID NO:1030, SEQ ID NO:1031, SEQ ID NO:1032, and SEQ ID NO:1033.

[0239] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 1060 when fitted to an HMM generated from the amino acid sequences set forth in Figure 34 are identified in the Sequence Listing of this application. Such

polypeptides include SEQ ID NO:1054, SEQ ID NO:1055, SEQ ID NO:1057, SEQ ID NO:1058, SEQ ID NO:1059, SEQ ID NO:1061, SEQ ID NO:1063, SEQ ID NO:1065, SEQ ID NO:1065, SEQ ID NO:1067, SEQ ID NO:1068, SEQ ID NO:1070, SEQ ID NO:1071, SEQ ID NO:1072, SEQ ID NO:1074, SEQ ID NO:1075, SEQ ID NO:1076, SEQ ID NO:1077, SEQ ID NO:1078, SEQ ID NO:1080, SEQ ID NO:1082, SEQ ID NO:1083, SEQ ID NO:1085, SEQ ID NO:1086, SEQ ID NO:1087, SEQ ID NO:1088, SEQ ID NO:1089, SEQ ID NO:1089, SEQ ID NO:1090, SEQ ID NO:1091, SEQ ID NO:1092, SEQ ID NO:1093, SEQ ID NO:1094, SEQ ID NO:1095, and SEQ ID NO:1097.

[0240] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 260 when fitted to an HMM generated from the amino acid sequences set forth in Figure 35 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:1099, SEQ ID NO:1101, SEQ ID NO:1103, SEQ ID NO:1104, SEQ ID NO:1105, SEQ ID NO:1106, SEQ ID NO:1108, SEQ ID NO:1109, and SEQ ID NO:1110.

[0241] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 150 when fitted to an HMM generated from the amino acid sequences set forth in Figure 36 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:1112, SEQ ID NO:1113, and SEQ ID NO:1114.

[0242] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 40 when fitted to an HMM generated from the amino acid sequences set forth in Figure 37 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:1116, SEQ ID NO:1118, SEQ ID NO:1120, SEQ ID NO:1122, SEQ ID NO:1123, SEQ ID NO:1125, SEQ ID NO:1126, SEQ ID NO:1128, SEQ ID NO:1129, SEQ ID NO:1131, SEQ ID NO:1132, SEQ ID NO:1133, SEQ ID NO:1134, SEQ ID NO:1136, SEQ ID NO:1138, SEQ ID NO:1140, SEQ ID NO:1141, SEQ ID NO:1142, SEQ ID NO:1143, SEQ ID NO:1144, SEQ ID NO:1145, SEQ ID NO:1147, SEQ ID NO:1149, SEQ ID NO:1151, SEQ ID NO:1153, and SEQ ID NO:1155.

[0243] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 450 when fitted to an HMM generated from the amino acid sequences set forth in Figure 38 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:1159, SEQ ID NO:1161, SEQ ID NO:1162, SEQ ID NO:1163, and SEQ ID NO:1164.

[0244] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 160 when fitted to an HMM generated from the amino acid sequences

set forth in Figure 39 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:1166, SEQ ID NO:1167, SEQ ID NO:1169, SEQ ID NO:1171, SEQ ID NO:1173, SEQ ID NO:1175, SEQ ID NO:1177, SEQ ID NO:1179, SEQ ID NO:1180, SEQ ID NO:1182, and SEQ ID NO:1183.

[0245] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 180 when fitted to an HMM generated from the amino acid sequences set forth in Figure 40 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:1185, SEQ ID NO:1187, SEQ ID NO:1189, SEQ ID NO:1190, SEQ ID NO:1191, and SEQ ID NO:1192.

[0246] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 670 when fitted to an HMM generated from the amino acid sequences set forth in Figure 41 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:1194, SEQ ID NO:1196, SEQ ID NO:1198, SEQ ID NO:1200, SEQ ID NO:1202, SEQ ID NO:1203, SEQ ID NO:1204, SEQ ID NO:1205, SEQ ID NO:1206, SEQ ID NO:1207, and SEQ ID NO:1208.

[0247] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 280 when fitted to an HMM generated from the amino acid sequences set forth in Figure 42 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:1210, SEQ ID NO:1211, SEQ ID NO:1213, SEQ ID NO:1215, SEQ ID NO:1216, SEQ ID NO:1218, SEQ ID NO:1220, SEQ ID NO:1222, SEQ ID NO:1224, SEQ ID NO:1226, SEQ ID NO:1228, SEQ ID NO:1229, SEQ ID NO:1230, SEQ ID NO:1232, SEQ ID NO:1233, SEQ ID NO:1234, SEQ ID NO:1235, SEQ ID NO:1236, SEQ ID NO:1237, SEQ ID NO:1238, SEQ ID NO:1239, SEQ ID NO:1240, SEQ ID NO:1241, SEQ ID NO:1242, SEQ ID NO:1243, SEQ ID NO:1244, SEQ ID NO:1245, SEQ ID NO:1246, SEQ ID NO:1247, SEQ ID NO:1248, SEQ ID NO:1249, SEQ ID NO:1251, SEQ ID NO:1253, SEQ ID NO:1255, SEQ ID NO:1257, SEQ ID NO:1259, SEQ ID NO:1261, SEQ ID NO:1263, SEQ ID NO:1264, SEQ ID NO:1265, SEQ ID NO:1266, SEQ ID NO:1267, SEQ ID NO:1268, SEQ ID NO:1269, SEQ ID NO:1270, SEQ ID NO:1271, and SEQ ID NO:1272.

[0248] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 700 when fitted to an HMM generated from the amino acid sequences set forth in Figure 43 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:1274, SEQ ID NO:1276, SEQ ID NO:1278, SEQ ID NO:1280, SEQ ID NO:1281, SEQ ID NO:1282, SEQ ID NO:1284, SEQ ID NO:1285, SEQ

ID NO:1287, SEQ ID NO:1289, SEQ ID NO:1291, SEQ ID NO:1293, SEQ ID NO:1294, SEQ ID NO:1295, SEQ ID NO:1296, SEQ ID NO:1297, SEQ ID NO:1298, and SEQ ID NO:1300.

[0249] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 920 when fitted to an HMM generated from the amino acid sequences set forth in Figure 44 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:1302, SEQ ID NO:1303, SEQ ID NO:1305, SEQ ID NO:1307, SEQ ID NO:1309, SEQ ID NO:1311, SEQ ID NO:1312, SEQ ID NO:1313, SEQ ID NO:1314, SEQ ID NO:1315, SEQ ID NO:1317, SEQ ID NO:1318, SEQ ID NO:1319, SEQ ID NO:1320, SEQ ID NO:1321, SEQ ID NO:1322, SEQ ID NO:1323, SEQ ID NO:1324, SEQ ID NO:1325, SEQ ID NO:1326, SEQ ID NO:1327, SEQ ID NO:1328, SEQ ID NO:1330, SEQ ID NO:1331, SEQ ID NO:1333, SEQ ID NO:1334, SEQ ID NO:1335, SEQ ID NO:1336, SEQ ID NO:1337, SEQ ID NO:1338, SEQ ID NO:1339, and SEQ ID NO:1340.

[0250] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 510 when fitted to an HMM generated from the amino acid sequences set forth in Figure 45 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:1342, SEQ ID NO:1344, SEQ ID NO:1346, SEQ ID NO:1348, SEQ ID NO:1350, SEQ ID NO:1352, SEQ ID NO:1354, SEQ ID NO:1355, SEQ ID NO:1357, SEQ ID NO:1358, SEQ ID NO:1360, SEQ ID NO:1361, SEQ ID NO:1362, SEQ ID NO:1363, SEQ ID NO:1364, SEQ ID NO:1366, SEQ ID NO:1367, SEQ ID NO:1369, SEQ ID NO:1370, SEQ ID NO:1371, SEQ ID NO:1372, SEQ ID NO:1373, SEQ ID NO:1374, SEQ ID NO:1375, SEQ ID NO:1376, SEQ ID NO:1377, SEQ ID NO:1378, SEQ ID NO:1379, SEQ ID NO:1380, SEQ ID NO:1381, SEQ ID NO:1382, and SEQ ID NO:1383.

[0251] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 140 when fitted to an HMM generated from the amino acid sequences set forth in Figure 46 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:1385, SEQ ID NO:1387, SEQ ID NO:1389, SEQ ID NO:1390, SEQ ID NO:1391, SEQ ID NO:1393, SEQ ID NO:1394, SEQ ID NO:1395, SEQ ID NO:1396, SEQ ID NO:1398, SEQ ID NO:1400, SEQ ID NO:1401, SEQ ID NO:1402, SEQ ID NO:1403, SEQ ID NO:1404, SEQ ID NO:1405, and SEQ ID NO:1407.

[0252] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 150 when fitted to an HMM generated from the amino acid sequences

set forth in Figure 47 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:1409, SEQ ID NO:1411, SEQ ID NO:1413, SEQ ID NO:1415, SEQ ID NO:1417, SEQ ID NO:1418, SEQ ID NO:1419, SEQ ID NO:1421, SEQ ID NO:1423, SEQ ID NO:1424, SEQ ID NO:1425, SEQ ID NO:1426.

[0253] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 190 when fitted to an HMM generated from the amino acid sequences set forth in Figure 48 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:1428, SEQ ID NO:1430, SEQ ID NO:1432, SEQ ID NO:1434, SEQ ID NO:1436, SEQ ID NO:1439, SEQ ID NO:1442, SEQ ID NO:1444, SEQ ID NO:1446, SEQ ID NO:1448, SEQ ID NO:1450, SEQ ID NO:1452, SEQ ID NO:1453, SEQ ID NO:1454, SEQ ID NO:1455, SEQ ID NO:1456, SEQ ID NO:1457, SEQ ID NO:1458, and SEQ ID NO:1459.

[0254] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 450 when fitted to an HMM generated from the amino acid sequences set forth in Figure 49 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:1463, SEQ ID NO:1465, SEQ ID NO:1467, SEQ ID NO:1469, SEQ ID NO:1471, SEQ ID NO:1473, SEQ ID NO:1474, SEQ ID NO:1475, SEQ ID NO:1476, and SEQ ID NO:1477.

[0255] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 580 when fitted to an HMM generated from the amino acid sequences set forth in Figure 50 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:1491, SEQ ID NO:1493, SEQ ID NO:1495, SEQ ID NO:1497, SEQ ID NO:1499, SEQ ID NO:1501, SEQ ID NO:1503, SEQ ID NO:1504, SEQ ID NO:1505, SEQ ID NO:1506, and SEQ ID NO:1508.

[0256] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 100 when fitted to an HMM generated from the amino acid sequences set forth in Figure 51 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:1510, SEQ ID NO:1512, SEQ ID NO:1514, SEQ ID NO:1516, SEQ ID NO:1518, SEQ ID NO:1520, SEQ ID NO:1522, and SEQ ID NO:1523.

[0257] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 800 when fitted to an HMM generated from the amino acid sequences set forth in Figure 52 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:1525, SEQ ID NO:1527, SEQ ID NO:1529, SEQ ID NO:1530, SEQ ID NO:1532, SEQ ID NO:1534, and SEQ ID NO:1535.

[0258] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 490 when fitted to an HMM generated from the amino acid sequences set forth in Figure 53 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:1537, SEQ ID NO:1539, SEQ ID NO:1540, SEQ ID NO:1541, SEQ ID NO:1543, SEQ ID NO:1545, SEQ ID NO:1547, SEQ ID NO:1548, SEQ ID NO:1550, SEQ ID NO:1552, SEQ ID NO:2386, SEQ ID NO:2388, SEQ ID NO:2390, SEQ ID NO:2391,, and SEQ ID NO:2392.

[0259] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 690 when fitted to an HMM generated from the amino acid sequences set forth in Figure 54 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:1554, SEQ ID NO:1555, SEQ ID NO:1557, SEQ ID NO:1559, SEQ ID NO:1561, SEQ ID NO:1563, SEQ ID NO:1565, SEQ ID NO:1567, SEQ ID NO:1569, SEQ ID NO:1571, SEQ ID NO:1572, SEQ ID NO:1573, SEQ ID NO:1574, and SEQ ID NO:1575.

[0260] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 380 when fitted to an HMM generated from the amino acid sequences set forth in Figure 55 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:1035, SEQ ID NO:1036, SEQ ID NO:1037, SEQ ID NO:1040, SEQ ID NO:1041, SEQ ID NO:1043, SEQ ID NO:1044, SEQ ID NO:1046, SEQ ID NO:1047, SEQ ID NO:1048, SEQ ID NO:1050, SEQ ID NO:1440, SEQ ID NO:1480, SEQ ID NO:1481, SEQ ID NO:1482, SEQ ID NO:1483, SEQ ID NO:1484, SEQ ID NO:1485, SEQ ID NO:1486, SEQ ID NO:1487, SEQ ID NO:1488, SEQ ID NO:1577, SEQ ID NO:1578, SEQ ID NO:1580, SEQ ID NO:1582, SEQ ID NO:1584, SEQ ID NO:1586, SEQ ID NO:1588, SEQ ID NO:1590, SEQ ID NO:1592, SEQ ID NO:1594, SEQ ID NO:1596, SEQ ID NO:1598, SEQ ID NO:1599, SEQ ID NO:1601, SEQ ID NO:1602, SEQ ID NO:1605, SEQ ID NO:1607, SEQ ID NO:1608, SEQ ID NO:1609, SEQ ID NO:1611, SEQ ID NO:1613, SEQ ID NO:1615, SEQ ID NO:1617, SEQ ID NO:1619, SEQ ID NO:1621, SEQ ID NO:1622, SEQ ID NO:1623, SEQ ID NO:1624, SEQ ID NO:1625, SEQ ID NO:1627, SEQ ID NO:1629, SEQ ID NO:1631, SEQ ID NO:1633, SEQ ID NO:1635, SEQ ID NO:1637, SEQ ID NO:1639, SEQ ID NO:1643, SEQ ID NO:1645, SEQ ID NO:1648, SEQ ID NO:1649, SEQ ID NO:1651, and SEQ ID NO:1653.

[0261] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 870 when fitted to an HMM generated from the amino acid sequences set forth in Figure 56 are identified in the Sequence Listing of this application. Such

polypeptides include SEQ ID NO:173, SEQ ID NO:212, SEQ ID NO:361, SEQ ID NO:421, SEQ ID NO:443, SEQ ID NO:740, SEQ ID NO:744, SEQ ID NO:942, SEQ ID NO:1437, and SEQ ID NO:1461.

[0262] Examples of polypeptides are shown in the sequence listing that have HMM bit scores greater than 140 when fitted to an HMM generated from the amino acid sequences set forth in Figure 57 are identified in the Sequence Listing of this application. Such polypeptides include SEQ ID NO:97, SEQ ID NO:2010, SEQ ID NO:2011, SEQ ID NO:2013, SEQ ID NO:2015, and SEQ ID NO:2017.

D. Percent Identity

[0263] In some embodiments, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with at least 20% sequence identity, *e.g.*, at least 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to one of the amino acid sequences set forth in SEQ ID NO:3, SEQ ID NO:49, SEQ ID NO:77, SEQ ID NO:97, SEQ ID NO:100, SEQ ID NO:152, SEQ ID NO:166, SEQ ID NO:186, SEQ ID NO:208, SEQ ID NO:218, SEQ ID NO:234, SEQ ID NO:246, SEQ ID NO:300, SEQ ID NO:332, SEQ ID NO:368, SEQ ID NO:510, SEQ ID NO:533, SEQ ID NO:556, SEQ ID NO:558, SEQ ID NO:593, SEQ ID NO:613, SEQ ID NO:646, SEQ ID NO:687, SEQ ID NO:730, SEQ ID NO:746, SEQ ID NO:769, SEQ ID NO:792, SEQ ID NO:824, SEQ ID NO:828, SEQ ID NO:853, SEQ ID NO:855, SEQ ID NO:891, SEQ ID NO:917, SEQ ID NO:944, SEQ ID NO:976, SEQ ID NO:982, SEQ ID NO:1054, SEQ ID NO:1099, SEQ ID NO:1112, SEQ ID NO:1116, SEQ ID NO:1157, SEQ ID NO:1159, SEQ ID NO:1166, SEQ ID NO:1185, SEQ ID NO:1194, SEQ ID NO:1210, SEQ ID NO:1274, SEQ ID NO:1302, SEQ ID NO:1342, SEQ ID NO:1385, SEQ ID NO:1409, SEQ ID NO:1428, SEQ ID NO:1437, SEQ ID NO:1463, SEQ ID NO:1491, SEQ ID NO:1510, SEQ ID NO:1525, SEQ ID NO:1537, SEQ ID NO:1554, and SEQ ID NO:1577. Polypeptides having such a percent sequence identity often have a domain indicative of a low nitrogen tolerance-modulating polypeptide and/or have an HMM bit score that is greater than 20, as discussed above. Amino acid sequences of low nitrogen tolerance-modulating polypeptides having at least 20% sequence identity to one of the amino acid sequences set forth in SEQ ID NO:3, SEQ ID NO:49, SEQ ID NO:77, SEQ ID NO:97, SEQ ID NO:100, SEQ ID NO:152, SEQ ID NO:166, SEQ ID NO:186, SEQ ID NO:208, SEQ ID NO:218, SEQ ID NO:234, SEQ ID NO:246, SEQ ID NO:300, SEQ ID NO:332, SEQ ID NO:368, SEQ ID NO:510, SEQ ID NO:533, SEQ ID NO:556, SEQ ID NO:558, SEQ ID NO:593, SEQ ID NO:613, SEQ ID

NO:646, SEQ ID NO:687, SEQ ID NO:730, SEQ ID NO:746, SEQ ID NO:769, SEQ ID NO:792, SEQ ID NO:824, SEQ ID NO:828, SEQ ID NO:853, SEQ ID NO:855, SEQ ID NO:891, SEQ ID NO:917, SEQ ID NO:944, SEQ ID NO:976, SEQ ID NO:982, SEQ ID NO:1054, SEQ ID NO:1099, SEQ ID NO:1112, SEQ ID NO:1116, SEQ ID NO:1157, SEQ ID NO:1159, SEQ ID NO:1166, SEQ ID NO:1185, SEQ ID NO:1194, SEQ ID NO:1210, SEQ ID NO:1274, SEQ ID NO:1302, SEQ ID NO:1342, SEQ ID NO:1385, SEQ ID NO:1409, SEQ ID NO:1428, SEQ ID NO:1437, SEQ ID NO:1463, SEQ ID NO:1491, SEQ ID NO:1510, SEQ ID NO:1525, SEQ ID NO:1537, SEQ ID NO:1554, and SEQ ID NO:1577are provided in Figures 1-57 and in the Sequence Listing.

[0264] "Percent sequence identity" refers to the degree of sequence identity between any given reference sequence, *e.g.*, SEQ ID NO:3, and a candidate low nitrogen tolerance-modulating sequence. A candidate sequence typically has a length that is from 80 percent to 200 percent of the length of the reference sequence, *e.g.*, 82, 85, 87, 89, 90, 93, 95, 97, 99, 100, 105, 110, 115, 120, 130, 140, 150, 160, 170, 180, 190, or 200 percent of the length of the reference sequence. A percent identity for any candidate nucleic acid or polypeptide relative to a reference nucleic acid or polypeptide can be determined as follows. A reference sequence (*e.g.*, a nucleic acid sequence or an amino acid sequence) is aligned to one or more candidate sequences using the computer program ClustalW (version 1.83, default parameters), which allows alignments of nucleic acid or polypeptide sequences to be carried out across their entire length (global alignment). Chenna et al. (2003) *Nucleic Acids Res.*, 31(13):3497-500.

[0265] ClustalW calculates the best match between a reference and one or more candidate sequences, and aligns them so that identities, similarities and differences can be determined. Gaps of one or more residues can be inserted into a reference sequence, a candidate sequence, or both, to maximize sequence alignments. For fast pairwise alignment of nucleic acid sequences, the following default parameters are used: word size: 2; window size: 4; scoring method: percentage; number of top diagonals: 4; and gap penalty: 5. For multiple alignment of nucleic acid sequences, the following parameters are used: gap opening penalty: 10.0; gap extension penalty: 5.0; and weight transitions: yes. For fast pairwise alignment of protein sequences, the following parameters are used: word size: 1; window size: 5; scoring method: percentage; number of top diagonals: 5; gap penalty: 3. For multiple alignment of protein sequences, the following parameters are used: weight matrix: blosum; gap opening penalty: 10.0; gap extension penalty: 0.05; hydrophilic gaps: on; hydrophilic residues: Gly, Pro, Ser, Asn, Asp, Gln, Glu, Arg, and Lys; residue-specific gap penalties: on.

The ClustalW output is a sequence alignment that reflects the relationship between sequences. ClustalW can be run, for example, at the Baylor College of Medicine Search Launcher site (searchlauncher.bcm.tmc.edu/multi-align/multi-align.html) and at the European Bioinformatics Institute site on the World Wide Web (ebi.ac.uk/clustalw).

[0266] To determine percent identity of a candidate nucleic acid or amino acid sequence to a reference sequence, the sequences are aligned using ClustalW, the number of identical matches in the alignment is divided by the length of the reference sequence, and the result is multiplied by 100. It is noted that the percent identity value can be rounded to the nearest tenth. For example, 78.11, 78.12, 78.13, and 78.14 are rounded down to 78.1, while 78.15, 78.16, 78.17, 78.18, and 78.19 are rounded up to 78.2.

[0267] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:3, and preferably has at least 20% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:3. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:3 are provided in Figure 1 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, and SEQ ID NO:47.

[0268] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:49, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:49. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:49 are provided in Figure 2 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, and SEQ ID NO:75.

[0269] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino

acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:77, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:77. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:77 are provided in Figure 3 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:1479.

[0270] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:100, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:100. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO: 100 are provided in Figure 4 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, and SEQ ID NO:150.

[0271] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:152, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:152. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:152 are provided in Figure 5 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, and SEQ ID NO:164.

[0272] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:166, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%,

80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:166. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:166 are provided in Figure 6 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184.

[0273] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:186, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:186. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:186 are provided in Figure 7 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, and SEQ ID NO:206.

[0274] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:208, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:208. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:208 are provided in Figure 8 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:214, and SEQ ID NO:216.

[0275] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:218, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:218. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:218 are provided in Figure 9 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:1039, SEQ ID NO:1049, and SEQ ID NO:1052.

[0276] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:234, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:234. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:234 are provided in Figure 10 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:236, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, and SEQ ID NO:244.

[0277] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:246, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:246. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:246 are provided in Figure 11 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:248, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:262, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:268, SEQ ID NO:270, SEQ ID NO:272, SEQ ID NO:274, SEQ ID NO:276, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID NO:296, and SEQ ID NO:298.

[0278] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:300, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:300. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:300 are provided in Figure 12 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:302, SEQ ID NO:304, SEQ ID NO:306, SEQ ID NO:308, SEQ ID NO:310, SEQ ID NO:312, SEQ ID NO:314, SEQ ID NO:316, SEQ ID NO:318, SEQ ID NO:319, SEQ ID NO:320, SEQ ID NO:321, SEQ ID NO:322, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, and SEQ ID NO:329.

[0279] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino

acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:332, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:332. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:332 are provided in Figure 13 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:332, SEQ ID NO:334, SEQ ID NO:335, SEQ ID NO:336, SEQ ID NO:338, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:342, SEQ ID NO:343, SEQ ID NO:344, SEQ ID NO:345, SEQ ID NO:346, SEQ ID NO:347, SEQ ID NO:348, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:352, SEQ ID NO:353, SEQ ID NO:354, SEQ ID NO:355, SEQ ID NO:356, SEQ ID NO:357, SEQ ID NO:358, SEQ ID NO:359, SEQ ID NO:360, SEQ ID NO:362, SEQ ID NO:363, SEQ ID NO:364, SEQ ID NO:365, SEQ ID NO:366, SEQ ID NO:2541, SEQ ID NO:2542, SEQ ID NO:2543, SEQ ID NO:2544, SEQ ID NO:2546, SEQ ID NO:2548, SEQ ID NO:2549, SEQ ID NO:2550, SEQ ID NO:2551, SEQ ID NO:2552, and SEQ ID NO:2553.

[0280] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:368, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:368. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:368 are provided in Figure 14 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:369, SEQ ID NO:370, SEQ ID NO:371, SEQ ID NO:372, SEQ ID NO:373, SEQ ID NO:374, SEQ ID NO:376, SEQ ID NO:378, SEQ ID NO:380, SEQ ID NO:382, SEQ ID NO:384, SEQ ID NO:386, SEQ ID NO:388, SEQ ID NO:390, SEQ ID NO:392, SEQ ID NO:394, SEQ ID NO:396, SEQ ID NO:398, SEQ ID NO:399, SEQ ID NO:401, SEQ ID NO:403, SEQ ID NO:404, SEQ ID NO:406, SEQ ID NO:408, SEQ ID NO:410, SEQ ID NO:412, SEQ ID NO:414, SEQ ID NO:416, SEQ ID NO:418, SEQ ID NO:419, SEQ ID NO:420, SEQ ID NO:422, SEQ ID NO:423, SEQ ID NO:425, SEQ ID NO:427, SEQ ID NO:428, SEQ ID NO:430, SEQ ID NO:432, SEQ ID NO:433, SEQ ID NO:434, SEQ ID NO:435, SEQ ID NO:436, SEQ ID NO:437, SEQ ID NO:438, SEQ ID NO:439, SEQ ID NO:440, SEQ ID NO:441, SEQ ID NO:444, SEQ ID NO:445, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:449, SEQ ID NO:450, SEQ ID NO:451, SEQ ID NO:452, SEQ ID NO:453, SEQ ID NO:454, SEQ ID NO:455, SEQ ID NO:456, SEQ ID NO:458, SEQ ID

NO:459, SEQ ID NO:461, SEQ ID NO:463, SEQ ID NO:465, SEQ ID NO:467, SEQ ID NO:469, SEQ ID NO:471, SEQ ID NO:473, SEQ ID NO:474, SEQ ID NO:475, SEQ ID NO:477, SEQ ID NO:479, SEQ ID NO:481, SEQ ID NO:483, SEQ ID NO:485, SEQ ID NO:487, SEQ ID NO:488, SEQ ID NO:489, SEQ ID NO:490, SEQ ID NO:491, SEQ ID NO:492, SEQ ID NO:494, SEQ ID NO:495, SEQ ID NO:496, SEQ ID NO:497, SEQ ID NO:498, SEQ ID NO:499, SEQ ID NO:500, SEQ ID NO:501, SEQ ID NO:502, SEQ ID NO:504, SEQ ID NO:505, SEQ ID NO:506, SEQ ID NO:507, and SEQ ID NO:508.

[0281] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:510, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:510. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:510 are provided in Figure 15 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:511, SEQ ID NO:513, SEQ ID NO:515, SEQ ID NO:517, SEQ ID NO:521, SEQ ID NO:523, SEQ ID NO:525, SEQ ID NO:527, SEQ ID NO:529, SEQ ID NO:530, and SEQ ID NO:531.

[0282] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:533, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:533. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:533 are provided in Figure 16 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:541, SEQ ID NO:542, SEQ ID NO:543, SEQ ID NO:544, SEQ ID NO:545, SEQ ID NO:546, SEQ ID NO:547, SEQ ID NO:548, SEQ ID NO:550, SEQ ID NO:552, SEQ ID NO:553, and SEQ ID NO:554.

[0283] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:558, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:558. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:558 are provided in Figure 17 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:559, SEQ ID NO:560, SEQ ID NO:561, SEQ ID NO:562, SEQ ID NO:563, SEQ ID NO:564, SEQ ID

NO:565, SEQ ID NO:566, SEQ ID NO:567, SEQ ID NO:569, SEQ ID NO:571, SEQ ID NO:572, SEQ ID NO:573, SEQ ID NO:575, SEQ ID NO:576, SEQ ID NO:577, SEQ ID NO:578, SEQ ID NO:579, SEQ ID NO:581, SEQ ID NO:583, SEQ ID NO:584, SEQ ID NO:585, SEQ ID NO:586, SEQ ID NO:588, SEQ ID NO:589, SEQ ID NO:590, and SEQ ID NO:591.

[0284] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:593, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:593. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:593 are provided in Figure 18 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:595, SEQ ID NO:597, SEQ ID NO:599, SEQ ID NO:601, SEQ ID NO:603, SEQ ID NO:605, SEQ ID NO:607, SEQ ID NO:609, SEQ ID NO:610, and SEQ ID NO:611.

[0285] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:613, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:613. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:613 are provided in Figure 19 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:615, SEQ ID NO:617, SEQ ID NO:618, SEQ ID NO:620, SEQ ID NO:622, SEQ ID NO:624, SEQ ID NO:626, SEQ ID NO:628, SEQ ID NO:630, SEQ ID NO:632, SEQ ID NO:634, SEQ ID NO:636, SEQ ID NO:638, SEQ ID NO:640, SEQ ID NO:642, SEQ ID NO:643, and SEQ ID NO:644.

[0286] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:646, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:646. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:646 are provided in Figure 20 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:648, SEQ ID NO:650, SEQ ID NO:652, SEQ ID NO:654, SEQ ID NO:656, SEQ ID NO:658, SEQ ID NO:660, SEQ ID NO:662, SEQ ID NO:664, SEQ ID NO:666, SEQ ID NO:668, SEQ ID

NO:670, SEQ ID NO:672, SEQ ID NO:674, SEQ ID NO:676, SEQ ID NO:678, SEQ ID NO:679, SEQ ID NO:680, SEQ ID NO:681, SEQ ID NO:682, SEQ ID NO:683, and SEQ ID NO:685.

[0287] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:687, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:687. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:687 are provided in Figure 21 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:689, SEQ ID NO:691, SEQ ID NO:693, SEQ ID NO:694, SEQ ID NO:696, SEQ ID NO:697, SEQ ID NO:699, SEQ ID NO:701, SEQ ID NO:703, SEQ ID NO:705, SEQ ID NO:706, SEQ ID NO:708, SEQ ID NO:710, SEQ ID NO:712, SEQ ID NO:714, SEQ ID NO:716, SEQ ID NO:718, SEQ ID NO:720, SEQ ID NO:721, SEQ ID NO:722, SEQ ID NO:723, SEQ ID NO:724, SEQ ID NO:725, SEQ ID NO:726, SEQ ID NO:727, and SEQ ID NO:728.

[0288] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:730, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:730. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:730 are provided in Figure 22 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:732, SEQ ID NO:733, SEQ ID NO:735, SEQ ID NO:737, SEQ ID NO:738, and SEQ ID NO:742.

[0289] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:746, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:746. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:746 are provided in Figure 23 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:748, SEQ ID NO:750, SEQ ID NO:751, SEQ ID NO:753, SEQ ID NO:755, SEQ ID NO:757, SEQ ID NO:758, SEQ ID NO:760, SEQ ID NO:761, SEQ ID NO:762, SEQ ID NO:763, SEQ ID NO:765, and SEQ ID NO:767.

[0290] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino

acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:769, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:769. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:769 are provided in Figure 24 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:771, SEQ ID NO:773, SEQ ID NO:775, SEQ ID NO:777, SEQ ID NO:779, SEQ ID NO:781, SEQ ID NO:783, SEQ ID NO:785, SEQ ID NO:787, SEQ ID NO:789, and SEQ ID NO:790.

[0291] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:792, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:792. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:792 are provided in Figure 25 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:794, SEQ ID NO:796, SEQ ID NO:798, SEQ ID NO:799, SEQ ID NO:801, SEQ ID NO:803, SEQ ID NO:805, SEQ ID NO:807, SEQ ID NO:808, SEQ ID NO:810, SEQ ID NO:812, SEQ ID NO:814, SEQ ID NO:816, SEQ ID NO:818, SEQ ID NO:819, SEQ ID NO:820, SEQ ID NO:821, and SEQ ID NO:822.

[0292] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:824, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:824. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:824 are provided in Figure 26 and in the Sequence Listing. Such polypeptides include, but not limited to, SEQ ID NO:826, SEQ ID NO:1696, SEQ ID NO:1698, SEQ ID NO:1700, SEQ ID NO:1702, SEQ ID NO:1704, SEQ ID NO:1706, SEQ ID NO:1708, SEQ ID NO:1710, SEQ ID NO:1711, SEQ ID NO:1713, SEQ ID NO:1714, SEQ ID NO:1715, and SEQ ID NO:1716.

[0293] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:828, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:828. Amino acid sequences of polypeptides having greater than 20%

sequence identity to the polypeptide set forth in SEQ ID NO:828 are provided in Figure 27 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:830, SEQ ID NO:832, SEQ ID NO:834, SEQ ID NO:836, SEQ ID NO:837, SEQ ID NO:838, SEQ ID NO:839, SEQ ID NO:840, SEQ ID NO:842, SEQ ID NO:844, SEQ ID NO:845, SEQ ID NO:846, SEQ ID NO:847, SEQ ID NO:848, SEQ ID NO:849, SEQ ID NO:850, and SEQ ID NO:851.

[0294] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:855, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:855. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:855 are provided in Figure 28 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:856, SEQ ID NO:858, SEQ ID NO:860, SEQ ID NO:862, SEQ ID NO:864, SEQ ID NO:866, SEQ ID NO:868, SEQ ID NO:870, SEQ ID NO:872, SEQ ID NO:874, SEQ ID NO:876, SEQ ID NO:878, SEQ ID NO:880, SEQ ID NO:882, SEQ ID NO:884, SEQ ID NO:885, SEQ ID NO:886, SEQ ID NO:887, SEQ ID NO:888, and SEQ ID NO:889.

[0295] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:891, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:891. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:891 are provided in Figure 29 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:893, SEQ ID NO:894, SEQ ID NO:895, SEQ ID NO:896, SEQ ID NO:898, SEQ ID NO:900, SEQ ID NO:901, SEQ ID NO:902, SEQ ID NO:903, SEQ ID NO:904, SEQ ID NO:905, SEQ ID NO:907, SEQ ID NO:908, SEQ ID NO:909, SEQ ID NO:910, SEQ ID NO:911, SEQ ID NO:912, SEQ ID NO:913, SEQ ID NO:914, and SEQ ID NO:915.

[0296] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:917, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:917. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:917 are provided in Figure 30

and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:919, SEQ ID NO:921, SEQ ID NO:923, SEQ ID NO:925, SEQ ID NO:927, SEQ ID NO:929, SEQ ID NO:931, SEQ ID NO:933, SEQ ID NO:935, SEQ ID NO:937, SEQ ID NO:939, and SEQ ID NO:940.

[0297] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:944, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:944. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:944 are provided in Figure 31 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:946, SEQ ID NO:947, SEQ ID NO:948, SEQ ID NO:950, SEQ ID NO:952, SEQ ID NO:954, SEQ ID NO:956, SEQ ID NO:958, SEQ ID NO:960, SEQ ID NO:962, SEQ ID NO:964, SEQ ID NO:966, SEQ ID NO:967, SEQ ID NO:968, SEQ ID NO:969, SEQ ID NO:970, SEQ ID NO:972, and SEQ ID NO:974.

[0298] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:976, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:976. Amino acid sequences of polypeptides having greater than 45% sequence identity to the polypeptide set forth in SEQ ID NO:976 are provided in Figure 32 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:978 and SEQ ID NO:980.

[0299] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:982, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:982. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:982 are provided in Figure 33 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:984, SEQ ID NO:985, SEQ ID NO:986, SEQ ID NO:987, SEQ ID NO:988, SEQ ID NO:989, SEQ ID NO:990, SEQ ID NO:991, SEQ ID NO:992, SEQ ID NO:993, SEQ ID NO:995, SEQ ID NO:996, SEQ ID NO:998, SEQ ID NO:1000, SEQ ID NO:1001, SEQ ID NO:1003, SEQ ID NO:1005, SEQ ID NO:1007, SEQ ID NO:1008, SEQ ID NO:1009, SEQ ID NO:1011, SEQ

ID NO:1013, SEQ ID NO:1015, SEQ ID NO:1016, SEQ ID NO:1018, SEQ ID NO:1019, SEQ ID NO:1021, SEQ ID NO:1023, SEQ ID NO:1025, SEQ ID NO:1026, SEQ ID NO:1027, SEQ ID NO:1028, SEQ ID NO:1029, SEQ ID NO:1030, SEQ ID NO:1031, SEQ ID NO:1032, and SEQ ID NO:1033.

[0300] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:1054, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1054. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1054 are provided in Figure 34 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:1055, SEQ ID NO:1057, SEQ ID NO:1058, SEQ ID NO:1059, SEQ ID NO:1061, SEQ ID NO:1063, SEQ ID NO:1065, SEQ ID NO:1065, SEQ ID NO:1067, SEQ ID NO:1068, SEQ ID NO:1070, SEQ ID NO:1071, SEQ ID NO:1072, SEQ ID NO:1074, SEQ ID NO:1075, SEQ ID NO:1076, SEQ ID NO:1077, SEQ ID NO:1078, SEQ ID NO:1080, SEQ ID NO:1082, SEQ ID NO:1083, SEQ ID NO:1085, SEQ ID NO:1086, SEQ ID NO:1087, SEQ ID NO:1088, SEQ ID NO:1089, SEQ ID NO:1089, SEQ ID NO:1090, SEQ ID NO:1091, SEQ ID NO:1092, SEQ ID NO:1093, SEQ ID NO:1094, SEQ ID NO:1095, and SEQ ID NO:1097.

[0301] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:1099, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1099. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1099 are provided in Figure 35 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:1101, SEQ ID NO:1103, SEQ ID NO:1104, SEQ ID NO:1105, SEQ ID NO:1106, SEQ ID NO:1108, SEQ ID NO:1109, and SEQ ID NO:1110.

[0302] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:1112, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1112. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1112 are provided in Figure 36

and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:1113 and SEQ ID NO:1114.

[0303] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:1116, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1116. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1116 are provided in Figure 37 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:1118, SEQ ID NO:1120, SEQ ID NO:1122, SEQ ID NO:1123, SEQ ID NO:1125, SEQ ID NO:1126, SEQ ID NO:1128, SEQ ID NO:1129, SEQ ID NO:1131, SEQ ID NO:1132, SEQ ID NO:1133, SEQ ID NO:1134, SEQ ID NO:1136, SEQ ID NO:1138, SEQ ID NO:1140, SEQ ID NO:1141, SEQ ID NO:1142, SEQ ID NO:1143, SEQ ID NO:1144, SEQ ID NO:1145, SEQ ID NO:1147, SEQ ID NO:1149, SEQ ID NO:1151, SEQ ID NO:1153, and SEQ ID NO:1155.

[0304] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:1159, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1159. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1159 are provided in Figure 38 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:1161, SEQ ID NO:1162, SEQ ID NO:1163, and SEQ ID NO:1164.

[0305] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:1166, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1166. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1166 are provided in Figure 39 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:1167, SEQ ID NO:1169, SEQ ID NO:1171, SEQ ID NO:1173, SEQ ID NO:1175, SEQ ID NO:1177, SEQ ID NO:1179, SEQ ID NO:1180, SEQ ID NO:1182, and SEQ ID NO:1183.

[0306] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID

NO:1185, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1185. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1185 are provided in Figure 40 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:1187, SEQ ID NO:1189, SEQ ID NO:1190, SEQ ID NO:1191, and SEQ ID NO:1192.

[0307] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:1194, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1194. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1194 are provided in Figure 41 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:1196, SEQ ID NO:1198, SEQ ID NO:1200, SEQ ID NO:1202, SEQ ID NO:1203, SEQ ID NO:1204, SEQ ID NO:1205, SEQ ID NO:1206, SEQ ID NO:1207, and SEQ ID NO:1208.

[0308] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:1210, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1210. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1210 are provided in Figure 42 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:1211, SEQ ID NO:1213, SEQ ID NO:1215, SEQ ID NO:1216, SEQ ID NO:1218, SEQ ID NO:1220, SEQ ID NO:1222, SEQ ID NO:1224, SEQ ID NO:1226, SEQ ID NO:1228, SEQ ID NO:1229, SEQ ID NO:1230, SEQ ID NO:1232, SEQ ID NO:1233, SEQ ID NO:1234, SEQ ID NO:1235, SEQ ID NO:1236, SEQ ID NO:1237, SEQ ID NO:1238, SEQ ID NO:1239, SEQ ID NO:1240, SEQ ID NO:1241, SEQ ID NO:1242, SEQ ID NO:1243, SEQ ID NO:1244, SEQ ID NO:1245, SEQ ID NO:1246, SEQ ID NO:1247, SEQ ID NO:1248, SEQ ID NO:1249, SEQ ID NO:1251, SEQ ID NO:1253, SEQ ID NO:1255, SEQ ID NO:1257, SEQ ID NO:1259, SEQ ID NO:1261, SEQ ID NO:1263, SEQ ID NO:1264, SEQ ID NO:1265, SEQ ID NO:1266, SEQ ID NO:1267, SEQ ID NO:1268, SEQ ID NO:1269, SEQ ID NO:1270, SEQ ID NO:1271, and SEQ ID NO:1272.

[0309] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID

NO:1274, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1274. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1274 are provided in Figure 43 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:1276, SEQ ID NO:1278, SEQ ID NO:1280, SEQ ID NO:1281, SEQ ID NO:1282, SEQ ID NO:1284, SEQ ID NO:1285, SEQ ID NO:1287, SEQ ID NO:1289, SEQ ID NO:1291, SEQ ID NO:1293, SEQ ID NO:1294, SEQ ID NO:1295, SEQ ID NO:1296, SEQ ID NO:1297, SEQ ID NO:1298, and SEQ ID NO:1300.

[0310] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:1302, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1302. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1302 are provided in Figure 44 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:1303, SEQ ID NO:1305, SEQ ID NO:1307, SEQ ID NO:1309, SEQ ID NO:1311, SEQ ID NO:1312, SEQ ID NO:1313, SEQ ID NO:1314, SEQ ID NO:1315, SEQ ID NO:1317, SEQ ID NO:1318, SEQ ID NO:1319, SEQ ID NO:1320, SEQ ID NO:1321, SEQ ID NO:1322, SEQ ID NO:1323, SEQ ID NO:1324, SEQ ID NO:1325, SEQ ID NO:1326, SEQ ID NO:1327, SEQ ID NO:1328, SEQ ID NO:1330, SEQ ID NO:1331, SEQ ID NO:1333, SEQ ID NO:1334, SEQ ID NO:1335, SEQ ID NO:1336, SEQ ID NO:1337, SEQ ID NO:1338, SEQ ID NO:1339, and SEQ ID NO:1340.

[0311] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:1342, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1342. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1342 are provided in Figure 45 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:1344, SEQ ID NO:1346, SEQ ID NO:1348, SEQ ID NO:1350, SEQ ID NO:1352, SEQ ID NO:1354, SEQ ID NO:1355, SEQ ID NO:1357, SEQ ID NO:1358, SEQ ID NO:1360, SEQ ID NO:1361, SEQ ID NO:1362, SEQ ID NO:1363, SEQ ID NO:1364, SEQ ID NO:1366, SEQ ID NO:1367, SEQ ID NO:1369, SEQ ID NO:1370, SEQ ID NO:1371, SEQ ID NO:1372,

SEQ ID NO:1373, SEQ ID NO:1374, SEQ ID NO:1375, SEQ ID NO:1376, SEQ ID NO:1377, SEQ ID NO:1378, SEQ ID NO:1379, SEQ ID NO:1380, SEQ ID NO:1381, SEQ ID NO:1382, and SEQ ID NO:1383.

[0312] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:1385, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1385. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1385 are provided in Figure 46 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:1387, SEQ ID NO:1389, SEQ ID NO:1390, SEQ ID NO:1391, SEQ ID NO:1393, SEQ ID NO:1394, SEQ ID NO:1395, SEQ ID NO:1396, SEQ ID NO:1398, SEQ ID NO:1400, SEQ ID NO:1401, SEQ ID NO:1402, SEQ ID NO:1403, SEQ ID NO:1404, SEQ ID NO:1405, and SEQ ID NO:1407.

[0313] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:1409, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1409. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1409 are provided in Figure 47 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:1411, SEQ ID NO:1413, SEQ ID NO:1415, SEQ ID NO:1417, SEQ ID NO:1418, SEQ ID NO:1419, SEQ ID NO:1421, SEQ ID NO:1423, SEQ ID NO:1424, SEQ ID NO:1425, and SEQ ID NO:1426.

[0314] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:1428, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1428. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1428 are provided in Figure 48 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:1430, SEQ ID NO:1432, SEQ ID NO:1434, SEQ ID NO:1436, SEQ ID NO:1439, SEQ ID NO:1442, SEQ ID NO:1444, SEQ ID NO:1446, SEQ ID NO:1448, SEQ ID NO:1450, SEQ ID NO:1452, SEQ ID NO:1453, SEQ ID NO:1454, SEQ ID NO:1455, SEQ ID NO:1456, SEQ

ID NO:1457, SEQ ID NO:1458, and SEQ ID NO:1459.

[0315] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:1463, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1463. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1463 are provided in Figure 49 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:1465, SEQ ID NO:1467, SEQ ID NO:1469, SEQ ID NO:1471, SEQ ID NO:1473, SEQ ID NO:1474, SEQ ID NO:1475, SEQ ID NO:1476, and SEQ ID NO:1477.

[0316] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:1491, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1491. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1491 are provided in Figure 50 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:1493, SEQ ID NO:1495, SEQ ID NO:1497, SEQ ID NO:1499, SEQ ID NO:1501, SEQ ID NO:1503, SEQ ID NO:1504, SEQ ID NO:1505, SEQ ID NO:1506, and SEQ ID NO:1508.

[0317] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:1510, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1510. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1510 are provided in Figure 51 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:1512, SEQ ID NO:1514, SEQ ID NO:1516, SEQ ID NO:1518, SEQ ID NO:1520, SEQ ID NO:1522, and SEQ ID NO:1523.

[0318] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:1525, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1525. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1525 are provided in Figure 52

and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:1527, SEQ ID NO:1529, SEQ ID NO:1530, SEQ ID NO:1532, SEQ ID NO:1534, and SEQ ID NO:1535.

[0319] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:1537, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1537. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1537 are provided in Figure 53 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:1539, SEQ ID NO:1540, SEQ ID NO:1541, SEQ ID NO:1543, SEQ ID NO:1545, SEQ ID NO:1547, SEQ ID NO:1548, SEQ ID NO:1550, SEQ ID NO:1552, SEQ ID NO:2386, SEQ ID NO:2388, SEQ ID NO:2390, SEQ ID NO:2391,, and SEQ ID NO:2392.

[0320] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:1554, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1554. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1554 are provided in Figure 54 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:1555, SEQ ID NO:1557, SEQ ID NO:1559, SEQ ID NO:1561, SEQ ID NO:1563, SEQ ID NO:1565, SEQ ID NO:1567, SEQ ID NO:1569, SEQ ID NO:1571, SEQ ID NO:1572, SEQ ID NO:1573, SEQ ID NO:1574, and SEQ ID NO:1575.

[0321] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:1577, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1577. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1577 are provided in Figure 55 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:1035, SEQ ID NO:1036, SEQ ID NO:1037, SEQ ID NO:1040, SEQ ID NO:1041, SEQ ID NO:1043, SEQ ID NO:1044, SEQ ID NO:1046, SEQ ID NO:1047, SEQ ID NO:1048, SEQ ID NO:1050, SEQ ID NO:1440, SEQ ID NO:1480, SEQ ID NO:1481, SEQ ID NO:1482, SEQ ID NO:1483, SEQ ID NO:1484, SEQ ID NO:1485, SEQ ID NO:1486, SEQ ID NO:1487,

SEQ ID NO:1488, SEQ ID NO:1578, SEQ ID NO:1580, SEQ ID NO:1582, SEQ ID NO:1584, SEQ ID NO:1586, SEQ ID NO:1588, SEQ ID NO:1590, SEQ ID NO:1592, SEQ ID NO:1594, SEQ ID NO:1596, SEQ ID NO:1598, SEQ ID NO:1599, SEQ ID NO:1601, SEQ ID NO:1602, SEQ ID NO:1605, SEQ ID NO:1607, SEQ ID NO:1608, SEQ ID NO:1609, SEQ ID NO:1611, SEQ ID NO:1613, SEQ ID NO:1615, SEQ ID NO:1617, SEQ ID NO:1619, SEQ ID NO:1621, SEQ ID NO:1622, SEQ ID NO:1623, SEQ ID NO:1624, SEQ ID NO:1625, SEQ ID NO:1627, SEQ ID NO:1629, SEQ ID NO:1631, SEQ ID NO:1633, SEQ ID NO:1635, SEQ ID NO:1637, SEQ ID NO:1639, SEQ ID NO:1643, SEQ ID NO:1645, SEQ ID NO:1648, SEQ ID NO:1649, SEQ ID NO:1651, SEQ ID NO:1653.

[0322] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:1437, and preferably has at least 20%, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1437. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1437 are provided in Figure 56 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:173, SEQ ID NO:212, SEQ ID NO:361, SEQ ID NO:421, SEQ ID NO:443, SEQ ID NO:740, SEQ ID NO:744, SEQ ID NO:942, SEQ ID NO:1461.

[0323] In some cases, a low nitrogen tolerance-modulating polypeptide has an amino acid sequence with sequence similarity to the amino acid sequence set forth in SEQ ID NO:97, and preferably has at least 20%, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:97. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:1437 are provided in Figure 57 and in the Sequence Listing. Examples of such polypeptides include SEQ ID NO:2010, SEQ ID NO:2011, SEQ ID NO:2013, SEQ ID NO:2015, and SEQ ID NO:2017

E. Other Sequences

[0324] It should be appreciated that a low nitrogen tolerance-modulating polypeptide can include additional amino acids that are not involved in low nitrogen tolerance-modulation, and thus such a polypeptide can be longer than would otherwise be the case. For example, a low nitrogen tolerance-modulating polypeptide can include a purification tag, a chloroplast transit peptide, a mitochondrial transit peptide, an amyloplast peptide, or a leader sequence added to the amino or carboxy terminus. In some embodiments, a low nitrogen

tolerance-modulating polypeptide includes an amino acid sequence that functions as a reporter, *e.g.*, a green fluorescent protein or yellow fluorescent protein.

III. Nucleic Acids

[0325] Nucleic acids described herein include nucleic acids that are effective to modulate low-nitrogen tolerance levels when transcribed in a plant or plant cell. Such nucleic acids include, without limitation, those that encode a low nitrogen tolerance-modulating polypeptide and those that can be used to inhibit expression of low nitrogen tolerance-modulating polypeptide via a nucleic acid based method.

A. Nucleic acids encoding low nitrogen tolerance-modulating polypeptides

[0326] Nucleic acids encoding low nitrogen tolerance-modulating polypeptides are described herein. Examples of such nucleic acids include SEQ ID NO:1, SEQ ID NO:48, SEQ ID NO:76, SEQ ID NO:96, SEQ ID NO:99, SEQ ID NO:151, SEQ ID NO:165, SEQ ID NO:175, SEQ ID NO:185, SEQ ID NO:207, SEQ ID NO:217, SEQ ID NO:233, SEQ ID NO:245, SEQ ID NO:299, SEQ ID NO:331, SEQ ID NO:367, SEQ ID NO:509, SEQ ID NO:532, SEQ ID NO:555, SEQ ID NO:557, SEQ ID NO:592, SEQ ID NO:612, SEQ ID NO:645, SEQ ID NO:686, SEQ ID NO:729, SEQ ID NO:745, SEQ ID NO:768, SEQ ID NO:791, SEQ ID NO:823, SEQ ID NO:827, SEQ ID NO:852, SEQ ID NO:854, SEQ ID NO:890, SEQ ID NO:916, SEQ ID NO:943, SEQ ID NO:975, SEQ ID NO:981, SEQ ID NO:1053, SEQ ID NO:1098, SEQ ID NO:1111, SEQ ID NO:1115, SEQ ID NO:1156, SEQ ID NO:1158, SEQ ID NO:1165, SEQ ID NO:1184, SEQ ID NO:1193, SEQ ID NO:1209, SEQ ID NO:1273, SEQ ID NO:1301, SEQ ID NO:1341, SEQ ID NO:1384, SEQ ID NO:1408, SEQ ID NO:1427, SEQ ID NO:1462, SEQ ID NO:1490, SEQ ID NO:1509, SEQ ID NO:1524, SEQ ID NO:1536, SEQ ID NO:1553, and SEQ ID NO:1576, as described in more detail below. A nucleic acid also can be a fragment that is at least 40% (*e.g.*, at least 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 99%) of the length of the full-length nucleic acid set forth in SEQ ID NO:1, SEQ ID NO:48, SEQ ID NO:76, SEQ ID NO:96, SEQ ID NO:99, SEQ ID NO:151, SEQ ID NO:165, SEQ ID NO:175, SEQ ID NO:185, SEQ ID NO:207, SEQ ID NO:217, SEQ ID NO:233, SEQ ID NO:245, SEQ ID NO:299, SEQ ID NO:331, SEQ ID NO:367, SEQ ID NO:509, SEQ ID NO:532, SEQ ID NO:555, SEQ ID NO:557, SEQ ID NO:592, SEQ ID NO:612, SEQ ID NO:645, SEQ ID NO:686, SEQ ID NO:729, SEQ ID NO:745, SEQ ID NO:768, SEQ ID NO:791, SEQ ID NO:823, SEQ ID NO:827, SEQ ID NO:852, SEQ ID NO:854, SEQ ID NO:890, SEQ ID NO:916, SEQ ID NO:943,

SEQ ID NO:975, SEQ ID NO:981, SEQ ID NO:1053, SEQ ID NO:1098, SEQ ID NO:1111, SEQ ID NO:1115, SEQ ID NO:1156, SEQ ID NO:1158, SEQ ID NO:1165, SEQ ID NO:1184, SEQ ID NO:1193, SEQ ID NO:1209, SEQ ID NO:1273, SEQ ID NO:1301, SEQ ID NO:1341, SEQ ID NO:1384, SEQ ID NO:1408, SEQ ID NO:1427, SEQ ID NO:1462, SEQ ID NO:1490, SEQ ID NO:1509, SEQ ID NO:1524, SEQ ID NO:1536, SEQ ID NO:1553, and SEQ ID NO:1576.

[0327] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:2. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:2.

[0328] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO: 48. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO: 48. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO: 48.

[0329] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:76. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:76. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:76.

[0330] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:96. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:96. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:96.

[0331] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:99. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:99. For example, a low nitrogen tolerance-modulating nucleic acid can have a

nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:99.

[0332] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:151. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:151. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:151.

[0333] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:165. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:165. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:165.

[0334] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:175. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:175. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:175.

[0335] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:185. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:185. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:185.

[0336] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:207. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:207. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:207.

[0337] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:217. Alternatively, a low nitrogen tolerance-modulating

nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:217. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:217.

[0338] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:233. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:233. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:233.

[0339] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:245. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:245. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:245.

[0340] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:299. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:299. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:299.

[0341] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:331. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:331. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:331.

[0342] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:367. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:367. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:367.

[0343] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:509. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:509. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:509.

[0344] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:532. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:532. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:532.

[0345] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:555. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:555. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:555.

[0346] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:557. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:557. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:557.

[0347] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:592. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:592. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:592.

[0348] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:612. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:612. For example, a low nitrogen tolerance-modulating nucleic acid can have a

nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:612.

[0349] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:645. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:645. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:645.

[0350] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:686. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:686. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:686.

[0351] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:729. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:729. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:729.

[0352] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:745. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:745. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:745.

[0353] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:768. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:768. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:768.

[0354] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:791. Alternatively, a low nitrogen tolerance-modulating

nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:791. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:791.

[0355] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:823. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:823. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:823.

[0356] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:827. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:827. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:827.

[0357] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:852. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:852. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:852.

[0358] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:854. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:854. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:854.

[0359] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:890. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:890. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:890.

[0360] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:916. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:916. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:916.

[0361] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:943. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:943. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:943.

[0362] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:975. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:975. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:975.

[0363] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:981. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:981. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:981.

[0364] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO: 1034. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO: 1034. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO: 1034.

[0365] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1053. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1053. For example, a low nitrogen tolerance-modulating nucleic acid can have a

nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1053.

[0366] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1098. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1098. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1098.

[0367] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1111. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1111. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1111.

[0368] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1115. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1115. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1115.

[0369] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1156. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1156. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1156.

[0370] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1158. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1158. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1158.

[0371] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1165. Alternatively, a low nitrogen tolerance-modulating

nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1165. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1165.

[0372] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1184. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1184. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1184.

[0373] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1193. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1193. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1193.

[0374] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO: 1209. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO: 1209. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO: 1209.

[0375] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1273. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1273. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1273.

[0376] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1301. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1301. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1301.

[0377] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1341. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1341. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1341.

[0378] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1384. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1384. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1384.

[0379] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1408. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1408. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1408.

[0380] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1427. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1427. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1427.

[0381] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1462. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1462. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1462.

[0382] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1490. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1490. For example, a low nitrogen tolerance-modulating nucleic acid can have a

nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1490.

[0383] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1509. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1509. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1509.

[0384] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1524. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1524. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1524.

[0385] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1536. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1536. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1536.

[0386] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1553. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1553. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1553.

[0387] A low nitrogen tolerance-modulating nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1576. Alternatively, a low nitrogen tolerance-modulating nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1576. For example, a low nitrogen tolerance-modulating nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1576.

[0388] Isolated nucleic acid molecules can be produced by standard techniques. For example, polymerase chain reaction (PCR) techniques can be used to obtain an isolated

nucleic acid containing a nucleotide sequence described herein. PCR can be used to amplify specific sequences from DNA as well as RNA, including sequences from total genomic DNA or total cellular RNA. Various PCR methods are described, for example, in PCR Primer: A Laboratory Manual, Dieffenbach and Dveksler, eds., Cold Spring Harbor Laboratory Press, 1995. Generally, sequence information from the ends of the region of interest or beyond is employed to design oligonucleotide primers that are identical or similar in sequence to opposite strands of the template to be amplified. Various PCR strategies also are available by which site-specific nucleotide sequence modifications can be introduced into a template nucleic acid. Isolated nucleic acids also can be chemically synthesized, either as a single nucleic acid molecule (*e.g.*, using automated DNA synthesis in the 3′ to 5′ direction using phosphoramidite technology) or as a series of oligonucleotides. For example, one or more pairs of long oligonucleotides (*e.g.*, >100 nucleotides) can be synthesized that contain the desired sequence, with each pair containing a short segment of complementarity (*e.g.*, about 15 nucleotides) such that a duplex is formed when the oligonucleotide pair is annealed. DNA polymerase is used to extend the oligonucleotides, resulting in a single, double-stranded nucleic acid molecule per oligonucleotide pair, which then can be ligated into a vector. Isolated nucleic acids of the invention also can be obtained by mutagenesis of, *e.g.*, a naturally occurring DNA.

B. Use of Nucleic Acids to Modulate Expression of Polypeptides

i. Expression of a Low Nitrogen Tolerance-Modulating Polypeptide

[0389] A nucleic acid encoding one of the low nitrogen tolerance-modulating polypeptides described herein can be used to express the polypeptide in a plant species of interest, typically by transforming a plant cell with a nucleic acid having the coding sequence for the polypeptide operably linked in sense orientation to one or more regulatory regions. It will be appreciated that because of the degeneracy of the genetic code, a number of nucleic acids can encode a particular low nitrogen tolerance-modulating polypeptide; *i.e.*, for many amino acids, there is more than one nucleotide triplet that serves as the codon for the amino acid. Thus, codons in the coding sequence for a given low nitrogen tolerance-modulating polypeptide can be modified such that optimal expression in a particular plant species is obtained, using appropriate codon bias tables for that species.

[0390] In some cases, expression of a low nitrogen tolerance-modulating polypeptide inhibits one or more functions of an endogenous polypeptide. For example, a nucleic acid that encodes a dominant negative polypeptide can be used to inhibit protein function. A

dominant negative polypeptide typically is mutated or truncated relative to an endogenous wild type polypeptide, and its presence in a cell inhibits one or more functions of the wild type polypeptide in that cell, *i.e.*, the dominant negative polypeptide is genetically dominant and confers a loss of function. The mechanism by which a dominant negative polypeptide confers such a phenotype can vary but often involves a protein-protein interaction or a protein-DNA interaction. For example, a dominant negative polypeptide can be an enzyme that is truncated relative to a native wild type enzyme, such that the truncated polypeptide retains domains involved in binding a first protein but lacks domains involved in binding a second protein. The truncated polypeptide is thus unable to properly modulate the activity of the second protein. See, *e.g.*, US 2007/0056058. As another example, a point mutation that results in a non-conservative amino acid substitution in a catalytic domain can result in a dominant negative polypeptide. See, *e.g.*, US 2005/032221. As another example, a dominant negative polypeptide can be a transcription factor that is truncated relative to a native wild type transcription factor, such that the truncated polypeptide retains the DNA binding domain(s) but lacks the activation domain(s). Such a truncated polypeptide can inhibit the wild type transcription factor from binding DNA, thereby inhibiting transcription activation.

ii. Inhibition of Expression of a Low Nitrogen Tolerance-Modulating Polypeptide

[0391] Polynucleotides and recombinant constructs described herein can be used to inhibit expression of a low nitrogen tolerance-modulating polypeptide in a plant species of interest. See, *e.g.*, Matzke and Birchler, Nature Reviews Genetics 6:24-35 (2005); Akashi et al., Nature Reviews Mol. Cell Biology 6:413-422 (2005); Mittal, Nature Reviews Genetics 5:355-365 (2004); Dorsett and Tuschl, Nature Reviews Drug Discovery 3: 318-329 (2004); and Nature Reviews RNA interference collection, Oct. 2005 at nature.com/reviews/focus/mai. A number of nucleic acid based methods, including antisense RNA, ribozyme directed RNA cleavage, post-transcriptional gene silencing (PTGS), *e.g.*, RNA interference (RNAi), and transcriptional gene silencing (TGS) are known to inhibit gene expression in plants. Suitable polynucleotides include full-length nucleic acids encoding low nitrogen tolerance-modulating polypeptides or fragments of such full-length nucleic acids. In some embodiments, a complement of the full-length nucleic acid or a fragment thereof can be used. Typically, a fragment is at least 10 nucleotides, *e.g.*, at least 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 30, 35, 40, 50, 80, 100, 200, 500 nucleotides or more. Generally, higher homology can be used to compensate for the use of a shorter sequence.

[0392] Antisense technology is one well-known method. In this method, a nucleic acid of a gene to be repressed is cloned and operably linked to a regulatory region and a transcription termination sequence so that the antisense strand of RNA is transcribed. The recombinant construct is then transformed into plants, as described herein, and the antisense strand of RNA is produced. The nucleic acid need not be the entire sequence of the gene to be repressed, but typically will be substantially complementary to at least a portion of the sense strand of the gene to be repressed.

[0393] In another method, a nucleic acid can be transcribed into a ribozyme, or catalytic RNA, that affects expression of an mRNA. *See*, U.S. Patent No. 6,423,885. Ribozymes can be designed to specifically pair with virtually any target RNA and cleave the phosphodiester backbone at a specific location, thereby functionally inactivating the target RNA. Heterologous nucleic acids can encode ribozymes designed to cleave particular mRNA transcripts, thus preventing expression of a polypeptide. Hammerhead ribozymes are useful for destroying particular mRNAs, although various ribozymes that cleave mRNA at site-specific recognition sequences can be used. Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. The sole requirement is that the target RNA contains a 5´-UG-3´ nucleotide sequence. The construction and production of hammerhead ribozymes is known in the art. *See*, for example, U.S. Patent No. 5,254,678 and WO 02/46449 and references cited therein. Hammerhead ribozyme sequences can be embedded in a stable RNA such as a transfer RNA (tRNA) to increase cleavage efficiency *in vivo*. Perriman *et al.* (1995) *Proc. Natl. Acad. Sci. USA*, 92(13):6175-6179; de Feyter and Gaudron, Methods in Molecular Biology, Vol. 74, Chapter 43, "Expressing Ribozymes in Plants", Edited by Turner, P.C., Humana Press Inc., Totowa, NJ. RNA endoribonucleases which have been described, such as the one that occurs naturally in *Tetrahymena thermophila*, can be useful. *See*, for example, U.S. Patent No. 4,987,071 and 6,423,885.

[0394] PTGS, *e.g.*, RNAi, can also be used to inhibit the expression of a gene. For example, a construct can be prepared that includes a sequence that is transcribed into an RNA that can anneal to itself, *e.g.*, a double stranded RNA having a stem-loop structure. In some embodiments, one strand of the stem portion of a double stranded RNA comprises a sequence that is similar or identical to the sense coding sequence or a fragment thereof of a low nitrogen tolerance-modulating polypeptide, and that is from about 10 nucleotides to about 2,500 nucleotides in length. The length of the sequence that is similar or identical to the sense coding sequence can be from 10 nucleotides to 500 nucleotides, from 15 nucleotides to

300 nucleotides, from 20 nucleotides to 100 nucleotides, or from 25 nucleotides to 100 nucleotides. The other strand of the stem portion of a double stranded RNA comprises a sequence that is similar or identical to the antisense strand or a fragment thereof of the coding sequence of the low nitrogen tolerance-modulating polypeptide, and can have a length that is shorter, the same as, or longer than the corresponding length of the sense sequence. In some cases, one strand of the stem portion of a double stranded RNA comprises a sequence that is similar or identical to the 3´ or 5´ untranslated region, or a fragment thereof, of an mRNA encoding a low nitrogen tolerance-modulating polypeptide, and the other strand of the stem portion of the double stranded RNA comprises a sequence that is similar or identical to the sequence that is complementary to the 3´ or 5´ untranslated region, respectively, or a fragment thereof , of the mRNA encoding the low nitrogen tolerance-modulating polypeptide. In other embodiments, one strand of the stem portion of a double stranded RNA comprises a sequence that is similar or identical to the sequence of an intron, or a fragment thereof, in the pre-mRNA encoding a low nitrogen tolerance-modulating polypeptide, and the other strand of the stem portion comprises a sequence that is similar or identical to the sequence that is complementary to the sequence of the intron, or a fragment thereof, in the pre-mRNA.

[0395] The loop portion of a double stranded RNA can be from 3 nucleotides to 5,000 nucleotides, *e.g.*, from 3 nucleotides to 25 nucleotides, from 15 nucleotides to 1,000 nucleotides, from 20 nucleotides to 500 nucleotides, or from 25 nucleotides to 200 nucleotides. The loop portion of the RNA can include an intron or a fragment thereof. A double stranded RNA can have zero, one, two, three, four, five, six, seven, eight, nine, ten, or more stem-loop structures.

[0396] A construct including a sequence that is operably linked to a regulatory region and a transcription termination sequence, and that is transcribed into an RNA that can form a double stranded RNA, is transformed into plants as described herein. Methods for using RNAi to inhibit the expression of a gene are known to those of skill in the art. *See*, *e.g.*, U.S. Patents 5,034,323; 6,326,527; 6,452,067; 6,573,099; 6,753,139; and 6,777,588. *See* also WO 97/01952; WO 98/53083; WO 99/32619; WO 98/36083; and U.S. Patent Publications 20030175965, 20030175783, 20040214330, and 20030180945.

[0397] Constructs containing regulatory regions operably linked to nucleic acid molecules in sense orientation can also be used to inhibit the expression of a gene. The transcription product can be similar or identical to the sense coding sequence, or a fragment thereof, of a low nitrogen tolerance-modulating polypeptide. The transcription product also

can be unpolyadenylated, lack a 5′ cap structure, or contain an unspliceable intron. Methods of inhibiting gene expression using a full-length cDNA as well as a partial cDNA sequence are known in the art. *See*, *e.g.*, U.S. Patent No. 5,231,020.

[0398] In some embodiments, a construct containing a nucleic acid having at least one strand that is a template for both sense and antisense sequences that are complementary to each other is used to inhibit the expression of a gene. The sense and antisense sequences can be part of a larger nucleic acid molecule or can be part of separate nucleic acid molecules having sequences that are not complementary. The sense or antisense sequence can be a sequence that is identical or complementary to the sequence of an mRNA, the 3′ or 5′ untranslated region of an mRNA, or an intron in a pre-mRNA encoding a low nitrogen tolerance-modulating polypeptide, or a fragment of such sequences. In some embodiments, the sense or antisense sequence is identical or complementary to a sequence of the regulatory region that drives transcription of the gene encoding a low nitrogen tolerance-modulating polypeptide. In each case, the sense sequence is the sequence that is complementary to the antisense sequence.

[0399] The sense and antisense sequences can be any length greater than about 10 nucleotides (*e.g.*, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, or more nucleotides). For example, an antisense sequence can be 21 or 22 nucleotides in length. Typically, the sense and antisense sequences range in length from about 15 nucleotides to about 30 nucleotides, *e.g.*, from about 18 nucleotides to about 28 nucleotides, or from about 21 nucleotides to about 25 nucleotides.

[0400] In some embodiments, an antisense sequence is a sequence complementary to an mRNA sequence, or a fragment thereof, encoding a low nitrogen tolerance-modulating polypeptide described herein. The sense sequence complementary to the antisense sequence can be a sequence present within the mRNA of the low nitrogen tolerance-modulating polypeptide. Typically, sense and antisense sequences are designed to correspond to a 15-30 nucleotide sequence of a target mRNA such that the level of that target mRNA is reduced.

[0401] In some embodiments, a construct containing a nucleic acid having at least one strand that is a template for more than one sense sequence (*e.g.*, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more sense sequences) can be used to inhibit the expression of a gene. Likewise, a construct containing a nucleic acid having at least one strand that is a template for more than one antisense sequence (*e.g.*, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more antisense sequences) can be used to inhibit the expression of a gene. For example, a construct can contain a nucleic acid having at least one strand that is a template for two sense sequences and two antisense sequences.

The multiple sense sequences can be identical or different, and the multiple antisense sequences can be identical or different. For example, a construct can have a nucleic acid having one strand that is a template for two identical sense sequences and two identical antisense sequences that are complementary to the two identical sense sequences. Alternatively, an isolated nucleic acid can have one strand that is a template for (1) two identical sense sequences 20 nucleotides in length, (2) one antisense sequence that is complementary to the two identical sense sequences 20 nucleotides in length, (3) a sense sequence 30 nucleotides in length, and (4) three identical antisense sequences that are complementary to the sense sequence 30 nucleotides in length. The constructs provided herein can be designed to have any arrangement of sense and antisense sequences. For example, two identical sense sequences can be followed by two identical antisense sequences or can be positioned between two identical antisense sequences.

[0402] A nucleic acid having at least one strand that is a template for one or more sense and/or antisense sequences can be operably linked to a regulatory region to drive transcription of an RNA molecule containing the sense and/or antisense sequence(s). In addition, such a nucleic acid can be operably linked to a transcription terminator sequence, such as the terminator of the nopaline synthase (*nos*) gene. In some cases, two regulatory regions can direct transcription of two transcripts: one from the top strand, and one from the bottom strand. *See*, for example, Yan *et al.*, *Plant Physiol.*, 141:1508-1518 (2006). The two regulatory regions can be the same or different. The two transcripts can form double-stranded RNA molecules that induce degradation of the target RNA. In some cases, a nucleic acid can be positioned within a T-DNA or plant-derived transfer DNA (P-DNA) such that the left and right T-DNA border sequences, or the left and right border-like sequences of the P-DNA, flank or are on either side of the nucleic acid. See, US 2006/0265788. The nucleic acid sequence between the two regulatory regions can be from about 15 to about 300 nucleotides in length. In some embodiments, the nucleic acid sequence between the two regulatory regions is from about 15 to about 200 nucleotides in length, from about 15 to about 100 nucleotides in length, from about 15 to about 50 nucleotides in length, from about 18 to about 50 nucleotides in length, from about 18 to about 40 nucleotides in length, from about 18 to about 30 nucleotides in length, or from about 18 to about 25 nucleotides in length.

[0403] In some nucleic-acid based methods for inhibition of gene expression in plants, a suitable nucleic acid can be a nucleic acid analog. Nucleic acid analogs can be modified at the base moiety, sugar moiety, or phosphate backbone to improve, for example,

stability, hybridization, or solubility of the nucleic acid. Modifications at the base moiety include deoxyuridine for deoxythymidine, and 5-methyl-2'-deoxycytidine and 5-bromo-2'-deoxycytidine for deoxycytidine. Modifications of the sugar moiety include modification of the 2' hydroxyl of the ribose sugar to form 2'-O-methyl or 2'-O-allyl sugars. The deoxyribose phosphate backbone can be modified to produce morpholino nucleic acids, in which each base moiety is linked to a six-membered morpholino ring, or peptide nucleic acids, in which the deoxyphosphate backbone is replaced by a pseudopeptide backbone and the four bases are retained. *See*, for example, Summerton and Weller (1997) *Antisense Nucleic Acid Drug Dev.*, 7:187-195; Hyrup *et al.* (1996) *Bioorgan. Med. Chem.*, 4:5-23. In addition, the deoxyphosphate backbone can be replaced with, for example, a phosphorothioate or phosphorodithioate backbone, a phosphoroamidite, or an alkyl phosphotriester backbone.

C. Constructs/Vectors

[0404] Recombinant constructs provided herein can be used to transform plants or plant cells in order to modulate low-nitrogen tolerance levels. A recombinant nucleic acid construct can comprise a nucleic acid encoding a low nitrogen tolerance-modulating polypeptide as described herein, operably linked to a regulatory region suitable for expressing the low nitrogen tolerance-modulating polypeptide in the plant or cell. Thus, a nucleic acid can comprise a coding sequence that encodes any of the low nitrogen tolerance-modulating polypeptides as set forth in SEQ ID NO:3, SEQ ID NO:49, SEQ ID NO:77, SEQ ID NO:97, SEQ ID NO:100, SEQ ID NO:152, SEQ ID NO:166, SEQ ID NO:186, SEQ ID NO:208, SEQ ID NO:218, SEQ ID NO:234, SEQ ID NO:246, SEQ ID NO:300, SEQ ID NO:332, SEQ ID NO:368, SEQ ID NO:510, SEQ ID NO:533, SEQ ID NO:556, SEQ ID NO:558, SEQ ID NO:593, SEQ ID NO:613, SEQ ID NO:646, SEQ ID NO:687, SEQ ID NO:730, SEQ ID NO:746, SEQ ID NO:769, SEQ ID NO:792, SEQ ID NO:824, SEQ ID NO:828, SEQ ID NO:853, SEQ ID NO:855, SEQ ID NO:891, SEQ ID NO:917, SEQ ID NO:944, SEQ ID NO:976, SEQ ID NO:982, SEQ ID NO:1054, SEQ ID NO:1099, SEQ ID NO:1112, SEQ ID NO:1116, SEQ ID NO:1157, SEQ ID NO:1159, SEQ ID NO:1166, SEQ ID NO:1185, SEQ ID NO:1194, SEQ ID NO:1210, SEQ ID NO:1274, SEQ ID NO:1302, SEQ ID NO:1342, SEQ ID NO:1385, SEQ ID NO:1409, SEQ ID NO:1428, SEQ ID NO:1437, SEQ ID NO:1463, SEQ ID NO:1491, SEQ ID NO:1510, SEQ ID NO:1525, SEQ ID NO:1537, SEQ ID NO:1554, and SEQ ID NO:1577. Examples of nucleic acids encoding low nitrogen tolerance-modulating polypeptides are set forth in SEQ ID NO:1, SEQ ID

NO:48, SEQ ID NO:76, SEQ ID NO:96, SEQ ID NO:99, SEQ ID NO:151, SEQ ID NO:165, SEQ ID NO:175, SEQ ID NO:185, SEQ ID NO:207, SEQ ID NO:217, SEQ ID NO:233, SEQ ID NO:245, SEQ ID NO:299, SEQ ID NO:331, SEQ ID NO:367, SEQ ID NO:509, SEQ ID NO:532, SEQ ID NO:555, SEQ ID NO:557, SEQ ID NO:592, SEQ ID NO:612, SEQ ID NO:645, SEQ ID NO:686, SEQ ID NO:729, SEQ ID NO:745, SEQ ID NO:768, SEQ ID NO:791, SEQ ID NO:823, SEQ ID NO:827, SEQ ID NO:852, SEQ ID NO:854, SEQ ID NO:890, SEQ ID NO:916, SEQ ID NO:943, SEQ ID NO:975, SEQ ID NO:981, SEQ ID NO:1053, SEQ ID NO:1098, SEQ ID NO:1111, SEQ ID NO:1115, SEQ ID NO:1156, SEQ ID NO:1158, SEQ ID NO:1165, SEQ ID NO:1184, SEQ ID NO:1193, SEQ ID NO:1209, SEQ ID NO:1273, SEQ ID NO:1301, SEQ ID NO:1341, SEQ ID NO:1384, SEQ ID NO:1408, SEQ ID NO:1427, SEQ ID NO:1462, SEQ ID NO:1490, SEQ ID NO:1509, SEQ ID NO:1524, SEQ ID NO:1536, SEQ ID NO:1553, and SEQ ID NO:1576. The low nitrogen tolerance-modulating polypeptide encoded by a recombinant nucleic acid can be a native low nitrogen tolerance-modulating polypeptide, or can be heterologous to the cell. In some cases, the recombinant construct contains a nucleic acid that inhibits expression of a low nitrogen tolerance-modulating polypeptide, operably linked to a regulatory region. Examples of suitable regulatory regions are described in the section entitled "Regulatory Regions."

[0405] Vectors containing recombinant nucleic acid constructs such as those described herein also are provided. Suitable vector backbones include, for example, those routinely used in the art such as plasmids, viruses, artificial chromosomes, BACs, YACs, or PACs. Suitable expression vectors include, without limitation, plasmids and viral vectors derived from, for example, bacteriophage, baculoviruses, and retroviruses. Numerous vectors and expression systems are commercially available from such corporations as Novagen (Madison, WI), Clontech (Palo Alto, CA), Stratagene (La Jolla, CA), and Invitrogen/Life Technologies (Carlsbad, CA).

[0406] The vectors provided herein also can include, for example, origins of replication, scaffold attachment regions (SARs), and/or markers. A marker gene can confer a selectable phenotype on a plant cell. For example, a marker can confer biocide resistance, such as resistance to an antibiotic (*e.g.*, kanamycin, G418, bleomycin, or hygromycin), or an herbicide (*e.g.*, glyphosate, chlorsulfuron or phosphinothricin). In addition, an expression vector can include a tag sequence designed to facilitate manipulation or detection (*e.g.*, purification or localization) of the expressed polypeptide. Tag sequences, such as luciferase, β-glucuronidase (GUS), green fluorescent protein (GFP), glutathione S-transferase (GST),

polyhistidine, c-myc, hemagglutinin, or Flag™ tag (Kodak, New Haven, CT) sequences typically are expressed as a fusion with the encoded polypeptide. Such tags can be inserted anywhere within the polypeptide, including at either the carboxyl or amino terminus.

D. Regulatory regions

[0407] The choice of regulatory regions to be included in a recombinant construct depends upon several factors, including, but not limited to, efficiency, selectability, inducibility, desired expression level, and cell- or tissue-preferential expression. It is a routine matter for one of skill in the art to modulate the expression of a coding sequence by appropriately selecting and positioning regulatory regions relative to the coding sequence. Transcription of a nucleic acid can be modulated in a similar manner.

[0408] Some suitable regulatory regions initiate transcription only, or predominantly, in certain cell types. Methods for identifying and characterizing regulatory regions in plant genomic DNA are known, including, for example, those described in the following references: Jordano *et al.* (1989) *Plant Cell*, 1:855-866; Bustos *et al.* (1989) *Plant Cell*, 1:839-854; Green *et al.* (1988) *EMBO J.*, 7:4035-4044; Meier *et al.* (1991) *Plant Cell*, 3:309-316; and Zhang *et al.* (1996) *Plant Physiology*, 110:1069-1079.

[0409] Examples of various classes of regulatory regions are described below. Some of the regulatory regions indicated below as well as additional regulatory regions are described in more detail in U.S. Patent Application Ser. Nos. 60/505,689; 60/518,075; 60/544,771; 60/558,869; 60/583,691; 60/619,181; 60/637,140; 60/757,544; 60/776,307; 10/957,569; 11/058,689; 11/172,703; 11/208,308; 11/274,890; 60/583,609; 60/612,891; 11/097,589; 11/233,726; 11/408,791; 11/414,142; 10/950,321; 11/360,017; PCT/US05/011105; PCT/US05/23639; PCT/US05/034308; PCT/US05/034343; and PCT/US06/038236; PCT/US06/040572; and PCT/US07/62762.

[0410] For example, the sequences of regulatory regions p326, YP0144, YP0190, p13879, YP0050, p32449, 21876, YP0158, YP0214, YP0380, PT0848, PT0633, YP0128, YP0275, PT0660, PT0683, PT0758, PT0613, PT0672, PT0688, PT0837, YP0092, PT0676, PT0708, YP0396, YP0007, YP0111, YP0103, YP0028, YP0121, YP0008, YP0039, YP0115, YP0119, YP0120, YP0374, YP0101, YP0102, YP0110, YP0117, YP0137, YP0285, YP0212, YP0097, YP0107, YP0088, YP0143, YP0156, PT0650, PT0695, PT0723, PT0838, PT0879, PT0740, PT0535, PT0668, PT0886, PT0585, YP0381, YP0337, PT0710, YP0356, YP0385, YP0384, YP0286, YP0377, PD1367, PT0863, PT0829, PT0665, PT0678, YP0086, YP0188, YP0263, PT0743 and YP0096 are set forth in the sequence listing of PCT/US06/040572; the

sequence of regulatory region PT0625 is set forth in the sequence listing of PCT/US05/034343; the sequences of regulatory regions PT0623, YP0388, YP0087, YP0093, YP0108, YP0022 and YP0080 are set forth in the sequence listing of U.S. Patent Application Ser. No. 11/172,703; the sequence of regulatory region PR0924 is set forth in the sequence listing of PCT/US07/62762; and the sequences of regulatory regions p530c10, pOsFIE2-2, pOsMEA, pOsYp102, and pOsYp285 are set forth in the sequence listing of PCT/US06/038236.

[0411] It will be appreciated that a regulatory region may meet criteria for one classification based on its activity in one plant species, and yet meet criteria for a different classification based on its activity in another plant species.

i. Broadly Expressing Promoters

[0412] A promoter can be said to be "broadly expressing" when it promotes transcription in many, but not necessarily all, plant tissues. For example, a broadly expressing promoter can promote transcription of an operably linked sequence in one or more of the shoot, shoot tip (apex), and leaves, but weakly or not at all in tissues such as roots or stems. As another example, a broadly expressing promoter can promote transcription of an operably linked sequence in one or more of the stem, shoot, shoot tip (apex), and leaves, but can promote transcription weakly or not at all in tissues such as reproductive tissues of flowers and developing seeds. Non-limiting examples of broadly expressing promoters that can be included in the nucleic acid constructs provided herein include the p326, YP0144, YP0190, p13879, YP0050, p32449, 21876, YP0158, YP0214, YP0380, PT0848, and PT0633 promoters. Additional examples include the cauliflower mosaic virus (CaMV) 35S promoter, the mannopine synthase (MAS) promoter, the 1' or 2' promoters derived from T-DNA of *Agrobacterium tumefaciens*, the figwort mosaic virus 34S promoter, actin promoters such as the rice actin promoter, and ubiquitin promoters such as the maize ubiquitin-1 promoter. In some cases, the CaMV 35S promoter is excluded from the category of broadly expressing promoters.

ii. Root Promoters

[0413] Root-active promoters confer transcription in root tissue, *e.g.*, root endodermis, root epidermis, or root vascular tissues. In some embodiments, root-active promoters are root-preferential promoters, *i.e.*, confer transcription only or predominantly in root tissue. Root-preferential promoters include the YP0128, YP0275, PT0625, PT0660, PT0683, and PT0758 promoters. Other root-preferential promoters include the PT0613, PT0672 , PT0688, and PT0837 promoters, which drive transcription primarily in root tissue

and to a lesser extent in ovules and/or seeds. Other examples of root-preferential promoters include the root-specific subdomains of the CaMV 35S promoter (Lam *et al.* (1989) *Proc. Natl. Acad. Sci. USA*, 86:7890-7894), root cell specific promoters reported by Conkling *et al.* (1990) *Plant Physiol.*, 93:1203-1211, and the tobacco RD2 promoter.

iii. Maturing Endosperm Promoters

[0414] In some embodiments, promoters that drive transcription in maturing endosperm can be useful. Transcription from a maturing endosperm promoter typically begins after fertilization and occurs primarily in endosperm tissue during seed development and is typically highest during the cellularization phase. Most suitable are promoters that are active predominantly in maturing endosperm, although promoters that are also active in other tissues can sometimes be used. Non-limiting examples of maturing endosperm promoters that can be included in the nucleic acid constructs provided herein include the napin promoter, the Arcelin-5 promoter, the phaseolin promoter (Bustos *et al.* (1989) *Plant Cell*, 1(9):839-853), the soybean trypsin inhibitor promoter (Riggs *et al.* (1989) *Plant Cell*, 1(6):609-621), the ACP promoter (Baerson *et al.* (1993) *Plant Mol. Biol.*, 22(2):255-267), the stearoyl-ACP desaturase promoter (Slocombe *et al.* (1994) *Plant Physiol.*, 104(4):167-176), the soybean α' subunit of β-conglycinin promoter (Chen *et al.* (1986) *Proc. Natl. Acad. Sci. USA*, 83:8560-8564), the oleosin promoter (Hong *et al.* (1997) *Plant Mol. Biol.*, 34(3):549-555), and zein promoters, such as the 15 kD zein promoter, the 16 kD zein promoter, 19 kD zein promoter, 22 kD zein promoter and 27 kD zein promoter. Also suitable are the Osgt-1 promoter from the rice glutelin-1 gene (Zheng *et al.* (1993) *Mol. Cell Biol.*, 13:5829-5842), the beta-amylase promoter, and the barley hordein promoter. Other maturing endosperm promoters include the YP0092, PT0676, and PT0708 promoters.

iv. Ovary Tissue Promoters

[0415] Promoters that are active in ovary tissues such as the ovule wall and mesocarp can also be useful, *e.g.*, a polygalacturonidase promoter, the banana TRX promoter, the melon actin promoter, YP0396, and PT0623. Examples of promoters that are active primarily in ovules include YP0007, YP0111, YP0092, YP0103, YP0028, YP0121, YP0008, YP0039, YP0115, YP0119, YP0120, and YP0374.

v. Embryo Sac/Early Endosperm Promoters

[0416] To achieve expression in embryo sac/early endosperm, regulatory regions can be used that are active in polar nuclei and/or the central cell, or in precursors to polar nuclei, but not in egg cells or precursors to egg cells. Most suitable are promoters that drive expression only or predominantly in polar nuclei or precursors thereto and/or the central cell.

A pattern of transcription that extends from polar nuclei into early endosperm development can also be found with embryo sac/early endosperm-preferential promoters, although transcription typically decreases significantly in later endosperm development during and after the cellularization phase. Expression in the zygote or developing embryo typically is not present with embryo sac/early endosperm promoters.

[0417] Promoters that may be suitable include those derived from the following genes: *Arabidopsis* viviparous-1 (see, GenBank No. U93215); *Arabidopsis* atmycl (see, Urao (1996) *Plant Mol. Biol.*, 32:571-57; Conceicao (1994) *Plant*, 5:493-505); *Arabidopsis* FIE (GenBank No. AF129516); *Arabidopsis* MEA; *Arabidopsis* FIS2 (GenBank No. AF096096); and FIE 1.1 (U.S. Patent 6,906,244). Other promoters that may be suitable include those derived from the following genes: maize MAC1 (see, Sheridan (1996) *Genetics*, 142:1009-1020); maize Cat3 (see, GenBank No. L05934; Abler (1993) *Plant Mol. Biol.*, 22:10131-1038). Other promoters include the following *Arabidopsis* promoters: YP0039, YP0101, YP0102, YP0110, YP0117, YP0119, YP0137, DME, YP0285, and YP0212. Other promoters that may be useful include the following rice promoters: p530c10, pOsFIE2-2, pOsMEA, pOsYp102, and pOsYp285.

vi. Embryo Promoters

[0418] Regulatory regions that preferentially drive transcription in zygotic cells following fertilization can provide embryo-preferential expression. Most suitable are promoters that preferentially drive transcription in early stage embryos prior to the heart stage, but expression in late stage and maturing embryos is also suitable. Embryo-preferential promoters include the barley lipid transfer protein (Ltp1) promoter (*Plant Cell Rep* (2001) 20:647-654), YP0097, YP0107, YP0088, YP0143, YP0156, PT0650, PT0695, PT0723, PT0838, PT0879, and PT0740.

vii. Photosynthetic Tissue Promoters

[0419] Promoters active in photosynthetic tissue confer transcription in green tissues such as leaves and stems. Most suitable are promoters that drive expression only or predominantly in such tissues. Examples of such promoters include the ribulose-1,5-bisphosphate carboxylase (RbcS) promoters such as the RbcS promoter from eastern larch (*Larix laricina*), the pine cab6 promoter (Yamamoto *et al.* (1994) *Plant Cell Physiol.*, 35:773-778), the Cab-1 promoter from wheat (Fejes *et al.* (1990) *Plant Mol. Biol.*, 15:921-932), the CAB-1 promoter from spinach (Lubberstedt *et al.* (1994) *Plant Physiol.*, 104:997-1006), the cab1R promoter from rice (Luan *et al.* (1992) *Plant Cell*, 4:971-981), the pyruvate orthophosphate dikinase (PPDK) promoter from corn (Matsuoka *et al.* (1993) *Proc. Natl.*

Acad. Sci. USA, 90:9586-9590), the tobacco Lhcb1*2 promoter (Cerdan *et al.* (1997) *Plant Mol. Biol.*, 33:245-255), the *Arabidopsis thaliana* SUC2 sucrose-H+ symporter promoter (Truernit *et al.* (1995) *Planta*, 196:564-570), and thylakoid membrane protein promoters from spinach (psaD, psaF, psaE, PC, FNR, atpC, atpD, cab, rbcS). Other photosynthetic tissue promoters include PT0535, PT0668, PT0886, YP0144, YP0380 and PT0585.

viii. Vascular Tissue Promoters

[0420] Examples of promoters that have high or preferential activity in vascular bundles include YP0087, YP0093, YP0108, YP0022, and YP0080. Other vascular tissue-preferential promoters include the glycine-rich cell wall protein GRP 1.8 promoter (Keller and Baumgartner (1991) *Plant Cell*, 3(10):1051-1061), the Commelina yellow mottle virus (CoYMV) promoter (Medberry *et al.* (1992) *Plant Cell*, 4(2):185-192), and the rice tungro bacilliform virus (RTBV) promoter (Dai *et al.* (2004) *Proc. Natl. Acad. Sci. USA*, 101(2):687-692).

ix. Inducible Promoters

[0421] Inducible promoters confer transcription in response to external stimuli such as chemical agents or environmental stimuli. For example, inducible promoters can confer transcription in response to hormones such as giberellic acid or ethylene, or in response to light or drought. Examples of drought-inducible promoters include YP0380, PT0848, YP0381, YP0337, PT0633, YP0374, PT0710, YP0356, YP0385, YP0396, YP0388, YP0384, PT0688, YP0286, YP0377, PD1367, and PD0901. Examples of nitrogen-inducible promoters include PT0863, PT0829, PT0665, and PT0886. Examples of shade-inducible promoters include PR0924 and PT0678. An example of a promoter induced by salt is rd29A (Kasuga et al. (1999) *Nature Biotech* 17: 287-291).

x. Basal Promoters

[0422] A basal promoter is the minimal sequence necessary for assembly of a transcription complex required for transcription initiation. Basal promoters frequently include a "TATA box" element that may be located between about 15 and about 35 nucleotides upstream from the site of transcription initiation. Basal promoters also may include a "CCAAT box" element (typically the sequence CCAAT) and/or a GGGCG sequence, which can be located between about 40 and about 200 nucleotides, typically about 60 to about 120 nucleotides, upstream from the transcription start site.

xi. Stem Promoters

[0423] A stem promoter may be specific to one or more stem tissues or specific to stem and other plant parts. Stem promoters may have high or preferential activity in, for

example, epidermis and cortex, vascular cambium, procambium, or xylem. Examples of stem promoters include YP0018 which is disclosed in US20060015970 and CryIA(b) and CryIA(c) (Braga et al. 2003, Journal of New Seeds 5:209-221).

xii. Other Promoters

[0424] Other classes of promoters include, but are not limited to, shoot-preferential, callus-preferential, trichome cell-preferential, guard cell-preferential such as PT0678, tuber-preferential, parenchyma cell-preferential, and senescence-preferential promoters. Promoters designated YP0086, YP0188, YP0263, PT0758, PT0743, PT0829, YP0119, and YP0096, as described in the above-referenced patent applications, may also be useful.

xiii. Other Regulatory Regions

[0425] A 5´ untranslated region (UTR) can be included in nucleic acid constructs described herein. A 5´ UTR is transcribed, but is not translated, and lies between the start site of the transcript and the translation initiation codon and may include the +1 nucleotide. A 3´ UTR can be positioned between the translation termination codon and the end of the transcript. UTRs can have particular functions such as increasing mRNA stability or attenuating translation. Examples of 3´ UTRs include, but are not limited to, polyadenylation signals and transcription termination sequences, *e.g.*, a nopaline synthase termination sequence.

[0426] It will be understood that more than one regulatory region may be present in a recombinant polynucleotide, *e.g.*, introns, enhancers, upstream activation regions, transcription terminators, and inducible elements. Thus, for example, more than one regulatory region can be operably linked to the sequence of a polynucleotide encoding a low nitrogen tolerance-modulating polypeptide.

[0427] Regulatory regions, such as promoters for endogenous genes, can be obtained by chemical synthesis or by subcloning from a genomic DNA that includes such a regulatory region. A nucleic acid comprising such a regulatory region can also include flanking sequences that contain restriction enzyme sites that facilitate subsequent manipulation.

IV. Transgenic Plants and Plant Cells

A. Transformation

[0428] The invention also features transgenic plant cells and plants comprising at least one recombinant nucleic acid construct described herein. A plant or plant cell can be transformed by having a construct integrated into its genome, *i.e.*, can be stably transformed. Stably transformed cells typically retain the introduced nucleic acid with each cell division.

A plant or plant cell can also be transiently transformed such that the construct is not integrated into its genome. Transiently transformed cells typically lose all or some portion of the introduced nucleic acid construct with each cell division such that the introduced nucleic acid cannot be detected in daughter cells after a sufficient number of cell divisions. Both transiently transformed and stably transformed transgenic plants and plant cells can be useful in the methods described herein.

[0429] Transgenic plant cells used in methods described herein can constitute part or all of a whole plant. Such plants can be grown in a manner suitable for the species under consideration, either in a growth chamber, a greenhouse, or in a field. Transgenic plants can be bred as desired for a particular purpose, *e.g.*, to introduce a recombinant nucleic acid into other lines, to transfer a recombinant nucleic acid to other species, or for further selection of other desirable traits. Alternatively, transgenic plants can be propagated vegetatively for those species amenable to such techniques. As used herein, a transgenic plant also refers to progeny of an initial transgenic plant provided the progeny inherits the transgene. Seeds produced by a transgenic plant can be grown and then selfed (or outcrossed and selfed) to obtain seeds homozygous for the nucleic acid construct.

[0430] Transgenic plants can be grown in suspension culture, or tissue or organ culture. For the purposes of this invention, solid and/or liquid tissue culture techniques can be used. When using solid medium, transgenic plant cells can be placed directly onto the medium or can be placed onto a filter that is then placed in contact with the medium. When using liquid medium, transgenic plant cells can be placed onto a flotation device, *e.g.*, a porous membrane that contacts the liquid medium. A solid medium can be, for example, Murashige and Skoog (MS) medium containing agar and a suitable concentration of an auxin, *e.g.*, 2,4-dichlorophenoxyacetic acid (2,4-D), and a suitable concentration of a cytokinin, *e.g.*, kinetin.

[0431] When transiently transformed plant cells are used, a reporter sequence encoding a reporter polypeptide having a reporter activity can be included in the transformation procedure and an assay for reporter activity or expression can be performed at a suitable time after transformation. A suitable time for conducting the assay typically is about 1-21 days after transformation, *e.g.*, about 1-14 days, about 1-7 days, or about 1-3 days. The use of transient assays is particularly convenient for rapid analysis in different species, or to confirm expression of a heterologous low nitrogen tolerance-modulating polypeptide whose expression has not previously been confirmed in particular recipient cells.

[0432] Techniques for introducing nucleic acids into monocotyledonous and dicotyledonous plants are known in the art, and include, without limitation, *Agrobacterium*-

mediated transformation, viral vector-mediated transformation, electroporation and particle gun transformation, *e.g.*, U.S. Patents 5,538,880; 5,204,253; 6,329,571 and 6,013,863. If a cell or cultured tissue is used as the recipient tissue for transformation, plants can be regenerated from transformed cultures if desired, by techniques known to those skilled in the art.

B. Screening/selection

[0433] A population of transgenic plants can be screened and/or selected for those members of the population that have a trait or phenotype conferred by expression of the transgene. For example, a population of progeny of a single transformation event can be screened for those plants having a desired level of expression of a low nitrogen tolerance-modulating polypeptide or nucleic acid. Physical and biochemical methods can be used to identify expression levels. These include Southern analysis or PCR amplification for detection of a polynucleotide; Northern blots, S1 RNase protection, primer-extension, or RT-PCR amplification for detecting RNA transcripts; enzymatic assays for detecting enzyme or ribozyme activity of polypeptides and polynucleotides; and protein gel electrophoresis, Western blots, immunoprecipitation, and enzyme-linked immunoassays to detect polypeptides. Other techniques such as *in situ* hybridization, enzyme staining, and immunostaining also can be used to detect the presence or expression of polypeptides and/or polynucleotides. Methods for performing all of the referenced techniques are known. As an alternative, a population of plants comprising independent transformation events can be screened for those plants having a desired trait, such as a modulated level of low-nitrogen tolerance. Selection and/or screening can be carried out over one or more generations, and/or in more than one geographic location. In some cases, transgenic plants can be grown and selected under conditions which induce a desired phenotype or are otherwise necessary to produce a desired phenotype in a transgenic plant. In addition, selection and/or screening can be applied during a particular developmental stage in which the phenotype is expected to be exhibited by the plant. Selection and/or screening can be carried out to choose those transgenic plants having a statistically significant difference in low nitrogen tolerance level relative to a control plant that lacks the transgene. Selected or screened transgenic plants have an altered phenotype as compared to a corresponding control plant, as described in the "Transgenic Plant Phenotypes" section herein.

C. Plant Species

[0434] The polynucleotides and vectors described herein can be used to transform a number of monocotyledonous and dicotyledonous plants and plant cell systems, including species from one of the following families: *Acanthaceae*, *Alliaceae*, *Alstroemeriaceae*, *Amaryllidaceae*, *Apocynaceae*, *Arecaceae*, *Asteraceae*, *Berberidaceae*, *Bixaceae*, *Brassicaceae*, *Bromeliaceae*, *Cannabaceae*, *Caryophyllaceae*, *Cephalotaxaceae*, *Chenopodiaceae*, *Colchicaceae*, *Cucurbitaceae*, *Dioscoreaceae*, *Ephedraceae*, *Erythroxylaceae*, *Euphorbiaceae*, *Fabaceae*, *Lamiaceae*, *Linaceae*, *Lycopodiaceae*, *Malvaceae*, *Melanthiaceae*, *Musaceae*, *Myrtaceae*, *Nyssaceae*, *Papaveraceae*, *Pinaceae*, *Plantaginaceae*, *Poaceae*, *Rosaceae*, *Rubiaceae*, *Salicaceae*, *Sapindaceae*, *Solanaceae*, *Taxaceae*, *Theaceae*, or *Vitaceae*.

[0435] Suitable species may include members of the genus *Abelmoschus*, *Abies*, *Acer*, *Agrostis*, *Allium*, *Alstroemeria*, *Ananas*, *Andrographis*, *Andropogon*, *Artemisia*, *Arundo*, *Atropa*, *Berberis*, *Beta*, *Bixa*, *Brassica*, *Calendula*, *Camellia*, *Camptotheca*, *Cannabis*, *Capsicum*, *Carthamus*, *Catharanthus*, *Cephalotaxus*, *Chrysanthemum*, *Cinchona*, *Citrullus*, *Coffea*, *Colchicum*, *Coleus*, *Cucumis*, *Cucurbita*, *Cynodon*, *Datura*, *Dianthus*, *Digitalis*, *Dioscorea*, *Elaeis*, *Ephedra*, *Erianthus*, *Erythroxylum*, *Eucalyptus*, *Festuca*, *Fragaria*, *Galanthus*, *Glycine*, *Gossypium*, *Helianthus*, *Hevea*, *Hordeum*, *Hyoscyamus*, *Jatropha*, *Lactuca*, *Linum*, *Lolium*, *Lupinus*, *Lycopersicon*, *Lycopodium*, *Manihot*, *Medicago*, *Mentha*, *Miscanthus*, *Musa*, *Nicotiana*, *Oryza*, *Panicum*, *Papaver*, *Parthenium*, *Pennisetum*, *Petunia*, *Phalaris*, *Phleum*, *Pinus*, *Poa*, *Poinsettia*, *Populus*, *Rauwolfia*, *Ricinus*, *Rosa*, *Saccharum*, *Salix*, *Sanguinaria*, *Scopolia*, *Secale*, *Solanum*, *Sorghum*, *Spartina*, *Spinacea*, *Tanacetum*, *Taxus*, *Theobroma*, *Triticosecale*, *Triticum*, *Uniola*, *Veratrum*, *Vinca*, *Vitis*, and *Zea*.

[0436] Suitable species include *Panicum* spp. or hybrid thereof, *Sorghum* spp. or hybrid thereof, sudangrass, *Miscanthus* spp. or hybrid thereof, *Saccharum* spp. or hybrid thereof, *Erianthus* spp., *Populus* spp., *Andropogon gerardii* (big bluestem), *Pennisetum purpureum* (elephant grass)) or hybrid thereof (*e.g., Pennisetum purpureum x Pennisetum typhoidum*), *Phalaris arundinacea* (reed canarygrass), *Cynodon dactylon* (bermudagrass), *Festuca arundinacea* (tall fescue), *Spartina pectinata* (prairie cord-grass), *Medicago sativa* (alfalfa), *Arundo donax* (giant reed) or hybrid thereof, *Secale cereale* (rye), *Salix* spp. (willow), *Eucalyptus* spp. (eucalyptus), Triticosecale (triticum - wheat X rye), *Tripsicum dactyloides* (Eastern gammagrass), Leymus cinereus (basin wildrye), Leymus condensatus (giant wildrye) and bamboo.

[0437] In some embodiments, a suitable species can be a wild, weedy, or cultivated sorghum species such as, but not limited to, *Sorghum almum, Sorghum amplum, Sorghum angustum, Sorghum arundinaceum, Sorghum bicolor* (such as bicolor, guinea, caudatum, kafir, and durra), *Sorghum brachypodum, Sorghum bulbosum, Sorghum burmahicum, Sorghum controversum, Sorghum drummondii, Sorghum ecarinatum, Sorghum exstans, Sorghum grande, Sorghum halepense, Sorghum interjectum, Sorghum intrans, Sorghum laxiflorum, Sorghum leiocladum, Sorghum macrospermum, Sorghum matarankense, Sorghum miliaceum, Sorghum nigrum, Sorghum nitidum, Sorghum plumosum, Sorghum propinquum, Sorghum purpureosericeum, Sorghum stipoideum, Sorghum sudanensese, Sorghum timorense, Sorghum trichocladum, Sorghum versicolor, Sorghum virgatum, Sorghum vulgare,* or hybrids such as *Sorghum* × *almum, Sorghum* x sudangrass or *Sorghum* × *drummondii*.

[0438] Suitable species also include *Helianthus annuus* (sunflower), *Carthamus tinctorius* (safflower), *Jatropha curcas* (jatropha), *Ricinus communis* (castor), *Elaeis guineensis* (palm), *Linum usitatissimum* (flax), and *Brassica juncea*.

[0439] Suitable species also include *Beta vulgaris* (sugarbeet), and *Manihot esculenta* (cassava).

[0440] Suitable species also include *Lycopersicon esculentum* (tomato), *Lactuca sativa* (lettuce), *Musa paradisiaca* (banana), *Solanum tuberosum* (potato), *Brassica oleracea* (broccoli, cauliflower, Brussels sprouts), *Camellia sinensis* (tea), *Fragaria ananassa* (strawberry), *Theobroma cacao* (cocoa), *Coffea arabica* (coffee), *Vitis vinifera* (grape), *Ananas comosus* (pineapple), *Capsicum annum* (hot & sweet pepper), *Allium cepa* (onion), *Cucumis melo* (melon), *Cucumis sativus* (cucumber), *Cucurbita maxima* (squash), *Cucurbita moschata* (squash), *Spinacea oleracea* (spinach), *Citrullus lanatus* (watermelon), *Abelmoschus esculentus* (okra), and *Solanum melongena* (eggplant).

[0441] Suitable species also include *Papaver somniferum* (opium poppy), *Papaver orientale*, *Taxus baccata*, *Taxus brevifolia*, *Artemisia annua*, *Cannabis sativa*, *Camptotheca acuminate*, *Catharanthus roseus*, *Vinca rosea*, *Cinchona officinalis*, *Colchicum autumnale*, *Veratrum californica*, *Digitalis lanata*, *Digitalis purpurea*, *Dioscorea spp.*, *Andrographis paniculata*, *Atropa belladonna*, *Datura stomonium*, *Berberis spp.*, *Cephalotaxus spp.*, *Ephedra sinica*, *Ephedra spp.*, *Erythroxylum coca*, *Galanthus wornorii*, *Scopolia spp.*, *Lycopodium serratum* (= *Huperzia serrata*), *Lycopodium spp.*, *Rauwolfia serpentina*, *Rauwolfia spp.*, *Sanguinaria canadensis*, *Hyoscyamus spp.*, *Calendula officinalis*, *Chrysanthemum parthenium*, *Coleus forskohlii*, and *Tanacetum parthenium*.

[0442] Suitable species also include *Parthenium argentatum* (guayule), *Hevea* spp. (rubber), *Mentha spicata* (mint), *Mentha piperita* (mint), *Bixa orellana*, and *Alstroemeria* spp.

[0443] Suitable species also include *Rosa* spp. (rose), *Dianthus caryophyllus* (carnation), *Petunia* spp. (petunia) and *Poinsettia pulcherrima* (poinsettia).

[0444] Suitable species also include *Nicotiana tabacum* (tobacco), *Lupinus albus* (lupin), *Uniola paniculata* (oats), bentgrass (*Agrostis* spp.), *Populus tremuloides* (aspen), *Pinus* spp. (pine), *Abies* spp. (fir), *Acer* spp. (maple), *Hordeum vulgare* (barley), *Poa pratensis* (bluegrass), *Lolium* spp. (ryegrass) and *Phleum pratense* (timothy).

[0445] Thus, the methods and compositions can be used over a broad range of plant species, including species from the dicot genera *Brassica*, *Carthamus*, *Glycine*, *Gossypium*, *Helianthus*, *Jatropha*, *Parthenium*, *Populus*, and *Ricinus*; and the monocot genera *Elaeis*, *Festuca*, *Hordeum*, *Lolium*, *Oryza*, *Panicum*, *Pennisetum*, *Phleum*, *Poa*, *Saccharum*, *Secale*, *Sorghum*, *Triticosecale*, *Triticum*, and *Zea*. In some embodiments, a plant is a member of the species *Panicum virgatum* (switchgrass), *Sorghum bicolor* (sorghum, sudangrass), *Miscanthus giganteus* (miscanthus), *Saccharum* sp. (energycane), *Populus balsamifera* (poplar), *Zea mays* (corn), *Glycine max* (soybean), *Brassica napus* (canola), *Triticum aestivum* (wheat), *Gossypium hirsutum* (cotton), *Oryza sativa* (rice), *Helianthus annuus* (sunflower), *Medicago sativa* (alfalfa), *Beta vulgaris* (sugarbeet), or *Pennisetum glaucum* (pearl millet).

[0446] In certain embodiments, the polynucleotides and vectors described herein can be used to transform a number of monocotyledonous and dicotyledenous plants and plant cell systems, wherein such plants are hybrids of different species or varieties of a specific species (*e.g.*, *Saccharum* sp. X *Miscanthus* sp., *Panicum virgatum* x *Panicum amarum, Panicum virgatum* x *Panicum amarulum,* and *Pennisetum purpureum* x *Pennisetum typhoidum*).

D. Transgenic Plant Phenotypes

[0447] In some embodiments, a plant in which expression of a low nitrogen tolerance-modulating polypeptide is modulated can have increased levels of photosynthetic efficiency in seedlings. For example, a low nitrogen tolerance-modulating polypeptide described herein can be expressed in a transgenic plant, resulting in increased levels of photosynthetic efficiency in growth conditions with low nitrogen sources. The level of photosynthetic efficiency can be increased by at least 0.25 percent, *e.g.*, 0.25, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, or more than

60 percent, as compared to the level of photosynthetic efficiency in a corresponding control plant that does not express the transgene. In some embodiments, a plant in which expression of a low nitrogen tolerance-modulating polypeptide is modulated can have decreased levels of photosynthetic efficiency. The level of photosynthetic efficiency can be decreased by at least 0.25 percent, *e.g.*, 0.25, 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, or more than 35 percent, as compared to the level of photosynthetic in a corresponding control plant that does not express the transgene.

[0448] In some embodiments, a plant in which expression of a low nitrogen tolerance-modulating polypeptide is modulated can have increased or decreased levels of photosynthetic efficiency in one or more green tissues, *e.g.*, leaves, stems, bulbs, flowers, fruits, young seeds. For example, the level of photosynthetic efficiency can be increased by at least 0.25 percent, *e.g.*, 0.25, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, or more than 60 percent, as compared to the level of photosynthetic efficiency in a corresponding control plant that does not express the transgene. In some embodiments, a plant in which expression of a low nitrogen tolerance-modulating polypeptide is modulated can have decreased levels of photosynthetic efficiency in one or more green tissues. The level of photosynthetic efficiency can be decreased by at least 0.25 percent, *e.g.*, 0.25, 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, or more than 35 percent, as compared to the level of photosynthetic efficiency in a corresponding control plant that does not express the transgene.

[0449] Increases in photosynthetic efficiency in low-nitrogen growth conditions in such plants can provide improved plant growth in geographic locales where plant's intake of nitrogenous fertilizers is often insufficient. Decreases in photosynthetic efficiency, and hence less tolerance to low-nitrogen growth conditions in such plants can be useful for removing weeds and such from the environment, by applying to weeds and such. For example, a plant capable of inducing the decrease in photosynthetic efficiency can be prepared to apply for land improvements and such.

[0450] Typically, a difference in the level of photosynthetic efficiency in a transgenic plant or cell relative to a control plant or cell is considered statistically significant at $p \leq 0.05$ with an appropriate parametric or non-parametric statistic, *e.g.*, Chi-square test, Student's t-test, Mann-Whitney test, or F-test. In some embodiments, a difference in the level of photosynthetic is statistically significant at $p < 0.01$, $p < 0.005$, or $p < 0.001$. A statistically significant difference in, for example, the level of photosynthetic efficiency in a transgenic

plant compared to the amount in cells of a control plant indicates that the recombinant nucleic acid present in the transgenic plant results in altered levels of photosynthetic efficiency.

[0451] In some embodiments, a plant in which expression of a low nitrogen tolerance-modulating polypeptide is modulated can have increased growth rates in seedlings. For example, a low nitrogen tolerance-modulating polypeptide described herein can be expressed in a transgenic plant, resulting in increased growth rate in growth conditions of limiting nitrogen sources. The growth rate can be increased by at least 2 percent, *e.g.*, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, or more than 60 percent, as compared to the growth rate in a corresponding control plant that does not express the transgene. In some embodiments, a plant in which expression of a low nitrogen tolerance-modulating polypeptide is modulated can have decreased growth rates. The growth rate can be decreased by at least 2 percent, *e.g.*, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, or more than 35 percent, as compared to the growth rate in a corresponding control plant that does not express the transgene. Growth rate can be measured in seedlings, developing, or mature plants and measured for periods of time such as about 1 hour, 3 hours, 6 hours, 12 hours, 1 day, 3 days, 5 days, 10 days, 1 month, 3 months, 6 months, 12 months, or the entire lifespan of a plant.

[0452] In some embodiments, a plant in which expression of a low nitrogen tolerance-modulating polypeptide is modulated can have increased or decreased growth rates in one or more vegetative and reproductive tissues, *e.g.*, leaves, stems, flowers, bulbs, fruits, young seeds. For example, the growth rate can be increased by at least 2 percent, *e.g.*, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, or more than 60 percent, as compared to the growth rate in a corresponding control plant that does not express the transgene. In some embodiments, a plant in which expression of a low nitrogen tolerance-modulating polypeptide is modulated can have decreased levels of growth rate in one or more vegetative tissues. The growth rate can be decreased by at least 2 percent, *e.g.*, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, or more than 35 percent, as compared to the growth rate in a corresponding control plant that does not express the transgene.

[0453] Increases in growth rate in low-nitrogen conditions in such plants can provide improved plant growth and initial establishment in geographic locales where plant's intake of nitrogenous fertilizers is often insufficient. Decreases in growth rate, and hence less tolerance to low-nitrogen growth conditions in such plants can be useful for engineering slow-growing plants, by applying to ornamentals and such. For example, a plant capable of

inducing the decrease in growth rate can be prepared to apply for land improvements and such.

[0454] Typically, a difference in the growth rate of a transgenic plant or cell relative to a control plant or cell is considered statistically significant at $p \leq 0.05$ with an appropriate parametric or non-parametric statistic, *e.g.*, Chi-square test, Student's t-test, Mann-Whitney test, or F-test. In some embodiments, a difference in the growth rate is statistically significant at $p < 0.01$, $p < 0.005$, or $p < 0.001$. A statistically significant difference in, for example, the growth rate of a transgenic plant compared to the growth rate of a control plant indicates that the recombinant nucleic acid present in the transgenic plant results in altered growth rates.

[0455] The phenotype of a transgenic plant is evaluated relative to a control plant. A plant is said "not to express" a polypeptide when the plant exhibits less than 10%, *e.g.*, less than 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, 0.5%, 0.1%, 0.01%, or 0.001%, of the amount of polypeptide or mRNA encoding the polypeptide exhibited by the plant of interest. Expression can be evaluated using methods including, for example, RT-PCR, Northern blots, S1 RNase protection, primer extensions, Western blots, protein gel electrophoresis, immunoprecipitation, enzyme-linked immunoassays, chip assays, and mass spectrometry. It should be noted that if a polypeptide is expressed under the control of a tissue-preferential or broadly expressing promoter, expression can be evaluated in the entire plant or in a selected tissue. Similarly, if a polypeptide is expressed at a particular time, *e.g.*, at a particular time in development or upon induction, expression can be evaluated selectively at a desired time period.

V. Plant Breeding

[0456] Genetic polymorphisms are discrete allelic sequence differences in a population. Typically, an allele that is present at 1% or greater is considered to be a genetic polymorphism. The discovery that polypeptides disclosed herein can modulate photosynthetic efficiency and/or nitrogen content is useful in plant breeding, because genetic polymorphisms exhibiting a degree of linkage with loci for such polypeptides are more likely to be correlated with variation in a low-nitrogen tolerance trait. For example, genetic polymorphisms linked to the loci for such polypeptides are more likely to be useful in marker-assisted breeding programs to create lines having a desired modulation in the low-nitrogen tolerance trait.

[0457] Thus, one aspect of the invention includes methods of identifying whether one or more genetic polymorphisms are associated with variation in a low-nitrogen tolerance trait.

Such methods involve determining whether genetic polymorphisms in a given population exhibit linkage with the locus for one of the polypeptides depicted in Figures 1-57, SEQ ID NO:556, SEQ ID NO:853, SEQ ID NO:1157 and/or a functional homolog thereof, such as, but not limited to those identified in the Sequence Listing of this application. The correlation is measured between variation in the low-nitrogen tolerance trait in plants of the population and the presence of the genetic polymorphism(s) in plants of the population, thereby identifying whether or not the genetic polymorphism(s) are associated with variation for the trait. If the presence of a particular allele is statistically significantly correlated with a desired modulation in the low-nitrogen tolerance trait, the allele is associated with variation for the trait and is useful as a marker for the trait. If, on the other hand, the presence of a particular allele is not significantly correlated with the desired modulation, the allele is not associated with variation for the trait and is not useful as a marker.

[0458] Such methods are applicable to populations containing the naturally occurring endogenous polypeptide rather than an exogenous nucleic acid encoding the polypeptide, *i.e.*, populations that are not transgenic for the exogenous nucleic acid. It will be appreciated, however, that populations suitable for use in the methods may contain a transgene for another, different trait, *e.g.*, herbicide resistance.

[0459] Genetic polymorphisms that are useful in such methods include simple sequence repeats (SSRs, or microsatellites), rapid amplification of polymorphic DNA (RAPDs), single nucleotide polymorphisms (SNPs), amplified fragment length polymorphisms (AFLPs) and restriction fragment length polymorphisms (RFLPs). SSR polymorphisms can be identified, for example, by making sequence specific probes and amplifying template DNA from individuals in the population of interest by PCR. If the probes flank an SSR in the population, PCR products of different sizes will be produced. See, *e.g.*, U.S. Patent 5,766,847. Alternatively, SSR polymorphisms can be identified by using PCR product(s) as a probe against Southern blots from different individuals in the population. See, U.H. Refseth et al. (1997) *Electrophoresis* 18: 1519. The identification of RFLPs is discussed, for example, in Alonso-Blanco et al. (Methods in Molecular Biology, vol.82, "*Arabidopsis* Protocols", pp. 137-146, J.M. Martinez-Zapater and J. Salinas, eds., c. 1998 by Humana Press, Totowa, NJ); Burr ("Mapping Genes with Recombinant Inbreds", pp. 249-254, in Freeling, M. and V. Walbot (Ed.), The Maize Handbook, c. 1994 by Springer-Verlag New York, Inc.: New York, NY, USA; Berlin Germany; Burr et al. (1998) *Genetics* 118: 519; and Gardiner, J. et al. (1993) *Genetics* 134: 917). The identification of AFLPs is discussed, for example, in EP 0 534 858 and US Pat. 5,878,215.

[0460] In some embodiments, the methods are directed to breeding a plant line. Such methods use genetic polymorphisms identified as described above in a marker assisted breeding program to facilitate the development of lines that have a desired alteration in the low-nitrogen tolerance trait. Once a suitable genetic polymorphism is identified as being associated with variation for the trait, one or more individual plants are identified that possess the polymorphic allele correlated with the desired variation. Those plants are then used in a breeding program to combine the polymorphic allele with a plurality of other alleles at other loci that are correlated with the desired variation. Techniques suitable for use in a plant breeding program are known in the art and include, without limitation, backcrossing, mass selection, pedigree breeding, bulk selection, crossing to another population and recurrent selection. These techniques can be used alone or in combination with one or more other techniques in a breeding program. Thus, each identified plants is selfed or crossed a different plant to produce seed which is then germinated to form progeny plants. At least one such progeny plant is then selfed or crossed with a different plant to form a subsequent progeny generation. The breeding program can repeat the steps of selfing or outcrossing for an additional 0 to 5 generations as appropriate in order to achieve the desired uniformity and stability in the resulting plant line, which retains the polymorphic allele. In most breeding programs, analysis for the particular polymorphic allele will be carried out in each generation, although analysis can be carried out in alternate generations if desired.

[0461] In some cases, selection for other useful traits is also carried out, *e.g.*, selection for fungal resistance or bacterial resistance. Selection for such other traits can be carried out before, during or after identification of individual plants that possess the desired polymorphic allele.

VI. Articles of Manufacture

[0462] Transgenic plants provided herein have various uses in the agricultural and energy production industries. For example, transgenic plants described herein can be used to make animal feed and food products. Such plants, however, are often particularly useful as a feedstock for energy production.

[0463] Transgenic plants described herein often produce higher yields of grain and/or biomass per hectare, relative to control plants that lack the exogenous nucleic acid. In some embodiments, such transgenic plants provide equivalent or even increased yields of grain and/or biomass per hectare relative to control plants when grown under conditions of reduced inputs such as fertilizer and/or water. Thus, such transgenic plants can be used to provide

yield stability at a lower input cost and/or under environmentally stressful conditions such as drought or limiting nitrogen sources. In some embodiments, plants described herein have a composition that permits more efficient processing into free sugars, and subsequently ethanol, for energy production. In some embodiments, such plants provide higher yields of ethanol, butanol, dimethyl ether, other biofuel molecules, and/or sugar-derived co-products per kilogram of plant material, relative to control plants. Such processing efficiencies are believed to be derived from the nitrogenous composition of the plant material. By providing higher yields at an equivalent or even decreased cost of production, the transgenic plants described herein improve profitability for farmers and processors as well as decrease costs to consumers.

[0464] Seeds from transgenic plants described herein can be conditioned and bagged in packaging material by means known in the art to form an article of manufacture. Packaging material such as paper and cloth are well known in the art. A package of seed can have a label, *e.g.*, a tag or label secured to the packaging material, a label printed on the packaging material, or a label inserted within the package, that describes the nature of the seeds therein.

[0465] The invention will be further described in the following examples, which do not limit the scope of the invention described in the claims.

VII. Examples

Example 1 – Transgenic Arabidopsis plants

[0466] The following symbols are used in the Examples with respect to *Arabidopsis* transformation: T_1: first generation transformant; T_2: second generation, progeny of self-pollinated T_1 plants; T_3: third generation, progeny of self-pollinated T_2 plants; T_4: fourth generation, progeny of self-pollinated T_3 plants. Independent transformations are referred to as events.

[0467] The following is a list of nucleic acids that were isolated from *Arabidopsis thaliana* plants, CeresClone:29661 (SEQ ID NO:1), CeresClone:251343 (SEQ ID NO:48), CeresClone:19586 (SEQ ID NO:76), CeresClone:25136 (SEQ ID NO:96), CeresClone:1820 (SEQ ID NO:99), CeresClone:13102 (SEQ ID NO:151), CeresClone:15457 (SEQ ID NO:165), Ceres Annot:859276 (SEQ ID NO:175), CeresClone:17883 (SEQ ID NO:185), CeresClone:251590 (SEQ ID NO:207), CeresClone:4898 (SEQ ID NO:217), CeresClone:148977 (SEQ ID NO:233), CeresClone:24255 (SEQ ID NO:245), CeresClone:38432 (SEQ ID NO:299), Ceres Annot:553243 (SEQ ID NO:331),

CeresClone:1011900 (SEQ ID NO:367), CeresClone:5232 (SEQ ID NO:509), CeresClone:29302 (SEQ ID NO:532), CeresClone:93971 (SEQ ID NO:555), Ceres Annot:12669619_cDNA (SEQ ID NO:557), CeresClone:21608 (SEQ ID NO:592), CeresClone:2031 (SEQ ID NO:612), CeresClone:94503 (SEQ ID NO:645), CeresClone:21740 (SEQ ID NO:686), CeresClone:5609 (SEQ ID NO:729), CeresClone:3137 (SEQ ID NO:745), CeresClone:32430 (SEQ ID NO:768), CeresClone:101255 (SEQ ID NO:791), Ceres Annot:573161 (SEQ ID NO:854), Ceres Annot:552727 (SEQ ID NO:890), CeresClone:732 (SEQ ID NO:1193), CeresClone:2267 (SEQ ID NO:1209), CeresClone:39358 (SEQ ID NO:1273), CeresClone:115046 (SEQ ID NO:1301), Ceres Annot:850581 (SEQ ID NO:1427), Ceres Annot:862321 (SEQ ID NO:1462), Ceres Annot:839064 (SEQ ID NO:1478), Ceres Annot:864666 (SEQ ID NO:1490), Ceres Annot:875012 (SEQ ID NO:1509), Ceres Annot:874016 (SEQ ID NO:1524), Ceres Annot:827304 (SEQ ID NO:1536), Ceres Annot:869192 (SEQ ID NO:1553), and Ceres Annot:876419 (SEQ ID NO:1576). The nucleic acid designated Ceres Clone: 968180 (SEQ ID NO:1115) was isolated from the species *Brassica napus*. The nucleic acid designated Ceres Clone: 1017441 (SEQ ID NO:224) was isolated from the species *Triticum aesticum*. The following is a list of nucleic acids that were isolated from *Zea mays* plants, CeresClone:1387146 (SEQ ID NO:981), CeresClone:1408950 (SEQ ID NO:1098, CeresClone:208453 (SEQ ID NO:1111), CeresClone:208995 (SEQ ID NO:943), CeresClone:225681 (SEQ ID NO:975), CeresClone:239806 (SEQ ID NO:916), CeresClone:244306 (SEQ ID NO:1053), CeresClone:276809 (SEQ ID NO:823), CeresClone:324216 (SEQ ID NO:852), CeresClone:339439 (SEQ ID NO:1341), CeresClone:424522 (SEQ ID NO:827), CeresClone:896483 (SEQ ID NO:1384), CeresClone:986438 (SEQ ID NO:1156), CeresClone:988083 (SEQ ID NO:1184), CeresClone:995409 (SEQ ID NO:1408), CeresClone:996227 (SEQ ID NO:1158), and CeresClone:996263 (SEQ ID NO:1165).

[0468] With the exception of Ceres Clone:29661 (SEQ ID NO:1), each isolated nucleic acid described above was cloned into a Ti plasmid vector, CRS338, containing a phosphinothricin acetyltransferase gene which confers FINALE™ resistance to transformed plants. Constructs were made using CRS338 that contained SEQ ID NO:48, SEQ ID NO:76, SEQ ID NO:96, SEQ ID NO:99, SEQ ID NO:151, SEQ ID NO:165, SEQ ID NO:175, SEQ ID NO:185, SEQ ID NO:207, SEQ ID NO:217, SEQ ID NO:233, SEQ ID NO:245, SEQ ID NO:299, SEQ ID NO:331, SEQ ID NO:367, SEQ ID NO:509, SEQ ID NO:532, SEQ ID NO:555, SEQ ID NO:557, SEQ ID NO:592, SEQ ID NO:612, SEQ ID NO:645, SEQ ID

NO:686, SEQ ID NO:729, SEQ ID NO:745, SEQ ID NO:768, SEQ ID NO:791, SEQ ID NO:823, SEQ ID NO:827, SEQ ID NO:852, SEQ ID NO:854, SEQ ID NO:890, SEQ ID NO:916, SEQ ID NO:943, SEQ ID NO:975, SEQ ID NO:981, SEQ ID NO:1053, SEQ ID NO:1098, SEQ ID NO:1111, SEQ ID NO:1115, SEQ ID NO:1156, SEQ ID NO:1158, SEQ ID NO:1165, SEQ ID NO:1184, SEQ ID NO:1193, SEQ ID NO:1209, SEQ ID NO:1273, SEQ ID NO:1301, SEQ ID NO:1341, SEQ ID NO:1384, SEQ ID NO:1408, SEQ ID NO:1427, SEQ ID NO:1462, SEQ ID NO:1490, SEQ ID NO:1509, SEQ ID NO:1524, SEQ ID NO:1536, SEQ ID NO:1553, or SEQ ID NO:1576, each operably linked to a 35S promoter. Ceres Clone:29661 (SEQ ID NO:1) was cloned into a Ti plasmid vector, CRS 311, containing a phosphinothricin acetyltransferase gene, which confers FINALE™ resistance to transformed plants. SEQ ID NO:1 was operably linked to a p32449 promoter in the constructs made using the CRS 331 vector. Wild-type *Arabidopsis thaliana* ecotype Wassilewskija (Ws) plants were transformed separately with each construct. The transformations were performed essentially as described in Bechtold *et al.* (1993) *C.R. Acad. Sci. Paris*, 316:1194-1199.

[0469] Transgenic *Arabidopsis* lines containing SEQ ID NO:1, SEQ ID NO:48, SEQ ID NO:76, SEQ ID NO:96, SEQ ID NO:99, SEQ ID NO:151, SEQ ID NO:165, SEQ ID NO:185, SEQ ID NO:207, SEQ ID NO:217, SEQ ID NO:233, SEQ ID NO:245, SEQ ID NO:299, SEQ ID NO:331, SEQ ID NO:367, SEQ ID NO:509, SEQ ID NO:532, SEQ ID NO:555, SEQ ID NO:557, SEQ ID NO:592, SEQ ID NO:612, SEQ ID NO:645, SEQ ID NO:686, SEQ ID NO:729, SEQ ID NO:745, SEQ ID NO:768, SEQ ID NO:791, SEQ ID NO:823, SEQ ID NO:827, SEQ ID NO:852, SEQ ID NO:854, SEQ ID NO:890, SEQ ID NO:916, SEQ ID NO:943, SEQ ID NO:975, SEQ ID NO:981, SEQ ID NO:224, SEQ ID NO:1053, SEQ ID NO:1098, SEQ ID NO:1111, SEQ ID NO:1115, SEQ ID NO:1156, SEQ ID NO:1158, SEQ ID NO:1165, SEQ ID NO:1184, SEQ ID NO:1193, SEQ ID NO:1209, SEQ ID NO:1273, SEQ ID NO:1301, SEQ ID NO:1341, SEQ ID NO:1384, SEQ ID NO:1408, SEQ ID NO:1427, SEQ ID NO:1462, SEQ ID NO:1478, SEQ ID NO:1490, SEQ ID NO:1509, SEQ ID NO:1524, SEQ ID NO:1536, SEQ ID NO:1553, SEQ ID NO:1576, or SEQ ID NO:175 were designated ME00919, ME01312, ME01463, ME01821, ME01910, ME02538, ME02603, ME02613, ME02801, ME03123, ME04204, ME04477, ME04507, ME04587, ME04753, ME04772, ME04909, ME05033, ME05194, ME05267, ME05300, ME05341, ME05392, ME05429, ME05493, ME05885, ME07344, ME07859, ME08464, ME09939, ME11735, ME12910, ME12927, ME12929, ME12954, ME12970, ME13006, ME13021, ME13064, ME13071, ME13087, ME13106, ME13107, ME13108, ME13110,

ME13125, ME13149, ME13151, ME13153, ME13177, ME13200, ME13204, ME14649, ME16546, ME17457, ME17567, ME17932, ME17936, ME18275, ME18924, ME19182, or ME20628, respectively. The presence of each vector containing a nucleic acid described above in the respective transgenic *Arabidopsis* line transformed with the vector was confirmed by FINALE™ resistance, PCR amplification from green leaf tissue extract, and/or sequencing of PCR products. As controls, wild-type *Arabidopsis* ecotype Ws plants were transformed with the empty vector, either CRS338 or CRS311.

Example 2 – Screening for transgenic plants tolerant to low-nitrogen growth conditions

[0470] A low-nitrogen tolerance screen was carried out on seedlings in order to identify transgenic lines that showed increased photosynthesis efficiency or seedling size or greenness under limiting nitrogen conditions relative to the internal control plants. The media used for the low-nitrogen tolerance assay contained 0.5 % sucrose, 0.5X MS without nitrogen media (PhytoTech), 0.05% MES Hydrate, and 0.8% Phytagar. In addition, for low ammonium nitrate assay, 240μM NH4NO3 was used as nitrogen source. For low nitrate assay, nitrogen source was 300μM KNO3. pH of the media was adjusted to pH 5.7 using 10N KOH. Sterilized seeds were plated on agar plates and stratified for 2 days in the dark at 4oC to promote uniform germination. Agar plates with germinating seedlings were placed horizontally in a CONVIRON® growth chamber set at 22°C, 16:8 hour light:dark cycle, 70% humidity with a combination of incandescent and fluorescent lamps emitting a light intensity of ~100 μEinsteins. The control plates were placed randomly within the set. Screen the seedlings daily starting at 14 days. In this screen, seedlings that were larger or greener relative to the internal controls on low nitrogen growth media were selected. As they were found each day, candidate seedlings were aseptically transplanted to standard MS germination plates for recovery. This intermediate recovery step was necessary before transplanting to soil to minimize the overall candidate mortality rate. The scoring and transplanting of candidates were continued until all remaining plants were small and yellowed from nitrogen stress. On the very last day of scoring, each plate was scanned for photosynthetic efficiency (Fv/Fm) on the chlorophyll fluorescence (CF) imager and scored as candidates and transplanted any extreme outliers on the high end of Fv/Fm scores. Fv/Fm ratio typically provides an estimate of the photosystem II (PSII) maximum efficiency within dark-adapted material where Fv is variable fluorescence, i.e. difference between minimum (Fo) and maximum (Fm) fluorescence signal, from dark-adapted material. This could be done

visually by looking at the false color image for each seedling using the CF image analysis software (plants with high end Fv/Fm scores appear red). This step was typically done at ~24 days after germination. Seven days after being transferred to MS recovery plates, candidates were transplanted to soil (standard Sunshine:vermiculite 3:2 mix; Osmocote; Marathon). Five days after being transplanted to soil, candidates were sprayed with FINALE® [5 mL FINALE®/48 oz. water] to eliminate non-transgenics from the population. Two days after spraying with FINALE®, cauline leaf tissue of each candidate was collected for genomic DNA extraction, PCR, and sequencing to determine the identity of the transgene for each candidate.

Example 3 – Validation plate assay

[0471] This assay was designed to validate transgenic lines that showed increased photosynthesis or size under limiting nitrogen conditions relative to the internal control. The media used for the low-nitrogen tolerance assay contained 0.5 % sucrose, 0.5X MS without nitrogen media (PhytoTech), 0.05% MES Hydrate, and 0.8% Phytagar. pH of the media was adjusted to pH 5.7 using 10N KOH. In addition, for low ammonium nitrate assay, 240μM NH_4NO_3 was used as nitrogen source. For low nitrate assay, nitrogen source was 300μM KNO_3. Sterilized seeds were plated on agar plates and stratified for 2 days in the dark at 4°C to promote uniform germination. Agar plates with germinating seedlings were placed horizontally in a CONVIRON® growth chamber set at 22°C, 16:8 hour light:dark cycle, 70% humidity with a combination of incandescent and fluorescent lamps emitting a light intensity of ~100 μEinsteins. The control plates were placed randomly within the set. Plates were scanned every other day using the CF Imager (after 45 minute of dark-acclimation) and were completed after all wild-type plants have completely yellowed. After the plates were scanned on the last day, they were sprayed with FINALE® (10 mL FINALE® into 48 oz. full-strength MS liquid media). Two days after spraying, each plate was dark-acclimated for 45 minutes and scanned for Fv/Fm on the CF imager and scored for each of the plants at each time point. For each separate time point, the data for all the T_2 transgenic plants across an event was pooled and a one-tailed t-test was used to compare both the Fv/Fm ratios and rosette areas relative to the pooled non-transgenics across the same plate. Whenever possible, this process was repeated for the T_3 generation plants. A low nitrogen tolerant candidate was confirmed when the transgenic Fv/Fm ratio and/or rosette area was greater than the wild-type segregants with a p-value ≤ 0.05 in 2 or more events in both generations

Example 4 –Validation soil assay

[0472] A Low, Medium, and High Nitrogen experiment on soil was carried out to assess phenotypic characteristics at a mature point in the life cycle of *Arabidopsis*, as compared to seedling screens. The lines to be tested were originally identified through superpool screens for low nitrate and low ammonium nitrate tolerance. These lines were later individually assayed as seedlings on low nitrate and low ammonium nitrate agar. For this assay, MetroMix200 soil was mixed with vermiculite and Marathon™ (MetroMix200:vermiculite 3:2 mix; Osmocote; Marathon) autoclaved and cooled before use. Experimental plants and controls were randomized across the flats. Prior to sowing seed, each flat was watered with 3L filtered water. Flats with 24 wells were filled with the following 3:2 ratios of MetroMix200 to Thermorock vermiculite. At the beginning of the experiment no nitrogen was provided until 2 weeks after germination when ¼ Hoaglands supplemented with KNO_3 at 25 ppm, 250ppm, and 1500ppm were used to water the flats from beneath.

[0473] Seeds were stratified on soil and in the dark at 4°C for 3 days. After the cold treatment, flats were transferred to the growth chamber. Plants were grown for approximately 5 weeks, or until full grown/mature. Plants were then dark-acclimated for one hour. Chlorophyll fluorescence images were taken using a CF-Imager (Technologica, UK) according to the manufacturer's protocol to measure the performance and efficiency of photosystem II: 1) Fv/Fm, maximum photosystem II efficiency 2) Fq'/Fm', operating efficiency and 3) non-photochemical quenching (NPQ).

[0474] One week after watering with ¼ Hoaglands supplemented with various KNO_3 concentrations, plant rosette area measurements were taken using the WhinRhizo imaging software (Reagent Instruments, Canada). The plants were then collected in manila envelopes, placed in a 125 °C drying oven for 1-2 days and weighed.

Example 5 – Analysis of ME00919 Events

[0475] ME00919 contains Ceres Clone:29661 (At3g61880, SEQ ID NO:1) from *Arabidopsis thaliana*, which encodes a 534 amino acid cytochrome P450 protein. Evaluation of low-nitrogen tolerance for ME00919 in T_2 and T_3 was conducted under the same conditions as described in Example 2. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -01 and -03, showed significantly increased photosynthetic efficiency relative to the internal controls in both generations at $p \leq$

0.05 using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME00919 seedlings on low ammonium nitrate-containing media are shown in Table 1. Events -01 and -03 segregated 15:1 and 3:1 (R:S), respectively, for FINALE™ resistance in the T_2 generation. ME00919 events were also tested for enhanced growth on the low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 1. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME00919	ME00919-01 (T_2)	0.65641304	46	0.595818	11	$2.48x10^{-2}$
ME00919	ME00919-01 (T_3)	0.66348780	41	0.595818	11	$1.55x10^{-2}$
ME00919	ME00919-03 (T_2)	0.67212195	41	0.634026	38	$3.35x10^{-3}$
ME00919	ME00919-03 (T_3)	0.69278947	19	0.634026	38	$2.39x10^{-5}$

[0476] Events -01 and -03 of ME00919 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 6 – Analysis of ME01312 Events

[0477] ME01312 contains Ceres Clone:251343 (At3g21270, SEQ ID NO:48) from *Arabidopsis thaliana*, which encodes a 204 amino acid Dof zinc finger protein. Ceres Clone:251343 shares approximately 40% amino acid identity to the corn Dof1 gene, which when overexpressed in *Arabidopsis*, has shown to confer tolerance to plants receiving low nitrogen stress (Yanagisawa et al., 2004). Evaluation of low-nitrogen tolerance for ME01312 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -03 and -11, showed significantly enhanced photosynthetic efficiency on either low nitrate or low ammonium nitrate-containing media after 16 and 17 days compared to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test

assuming unequal variance. Event -03 had a slightly greater p-value than 0.05 in the T_3 generation for the low nitrate screen, significant at $p \leq 0.10$. A summary of photosynthetic efficiency of ME01312 seedlings on either low nitrate or low ammonium nitrate-containing media is shown in Table 2. Events -03 and -11 segregated 3:1 (R:S), respectively, for FINALE™ resistance in the T_2 generation.

Table 2A. T-test comparison of photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 16 days of growth on low nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME01312	ME01312-03 (T_2)	0.63	38	0.60	58	0.03
ME01312	ME01312-03 (T_3)	0.63	38	0.60	58	0.07
ME01312	ME01312-11 (T_2)	0.64	41	0.60	58	0.019
ME01312	ME01312-11 (T_3)	0.64	47	0.60	58	9.89×10^{-3}

Table 2B. T-test comparison of photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 17 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME01312	ME01312-03 (T_2)	0.64	36	0.61	88	2.64×10^{-3}
ME01312	ME01312-03 (T_3)	0.66	27	0.61	88	1.87×10^{-5}
ME01312	ME01312-11 (T_2)	0.65	35	0.61	88	7.06×10^{-4}
ME01312	ME01312-11 (T_3)	0.64	37	0.61	88	0.011

[0478] Events -03 -11 of ME01312 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 7 – Analysis of ME01463 Events

[0479] ME01463 contains Ceres Clone:19586 (At1g80600, SEQ ID NO:76) from *Arabidopsis thaliana*, which encodes a 457 acetylornithine aminotransferase, a member of the Class-III aminotransferase family. Evaluation of low-nitrogen tolerance for ME01463 in two generations was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Three events, -02, -06, and -10, showed significantly increased photosynthetic efficiency on

low ammonium nitrate containing-media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME01463 seedlings is shown in Table 3. Events -02, -06, and -10 segregated 2:1, 2:1 and 3:1 (R:S), respectively, for FINALE™ resistance in the T_2 generation. ME01463 events were also tested for enhanced growth on the low ammonium nitrate media. No significant differences between the transgenics and the controls were observed (data not shown).

Table 3. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME01463	ME01463-02 (T_3)	0.6815	26	0.6376	122	2.47×10^{-4}
ME01463	ME01463-02 (T_4)	0.6701	41	0.6376	122	1.57×10^{-3}
ME01463	ME01463-06 (T_3)	0.6615	31	0.6376	122	2.37×10^{-2}
ME01463	ME01463-06 (T_4)	0.6881	35	0.6376	122	5.85×10^{-6}
ME01463	ME01463-10 (T_2)	0.6699	33	0.6376	122	2.25×10^{-3}
ME01463	ME01463-10 (T_3)	0.6809	18	0.6376	122	4.60×10^{-4}

[0480] Events -02, -06, and -10 of ME01463 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 8 – Analysis of ME01821 Events

[0481] ME01821 contains Ceres Clone:25136 (At1g65500, SEQ ID NO:96) from *Arabidopsis thaliana*, which encodes a 86 amino acid protein of unknown function. Evaluation of low-nitrogen tolerance for ME01821 in T_2 generation was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Three events, -01, -04 and -05, showed significantly increased photosynthetic efficiency on low nitrate-containing media relative to the internal controls in T_2 generation. Two events, -04 and -05, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to

the internal controls in T_2 generation at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME01821 seedlings is shown in Table 4.

Table 4A. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME01821	ME01821-01 (T_2)	0.6745	15	0.6520	33	$3.76x10^{-2}$
ME01821	ME01821-04 (T_2)	0.6826	17	0.6614	14	$2.76x10^{-2}$
ME01821	ME01821-05 (T_2)	0.6826	20	0.6614	14	$3.74x10^{-2}$

Table 4B. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME01821	ME01821-04 (T_2)	0.7422	13	0.7166	21	$5.20x10^{-3}$
ME01821	ME01821-05 (T_2)	0.7426	19	0.7166	21	$6.07x10^{-3}$

[0482] A summary of the enhanced growth of ME01812 events on either low nitrate- or low ammonium nitrate-containing media is shown in Table 5. For two events -01 and -05, transgenic seedlings were found significantly larger than the pooled non-transgenic segregants after 14 days of growth on low nitrate-containing media (Table 5A). Transgenic seedlings of two events -02 and -05 were found significantly larger than the pooled non-transgenic segregants after 14 days of growth on low ammonium nitrate-containing media (Table 5B). In this study, the seedling area for transgenic plants within an event was compared to the seedling area for non-transgenic segregants pooled across the same line.

Table 5A. T-test comparison of seedling area between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Area	n	Area	n	p-value
ME01821	ME01821-01 (T_2)	0.0608	15	0.0555	33	$3.97x10^{-2}$
ME01821	ME01821-05 (T_2)	0.0666	20	0.0530	14	$3.05x10^{-6}$

Table 5B. T-test comparison of seedling area between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Area	n	Area	n	p-value
ME01821	ME01821-02 (T_2)	0.0750	19	0.0567	21	$8.94x10^{-5}$
ME01821	ME01821-05 (T_2)	0.0680	19	0.0567	21	$7.89x10^{-3}$

Example 9 – Analysis of ME01910 Events

[0483] ME01910 contains Ceres Clone:1820 (At2g30620, SEQ ID NO:99) from *Arabidopsis thaliana*, which encodes a 273 amino acid linker histone H1 and H5 family protein. Evaluation of low-nitrogen tolerance for ME01910 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -01 and -02, showed significantly increased photosynthetic efficiency relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME01910 seedlings is shown in Table 6. Events -01 and -02 segregated 3:1 (R:S) for FINALE™ resistance in the T_2 generation. ME01910 events were also tested for enhanced growth on the low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 6. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME01910	ME01910-01 (T_2)	0.60433	39	0.56396	27	2.03×10^{-2}
ME01910	ME01910-01 (T_3)	0.61274	31	0.56396	27	9.23×10^{-3}
ME01910	ME01910-02 (T_2)	0.62705	37	0.58083	29	7.39×10^{-3}
ME01910	ME01910-02 (T_3)	0.64146	24	0.58083	29	9.23×10^{-4}

[0484] Events -01 and -02 of ME01910 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 10 – Analysis of ME02538 Events

[0485] ME02538 contains Ceres Clone:13102 (At1g67920, SEQ ID NO:151) from *Arabidopsis thaliana*, which encodes a 67 amino acid protein of unknown function. Evaluation of low-nitrogen tolerance for ME02538 in T_2 generation was conducted under the same conditions as described in Example 2. In this study, the seedling photosynthetic

efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, --04 and -05, showed significantly increased photosynthetic efficiency relative to the internal controls in T_2 generation on both low nitrate-containing and ammonium nitrate-containing media at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME01821 seedlings is shown in Table 7.

Table 7A. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME02538	ME02538-04 (T_2)	0.6686	15	0.6171	24	1.92×10^{-4}
ME02538	ME02538-05 (T_2)	0.6420	20	0.6171	24	4.84×10^{-2}

Table 7B. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME02538	ME02538-04 (T_2)	0.7345	13	0.7080	22	4.45×10^{-3}
ME02538	ME02538-05 (T_2)	0.7356	20	0.7080	22	5.93×10^{-3}

[0486] ME02538 events were also tested for enhanced growth on the low ammonium nitrate media. A summary of the growth assay performed on ME01812 events is shown in Table 8. Transgenic seedlings of two events -01 and -02 were found significantly larger than the pooled non-transgenic segregants on both low nitrate- (Table 8A) and low ammonium nitrate-containing media (Table 8B).

Table 8A. T-test comparison of seedling area between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Area	n	Area	n	p-value
ME02538	ME02538-01 (T_2)	0.0655	16	0.0558	36	2.80×10^{-4}
ME02538	ME02538-02 (T_2)	0.0651	13	0.0601	20	1.32×10^{-2}

Table 8B. T-test comparison of seedling area between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Area	n	Area	n	p-value
ME02538	ME02538-01 (T_2)	0.0856	15	0.0737	39	8.60×10^{-3}
ME02538	ME02538-02 (T_2)	0.0864	14	0.0776	22	3.13×10^{-2}

Example 11 – Analysis of ME02603 Events

[0487] ME02603 contains Ceres Clone:15457 (At5g47610, SEQ ID NO:165) from *Arabidopsis thaliana*, which encodes a 166 amino acid zinc ion binding protein. Evaluation of low-nitrogen tolerance for ME02603 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -01 and -04, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME02603 seedlings is shown in Table 9. Events -01 and -04 segregated 3:1 (R:S) for FINALE™ resistance in the T_2 generation. Transgenic plants of two events -01 and -04 - were also tested for enhanced photosynthetic efficiency on the low nitrate media. No significant differences between the transgenics and the controls were observed.

Table 9. T-test comparison of photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 17 days (21 days for the T_2 generation of ME02603-01) of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME02603	ME02603-01 (T_2)	0.61	10	0.54	32	9.00×10^{-4}
ME02603	ME02603-01 (T_3)	0.67	28	0.65	62	6.11×10^{-3}
ME02603	ME02603-04 (T_2)	0.69	25	0.65	62	4.45×10^{-5}
ME02603	ME02603-04 (T_3)	0.68	24	0.65	62	7.53×10^{-3}

[0488] Events -01 and -04 of ME02603 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 12 – Analysis of ME02613 Events

[0489] ME02613 contains Ceres Clone:17883 (At3g13910, SEQ ID NO:185) from *Arabidopsis thaliana*, which encodes a 102 amino acid protein of unknown function. Evaluation of low-nitrogen tolerance for ME02613 in T_2 generation was conducted under the

same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. In T_2 generation, two events, -01 and -04, showed significantly increased photosynthetic efficiency on low nitrate containing-media relative to the internal controls in T_2 generation at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. Two events, -03 and -04, showed significantly increased photosynthetic efficiency on low ammonium nitrate containing-media relative to the internal controls in T_2 generation at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME02613 seedlings is shown in Table 10.

Table 10A. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME02613	ME02613-01 (T_2)	0.6979	16	0.6630	21	1.45×10^{-2}
ME02613	ME02613-04 (T_2)	0.7046	13	0.6630	21	5.73×10^{-4}

Table 10B. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME02613	ME02613-03 (T_2)	0.7270	9	0.7068	29	4.34×10^{-2}
ME02613	ME02613-04 (T_2)	0.7485	15	0.7068	29	7.09×10^{-5}

[0490] A summary of the enhanced growth of ME02613 events on either low nitrate- or low ammonium nitrate-containing media is shown in Table 11. For two events -01 and -03, transgenic seedlings were found significantly larger than the pooled non-transgenic segregants after 14 days of growth on low nitrate-containing media (Table 11A). Transgenic seedlings of two events -02 and -03 were found significantly larger than the pooled non-transgenic segregants after 14 days of growth on low ammonium nitrate-containing media (Table 11B).

Table 11A. T-test comparison of seedling area between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Area	n	Area	n	p-value
ME02613	ME02613-01 (T_2)	0.05706	16	0.05259	31	$4.71x10^{-2}$
ME02613	ME02613-03 (T_2)	0.06236	12	0.05789	29	$2.39x10^{-2}$

Table 1. T-test comparison of seedling area between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Area	n	Area	n	p-value
ME02613	ME02613-02 (T_2)	0.08324	14	0.07018	29	$2.72x10^{-4}$
ME02613	ME02613-03 (T_2)	0.08273	9	0.07018	29	$1.41x10^{-2}$

Example 13 – Analysis of ME02801 Events

[0491] ME02801 contains Ceres Clone:251590 (At3g53080, SEQ ID NO:207) from *Arabidopsis thaliana*, which encodes a 155 amino acid protein of unknown function. Evaluation of low-nitrogen tolerance for ME02801 in T_2 and T_3 was conducted under the same conditions as described in Example 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -02 and -04, showed significantly increased photosynthetic efficiency on low nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME02801 seedlings is shown in Table 12. Events -02 and -04 segregated 3:1 (R:S) for FINALE™ resistance in the T_2 generation. ME02801 events were also tested for enhanced growth on the low nitrate media and enhanced photosynthetic efficiency and growth on low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 12. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME02801	ME02801-02 (T_2)	0.536385	39	0.465903	113	$5.49x10^{-7}$
ME02801	ME02801-02 (T_3)	0.536465	43	0.465903	113	$5.11x10^{-7}$
ME02801	ME02801-04 (T_2)	0.532419	31	0.465903	113	$1.28x10^{-5}$
ME02801	ME02801-04 (T_3)	0.510406	32	0.465903	113	$1.74x10^{-2}$

[0492] Events -02 and -04 of ME02801 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic

plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 14 – Analysis of ME03123 Events

[0493] ME03123 contains Ceres Clone:4898 (At1g29970, SEQ ID NO:217) from *Arabidopsis thaliana*, which encodes a 158 amino acid protein of unknown function. Evaluation of low-nitrogen tolerance for ME03123 in T_2 and/or T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. A summary of photosynthetic efficiency of ME03123 seedlings is shown in Table 13. Two events, -01 and -10, showed significantly increased photosynthetic efficiency on low nitrate- or low ammonium nitrate-containing media relative to the internal controls in T_2 or T_3 generation at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance.

Table 13A. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME03123	ME03123-01 (T_2)	0.6282	15	0.5732	26	6.60×10^{-5}
ME03123	ME03123-10 (T_3)	0.6069	12	0.5732	26	1.05×10^{-2}

Table 13B. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME03123	ME03123-01 (T_2)	0.6736	17	0.6315	16	1.74×10^{-2}
ME03123	ME03123-10 (T_3)	0.6699	20	0.6315	16	1.60×10^{-2}

[0494] ME03123 events were also tested for enhanced growth on the low ammonium nitrate media. In this assay, transgenic seedlings of ME03123-02 and ME03123-04 (T_2) were significantly larger than the pooled non-transgenic segregants after 14 days of growth on low nitrate (Table 14).

Table 14. T-test comparison of seedling area between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Area	n	Area	n	p-value
ME03123	ME03123-02 (T_2)	0.07235	19	0.05623	20	$1.41x10^{-6}$
ME03123	ME03123-04 (T_3)	0.06571	7	0.05729	41	$7.74x10^{-3}$

Example 15 – Analysis of ME04204 Events

[0495] ME04204 contains Ceres Clone:148977 (At1g78770, SEQ ID NO:233) from *Arabidopsis thaliana*, which encodes a 159 amino acid anaphase promoting complex/cyclosome subunit protein. However, it is also possible that this is natural variant transcript produced by the plant, because multiple annotations for locus At1g78770 were found in public domain. Evaluation of low-nitrogen tolerance for ME04204 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -01 and -05, showed significantly increased photosynthetic efficiency relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME04204 seedlings is shown in Table 15. Events -01 and -05 segregated 3:1 (R:S) for FINALE™ resistance in the T_2 generation. ME04204 events were also tested for enhanced growth on the low nitrate media. No significant differences between the transgenics and the controls were observed.

Table 15. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME04204	ME04204-01 (T_2)	0.623676	34	0.585504	121	$2.15x10^{-4}$
ME04204	ME04204-01 (T_3)	0.627706	17	0.585504	121	$8.22x10^{-5}$
ME04204	ME04204-05 (T_2)	0.615857	35	0.585504	121	$9.41x10^{-3}$
ME04204	ME04204-05 (T_3)	0.611419	43	0.585504	121	$1.25x10^{-2}$

[0496] Events -01 and -05 of ME04204 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-

bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 16 – Analysis of ME04477 Events

[0497] ME04477 contains Ceres Clone:24255 (At2g36320, SEQ ID NO:245) from *Arabidopsis thaliana*, which encodes a 161 amino acid DNA binding / zinc ion binding protein. Evaluation of low-nitrogen tolerance for ME04477 in T_2 and T_3 was conducted under the same conditions as described in Example 2. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -01 and -05, showed significantly increased photosynthetic efficiency on low nitrate- containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME04477 seedlings is shown in Table 16. Events -01 and -05 segregated 3:1 (R:S) for FINALE™ resistance in the T_2 generation. ME04477 events were also tested for enhanced growth on the low nitrate media. No significant differences between the transgenics and the controls were observed.

Table 16. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME04204	ME04204-01 (T_2)	0.623676	34	0.585504	121	2.15×10^{-4}
ME04204	ME04204-01 (T_3)	0.627706	17	0.585504	121	8.22×10^{-5}
ME04204	ME04204-05 (T_2)	0.615857	35	0.585504	121	9.41×10^{-3}
ME04204	ME04204-05 (T_3)	0.611419	43	0.585504	121	1.25×10^{-2}

[0498] Events -01 and -05 of ME04477 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 17 – Analysis of ME04507 Events

[0499] ME04507 contains Ceres Clone:38432 (At4g38250, SEQ ID NO:299) from

Arabidopsis thaliana, which encodes a 436 amino acid transmembrane amino acid transporter protein. Evaluation of low-nitrogen tolerance for ME04507 in T_2 and T_3 was conducted under the same conditions as described in Example 2. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -03 and -04, showed significantly increased photosynthetic efficiency on low nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME04507 seedlings is shown in Table 17. Events -03 and -04 segregated 15:1 and 3:1 (R:S), respectively, for FINALE™ resistance in the T_2 generation. ME04507 events were also tested for enhanced growth on the low nitrate media. No significant differences between the transgenics and the controls were observed.

Table 17. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate media.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME04507	ME04507-03 (T_2)	0.57753	40	0.53084	103	4.90×10^{-4}
ME04507	ME04507-03 (T_3)	0.56318	39	0.53084	103	2.64×10^{-2}
ME04507	ME04507-04 (T_2)	0.57708	38	0.53084	103	6.12×10^{-3}
ME04507	ME04507-04 (T_3)	0.57277	22	0.53084	103	2.35×10^{-2}

[0500] Events -03 and -04 of ME04507 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 18 – Analysis of ME04587 Events

[0501] ME04587 contains Ceres Annot: 553243 (At2g27010, SEQ ID NO:331) from *Arabidopsis thaliana*, which encodes a 516 amino acid cytochrome P450 protein. Evaluation of low-nitrogen tolerance for ME04587 in T_2 and T_3 was conducted under the same conditions as described in Example 2. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -01 and -02, showed significantly

increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME04587 seedlings is shown in Table 18. In T_2 generation, events -01 and -02 segregated 1:1 and 47:1 respectively (R:S) for FINALE™ resistance. These two events segregated 2:1 and 7:1 respectively (R:S) for FINALE® resistance in the T_3 generation.

Table 18. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME04587	ME04587-01 (T_2)	0.6424	10	0.5437	30	2.48×10^{-3}
ME04587	ME04587-01 (T_3)	0.6165	25	0.5437	30	1.24×10^{-2}
ME04587	ME04587-02 (T_2)	0.6022	47	0.5437	30	3.08×10^{-2}
ME04587	ME04587-02 (T_3)	0.6310	43	0.5437	30	3.68×10^{-3}

[0502] ME04587 events were also tested for enhanced growth on the low ammonium nitrate media. In addition, these events were tested on low nitrate media for increased seedling area and photosynthetic efficiency. No statistically significant differences between the transgenics and the controls were observed.

[0503] Events -01 and –02 of ME04587 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 19 – Analysis of ME04753 Events

[0504] ME04753 contains Ceres Clone:1011900 (At2g21660, SEQ ID NO:367) from *Arabidopsis thaliana*, which encodes a 130 amino acid glycine-rich RNA binding protein. Evaluation of low-nitrogen tolerance for ME04753 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -01 and -02, showed significantly increased photosynthetic efficiency on low nitrate-containing media relative to

the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME04753 seedlings is shown in Table 19. Events -01 and -02 segregated 3:1 and 2:1 respectively (R:S) for FINALE™ resistance in the T_2 generation. ME04753 events were also tested for enhanced growth on the low nitrate media. No significant differences between the transgenics and the controls were observed.

Table 19. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate media.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME04753	ME04753-01 (T_2)	0.49323	39	0.45917	66	3.17×10^{-2}
ME04753	ME04753-01 (T_3)	0.50942	26	0.45917	66	1.80×10^{-2}
ME04753	ME04753-02 (T_2)	0.49856	34	0.45917	66	2.43×10^{-2}
ME04753	ME04753-02 (T_3)	0.51274	27	0.45917	66	1.15×10^{-2}

[0505] Events -01 and -02 of ME04753 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 20 – Analysis of ME04772 Events

[0506] ME04772 contains Ceres Clone:5232 (At1g13380, SEQ ID NO:509) from *Arabidopsis thaliana*, which encodes a 188 amino acid protein of unknown function. Evaluation of low-nitrogen tolerance for ME04772 in T_2 and T_3 was conducted under the same conditions as described in Example 2. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -02 and -04, showed significantly increased photosynthetic efficiency on low nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME04772 seedlings is shown in Table 20. Events -02 and -04 segregated 2:1 and 3:1 respectively (R:S) for FINALE™ resistance in the T_2 generation. ME04772 events were also tested for enhanced growth on the low nitrate media. No significant differences between the transgenics and the controls were observed.

Table 20. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate media.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME04772	ME04772-02 (T_2)	0.53708	25	0.46204	53	$3.36x10^{-5}$
ME04772	ME04772-02 (T_3)	0.53121	34	0.46204	53	$1.27x10^{-4}$
ME04772	ME04772-04 (T_2)	0.52921	34	0.46204	53	$3.71x10^{-4}$
ME04772	ME04772-04 (T_3)	0.50272	36	0.46204	53	$2.73x10^{-2}$

[0507] Events -02 and -04 of ME04772 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 21 – Analysis of ME04772 Events

[0508] ME04909 contains Ceres Clone:29302 (At1g49010, SEQ ID NO:532) from *Arabidopsis thaliana*, which encodes a 314 amino acid Myb-like DNA-binding domain protein. Evaluation of low-nitrogen tolerance for ME04909 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -01 and -03, showed significantly increased photosynthetic efficiency on low nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME04909 seedlings is shown in Table 21. Events -01 and -03 segregated 15:1 (R:S) for FINALE™ resistance in the T_2 generation. ME04909 events were also tested for enhanced growth on the low nitrate media. No significant differences between the transgenics and the controls were observed.

Table 21. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME04909	ME04909-01 (T_2)	0.587774	31	0.550342	111	$1.36x10^{-2}$
ME04909	ME04909-01 (T_3)	0.607452	31	0.550342	111	$1.28x10^{-3}$
ME04909	ME04909-03 (T_2)	0.581537	41	0.550342	111	$1.8x10^{-2}$
ME04909	ME04909-03 (T_3)	0.609806	31	0.550342	111	$4.3x10^{-5}$

[0509] Events -01 and -03 of ME04909 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 22 – Analysis of ME05033 Events

[0510] ME05033 contains Ceres Clone:93971 (At4g19095, SEQ ID NO:555) from *Arabidopsis thaliana*, which encodes a 188 amino acid protein of unknown function. Evaluation of low-nitrogen tolerance for ME05033 in T_2 and T_3 was conducted under the same conditions as described in Example 2. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -03 and -05, showed significantly increased photosynthetic efficiency on low nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME05033 seedlings is shown in Table 22. Events -03 and -05 segregated 15:1 and 2:1 respectively (R:S) for FINALE™ resistance in the T_2 generation. ME05033 events were also tested for enhanced growth on the low nitrate media. No significant differences between the transgenics and the controls were observed.

Table 22. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate media.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME05033	ME05033-03 (T_2)	0.65717	46	0.62621	132	9.20×10^{-5}
ME05033	ME05033-03 (T_3)	0.64956	39	0.62621	132	4.52×10^{-3}
ME05033	ME05033-05 (T_2)	0.64448	29	0.62621	132	3.46×10^{-2}
ME05033	ME05033-05 (T_3)	0.65537	30	0.62621	132	2.38×10^{-4}

[0511] Events -03 and -05 of ME05033 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical

differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 23 – Analysis of ME05194 Events

[0512] ME05194 contains Ceres cDNA:12669619 (At1g30710, SEQ ID NO:557) from *Arabidopsis thaliana*, which encodes a 531 amino acid electron carrier protein. Evaluation of low-nitrogen tolerance for ME05194 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. Two events, -03 and -05, showed significantly enhanced growth on low nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. In this study, the seedling area at 14 days for transgenic plants within an event was compared to the seedling area for non-transgenic segregants pooled across the same line. A summary of enhanced growth under low nitrate growth conditions of ME05194 seedlings is shown in Table 23. Events -03 and -05 segregated 1:1 (R:S) for FINALE™ resistance in the T_2 generation. ME05194 events were also tested for increased photosynthetic efficiency on the low nitrate media. No significant differences between the transgenics and the controls were observed.

Table 23. t-test comparison of seedling area between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Area	n	Area	n	p-value
ME05194	ME05194-03 (T_2)	0.051216	38	0.040874	82	2.54×10^{-5}
ME05194	ME05194-03 (T_3)	0.047042	45	0.040874	82	2.61×10^{-2}
ME05194	ME05194-05 (T_2)	0.048746	26	0.040874	82	6.15×10^{-3}
ME05194	ME05194-05 (T_3)	0.048457	14	0.040874	82	3.03×10^{-2}

[0513] Events -03 and -05 of ME05194 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 24 – Analysis of ME05267 Events

[0514] ME05267 contains Ceres Clone:21608 (At5g49510, SEQ ID NO:592) from *Arabidopsis thaliana*, which encodes a 195 amino acid von Hippel-Lindau binding protein. Evaluation of low-nitrogen tolerance for ME05267 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. Two events, -01 and -04, showed significantly enhanced growth on low nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. In this study, the seedling area at 14 days for transgenic plants within an event was compared to the seedling area for non-transgenic segregants pooled across the same line. A summary of enhanced growth under low nitrate growth conditions of ME05194 seedlings is shown in Table 24. Events -01 and -04 segregated 15:1 (R:S) for FINALE™ resistance in the T_2 generation. ME05267 events were also tested for increased photosynthetic efficiency on the low nitrate media. No significant differences between the transgenics and the controls were observed.

Table 24. t-test comparison of seedling area between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Area	n	Area	n	p-value
ME05267	ME05267-01 (T_2)	0.053263	46	0.0450197	122	$4.4x10^{-5}$
ME05267	ME05267-01 (T_3)	0.051135	26	0.0450197	122	$5.0x10^{-2}$
ME05267	ME05267-04 (T_2)	0.049977	44	0.0450197	122	$6.4x10^{-3}$
ME05267	ME05267-04 (T_3)	0.053084	38	0.0450197	122	$8.4x10^{-4}$

[0515] Events -01 and -04 of ME05267 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 25 – Analysis of ME05300 Events

[0516] ME05300 contains Ceres Clone:2031 (At1g72020, SEQ ID NO:612) from *Arabidopsis thaliana*, which encodes a 97 amino acid protein of unknown function. Evaluation of low-nitrogen tolerance for ME05300 in T_2 generation was conducted under the same conditions as described in Examples 2 and 3. A summary of photosynthetic efficiency

of ME05300 seedlings is shown in Table 25. Two events, -04 and -05, showed significantly increased photosynthetic efficiency on low nitrate- and low ammonium nitrate-containing media relative to the internal controls in T_2 generation at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. In addition, two events, -01 and -05, showed significantly enhanced growth on low nitrate- and low ammonium nitrate-containing media relative to the internal controls in T_2 generation at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. In this study, the seedling area for transgenic plants within an event was compared to the seedling area for non-transgenic segregants pooled across the same line. A summary of enhanced growth under low nitrate and low ammonium nitrate growth conditions of ME05300 seedlings is shown in Table 26.

Table 25A. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME05300	ME05300-04 (T_2)	0.6867	7	0.6488	27	1.65×10^{-2}
ME05300	ME05300-05 (T_2)	0.6839	16	0.6488	27	2.50×10^{-3}

Table 25B. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME05300	ME05300-04 (T_2)	0.6767	6	0.6323	32	1.68×10^{-2}
ME05300	ME05300-05 (T_2)	0.6934	11	0.6323	32	7.04×10^{-4}

Table 26A. T-test comparison of seedling area between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Area	n	Area	n	p-value
ME05300	ME05300-01 (T_2)	0.0737	18	0.0588	21	3.80×10^{-3}
ME05300	ME05300-05 (T_2)	0.0655	16	0.0570	27	1.59×10^{-2}

Table 26B. T-test comparison of seedling area between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Area	n	Area	n	p-value
ME05300	ME05300-01 (T_2)	0.0987	17	0.0776	29	3.89×10^{-3}
ME05300	ME05300-05 (T_2)	0.1082	11	0.0776	29	1.57×10^{-3}

Example 26 – Analysis of ME05341 Events

[0517] ME05341 contains Ceres Clone:94503 (At4g14420, SEQ ID NO:645) from *Arabidopsis thaliana*, which encodes a 158 amino acid elicitor-like protein. Evaluation of low-nitrogen tolerance for ME05341 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. Two events, -01 and -02, showed significantly enhanced growth on low nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. In this study, the seedling area at 14 days for transgenic plants within an event was compared to the seedling area for non-transgenic segregants pooled across the same line. A summary of photosynthetic efficiency of ME05341 seedlings is shown in Table 27. Events -01 and -02 segregated 15:1 (R:S) for FINALE™ resistance in the T_2 generation. ME05341 events were also tested for increased photosynthetic efficiency on the low nitrate media. No significant differences between the transgenics and the controls were observed.

Table 27. t-test comparison of seedling area between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Area	n	Area	n	p-value
ME05341	ME05341-01 (T_2)	0.06253	46	0.04988	143	4.17×10^{-10}
ME05341	ME05341-01 (T_3)	0.05876	38	0.04988	143	4.13×10^{-4}
ME05341	ME05341-02 (T_2)	0.06152	46	0.04988	143	2.91×10^{-7}
ME05341	ME05341-02 (T_3)	0.05572	48	0.04988	143	2.90×10^{-3}

[0518] Events -01 and -02 of ME05341 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 27 – Analysis of ME05392 Events

[0519] ME05392 contains Ceres Clone:21740 (At5g01610, SEQ ID NO:686) from *Arabidopsis thaliana*, which encodes a 170 amino acid protein of unknown function. Evaluation of low-nitrogen tolerance for ME05392 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-

transgenic segregants pooled across the same plate. Two events, -01 and -03, showed significantly increased photosynthetic efficiency on low nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME05392 seedlings is shown in Table 20. Events -01 and -03 segregated 2:1 (R:S) for FINALE™ resistance in the T_2 generation. ME05392 events were also tested for enhanced growth on the low nitrate media. No significant differences between the transgenics and the controls were observed.

Table 28. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate media.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME05392	ME05392-01 (T_2)	0.61759	32	0.60093	107	3.70×10^{-2}
ME05392	ME05392-01 (T_3)	0.63388	40	0.60093	107	5.05×10^{-5}
ME05392	ME05392-03 (T_2)	0.64335	23	0.60093	107	5.81×10^{-5}
ME05392	ME05392-03 (T_3)	0.63397	36	0.60093	107	4.30×10^{-5}

[0520] Events -01 and -03 of ME05392 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 28 – Analysis of ME05429 Events

[0521] ME05429 contains Ceres Clone:5609 (At3g60480, SEQ ID NO:729) from *Arabidopsis thaliana*, which encodes a 188 amino acid protein of unknown function. Evaluation of low-nitrogen tolerance for ME05429 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -06 and -08, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME05429 seedlings is shown in Table 29. Events -06 and -08 segregated 3:1 and 2:1 respectively (R:S) for FINALE™ resistance in the T_2 generation. ME05429 events were tested for enhanced

growth on the low ammonium nitrate media. In addition, these events were also tested for enhanced growth and photosynthetic efficiency on low nitrate media. No significant differences between the transgenics and the controls were observed.

Table 29. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME05429	ME05429-06 (T_2)	0.62521	28	0.59991	78	$2.85x10^{-2}$
ME05429	ME05429-06 (T_3)	0.63031	39	0.59991	78	$8.49x10^{-3}$
ME05429	ME05429-08 (T_2)	0.64526	23	0.59991	78	$1.67x10^{-3}$
ME05429	ME05429-08 (T_3)	0.65076	17	0.59991	78	$2.76x10^{-4}$

[0522] Events -06 and -08 of ME05429 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 29 – Analysis of ME05493 Events

[0523] ME05493 contains Ceres Clone:3137 (At3g43430, SEQ ID NO:745) from *Arabidopsis thaliana*, which encodes a 169 amino acid zinc finger family protein. Evaluation of low-nitrogen tolerance for ME05493 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -01 and -05, showed significantly increased photosynthetic efficiency on low nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME05493 seedlings is shown in Table 30. Events -01 and -05 segregated 15:1 (R:S) for FINALE™ resistance in the T_2 generation. ME05493 events were also tested for enhanced growth on the low nitrate media. No significant differences between the transgenics and the controls were observed.

Table 30. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate media.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME05493	ME05493-01 (T_2)	0.64121	32	0.61097	92	$1.13x10^{-3}$
ME05493	ME05493-01 (T_3)	0.64250	46	0.61097	92	$3.03x10^{-4}$
ME05493	ME05493-05 (T_2)	0.62865	43	0.61097	92	$1.75x10^{-2}$
ME05493	ME05493-05 (T_3)	0.63936	42	0.61097	92	$1.21x10^{-4}$

[0524] Events -01 and -05 of ME05493 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 30 – Analysis of ME05885 Events

[0525] ME05885 contains Ceres Clone:32430 (At1g16170, SEQ ID NO:768) from *Arabidopsis thaliana*, which encodes a 92 amino acid protein of unknown function. Evaluation of low-nitrogen tolerance for ME05885 in T_3 generation was conducted under the same conditions as described in Examples 2 and 3. A summary of photosynthetic efficiency of ME05885 seedlings is shown in Table 31. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -01 and -05, showed significantly increased photosynthetic efficiency on low nitrate-containing media and low ammonium nitrate-containing media relative to the internal controls in T_3 generation at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance.

Table 31A. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME05885	ME05885-01 (T_3)	0.6759	12	0.6533	28	$4.32x10^{-2}$
ME05885	ME05885-05 (T_3)	0.6831	7	0.6530	52	$3.68x10^{-6}$

Table 31B. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME05885	ME05885-01 (T_3)	0.6490	13	0.6135	30	$3.06x10^{-2}$
ME05885	ME05885-05 (T_3)	0.6810	9	0.6133	43	$6.77x10^{-5}$

[0526] ME05885 events were also tested for enhanced growth on the low nitrate and low ammonium nitrate media. A summary of enhanced growth under low nitrate and low ammonium nitrate growth conditions of ME05885 seedlings in T_3 generation is shown in Table 32. Two events, -03 and -05, showed significantly enhanced growth on low nitrate-containing media. Two events, -02 and -05, showed significantly enhanced growth on low ammonium nitrate-containing media relative to the internal controls at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. In this study, the seedling area for transgenic plants within an event was compared to the seedling area for non-transgenic segregants pooled across the same line.

Table 32A. T-test comparison of seedling area between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Area	n	Area	n	p-value
ME05885	ME05885-03 (T_3)	0.06245	6	0.05286	14	$1.42x10^{-2}$
ME05885	ME05885-05 (T_3)	0.05893	7	0.04725	12	$5.61x10^{-3}$

Table 32B. T-test comparison of seedling area between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Area	n	Area	n	p-value
ME05885	ME05885-02 (T_3)	0.0744	14	0.05595	6	$3.28x10^{-5}$
ME05885	ME05885-05 (T_3)	0.0753	9	0.06179	11	$5.08x10^{-3}$

Example 31 – Analysis of ME07344 Events

[0527] ME07344 contains Ceres Clone:101255 (At2g19810, SEQ ID NO:791) from *Arabidopsis thaliana*, which encodes a 359 amino acid CCCH-type zinc finger protein.

Evaluation of low-nitrogen tolerance for ME07344 in T_2 and T_3 was conducted under the same conditions as described in Example 4. In this study, the 4th true leaf from each plant was collected on day 38 and analyzed on the CF imager for its Fv/Fm value. Transgenic plants within an event were compared to all non-transgenic plants, including the non-transgenic segregants and external controls. Two events, -02 and -03, showed significantly increased photosynthetic efficiency relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME07344 seedlings is shown in Table 33. Events -02 and -03 segregated 3:1 (R:S) for FINALE™ resistance in the T_2 generation. ME07344 events were also tested for enhanced growth on the low nitrate media. No significant differences between the transgenics and the controls were observed.

Table 33. T-test comparison of photosynthetic efficiency between transgenic plants and non-transgenic controls after 38 days of growth on nitrogen-depleted soil.

		Transgenic		Non-Transgenic Controls		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME07344	ME07344-02 (T_2)	0.752	17	0.729	50	2.86×10^{-4}
ME07344	ME07344-02 (T_3)	0.750	16	0.729	50	1.11×10^{-4}
ME07344	ME07344-03 (T_2)	0.741	13	0.729	50	0.018
ME07344	ME07344-03 (T_3)	0.754	17	0.729	50	4.62×10^{-6}

[0528] Events -02 and -03 of ME07344 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 32 – Analysis of ME07859 Events

[0529] ME07859 contains Ceres Clone:276809 (SEQ ID NO:823) from *Zea mays*, which encodes a 135 amino acid sterol desaturase protein. Evaluation of low-nitrogen tolerance for ME07859 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -02 and -04, showed significantly increased photosynthetic efficiency on low nitrate-containing media relative to the internal controls in

both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME07859 seedlings is shown in Table 34. Events -02 and -04 segregated 1:1 and 2:1 respectively (R:S) for FINALE™ resistance in the T_2 generation. ME07859 events were also tested for enhanced growth on the low nitrate media as well as for enhanced growth and photosynthetic efficiency on low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 34. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate media.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME07859	ME07859-02 (T_2)	0.6598	24	0.6378	127	0.03
ME07859	ME07859-02 (T_3)	0.6825	14	0.6378	127	$1.3x10^{-3}$
ME07859	ME07859-04 (T_2)	0.6539	33	0.6378	127	0.05
ME07859	ME07859-04 (T_3)	0.6601	17	0.6378	127	0.05

[0530] Events -02 and -04 of ME07859 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 33 – Analysis of ME08464 Events

[0531] ME08464 contains Ceres Clone:424522 (SEQ ID NO:827)from *Zea mays*, which encodes a 500 amino acid unknown protein. Evaluation of low-nitrogen tolerance for ME08464 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -02 and -03, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME07859 seedlings is shown in Table 35. Events -02 and -03 segregated 3:1 (R:S) for FINALE™ resistance in the T_2 generation. ME08464 events were also tested for increased photosynthetic efficiency on the low nitrate media. No significant differences between the transgenics and the controls were observed.

Table 35. T-test comparison of photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 15 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME08464	ME08464-02 (T_2)	0.65	41	0.62	40	0.015
ME08464	ME08464-02 (T_3)	0.67	32	0.62	40	2.32×10^{-4}
ME08464	ME08464-03 (T_2)	0.65	43	0.62	40	0.013
ME08464	ME08464-03 (T_3)	0.65	42	0.62	40	6.85×10^{-3}

[0532] Events -02 and -03 of ME08464 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 34 – Analysis of ME09939 Events

[0533] ME09939 contains Ceres Clone:324216 (SEQ ID NO:852) from *Zea mays*, which encodes a 38 amino acid protein of unknown function. Evaluation of low-nitrogen tolerance for ME09939 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -04 and -05, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME09939 seedlings is shown in Table 36. Events -04 and -05 segregated 15:1 and 3:1 respectively (R:S) for FINALE™ resistance in the T_2 generation. ME09939 events were also tested for enhanced growth on the low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 36. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME09939	ME09939-04 (T_2)	0.49285	40	0.38571	7	0.05
ME09939	ME09939-04 (T_3)	0.50697	34	0.38571	7	$3.50x10^{-2}$
ME09939	ME09939-05 (T_2)	0.53487	39	0.47492	24	$1.19x10^{-2}$
ME09939	ME09939-05 (T_3)	0.55341	32	0.47492	24	$1.82x10^{-3}$

[0534] Events -04 and -05 of ME09939 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 35 – Analysis of ME11735 Events

[0535] ME11735 contains Ceres Annot:573161 (At5g43260, SEQ ID NO:854) from *Arabidopsis thaliana*, which encodes a 97 amino acid DnaJ-related chaperone protein. Evaluation of low-nitrogen tolerance for ME11735 in T_2 and T_3 was conducted under the same conditions as described in Example 2 and 3. A summary of the enhanced growth of ME11735 events on low nitrate-containing media is shown in Table 37. In this study, the seedling area for transgenic plants within an event was compared to the seedling area for non-transgenic segregants pooled across the same line. Two events, -04 and -05, were found significantly larger than the pooled non-transgenic segregants after 14 days of growth on low nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. ME11735 events were also tested for increased photosynthetic efficiency on the low nitrate media. No significant differences between the transgenics and the controls were observed. Events -04 and -05 segregated 40:1 and 4:1 respectively (R:S) for FINALE™ resistance in the T_2 generation.

Table 37. t-test comparison of seedling area between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Area	n	Area	n	p-value
ME11735	ME11735-04 (T_2)	0.05820	41	0.04994	127	$5.91x10^{-5}$

ME11735	ME11735-04 (T_3)	0.05553	42	0.04994	127	$1.26x10^{-2}$
ME11735	ME11735-05 (T_2)	0.05788	37	0.04994	127	$1.59x10^{-3}$
ME11735	ME11735-05 (T_3)	0.06011	13	0.04994	127	$1.64x10^{-2}$

[0536] Events -04 and -05 of ME11735 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 36 – Analysis of ME12910 Events

[0537] ME12910 contains Ceres Annot:552727 (At2g22930, SEQ ID NO:890) from *Arabidopsis thaliana*, which encodes a 442 amino acid UDP-glucoronosyl and UDP-glucosyl transferase family protein. Evaluation of low-nitrogen tolerance for ME12910 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -03 and -05, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME12910 seedlings is shown in Table 38. ME12910 events were also tested for enhanced growth on the low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 38. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME12910	ME12910-03 (T_2)	0.5851	39	0.5191	29	$1.54x10^{-3}$
ME12910	ME12910-03 (T_3)	0.5861	22	0.5191	29	$2.17x10^{-3}$
ME12910	ME12910-05 (T_2)	0.5523	44	0.4251	7	$1.23x10^{-2}$
ME12910	ME12910-05 (T_3)	0.5600	42	0.4251	7	$9.62x10^{-3}$

[0538] Events -03 and -05 segregated 3:1 and 15:1 respectively (R:S) for FINALE™ resistance in the T_2 generation.

[0539] Events -03 and -05 of ME12910 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 37 – Analysis of ME12927 Events

[0540] ME12927 contains Ceres Clone:239806 (SEQ ID NO:916) from *Zea mays*, which encodes a 201 amino acid lipoprotein amino terminal region. Evaluation of low-nitrogen tolerance for ME12927 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Three events, -02, -03 and -05, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$, using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME12927 seedlings is shown in Table 39.

Table 39. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME12927	ME12927-02 (T_2)	0.60843	44	0.47813	8	4.88×10^{-3}
ME12927	ME12927-02 (T_3)	0.60867	36	0.47813	8	5.23×10^{-3}
ME12927	ME12927-03 (T_2)	0.61906	32	0.57929	38	8.96×10^{-3}
ME12927	ME12927-03 (T_3)	0.63437	19	0.57929	38	5.35×10^{-4}
ME12927	ME12927-05 (T_2)	0.60581	43	0.53982	22	7.26×10^{-3}
ME12927	ME12927-05 (T_3)	0.63145	29	0.53982	22	5.83×10^{-4}

[0541] ME12927 events were also tested for enhanced growth on the low ammonium nitrate media. A summary of the enhanced growth of ME11735 events on low ammonium nitrate-containing media is shown in Table 40. In this study, the seedling area for transgenic plants within an event was compared to the seedling area for non-transgenic segregants pooled across the same line. Three events, -02, -03 and -05, were found significantly larger than the pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$, using a one-

tailed t-test assuming unequal variance.

Table 40. t-test comparison of seedling area between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Area	n	Area	n	p-value
ME12927	ME12927-02 (T_2)	0.066920	44	0.056585	117	$1.65x10^{-4}$
ME12927	ME12927-02 (T_3)	0.062119	36	0.056585	117	$3.51x10^{-2}$
ME12927	ME12927-03 (T_2)	0.068972	32	0.056585	117	$1.18x10^{-5}$
ME12927	ME12927-03 (T_3)	0.063716	19	0.056585	117	$1.98x10^{-2}$
ME12927	ME12927-05 (T_2)	0.069972	43	0.056585	117	$4.25x10^{-6}$
ME12927	ME12927-05 (T_3)	0.064014	29	0.056585	117	$8.49x10^{-3}$

[0542] Events 02, -03 and -05 segregated 15:1, 2:1 and 15:1 respectively (R:S) for FINALE™ resistance in the T_2 generation.

[0543] Events 02, -03 and -05 of ME12927 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill) in T_1 generation.

Example 38 – Analysis of ME12929 Events

[0544] ME12929 contains Ceres Clone:208995 (SEQ ID NO:943) from *Zea mays*, which encodes a 94 amino acid protein of unknown function. Evaluation of low-nitrogen tolerance for ME12929 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -03 and -04, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME12929 seedlings is shown in Table 41. ME12929 events were also tested for enhanced growth on the low ammonium nitrate media. No significant differences between the transgenics and the controls were observed. Events -03 and -04 segregated 1:1 and 3:1 respectively (R:S) for FINALE™ resistance in the T_2 generation.

[0545] Events -03 and -04 of ME12929 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Table 41. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME12929	ME12929-03 (T_2)	0.6410	33	0.5736	24	$9.44x10^{-4}$
ME12929	ME12929-03 (T_3)	0.6610	41	0.5736	24	$4.38x10^{-5}$
ME12929	ME12929-04 (T_2)	0.6544	47	0.5790	9	$3.68x10^{-2}$
ME12929	ME12929-04 (T_3)	0.6663	43	0.5790	9	$2.15x10^{-2}$

Example 39 – Analysis of ME12954 Events

[0546] ME12954 contains Ceres Clone:225681 (SEQ ID NO:975) from *Zea mays*, which encodes a 286 amino acid protein of unknown function. Evaluation of low-nitrogen tolerance for ME12954 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. Two events, -04 and -05, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. A summary of photosynthetic efficiency of ME12954 seedlings is shown in Table 42.

Table 42. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME12954	ME12954-04 (T_2)	0.6236	40	0.5973	152	$6.61x10^{-3}$
ME12954	ME12954-04 (T_3)	0.6200	39	0.5973	152	$1.97x10^{-2}$
ME12954	ME12954-05 (T_2)	0.6280	45	0.5973	152	$1.79x10^{-2}$
ME12954	ME12954-05 (T_3)	0.6315	35	0.5973	152	$2.85x10^{-2}$

[0547] ME12954 events were also tested for enhanced growth on the low ammonium

nitrate media. A summary of the enhanced growth of ME12954 events on low ammonium nitrate-containing media is shown in Table 43. In this study, the seedling area for transgenic plants within an event was compared to the seedling area for non-transgenic segregants pooled across the same line. Two events, -02 and -04, were found significantly larger than the pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$, using a one-tailed t-test assuming unequal variance.

Table 43. t-test comparison of seedling area between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Area	n	Area	n	p-value
ME12954	ME12954-02 (T_2)	0.06883	31	0.05579	152	$1.86x10^{-5}$
ME12954	ME12954-02 (T_3)	0.06604	26	0.05579	152	$1.48x10^{-3}$
ME12954	ME12954-04 (T_2)	0.06469	40	0.05579	152	$1.95x10^{-4}$
ME12954	ME12954-04 (T_3)	0.06301	39	0.05579	152	$3.32x10^{-3}$

[0548] Events -02, -04 and -05 segregated 2:1, 3:1 and 15:1 respectively (R:S) for FINALE™ resistance in the T2 generation.

[0549] Events -02, -04 and -05 of ME12954 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 40 – Analysis of ME12970 Events

[0550] ME12970 contains Ceres Clone:1387146 (SEQ ID NO:981) from *Zea mays*, which encodes a 147 amino acid C2 domain-containing protein. Evaluation of low-nitrogen tolerance for ME12970 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. Two events, -02 and -03, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. A summary of

photosynthetic efficiency of ME12970 seedlings is shown in Table 44. ME12970 events were also tested for enhanced growth on the low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 44. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME12970	ME12970-02 (T_2)	0.55136	44	0.52401	108	$3.78x10^{-2}$
ME12970	ME12970-02 (T_3)	0.58305	43	0.52401	108	$1.89x10^{-5}$
ME12970	ME12970-03 (T_2)	0.58759	37	0.52401	108	$2.14x10^{-6}$
ME12970	ME12970-03 (T_3)	0.59131	29	0.52401	108	$3.05x10^{-6}$

[0551] Events -02 and -03 segregated 15:1 and 3:1 respectively (R:S) for FINALE™ resistance in the T2 generation.

[0552] Events -02 and -03 of ME12970 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 41 – Analysis of ME13006 Events

[0553] ME13006 contains Ceres Clone:1017441 (SEQ ID NO:224) from *Triticum aestivum*, which encodes a 143 amino acid polypeptide, predicted to be a homolog of Ceres Clone:4898 (ME03123, SEQ ID NO:217). Evaluation of low-nitrogen tolerance for ME13006 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -01 and -03, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME13006 seedlings is shown in Table 45. ME13006 events were also tested for enhanced growth on the low nitrate media. No significant differences between the transgenics and the controls were observed.

Table 45. t-test comparison of seedling area between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Area	n	Area	n	p-value
ME13006	ME13006-01 (T_2)	0.0777	42	0.0648	7	$3.29x10^{-2}$
ME13006	ME13006-01 (T_3)	0.0660	28	0.0540	19	$1.49x10^{-3}$
ME13006	ME13006-03 (T_2)	0.0706	21	0.0601	29	$4.83x10^{-3}$
ME13006	ME13006-03 (T_3)	0.0758	14	0.0617	33	$2.60x10^{-3}$

[0554] Events -01 and -03 segregated 3:1 and 1:1 respectively (R:S) for FINALE™ resistance in the T_2 generation.

[0555] Events -01 and -03 of ME13006 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 42 – Analysis of ME13021 Events

[0556] ME13021 contains Ceres Clone:244306 (SEQ ID NO:1053) from *Zea mays*, which encodes a 572 amino acid TCP-1/cpn60 chaperonin family protein. Evaluation of low-nitrogen tolerance for ME13021 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -04 and -05, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME13021 seedlings is shown in Table 46. ME13021 events were also tested for enhanced growth on the low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 46. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME13021	ME13021-04 (T_2)	0.56697	39	0.49440	10	$2.47x10^{-2}$
ME13021	ME13021-04 (T_3)	0.59916	37	0.48685	13	$1.54x10^{-3}$
ME13021	ME13021-05 (T_2)	0.60575	32	0.50344	18	$6.05x10^{-4}$
ME13021	ME13021-05 (T_3)	0.64400	23	0.55638	26	$3.86x10^{-6}$

[0557] Events -04 and -05 segregated 3:1 and 2:1 respectively (R:S) for FINALE™ resistance in the T2 generation.

[0558] Events -04 and -05 of ME13021 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill) in T1 generation.

Example 43 – Analysis of ME13064 Events

[0559] ME13064 contains Ceres Clone:1408950 (SEQ ID NO:1098) from *Zea mays*, which encodes a 152 amino acid protein of unknown function. Evaluation of low-nitrogen tolerance for ME13064 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -03 and -04, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME13064 seedlings is shown in Table 47. ME13064 events were also tested for enhanced growth on the low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 47. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME13064	ME13064-03 (T_2)	0.59444	27	0.54793	28	$5.84x10^{-3}$
ME13064	ME13064-03 (T_3)	0.59676	29	0.54793	28	$1.25x10^{-2}$
ME13064	ME13064-04 (T_2)	0.58577	31	0.51053	40	$2.05x10^{-3}$
ME13064	ME13064-04 (T_3)	0.59128	25	0.51053	40	$8.93x10^{-4}$

[0560] Events -03 and -04 segregated 2:1 (R:S) for FINALE™ resistance in the T2 generation.

[0561] Events -03 and -04 of ME13064 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill) in T1 generation.

Example 44 – Analysis of ME13071 Events

[0562] ME13071 contains Ceres Clone:208453 (SEQ ID NO:1111) from *Zea mays*, which encodes a 74 amino acid protein of unknown function. Evaluation of low-nitrogen tolerance for ME13071 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. Two events, -03 and -05, showed significantly enhanced growth on low nitrate- and low ammonium nitrate-containing media relative to the internal controls in T_2 generation at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. In this study, the seedling area for transgenic plants within an event was compared to the seedling area for non-transgenic segregants pooled across the same line. A summary of enhanced growth under low ammonium nitrate growth conditions of ME13071 seedlings is shown in Table 48. ME13071 events were also tested for photosynthetic efficiency on the low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 48. t-test comparison of seedling area between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Area	n	Area	n	p-value
ME13071	ME13071-03 (T_2)	0.06694	26	0.05915	19	$3.55x10^{-3}$
ME13071	ME13071-03 (T_3)	0.07787	24	0.07040	22	$3.65x10^{-2}$
ME13071	ME13071-05 (T_2)	0.06232	32	0.05491	16	$2.07x10^{-3}$
ME13071	ME13071-05 (T_3)	0.06335	22	0.05626	28	$1.09x10^{-2}$

[0563] Events -03 and -05 segregated 1:1 and 2:1 respectively (R:S) for FINALE™ resistance in the T2 generation.

[0564] Events -03 and -05 of ME13071 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 45 – Analysis of ME13087 Events

[0565] ME13087 contains Ceres Clone:968180 (SEQ ID NO:1115) from *Brassica napus*, which encodes a 159 amino acid zinc finger protein. Evaluation of low-nitrogen tolerance for ME13087 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Four events, -01, -02, -03 and -04, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME13087 seedlings is shown in Table 49. ME13087 events were also tested for enhanced growth on the low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 49. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME13087	ME13087-01 (T_2)	0.59761	23	0.56163	38	$9.61x10^{-3}$
ME13087	ME13087-01 (T_3)	0.61247	15	0.56163	38	$5.99x10^{-4}$
ME13087	ME13087-02 (T_2)	0.63400	39	0.58532	34	$9.30x10^{-3}$
ME13087	ME13087-02 (T_3)	0.63442	26	0.58532	34	$1.22x10^{-2}$
ME13087	ME13087-03 (T_2)	0.61429	38	0.55533	24	$5.04x10^{-3}$
ME13087	ME13087-03 (T_3)	0.62283	35	0.55533	24	$3.31x10^{-3}$
ME13087	ME13087-04 (T_2)	0.62714	28	0.60068	56	$3.02x10^{-2}$
ME13087	ME13087-04 (T_3)	0.64543	7	0.60068	56	$9.04x10^{-3}$

[0566] Events -01, -02, -03 and -04 segregated 2:1, 3:1, 3:1 and 2:1 respectively (R:S) for FINALE™ resistance in the T2 generation.

[0567] Events -01, -02, -03 and -04 of ME13087 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill) in T1 generation.

Example 46 – Analysis of ME13106 Events

[0568] ME13106 contains Ceres Clone:986438 (SEQ ID NO:1156) from *Zea mays,* which encodes a 188 amino acid protein of unknown function. Evaluation of low-nitrogen tolerance for ME13106 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -03 and -04, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME13106 seedlings is shown in Table 50. ME13106 events were also tested for enhanced growth on the low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 50. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME13106	ME13106-03 (T_2)	0.62726	27	0.58600	43	$1.50x10^{-2}$
ME13106	ME13106-03 (T_3)	0.65163	30	0.58600	43	$1.69x10^{-4}$
ME13106	ME13106-04 (T_2)	0.60836	36	0.55876	25	$2.62x10^{-2}$
ME13106	ME13106-04 (T_3)	0.64250	38	0.55876	25	$5.01x10^{-4}$

[0569] Events -03 and -04 segregated 1:1 and 3:1 respectively (R:S) for FINALE™ resistance in the T_2 generation.

[0570] Events -03 and -04 of ME13106 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 47 – Analysis of ME13107 Events

[0571] ME13107 contains Ceres Clone:996227 (SEQ ID NO:1158) from *Zea mays,* which encodes a 240 amino acid zein seed storage protein. Evaluation of low-nitrogen tolerance for ME13107 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Three events, -02, -04 and -05, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME13107 seedlings is shown in Table 51.

Table 51. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME13107	ME13107-02 (T_2)	0.63122	37	0.56643	21	$1.07x10^{-2}$
ME13107	ME13107-02 (T_3)	0.63848	29	0.56643	21	$6.03x10^{-3}$
ME13107	ME13107-04 (T_2)	0.62948	27	0.55918	50	$2.07x10^{-5}$
ME13107	ME13107-04 (T_3)	0.63019	21	0.55918	50	$6.72x10^{-5}$
ME13107	ME13107-05 (T_2)	0.61952	29	0.54440	48	$7.85x10^{-5}$
ME13107	ME13107-05 (T_3)	0.62185	20	0.54440	48	$4.02x10^{-5}$

[0572] ME13107 events were also tested for enhanced growth on the low ammonium nitrate media. Two events, -02 and -04, showed significantly enhanced growth on low ammonium nitrate-containing media relative to the internal controls in T_2 generation at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. In this study, the seedling area for transgenic plants within an event was compared to the seedling area for non-transgenic segregants pooled across the same line. A summary of enhanced growth under low ammonium nitrate growth conditions of ME13071 seedlings is shown in Table 52.

Table 2. t-test comparison of seedling area between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Area	n	Area	n	p-value
ME13107	ME13107-02 (T_2)	0.07738	37	0.06919	203	$3.63x10^{-2}$
ME13107	ME13107-02 (T_3)	0.07688	29	0.06919	203	$4.60x10^{-2}$
ME13107	ME13107-04 (T_2)	0.07514	27	0.06919	203	$3.18x10^{-2}$
ME13107	ME13107-04 (T_3)	0.07585	21	0.06919	203	$2.27x10^{-2}$

[0573] Events -02, -04 and -05 segregated 3:1, 1:1 and 2:1 respectively (R:S) for FINALE™ resistance in the T_2 generation.

[0574] Events -02, -04 and -05 of ME13107 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 48 – Analysis of ME13108 Events

[0575] ME13108 contains Ceres Clone:996263 (SEQ ID NO:1165) from *Zea mays*, which encodes an 84 amino acid BRICK1 protein. Evaluation of low-nitrogen tolerance for ME13108 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Three events, -01, -04 and -05, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME13108 seedlings is shown in Table 53. ME13108 events were also tested for enhanced growth on the low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 53. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME13108	ME13108-01 (T_2)	0.56703	36	0.53932	195	1.97×10^{-2}
ME13108	ME13108-01 (T_3)	0.59250	26	0.53932	195	3.64×10^{-4}
ME13108	ME13108-04 (T_2)	0.60032	37	0.53932	195	3.37×10^{-7}
ME13108	ME13108-04 (T_3)	0.60463	30	0.53932	195	4.10×10^{-5}
ME13108	ME13108-05 (T_2)	0.60727	30	0.53932	195	4.97×10^{-9}
ME13108	ME13108-05 (T_3)	0.61850	32	0.53932	195	2.35×10^{-9}

[0576] Events -01, -04 and -05 segregated 3:1 (R:S) for FINALE™ resistance in the T_2 generation.

[0577] Events -01, -04 and -05 of ME13108 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 49 – Analysis of ME13110 Events

[0578] ME13110 contains Ceres Clone:988083 (SEQ ID NO:1184) from *Zea mays*, which encodes a 188 amino acid protein of unknown function. Evaluation of low-nitrogen

tolerance for ME13110 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Three events, -03, -04 and -05, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME13110 seedlings is shown in Table 54. ME13110 events were also tested for enhanced growth on the low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 54. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME13110	ME13110-03 (T_2)	0.5721	34	0.3948	16	8.92×10^{-3}
ME13110	ME13110-03 (T_3)	0.5773	24	0.4583	26	4.58×10^{-4}
ME13110	ME13110-04 (T_2)	0.5651	35	0.4243	15	4.34×10^{-2}
ME13110	ME13110-04 (T_3)	0.6000	10	0.4594	40	3.29×10^{-3}
ME13110	ME13110-05 (T_2)	0.5143	28	0.3809	22	2.24×10^{-2}
ME13110	ME13110-05 (T_3)	0.5278	28	0.3688	21	1.28×10^{-2}

[0579] Events -03, -04 and -05 segregated 3:1, 1:1 and 3:1 respectively (R:S) for FINALE™ resistance in the T_2 generation.

[0580] Events -03, -04 and -05 of ME13110 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 50 – Analysis of ME13125 Events

[0581] ME13125 contains Ceres Clone:732 (At3g50880, SEQ ID NO:1193) from *Arabidopsis thaliana*, which encodes a 188 amino acid protein of unknown function. Evaluation of low-nitrogen tolerance for ME13125 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic

efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Three events, -01, -03 and -05, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME13125 seedlings is shown in Table 55. ME13125 events were also tested for enhanced growth on the low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 55. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME13125	ME13125-01 (T_2)	0.61129	42	0.53829	125	4.82×10^{-7}
ME13125	ME13125-01 (T_3)	0.61929	38	0.53829	125	1.96×10^{-7}
ME13125	ME13125-03 (T_2)	0.63360	45	0.53829	125	3.05×10^{-13}
ME13125	ME13125-03 (T_3)	0.62218	44	0.53829	125	3.81×10^{-9}
ME13125	ME13125-05 (T_2)	0.61565	31	0.53829	125	4.12×10^{-8}
ME13125	ME13125-05 (T_3)	0.58469	16	0.53829	125	0.05

[0582] Events -01, -03 and -05 segregated 3:1, 15:1 and 2:1 respectively (R:S) for FINALE™ resistance in the T_2 generation.

[0583] Events -01, -03 and -05 of ME13125 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 51 – Analysis of ME13149 Events

[0584] ME13149 contains Ceres Clone:2267 (At2g24765, SEQ ID NO:1209) from *Arabidopsis thaliana*, which encodes a 182 amino acid ADP-ribosylation factor 3 protein. Evaluation of low-nitrogen tolerance for ME13149 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -02 and -03, showed

significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME13149 seedlings is shown in Table 56. ME13149 events were also tested for enhanced growth on the low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 56. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME13149	ME13149-02 (T_2)	0.55623	30	0.51138	55	$2.29x10^{-2}$
ME13149	ME13149-02 (T_3)	0.54818	17	0.51138	55	$4.56x10^{-2}$
ME13149	ME13149-03 (T_2)	0.55998	42	0.51138	55	$5.11x10^{-3}$
ME13149	ME13149-03 (T_3)	0.58450	24	0.51138	55	$2.77x10^{-4}$

[0585] Events -02 and -03 segregated 2:1 and 15:1 respectively (R:S) for FINALE™ resistance in the T_2 generation.

[0586] Events -02 and -03 of ME13149 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 52 – Analysis of ME13151 Events

[0587] ME13151 contains Ceres Clone:39358 (At3g25150, SEQ ID NO:1273) from *Arabidopsis thaliana*, which encodes a 488 amino acid nuclear transport factor 2 (NTF2) domain protein. Evaluation of low-nitrogen tolerance for ME13151 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -01 and -02, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of

ME13151 seedlings is shown in Table 57. ME13151 events were also tested for enhanced growth on the low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 57. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME13151	ME13151-01 (T_2)	0.62593	44	0.53141	17	$8.58x10^{-4}$
ME13151	ME13151-01 (T_3)	0.59936	33	0.53141	17	$1.21x10^{-2}$
ME13151	ME13151-02 (T_2)	0.59879	39	0.46956	16	$3.08x10^{-5}$
ME13151	ME13151-02 (T_3)	0.59566	32	0.46956	16	$4.28x10^{-5}$

[0588] Events -01 and -02 segregated 9:1 and 6:1 respectively (R:S) for FINALE™ resistance in the T2 generation.

[0589] Events -01 and -02 of ME13151 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 53 – Analysis of ME13153 Events

[0590] ME13153 contains Ceres Clone:115046 (At3g17760, SEQ ID NO:1301) from *Arabidopsis thaliana*, which encodes a 494 amino acid glutamate decarboxylase. Evaluation of low-nitrogen tolerance for ME13153 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -03 and -04, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME13153 seedlings is shown in Table 58. ME13153 events were also tested for increased photosynthetic efficiency on the low nitrate media. No significant differences between the transgenics and the controls were observed.

Table 58. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and non-transgenic segregants after 14 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME13153	ME13153-03 (T_2)	0.62	34	0.56	16	$3.0x10^{-2}$
ME13153	ME13153-03 (T_3)	0.60	19	0.54	22	$2.9x10^{-2}$
ME13153	ME13153-04 (T_2)	0.57	32	0.50	18	$4.3x10^{-2}$
ME13153	ME13153-04 (T_3)	0.61	24	0.55	24	$2.1x10^{-2}$

[0591] Events -03 and -04 segregated 3:1 (R:S) for FINALE™ resistance in the T_2 generation.

[0592] Events -03 and -04 of ME13153 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting. Events -03 and -04 yielded slightly less seed per plant compared to the controls, but these differences are not significant at $p \leq 0.10$.

Example 54 – Analysis of ME13177 Events

[0593] ME13177 contains Ceres Clone:339439 (SEQ ID NO:1341) from *Zea mays*, which encodes a 345 amino acid cyclin C-terminal domain protein. Evaluation of low-nitrogen tolerance for ME13177 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -01 and -02, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME13177 seedlings is shown in Table 59. ME13177 events were also tested for enhanced growth on the low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 59. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME13177	ME13177-01 (T_2)	0.6315	32	0.6112	175	$2.43x10^{-2}$
ME13177	ME13177-01 (T_3)	0.6407	29	0.6112	175	$7.33x10^{-3}$
ME13177	ME13177-02 (T_2)	0.6400	41	0.6112	175	$1.23x10^{-3}$
ME13177	ME13177-02 (T_3)	0.6499	20	0.6112	175	$6.47x10^{-3}$

[0594] Events -01 and -02 segregated 2:1 and 3:1 respectively (R:S) for FINALE™ resistance in the T_2 generation.

[0595] Events -01 and -02 of ME13177 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 55 – Analysis of ME13200 Events

[0596] ME13200 contains Ceres Clone:896483 (SEQ ID NO:1384) from *Zea mays*, which encodes an 85 amino acid myb family transcription factor. Evaluation of low-nitrogen tolerance for ME13200 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. A summary of the enhanced growth of ME13200 events on low ammonium nitrate-containing media is shown in Table 60. In this study, the seedling area for transgenic plants within an event was compared to the seedling area for non-transgenic segregants pooled across the same line. Two events, -03 and -04, were found significantly larger than the pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. ME13200 events were also tested for increased photosynthetic efficiency on the low ammonium nitrate media as well as for enhanced photosynthesis and growth on low nitrate media. No significant differences between the transgenics and the controls were observed.

Table 60. t-test comparison of seedling area between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Area	n	Area	n	p-value
ME13200	ME13200-03 (T_2)	0.07366	43	0.06342	35	$4.09x10^{-4}$
ME13200	ME13200-03 (T_3)	0.08193	34	0.06342	35	$2.37x10^{-5}$
ME13200	ME13200-04 (T_2)	0.07377	48	0.06342	35	$4.87x10^{-4}$
ME13200	ME13200-04 (T_3)	0.07530	47	0.06342	35	$1.88x10^{-4}$

[0597] Events -03 and -04 segregated 3:1 and 15:1 respectively respectively (R:S) for FINALE™ resistance in the T_2 generation.

[0598] Events -03 and -04 of ME13200 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 56 – Analysis of ME13204 Events

[0599] ME13204 contains Ceres Clone:995409 (SEQ ID NO:1408) from *Zea mays*, which encodes a 178 amino acid protein of unknown function. Evaluation of low-nitrogen tolerance for ME13204 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -01 and -05, showed significantly increased photosynthetic efficiency on low nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME13204 seedlings is shown in Table 61. ME13204 events were also tested for enhanced growth on the low nitrate media as well as for enhanced growth and photosynthetic efficiency on low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 61. T-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate media.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME13204	ME13204-01 (T_2)	0.5874	45	0.5354	46	$1.41x10^{-2}$
ME13204	ME13204-01 (T_3)	0.5932	36	0.5354	46	$9.85x10^{-3}$
ME13204	ME13204-05 (T_2)	0.5855	34	0.5354	46	$2.00x10^{-2}$
ME13204	ME13204-05 (T_3)	0.5998	20	0.5354	46	$5.58x10^{-3}$

[0600] Events -01 and -05 segregated 9:1 and 3:1 respectively (R:S) for FINALE™ resistance in the T_2 generation.

[0601] Events -01 and -05 of ME13204 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 57 – Analysis of ME14649 Events

[0602] ME14649 contains Ceres Annot:850581 (At5g01880, SEQ ID NO:1427) from *Arabidopsis thaliana*, which encodes a 159 amino acid zinc finger protein. Evaluation of low-nitrogen tolerance for ME14649 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -02 and -03, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME14649 seedlings is shown in Table 62. ME14649 events were also tested for enhanced growth on the low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 62. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME14649	ME14649-02 (T_2)	0.59789	35	0.54533	30	$1.54x10^{-4}$
ME14649	ME14649-02 (T_3)	0.58154	26	0.54533	30	$3.42x10^{-2}$
ME14649	ME14649-03 (T_2)	0.61875	28	0.56539	33	$2.03x10^{-3}$
ME14649	ME14649-03 (T_3)	0.62630	27	0.56539	33	$9.18x10^{-4}$

[0603] Events -02 and -03 segregated 3:1 and 2:1 respectively (R:S) for FINALE™ resistance in the T_2 generation.

[0604] Events -02 and -03 of ME14649 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill) in T1 generation.

Example 58 – Analysis of ME16546 Events

[0605] ME16546 contains Ceres Annot:862321 (At2g45360, SEQ ID NO:1462) from *Arabidopsis thaliana*, which encodes a 215 amino acid protein of unknown function. Evaluation of low-nitrogen tolerance for ME16546 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -04 and -05, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME16546 seedlings is shown in Table 63. ME16546 events were also tested for enhanced growth on the low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 63. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME16546	ME16546-04 (T_2)	0.59891	33	0.56124	130	$2.21x10^{-4}$
ME16546	ME16546-04 (T_3)	0.57924	41	0.56124	130	$3.77x10^{-2}$
ME16546	ME16546-05 (T_2)	0.58861	36	0.56124	130	$7.17x10^{-3}$
ME16546	ME16546-05 (T_3)	0.61763	27	0.56124	130	$3.25x10^{-6}$

[0606] Events -04 and -05 segregated 2:1 and 3:1 respectively (R:S) for FINALE™ resistance in the T_2 generation.

[0607] Events -04 and -05 of ME16546 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 59 – Analysis of ME17457 Events

[0608] ME17457 contains Ceres Annot:839064 (At1g80600, SEQ ID NO:1478) from *Arabidopsis thaliana*, which encodes a 457 acetylornithine aminotransferase, a member of the Class-III aminotransferase family. This is a homolog of Ceres Clone:19586 (ME01463, SEQ ID NO:76). Evaluation of low-nitrogen tolerance for ME17457 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Four events, -02, -03, -05 and -06, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME17457 seedlings is shown in Table 64. ME17457 events were also tested for enhanced growth on the low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 64. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME17457	ME17457-02 (T_2)	0.60800	21	0.50878	46	$6.99x10^{-4}$
ME17457	ME17457-02 (T_3)	0.59539	18	0.50878	46	$9.02x10^{-3}$
ME17457	ME17457-03 (T_2)	0.55164	11	0.49673	45	$3.45x10^{-2}$
ME17457	ME17457-03 (T_3)	0.57356	18	0.49673	45	$2.49x10^{-3}$
ME17457	ME17457-05 (T_2)	0.52928	18	0.42672	32	$2.23x10^{-3}$
ME17457	ME17457-05 (T_3)	0.56660	25	0.42672	32	$5.97x10^{-5}$
ME17457	ME17457-06 (T_2)	0.54088	33	0.47350	30	$3.59x10^{-4}$
ME17457	ME17457-06 (T_3)	0.52210	21	0.47350	30	$2.03x10^{-2}$

[0609] Events -02, -03 and -05 segregated 1:1, and Event -06 segregated 3:1 (R:S) for FINALE™ resistance in the T_2 generation.

[0610] Events -02, -03, -05 and -06 of ME17457 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 60 – Analysis of ME17567 Events

[0611] ME17567 contains Ceres Annot:864666 (At1g16320, SEQ ID NO:1490) from *Arabidopsis thaliana*, which encodes a 273 amino acid protein of unknown function. Evaluation of low-nitrogen tolerance for ME17567 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -01 and -04, showed significantly increased photosynthetic efficiency on low nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME17567 seedlings is shown in Table 65. ME17567 events were also tested for enhanced growth on the low nitrate media as well as enhanced photosynthetic efficiency and growth on low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 65. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME17567	ME17567-01 (T_2)	0.605455	33	0.474791	67	$9.69x10^{-10}$
ME17567	ME17567-01 (T_3)	0.6244	20	0.474791	67	$6.79x10^{-13}$
ME17567	ME17567-04 (T_2)	0.57727	37	0.474791	67	$1.22x10^{-7}$
ME17567	ME17567-04 (T_3)	0.615143	35	0.474791	67	$5.95x10^{-13}$

[0612] Events -01 and -04 segregated 2:1 and 3:1 respectively (R:S) for FINALE™ resistance in the T_2 generation.

[0613] Events -01 and -04 of ME17567 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 61 – Analysis of ME17932 Events

[0614] ME17932 contains Ceres Annot:875012 (At3g53560, SEQ ID NO:1509) from *Arabidopsis thaliana*, which encodes a 340 amino acid chloroplast lumen common family protein. Evaluation of low-nitrogen tolerance for ME17932 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Four events, -01, -02, -03 and -05, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME17932 seedlings is shown in Table 66. ME17932 events were also tested for enhanced growth on the low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 66. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME17932	ME17932-01 (T_2)	0.6292	36	0.6094	194	0.050
ME17932	ME17932-01 (T_3)	0.6640	22	0.6094	194	$2.82x10^{-6}$
ME17932	ME17932-02 (T_2)	0.6351	32	0.6094	194	$1.05x10^{-2}$
ME17932	ME17932-02 (T_3)	0.6373	20	0.6094	194	$2.82x10^{-2}$
ME17932	ME17932-03 (T_2)	0.6504	45	0.6094	194	$1.80x10^{-5}$
ME17932	ME17932-03 (T_3)	0.6708	20	0.6094	194	$8.38x10^{-4}$
ME17932	ME17932-05 (T_2)	0.6349	24	0.6094	194	$3.23x10^{-2}$
ME17932	ME17932-05 (T_3)	0.6615	11	0.6094	194	$1.16x10^{-3}$

[0615] Events -01, -02, -03 and -05 segregated 3:1, 2:1, 15:1 and 1:1 respectively (R:S) for FINALE™ resistance in the T_2 generation.

[0616] Events -01, -02, -03 and -05 of ME17932 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 62 – Analysis of ME17936 Events

[0617] ME17936 contains Ceres Annot:874016 (At3g42800, SEQ ID NO:1524) from *Arabidopsis thaliana*, which encodes a 341 amino acid protein of unknown function. Evaluation of low-nitrogen tolerance for ME17936 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -01 and -05, showed significantly increased photosynthetic efficiency on low nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME17936 seedlings is shown in Table 67. ME17936 events were also tested for for enhanced growth on the low nitrate media as well as for increased photosynthetic efficiency and enhanced growth on low ammonium nitrate media. No significant differences between the transgenics and the controls were

observed.

Table 67. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate media.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME17936	ME17936-01 (T_2)	0.64778	36	0.61762	39	$4.68x10^{-3}$
ME17936	ME17936-01 (T_3)	0.66081	21	0.61762	39	$4.33x10^{-5}$
ME17936	ME17936-05 (T_2)	0.63189	35	0.61444	50	$2.73x10^{-2}$
ME17936	ME17936-05 (T_3)	0.64257	14	0.61444	50	$2.56x10^{-2}$

[0618] Events -01 and -05 segregated 3:1 (R:S) for FINALE™ resistance in the T_2 generation.

[0619] Events -01 and -05 of ME17936 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 63 – Analysis of ME18275 Events

[0620] ME18275 contains Ceres Annot:827304 (At2g18300, SEQ ID NO:1536) from *Arabidopsis thaliana*, which encodes a 335 amino acid helix-loop-helix DNA-binding domain. Evaluation of low-nitrogen tolerance for ME18275 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. A summary of the enhanced growth of ME18275 events on low nitrate-containing media is shown in Table 68. In this study, the seedling area for transgenic plants within an event was compared to the seedling area for non-transgenic segregants pooled across the same line. Three events, -01, -02 and -03, were found significantly larger than the pooled non-transgenic segregants after 14 days of growth on low nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$, using a one-tailed t-test assuming unequal variance. ME18275 events were also tested for photosynthetic efficiency on the low nitrate media as well as for increased photosynthetic efficiency and enhanced growth on low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 68. t-test comparison of seedling area between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Area	n	Area	n	p-value
ME18275	ME18275-01 (T_2)	0.09574	40	0.05961	10	$3.24x10^{-10}$
ME18275	ME18275-01 (T_3)	0.07807	32	0.05142	15	$3.71x10^{-4}$
ME18275	ME18275-02 (T_2)	0.11903	33	0.05884	16	$6.21x10^{-14}$
ME18275	ME18275-02 (T_3)	0.08552	22	0.04208	24	$2.82x10^{-5}$
ME18275	ME18275-03 (T_2)	0.10281	39	0.06789	9	$9.48x10^{-8}$
ME18275	ME18275-03 (T_3)	0.09136	20	0.05646	26	$9.46x10^{-4}$

[0621] Events -01, -02 and -03 segregated 3:1 (R:S) for FINALE™ resistance in the T_2 generation.

[0622] Events -01, -02 and -03 of ME18275 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 64 – Analysis of ME18924 Events

[0623] ME18924 contains Ceres Annot:869192 (At1g72160, SEQ ID NO:1553) from *Arabidopsis thaliana*, which encodes a 490 amino acid emp24/gp25L/p24 family protein. Evaluation of low-nitrogen tolerance for ME18924 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. A summary of photosynthetic efficiency of ME18924 seedlings is shown in Table 69. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Three events, -02, -04 and -05, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$, using a one-tailed t-test assuming unequal variance.

Table 69. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME18924	ME18924-02 (T_2)	0.6515	46	0.6223	138	$6.43x10^{-3}$
ME18924	ME18924-02 (T_3)	0.6639	45	0.6223	138	$1.52x10^{-4}$
ME18924	ME18924-04 (T_2)	0.6489	33	0.6223	138	$2.72x10^{-3}$
ME18924	ME18924-04 (T_3)	0.6517	21	0.6223	138	$1.58x10^{-2}$
ME18924	ME18924-05 (T_2)	0.6602	35	0.6223	138	$5.55x10^{-5}$
ME18924	ME18924-05 (T_3)	0.6488	31	0.6223	138	$4.25x10^{-2}$

[0624] ME18924 events were also tested for enhanced growth on the low ammonium nitrate media. A summary of the enhanced growth of ME18924 events on low nitrate-containing media is shown in Table 70. In this study, the seedling area for transgenic plants within an event was compared to the seedling area for non-transgenic segregants pooled across the same line. Two events, -01 and -04, were found significantly larger than the pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$, using a one-tailed t-test assuming unequal variance.

Table 70. t-test comparison of seedling area between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Area	n	Area	n	p-value
ME18924	ME18924-01 (T_2)	0.06881	37	0.06311	138	$1.31x10^{-2}$
ME18924	ME18924-01 (T_3)	0.07164	34	0.06311	138	$7.43x10^{-3}$
ME18924	ME18924-04 (T_2)	0.08401	33	0.06311	138	$5.64x10^{-8}$
ME18924	ME18924-04 (T_3)	0.07365	21	0.06311	138	$3.82x10^{-2}$

[0625] Events -01, -02, -04 and -05 segregated 3:1, 15:1, 2:1 and 2:1 respectively (R:S) for FINALE™ resistance in the T_2 generation.

[0626] Events -01, -02, -04 and -05 of ME18924 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 65 – Analysis of ME19182 Events

[0627] ME19182 contains Ceres Annot:876419 (At4g01480, SEQ ID NO:1576) from *Arabidopsis thaliana*, which encodes a 216 amino acid inorganic pyrophosphatase protein. Evaluation of low-nitrogen tolerance for ME19182 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -01 and -03, showed significantly increased photosynthetic efficiency on low ammonium nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME19182 seedlings is shown in Table 71. ME19182 events were also tested for enhanced growth on the low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 71. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 18 days of growth on low ammonium nitrate.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME19182	ME19182-01 (T_2)	0.64938	24	0.61988	154	2.47×10^{-2}
ME19182	ME19182-01 (T_3)	0.65546	13	0.61988	154	1.08×10^{-2}
ME19182	ME19182-03 (T_2)	0.64797	37	0.61988	154	3.84×10^{-3}
ME19182	ME19182-03 (T_3)	0.65388	26	0.61988	154	3.15×10^{-3}

[0628] Events -01 and -03 segregated 2:1 and 3:1 respectively (R:S) for FINALE™ resistance in the T2 generation.

[0629] Events -01 and -03 of ME19182 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 66 – Analysis of ME20628 Events

[0630] ME20628 contains Ceres Annot:859276 (At2g21230, SEQ ID NO:175) from *Arabidopsis thaliana*, which encodes a 188 amino acid protein of unknown function.

Evaluation of low-nitrogen tolerance for ME20628 in T_2 and T_3 was conducted under the same conditions as described in Examples 2 and 3. In this study, the seedling photosynthetic efficiency was measured as Fv/Fm comparing transgenic plants within an event to non-transgenic segregants pooled across the same plate. Two events, -03 and -04, showed significantly increased photosynthetic efficiency on low nitrate-containing media relative to the internal controls in both generations at $p \leq 0.05$ using a one-tailed t-test assuming unequal variance. A summary of photosynthetic efficiency of ME20628 seedlings is shown in Table 72. ME20628 events were also tested for enhanced growth on the low nitrate media as well as for increased photosynthetic efficiency and enhanced growth on low ammonium nitrate media. No significant differences between the transgenics and the controls were observed.

Table 72. t-test comparison of seedling photosynthetic efficiency between transgenic seedlings and pooled non-transgenic segregants after 14 days of growth on low nitrate media.

		Transgenic		Pooled Non-Transgenics		t-test
Line	Events	Fv/Fm	n	Fv/Fm	n	p-value
ME20628	ME20628-03 (T_2)	0.62771	42	0.58957	7	$9.94x10^{-3}$
ME20628	ME20628-03 (T_3)	0.64375	20	0.61914	28	$2.97x10^{-2}$
ME20628	ME20628-04 (T_2)	0.62439	38	0.59667	12	$4.78x10^{-2}$
ME20628	ME20628-04 (T_3)	0.64768	22	0.61360	25	$9.93x10^{-4}$

[0631] Events -03 and -04 segregated 3:1 (R:S) for FINALE™ resistance in the T_2 generation.

[0632] Events -03 and -04 of ME20628 exhibited no statistically relevant negative phenotypes. That is, there was no detectable reduction in germination rate, the transgenic plants appeared wild type in all instances; there was no observable or statistical differences between transgenics and controls in days to flowering; there was no observable or statistical differences between transgenics and controls in the size of the rosette area 7 days post-bolting; and there was no observable or statistical differences between transgenics and controls in fertility (silique number and seed fill).

Example 67 – Determination of Functional Homologs by Reciprocal BLAST

[0633] A candidate sequence was considered a functional homolog of a reference sequence if the candidate and reference sequences encoded proteins having a similar function and/or activity. A process known as Reciprocal BLAST (Rivera *et al.* (1998) *Proc. Natl. Acad. Sci. USA*, 95:6239-6244) was used to identify potential functional homolog sequences from databases consisting of all available public and proprietary peptide sequences, including NR from NCBI and peptide translations from Ceres clones.

[0634] Before starting a Reciprocal BLAST process, a specific reference polypeptide was searched against all peptides from its source species using BLAST in order to identify polypeptides having BLAST sequence identity of 80% or greater to the reference polypeptide and an alignment length of 85% or greater along the shorter sequence in the alignment. The reference polypeptide and any of the aforementioned identified polypeptides were designated as a cluster.

[0635] The BLASTP version 2.0 program from Washington University at Saint Louis, Missouri, USA was used to determine BLAST sequence identity and E-value. The BLASTP version 2.0 program includes the following parameters: 1) an E-value cutoff of 1.0e-5; 2) a word size of 5; and 3) the -postsw option. The BLAST sequence identity was calculated based on the alignment of the first BLAST HSP (High-scoring Segment Pairs) of the identified potential functional homolog sequence with a specific reference polypeptide. The number of identically matched residues in the BLAST HSP alignment was divided by the HSP length, and then multiplied by 100 to get the BLAST sequence identity. The HSP length typically included gaps in the alignment, but in some cases gaps were excluded.

[0636] The main Reciprocal BLAST process consists of two rounds of BLAST searches; forward search and reverse search. In the forward search step, a reference polypeptide sequence, "polypeptide A," from source species SA was BLASTed against all protein sequences from a species of interest. Top hits were determined using an E-value cutoff of 10^{-5} and a sequence identity cutoff of 35%. Among the top hits, the sequence having the lowest E-value was designated as the best hit, and considered a potential functional homolog or ortholog. Any other top hit that had a sequence identity of 80% or greater to the best hit or to the original reference polypeptide was considered a potential functional homolog or ortholog as well. This process was repeated for all species of interest.

[0637] In the reverse search round, the top hits identified in the forward search from all species were BLASTed against all protein sequences from the source species SA. A top hit from the forward search that returned a polypeptide from the aforementioned cluster as its best hit was also considered as a potential functional homolog.

[0638] Functional homologs were identified by manual inspection of potential functional homolog sequences. Representative functional homologs for SEQ ID NO:3, SEQ ID NO:49, SEQ ID NO:77, SEQ ID NO:100, SEQ ID NO:152, SEQ ID NO:166, SEQ ID NO:186, SEQ ID NO:208, SEQ ID NO:218, SEQ ID NO:234, SEQ ID NO:246, SEQ ID NO:300, SEQ ID NO:332, SEQ ID NO:368, SEQ ID NO:510, SEQ ID NO:533, SEQ ID NO:558, SEQ ID NO:593, SEQ ID NO:613, SEQ ID NO:646, SEQ ID NO:687, SEQ ID

NO:730, SEQ ID NO:746, SEQ ID NO:769, SEQ ID NO:792, SEQ ID NO:824, SEQ ID NO:828, SEQ ID NO:855, SEQ ID NO:891, SEQ ID NO:917, SEQ ID NO:944, SEQ ID NO:976, SEQ ID NO:982, SEQ ID NO:1054, SEQ ID NO:1099, SEQ ID NO:1112, SEQ ID NO:1116, SEQ ID NO:1159, SEQ ID NO:1166, SEQ ID NO:1185, SEQ ID NO:1194, SEQ ID NO:1210, SEQ ID NO:1274, SEQ ID NO:1302, SEQ ID NO:1342, SEQ ID NO:1385, SEQ ID NO:1409, SEQ ID NO:1428, SEQ ID NO:1463, SEQ ID NO:1491, SEQ ID NO:1510, SEQ ID NO:1525, SEQ ID NO:1537, SEQ ID NO:1554, SEQ ID NO:1577, and SEQ ID NO:1437 are shown in Figures 1-57, respectively. Additional exemplary homologs are correlated to certain Figures in the Sequence Listing.

Example 68 – Determination of Functional Homologs by Hidden Markov Models

[0639] Hidden Markov Models (HMMs) were generated by the program HMMER 2.3.2. To generate each HMM, the default HMMER 2.3.2 program parameters, configured for global alignments, were used.

[0640] An HMM was generated using the sequences shown in Figure 1 as input. These sequences were fitted to the model and a representative HMM bit score for each sequence is shown in the Sequence Listing. Additional sequences were fitted to the model, and representative HMM bit scores for any such additional sequences are shown in the Sequence Listing. The results indicate that these additional sequences are functional homologs of SEQ ID NO:3.

[0641] The procedure above was repeated and an HMM was generated for each group of sequences shown in Figures 2-57, using the sequences shown in each Figure as input for that HMM. A representative bit score for each sequence is shown in the Sequence Listing. Additional sequences were fitted to certain HMMs, and representative HMM bit scores for such additional sequences are shown in the Sequence Listing. The results indicate that these additional sequences are functional homologs of the sequences used to generate that HMM.

VIII. Other Embodiments

[0642] It is to be understood that while the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

CLAIMS

WHAT IS CLAIMED IS:

1. A method of producing a plant, said method comprising growing a plant cell comprising an exogenous nucleic acid, said exogenous nucleic acid comprising a regulatory region operably linked to a nucleotide sequence encoding a polypeptide, wherein the HMM bit score of the amino acid sequence of said polypeptide is greater than about 20, said HMM based on the amino acid sequences depicted in one of Figures 1-57, and wherein said plant has a difference in the level of low-nitrogen tolerance as compared to the corresponding level of low-nitrogen tolerance of a control plant that does not comprise said nucleic acid.

2. A method of producing a plant, said method comprising growing a plant cell comprising an exogenous nucleic acid, said exogenous nucleic acid comprising a regulatory region operably linked to a nucleotide sequence encoding a polypeptide having 80 percent or greater sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:49, SEQ ID NO:77, SEQ ID NO:97, SEQ ID NO:100, SEQ ID NO:152, SEQ ID NO:166, SEQ ID NO:186, SEQ ID NO:208, SEQ ID NO:218, SEQ ID NO:234, SEQ ID NO:246, SEQ ID NO:300, SEQ ID NO:332, SEQ ID NO:368, SEQ ID NO:510, SEQ ID NO:533, SEQ ID NO:556, SEQ ID NO:558, SEQ ID NO:593, SEQ ID NO:613, SEQ ID NO:646, SEQ ID NO:687, SEQ ID NO:730, SEQ ID NO:746, SEQ ID NO:769, SEQ ID NO:792, SEQ ID NO:824, SEQ ID NO:828, SEQ ID NO:853, SEQ ID NO:855, SEQ ID NO:891, SEQ ID NO:917, SEQ ID NO:944, SEQ ID NO:976, SEQ ID NO:982, SEQ ID NO:1054, SEQ ID NO:1099, SEQ ID NO:1112, SEQ ID NO:1116, SEQ ID NO:1157, SEQ ID NO:1159, SEQ ID NO:1166, SEQ ID NO:1185, SEQ ID NO:1194, SEQ ID NO:1210, SEQ ID NO:1274, SEQ ID NO:1302, SEQ ID NO:1342, SEQ ID NO:1385, SEQ ID NO:1409, SEQ ID NO:1428, SEQ ID NO:1437, SEQ ID NO:1463, SEQ ID NO:1491, SEQ ID NO:1510, SEQ ID NO:1525, SEQ ID NO:1537, SEQ ID NO:1554, and SEQ ID NO:1577, wherein a plant produced from said plant cell has a difference in the level of low-nitrogen tolerance as compared to the corresponding level of low-nitrogen tolerance of a control plant that does not comprise said nucleic acid.

3. The method of claim 1 or 2, wherein the polypeptide comprises a Pfam domain having 70 percent or greater sequence identity to a Pfam domain in any one of the polypeptides in the sequence listing.

4. A method of producing a plant, said method comprising growing a plant cell comprising an exogenous nucleic acid, said exogenous nucleic acid comprising a regulatory region operably linked to a nucleotide sequence having 80 percent or greater sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:48, SEQ ID NO:76, SEQ ID NO:96, SEQ ID NO:99, SEQ ID NO:151, SEQ ID NO:165, SEQ ID NO:175, SEQ ID NO:185, SEQ ID NO:207, SEQ ID NO:217, SEQ ID NO:233, SEQ ID NO:245, SEQ ID NO:299, SEQ ID NO:331, SEQ ID NO:367, SEQ ID NO:509, SEQ ID NO:532, SEQ ID NO:555, SEQ ID NO:557, SEQ ID NO:592, SEQ ID NO:612, SEQ ID NO:645, SEQ ID NO:686, SEQ ID NO:729, SEQ ID NO:745, SEQ ID NO:768, SEQ ID NO:791, SEQ ID NO:823, SEQ ID NO:827, SEQ ID NO:852, SEQ ID NO:854, SEQ ID NO:890, SEQ ID NO:916, SEQ ID NO:943, SEQ ID NO:975, SEQ ID NO:981, SEQ ID NO:1053, SEQ ID NO:1098, SEQ ID NO:1111, SEQ ID NO:1115, SEQ ID NO:1156, SEQ ID NO:1158, SEQ ID NO:1165, SEQ ID NO:1184, SEQ ID NO:1193, SEQ ID NO:1209, SEQ ID NO:1273, SEQ ID NO:1301, SEQ ID NO:1341, SEQ ID NO:1384, SEQ ID NO:1408, SEQ ID NO:1427, SEQ ID NO:1462, SEQ ID NO:1490, SEQ ID NO:1509, SEQ ID NO:1524, SEQ ID NO:1536, SEQ ID NO:1553, and SEQ ID NO:1576, or a fragment thereof, wherein a tissue of a plant produced from said plant cell has a difference in the level of low-nitrogen tolerance as compared to the corresponding level of low-nitrogen tolerance of a control plant that does not comprise said nucleic acid.

5. A method of producing a plant, said method comprising growing a plant cell comprising an exogenous nucleic acid, said exogenous nucleic acid effective for downregulating an endogenous nucleic acid in the plant cell, wherein the endogenous nucleic acid encodes a polypeptide, and wherein the HMM bit score of the amino acid sequence of the polypeptide is greater than about 20, said HMM based on the amino acid sequences depicted in one of Figures 1-57.

6. A method of modulating the level of low-nitrogen tolerance in a plant, said method comprising introducing into a plant cell an exogenous nucleic acid, said exogenous nucleic acid comprising a regulatory region operably linked to a nucleotide sequence encoding a polypeptide, wherein the HMM bit score of the amino acid sequence of said polypeptide is greater than about 20, said HMM based on the amino acid sequences depicted in one of Figures 1-57, and wherein a tissue of a plant produced from said plant cell has a difference in the level of low-nitrogen tolerance as compared to the corresponding level of low-nitrogen

tolerance of a control plant that does not comprise said exogenous nucleic acid.

7. A method of modulating the level of low-nitrogen tolerance in a plant, said method comprising introducing into a plant cell an exogenous nucleic acid, said exogenous nucleic acid comprising a regulatory region operably linked to a nucleotide sequence encoding a polypeptide having 80 percent or greater sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:49, SEQ ID NO:77, SEQ ID NO:97, SEQ ID NO:100, SEQ ID NO:152, SEQ ID NO:166, SEQ ID NO:186, SEQ ID NO:208, SEQ ID NO:218, SEQ ID NO:234, SEQ ID NO:246, SEQ ID NO:300, SEQ ID NO:332, SEQ ID NO:368, SEQ ID NO:510, SEQ ID NO:533, SEQ ID NO:556, SEQ ID NO:558, SEQ ID NO:593, SEQ ID NO:613, SEQ ID NO:646, SEQ ID NO:687, SEQ ID NO:730, SEQ ID NO:746, SEQ ID NO:769, SEQ ID NO:792, SEQ ID NO:824, SEQ ID NO:828, SEQ ID NO:853, SEQ ID NO:855, SEQ ID NO:891, SEQ ID NO:917, SEQ ID NO:944, SEQ ID NO:976, SEQ ID NO:982, SEQ ID NO:1054, SEQ ID NO:1099, SEQ ID NO:1112, SEQ ID NO:1116, SEQ ID NO:1157, SEQ ID NO:1159, SEQ ID NO:1166, SEQ ID NO:1185, SEQ ID NO:1194, SEQ ID NO:1210, SEQ ID NO:1274, SEQ ID NO:1302, SEQ ID NO:1342, SEQ ID NO:1385, SEQ ID NO:1409, SEQ ID NO:1428, SEQ ID NO:1437, SEQ ID NO:1463, SEQ ID NO:1491, SEQ ID NO:1510, SEQ ID NO:1525, SEQ ID NO:1537, SEQ ID NO:1554, and SEQ ID NO:1577, wherein a tissue of a plant produced from said plant cell has a difference in the level of low-nitrogen tolerance as compared to the corresponding level of low-nitrogen tolerance of a control plant that does not comprise said nucleic acid.

8. The method of any one of claims 1 to 7, wherein said polypeptide is selected from the group consisting of SEQ ID NO:3, SEQ ID NO:49, SEQ ID NO:77, SEQ ID NO:97, SEQ ID NO:100, SEQ ID NO:152, SEQ ID NO:166, SEQ ID NO:186, SEQ ID NO:208, SEQ ID NO:218, SEQ ID NO:234, SEQ ID NO:246, SEQ ID NO:300, SEQ ID NO:332, SEQ ID NO:368, SEQ ID NO:510, SEQ ID NO:533, SEQ ID NO:556, SEQ ID NO:558, SEQ ID NO:593, SEQ ID NO:613, SEQ ID NO:646, SEQ ID NO:687, SEQ ID NO:730, SEQ ID NO:746, SEQ ID NO:769, SEQ ID NO:792, SEQ ID NO:824, SEQ ID NO:828, SEQ ID NO:853, SEQ ID NO:855, SEQ ID NO:891, SEQ ID NO:917, SEQ ID NO:944, SEQ ID NO:976, SEQ ID NO:982, SEQ ID NO:1054, SEQ ID NO:1099, SEQ ID NO:1112, SEQ ID NO:1116, SEQ ID NO:1157, SEQ ID NO:1159, SEQ ID NO:1166, SEQ ID NO:1185, SEQ ID NO:1194, SEQ ID NO:1210, SEQ ID NO:1274, SEQ ID NO:1302, SEQ ID NO:1342,

SEQ ID NO:1385, SEQ ID NO:1409, SEQ ID NO:1428, SEQ ID NO:1437, SEQ ID NO:1463, SEQ ID NO:1491, SEQ ID NO:1510, SEQ ID NO:1525, SEQ ID NO:1537, SEQ ID NO:1554, and SEQ ID NO:1577.

9. A method of modulating the level of low-nitrogen tolerance in a plant, said method comprising introducing into a plant cell an exogenous nucleic acid, said exogenous nucleic acid comprising a regulatory region operably linked to a nucleotide sequence having 80 percent or greater sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:48, SEQ ID NO:76, SEQ ID NO:96, SEQ ID NO:99, SEQ ID NO:151, SEQ ID NO:165, SEQ ID NO:175, SEQ ID NO:185, SEQ ID NO:207, SEQ ID NO:217, SEQ ID NO:233, SEQ ID NO:245, SEQ ID NO:299, SEQ ID NO:331, SEQ ID NO:367, SEQ ID NO:509, SEQ ID NO:532, SEQ ID NO:555, SEQ ID NO:557, SEQ ID NO:592, SEQ ID NO:612, SEQ ID NO:645, SEQ ID NO:686, SEQ ID NO:729, SEQ ID NO:745, SEQ ID NO:768, SEQ ID NO:791, SEQ ID NO:823, SEQ ID NO:827, SEQ ID NO:852, SEQ ID NO:854, SEQ ID NO:890, SEQ ID NO:916, SEQ ID NO:943, SEQ ID NO:975, SEQ ID NO:981, SEQ ID NO:1053, SEQ ID NO:1098, SEQ ID NO:1111, SEQ ID NO:1115, SEQ ID NO:1156, SEQ ID NO:1158, SEQ ID NO:1165, SEQ ID NO:1184, SEQ ID NO:1193, SEQ ID NO:1209, SEQ ID NO:1273, SEQ ID NO:1301, SEQ ID NO:1341, SEQ ID NO:1384, SEQ ID NO:1408, SEQ ID NO:1427, SEQ ID NO:1462, SEQ ID NO:1490, SEQ ID NO:1509, SEQ ID NO:1524, SEQ ID NO:1536, SEQ ID NO:1553, and SEQ ID NO:1576, or a fragment thereof, wherein a tissue of a plant produced from said plant cell has a difference in the level of low-nitrogen tolerance as compared to the corresponding level of low-nitrogen tolerance of a control plant that does not comprise said nucleic acid.

10. A plant cell comprising an exogenous nucleic acid, said exogenous nucleic acid comprising a regulatory region operably linked to a nucleotide sequence encoding a polypeptide, wherein the HMM bit score of the amino acid sequence of said polypeptide is greater than about 20, said HMM based on the amino acid sequences depicted in one of Figures 1-57, and wherein said plant cell has a difference in the level of low-nitrogen tolerance as compared to the corresponding level of low-nitrogen tolerance of a control plant that does not comprise said nucleic acid.

11. A plant cell comprising an exogenous nucleic acid said exogenous nucleic acid

comprising a regulatory region operably linked to a nucleotide sequence encoding a polypeptide having 80 percent or greater sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:49, SEQ ID NO:77, SEQ ID NO:97, SEQ ID NO:100, SEQ ID NO:152, SEQ ID NO:166, SEQ ID NO:186, SEQ ID NO:208, SEQ ID NO:218, SEQ ID NO:234, SEQ ID NO:246, SEQ ID NO:300, SEQ ID NO:332, SEQ ID NO:368, SEQ ID NO:510, SEQ ID NO:533, SEQ ID NO:556, SEQ ID NO:558, SEQ ID NO:593, SEQ ID NO:613, SEQ ID NO:646, SEQ ID NO:687, SEQ ID NO:730, SEQ ID NO:746, SEQ ID NO:769, SEQ ID NO:792, SEQ ID NO:824, SEQ ID NO:828, SEQ ID NO:853, SEQ ID NO:855, SEQ ID NO:891, SEQ ID NO:917, SEQ ID NO:944, SEQ ID NO:976, SEQ ID NO:982, SEQ ID NO:1054, SEQ ID NO:1099, SEQ ID NO:1112, SEQ ID NO:1116, SEQ ID NO:1157, SEQ ID NO:1159, SEQ ID NO:1166, SEQ ID NO:1185, SEQ ID NO:1194, SEQ ID NO:1210, SEQ ID NO:1274, SEQ ID NO:1302, SEQ ID NO:1342, SEQ ID NO:1385, SEQ ID NO:1409, SEQ ID NO:1428, SEQ ID NO:1437, SEQ ID NO:1463, SEQ ID NO:1491, SEQ ID NO:1510, SEQ ID NO:1525, SEQ ID NO:1537, SEQ ID NO:1554, and SEQ ID NO:1577, wherein a tissue of a plant produced from said plant cell has a difference in the level of low-nitrogen tolerance as compared to the corresponding level of low-nitrogen tolerance of a control plant that does not comprise said nucleic acid.

12. A plant cell comprising an exogenous nucleic acid said exogenous nucleic acid comprising a regulatory region operably linked to a nucleotide sequence having 80 percent or greater sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:48, SEQ ID NO:76, SEQ ID NO:96, SEQ ID NO:99, SEQ ID NO:151, SEQ ID NO:165, SEQ ID NO:175, SEQ ID NO:185, SEQ ID NO:207, SEQ ID NO:217, SEQ ID NO:233, SEQ ID NO:245, SEQ ID NO:299, SEQ ID NO:331, SEQ ID NO:367, SEQ ID NO:509, SEQ ID NO:532, SEQ ID NO:555, SEQ ID NO:557, SEQ ID NO:592, SEQ ID NO:612, SEQ ID NO:645, SEQ ID NO:686, SEQ ID NO:729, SEQ ID NO:745, SEQ ID NO:768, SEQ ID NO:791, SEQ ID NO:823, SEQ ID NO:827, SEQ ID NO:852, SEQ ID NO:854, SEQ ID NO:890, SEQ ID NO:916, SEQ ID NO:943, SEQ ID NO:975, SEQ ID NO:981, SEQ ID NO:1053, SEQ ID NO:1098, SEQ ID NO:1111, SEQ ID NO:1115, SEQ ID NO:1156, SEQ ID NO:1158, SEQ ID NO:1165, SEQ ID NO:1184, SEQ ID NO:1193, SEQ ID NO:1209, SEQ ID NO:1273, SEQ ID NO:1301, SEQ ID NO:1341, SEQ ID NO:1384, SEQ ID NO:1408, SEQ ID NO:1427, SEQ ID NO:1462, SEQ ID NO:1490, SEQ ID NO:1509, SEQ ID NO:1524, SEQ ID NO:1536, SEQ ID NO:1553, and SEQ ID

NO:1576, or a fragment thereof, wherein a tissue of a plant produced from said plant cell has a difference in the level of low-nitrogen tolerance as compared to the corresponding level of low-nitrogen tolerance of a control plant that does not comprise said nucleic acid.

13. A transgenic plant comprising the plant cell of any one of claims 10-12.

14. The transgenic plant of claim 13, wherein said plant is a member of a species selected from the group consisting of *Panicum virgatum* (switchgrass), *Sorghum bicolor* (sorghum, sudangrass), *Miscanthus giganteus* (miscanthus), *Saccharum* sp. (energycane), *Populus balsamifera* (poplar), *Zea mays* (corn), *Glycine max* (soybean), *Brassica napus* (canola), *Triticum aestivum* (wheat), *Gossypium hirsutum* (cotton), *Oryza sativa* (rice), *Helianthus annuus* (sunflower), *Medicago sativa* (alfalfa), *Beta vulgaris* (sugarbeet), or *Pennisetum glaucum* (pearl millet).

15. A transgenic plant of claim 13, wherein said polypeptide is any one of the polypeptides in the sequence listing.

16. A product comprising plant tissue from a transgenic plant according to claims 14.

17. An isolated nucleic acid comprising a nucleotide sequence having 95% or greater sequence identity to the nucleotide sequence set forth in SEQ ID NOs: 5, 7, 37, 50, 52, 54, 66, 79, 86, 91, 103, 105, 107, 109, 112, 114, 124, 127, 136, 140, 143, 153, 155, 157, 159, 161, 163, 167, 169, 171, 175, 176, 178, 187, 189, 202, 215, 219, 221, 226, 228, 235, 237, 240, 247, 250, 252, 258, 261, 269, 273, 280, 301, 303, 305, 307, 311, 313, 315, 317, 330, 331, 333, 379, 387, 389, 397, 429, 431, 442, 457, 462, 466, 470, 472, 480, 486, 512, 514, 516, 518, 520, 522, 524, 526, 528, 534, 537, 540, 551, 557, 568, 570, 574, 582, 587, 594, 596, 598, 600, 602, 604, 606, 608, 614, 616, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 673, 677, 688, 690, 692, 698, 700, 702, 704, 709, 711, 713, 715, 717, 719, 731, 734, 736, 739, 743, 747, 749, 756, 759, 780, 795, 797, 811, 829, 831, 835, 841, 843, 852, 854, 857, 859, 861, 863, 867, 869, 871, 875, 879, 881, 883, 890, 892, 897, 899, 918, 922, 924, 930, 934, 936, 938, 941, 945, 949, 951, 955, 959, 961, 963, 965, 975, 979, 981, 983, 994, 1002, 1006, 1010, 1014, 1017, 1020, 1022, 1024, 1038, 1042, 1056, 1060, 1062, 1064, 1066, 1073, 1079, 1100, 1107, 1117, 1119, 1121, 1127, 1130, 1137, 1160, 1165, 1168, 1170, 1172, 1176, 1178, 1181, 1186,

1195, 1197, 1199, 1201, 1212, 1214, 1217, 1227, 1231, 1250, 1252, 1254, 1256, 1258, 1260, 1262, 1275, 1277, 1279, 1283, 1286, 1288, 1290, 1292, 1304, 1306, 1308, 1310, 1332, 1343, 1353, 1386, 1388, 1408, 1410, 1412, 1414, 1416, 1420, 1422, 1427, 1429, 1431, 1433, 1435, 1438, 1441, 1443, 1449, 1451, 1462, 1464, 1466, 1468, 1470, 1472, 1478, 1489, 1490, 1492, 1494, 1498, 1500, 1509, 1511, 1513, 1519, 1524, 1526, 1528, 1536, 1538, 1542, 1544, 1546, 1549, 1553, 1556, 1558, 1560, 1562, 1564, 1568, 1570, 1576, 1579, 1581, 1583, 1585, 1587, 1593, 1600, 1606, 1610, 1614, 1620, 1630, 1632, 1640, 1642, 1644, 1646, 1654.

18. An isolated nucleic acid comprising a nucleotide sequence encoding a polypeptide having 80% or greater sequence identity to the amino acid sequence set forth in SEQ ID NOs: 6, 8, 38, 51, 53, 55, 67, 80, 87, 92, 100, 104, 106, 108, 110, 113, 115, 125, 128, 137, 141, 144, 154, 156, 158, 160, 162, 164, 168, 170, 172, 177, 179, 188, 190, 203, 216, 220, 222, 227, 229, 236, 238, 241, 248, 251, 253, 259, 262, 270, 274, 279, 281, 302, 304, 306, 308, 312, 314, 316, 318, 332, 334, 338, 368, 380, 384, 388, 390, 398, 430, 432, 443, 458, 463, 467, 471, 473, 481, 487, 513, 515, 517, 521, 523, 525, 527, 529, 535, 538, 541, 552, 558, 569, 571, 575, 583, 588, 595, 597, 599, 601, 603, 605, 607, 609, 615, 617, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 674, 678, 687, 689, 691, 693, 699, 701, 703, 705, 710, 712, 714, 716, 718, 720, 732, 735, 737, 740, 744, 748, 750, 760, 769, 781, 796, 798, 812, 830, 832, 836, 842, 844, 853, 855, 858, 860, 862, 864, 868, 870, 876, 880, 882, 884, 891, 893, 898, 900, 919, 923, 925, 931, 935, 937, 939, 942, 946, 950, 952, 956, 960, 962, 964, 966, 976, 980, 982, 984, 995, 1003, 1007, 1011, 1015, 1018, 1021, 1023, 1025, 1039, 1043, 1057, 1061, 1063, 1065, 1067, 1074, 1080, 1099, 1101, 1108, 1116, 1118, 1120, 1122, 1128, 1131, 1138, 1161, 1166, 1169, 1171, 1173, 1175, 1177, 1179, 1182, 1187, 1196, 1198, 1200, 1202, 1203, 1213, 1215, 1218, 1228, 1232, 1251, 1253, 1255, 1257, 1259, 1261, 1263, 1276, 1278, 1280, 1287, 1289, 1291, 1293, 1305, 1307, 1309, 1311, 1333, 1344, 1354, 1366, 1387, 1389, 1409, 1411, 1413, 1415, 1417, 1421, 1428, 1430, 1432, 1434, 1436, 1437, 1439, 1442, 1450, 1452, 1463, 1465, 1467, 1469, 1471, 1473, 1479, 1480, 1486, 1491, 1493, 1495, 1499, 1501, 1510, 1512, 1514, 1520, 1525, 1527, 1529, 1537, 1539, 1543, 1545, 1547, 1550, 1554, 1557, 1559, 1561, 1563, 1565, 1569, 1571, 1577, 1580, 1582, 1584, 1586, 1588, 1594, 1601, 1607, 1611, 1615, 1621, 1627, 1631, 1633, 1635, 1643, 1645.

19. A method of identifying whether a polymorphism is associated with variation in a trait, said method comprising:

a) determining whether one or more genetic polymorphisms in a population of plants is associated with the locus for a polypeptide selected from the group consisting of the polypeptides depicted in Figures 1-57, SEQ ID NO:556, SEQ ID NO:853, and SEQ ID NO:1157 and functional homologs thereof; and

b) measuring the correlation between variation in said trait in plants of said population and the presence of said one or more genetic polymorphisms in plants of said population, thereby identifying whether or not said one or more genetic polymorphisms are associated with variation in said trait.

20. A method of identifying whether a polymorphism is associated with variation in a trait, said method comprising:

a) screening a population of plants to determine whether one or more genetic polymorphisms in said population of plants is associated with the locus for a polypeptide selected from the group consisting of the polypeptides depicted in Figures 1-57; SEQ ID NO: 556, SEQ ID NO: 853, and SEQ ID NO: 1157 and functional homologs thereof;

b) measuring the correlation between variation in said trait in plants of said population and the presence of said one or more genetic polymorphisms in plants of said population, thereby identifying whether or not said one or more genetic polymorphisms are associated with variation in said trait;

c) selecting from said population of plants a sub-population of plants that possess said one or more genetic polymorphisms associated with said trait; and

d) crossing one or more plants from said sub-population of plants.

21. The method according to claim 20, further comprising breeding said sub-population of plants to produce a plant line which comprises said polymorphism.

22. A method of making a plant line, said method comprising:

a) determining whether one or more genetic polymorphisms in a population of plants is associated with the locus for a polypeptide selected from the group consisting of the polypeptides depicted in Figures 1-57, SEQ ID NO:556, SEQ ID NO:853, and SEQ ID NO:1157 and functional homologs thereof;

b) identifying one or more plants in said population in which the presence of at least one allele at said one or more genetic polymorphisms is associated with variation in a trait;

c) crossing each said one or more identified plants with itself or a different plant to produce

seed;

d) crossing at least one progeny plant grown from said seed with itself or a different plant; and

e) repeating steps c) and d) for an additional 0-5 generations to make said plant line, wherein said at least one allele is present in said plant line.

23. The method of any one of claims 19-22, wherein said trait is the level of low-nitrogen tolerance.

24. The method of any one of claims 19-22, wherein said population is a population of switchgrass, sorghum, sugar cane, or miscanthus plants.

Figure 1

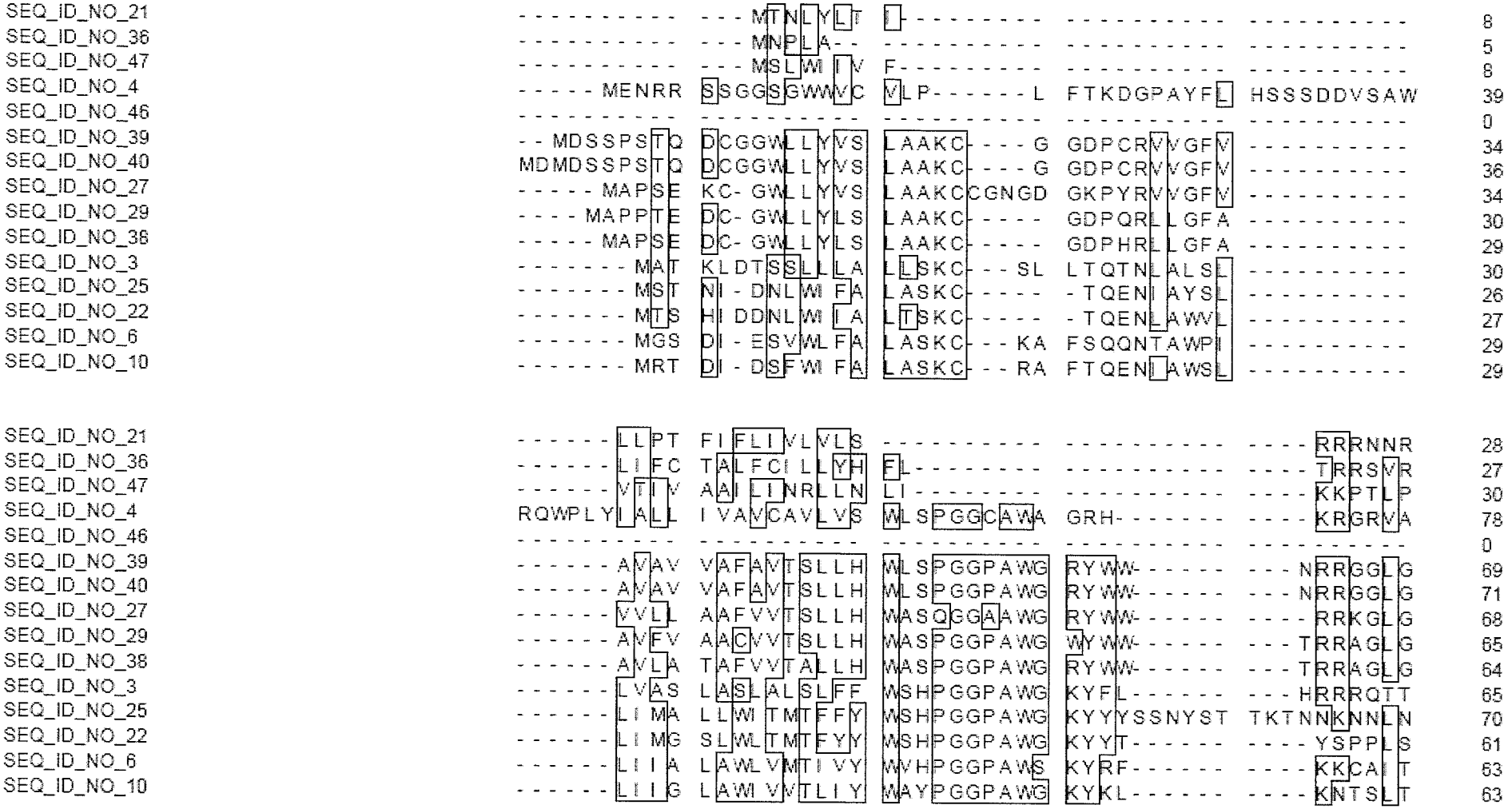
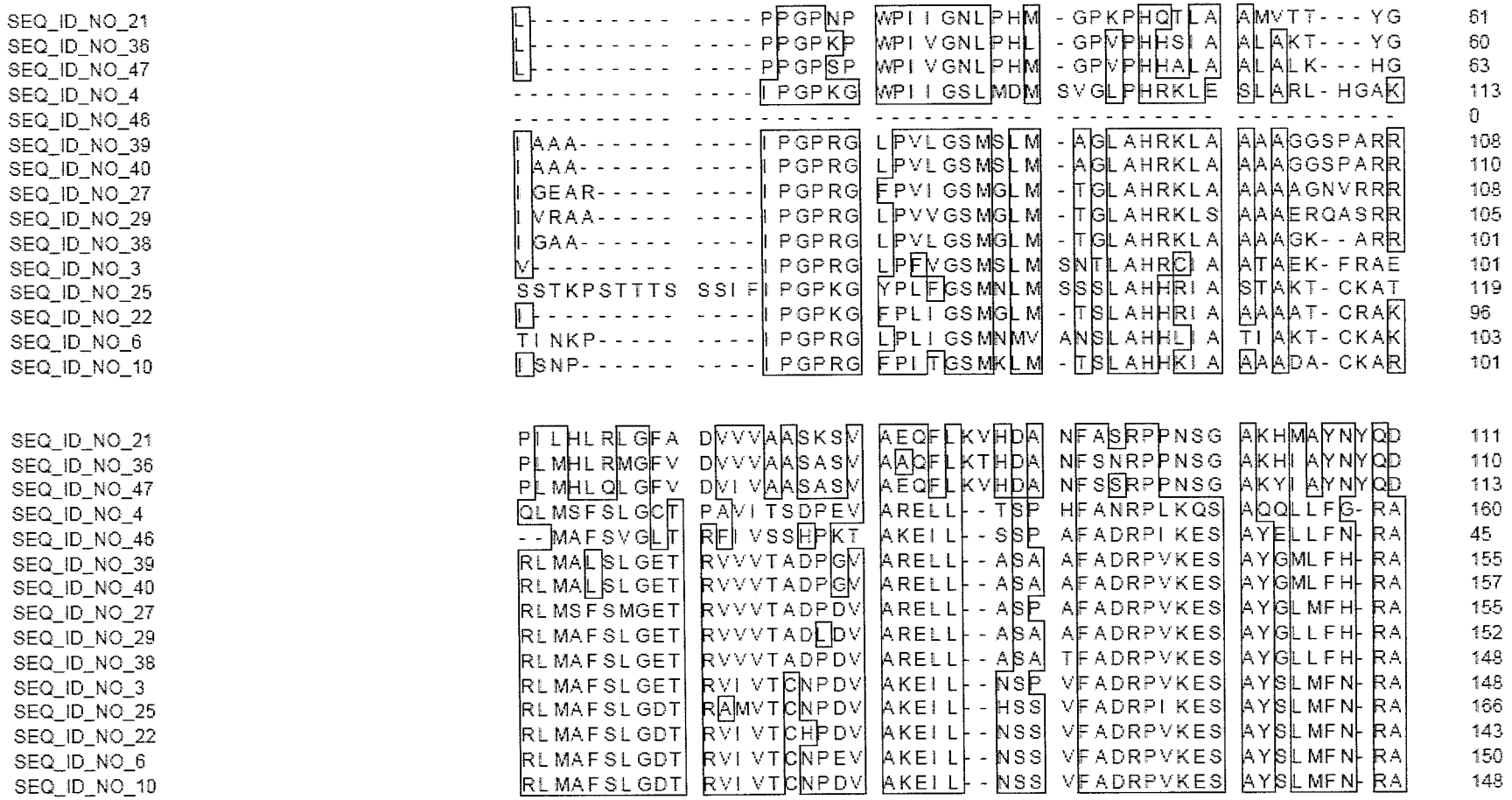

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SEQ_ID_NO_27
SEQ_ID_NO_29
SEQ_ID_NO_38
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SEQ_ID_NO_25
SEQ_ID_NO_22
SEQ_ID_NO_6
SEQ_ID_NO_10

Figure 1 (continued)




SEQ_ID_NO_21 159
SEQ_ID_NO_36 158
SEQ_ID_NO_47 161
SEQ_ID_NO_4 208
SEQ_ID_NO_46 93
SEQ_ID_NO_39 205
SEQ_ID_NO_40 207
SEQ_ID_NO_27 203
SEQ_ID_NO_29 200
SEQ_ID_NO_38 198
SEQ_ID_NO_3 196
SEQ_ID_NO_25 214
SEQ_ID_NO_22 191
SEQ_ID_NO_6 198
SEQ_ID_NO_10 196
SEQ_ID_NO_21 201
SEQ_ID_NO_36 203
SEQ_ID_NO_47 208
SEQ_ID_NO_4 252
SEQ_ID_NO_46 135
SEQ_ID_NO_39 250
SEQ_ID_NO_40 252
SEQ_ID_NO_27 249
SEQ_ID_NO_29 244
SEQ_ID_NO_38 245
SEQ_ID_NO_3 240
SEQ_ID_NO_25 257
SEQ_ID_NO_22 233
SEQ_ID_NO_6 241
SEQ_ID_NO_10 238

Figure 1 (continued)

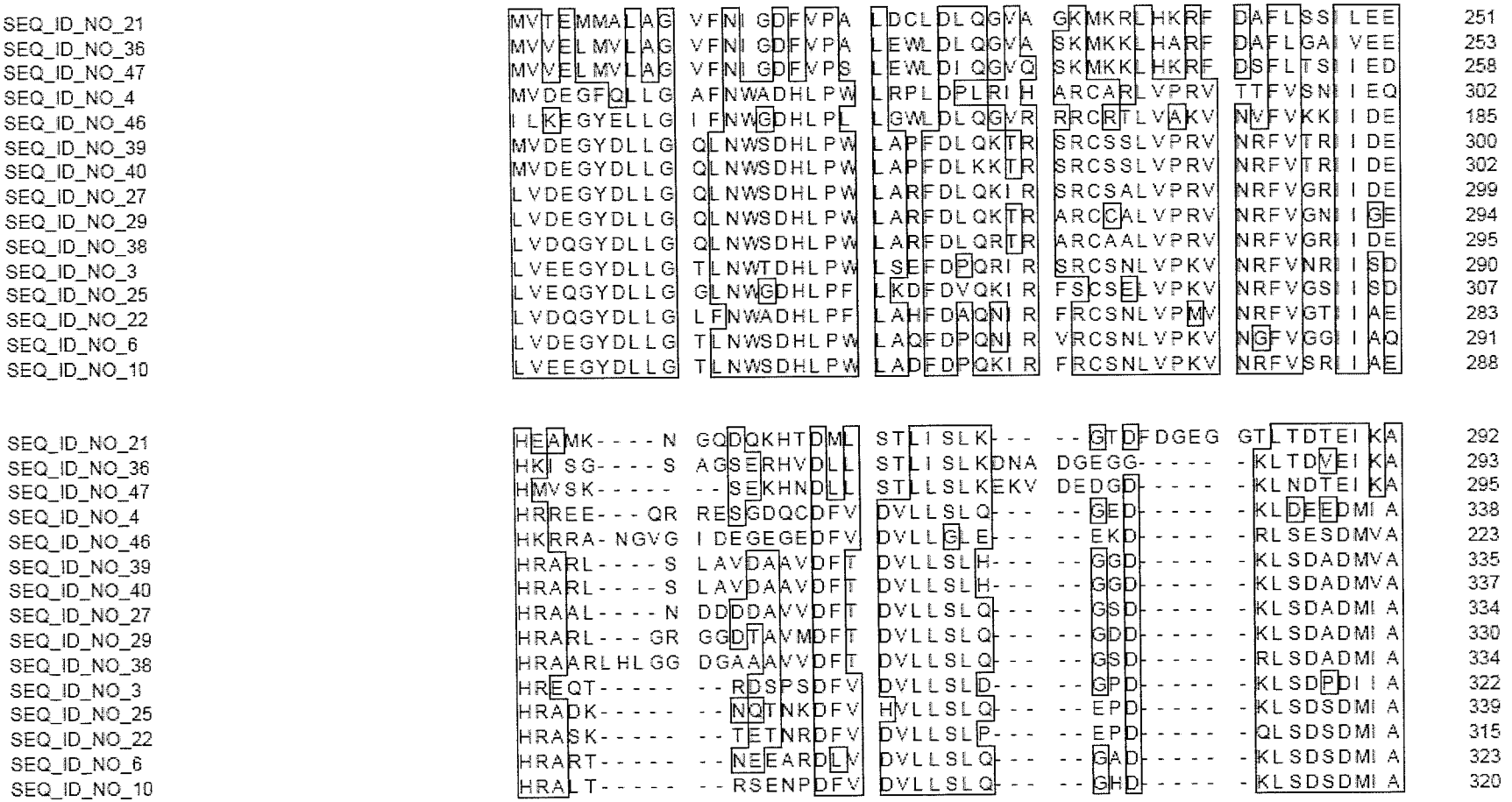


Figure 1 (continued)

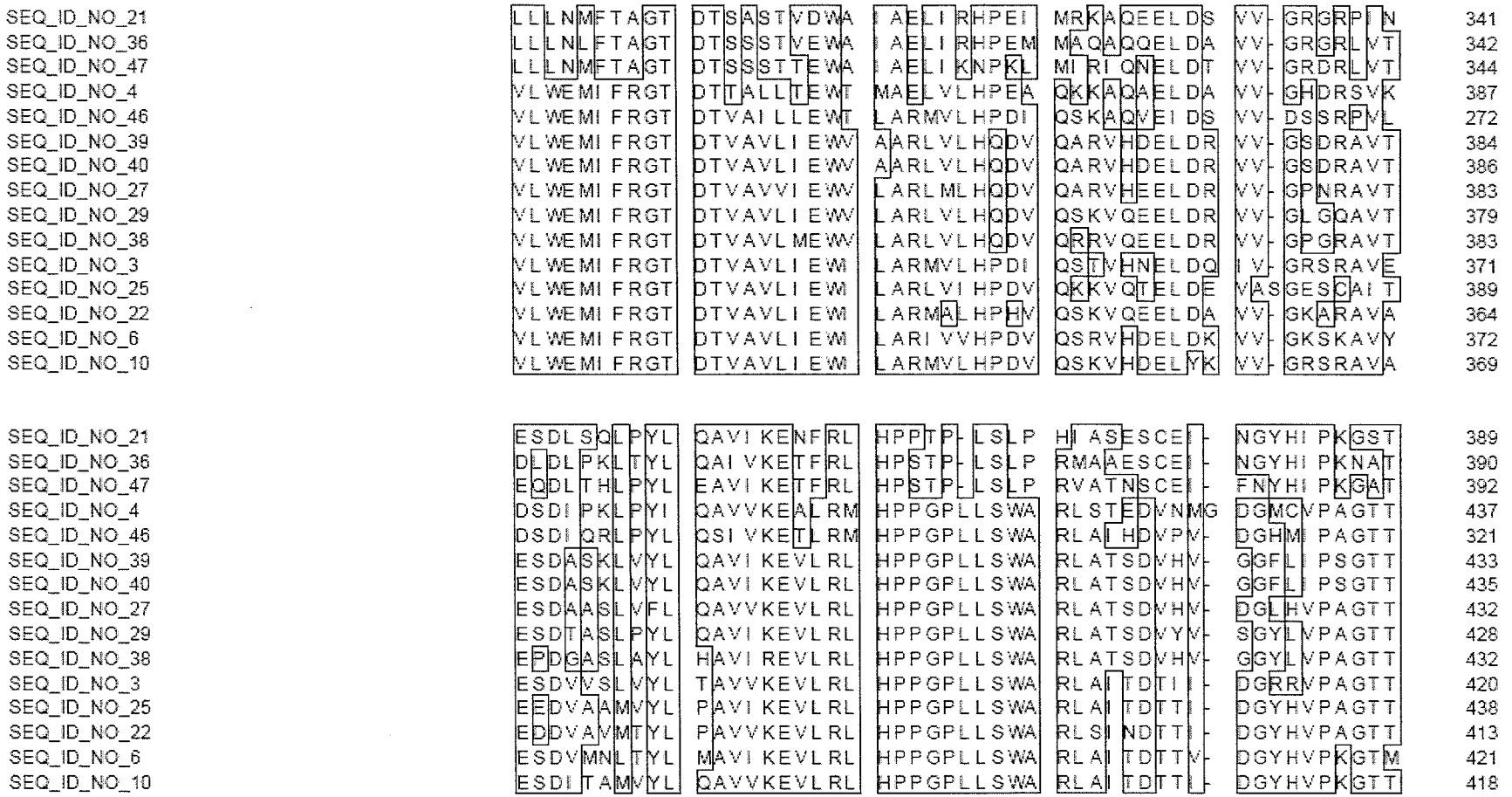


Figure 1 (continued)



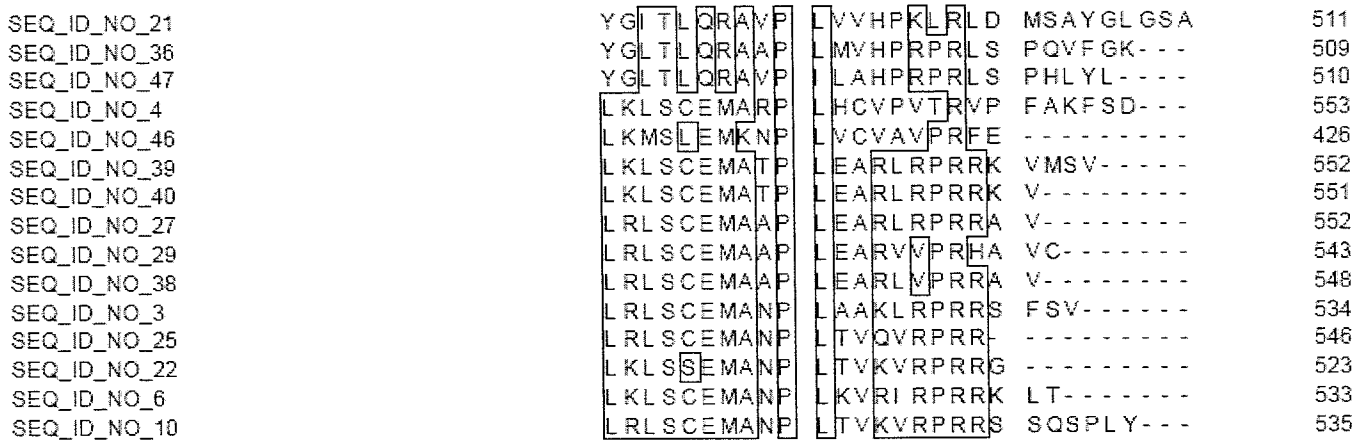

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SEQ_ID_NO_36 YGLTLQRAAP LMVHPRPRLS PQVFGK--- 509
SEQ_ID_NO_47 YGLTLQRAVP ILAHPRPRLS PHLYL---- 510
SEQ_ID_NO_4 LKLSCEMARP LHCVPVTRVP FAKFSD--- 553
SEQ_ID_NO_46 LKMSLEMKNP LVCVAVPRFE ---------- 426
SEQ_ID_NO_39 LKLSCEMATP LEARLRPRRK VMSV----- 552
SEQ_ID_NO_40 LKLSCEMATP LEARLRPRRK V--------- 551
SEQ_ID_NO_27 LRLSCEMAAP LEARLRPRRA V--------- 552
SEQ_ID_NO_29 LRLSCEMAAP LEARVVPRHA VC------- 543
SEQ_ID_NO_38 LRLSCEMAAP LEARLVPRRA V--------- 548
SEQ_ID_NO_3 LRLSCEMANP LAAKLRPRRS FSV------ 534
SEQ_ID_NO_25 LRLSCEMANP LTVQVRPRR- ---------- 546
SEQ_ID_NO_22 LKLSSEMANP LTVKVRPRRG ---------- 523
SEQ_ID_NO_6 LKLSCEMANP LKVRIRPRRK LT------- 533
SEQ_ID_NO_10 LRLSCEMANP LTVKVRPRRS SQSPLY--- 535

Figure 2

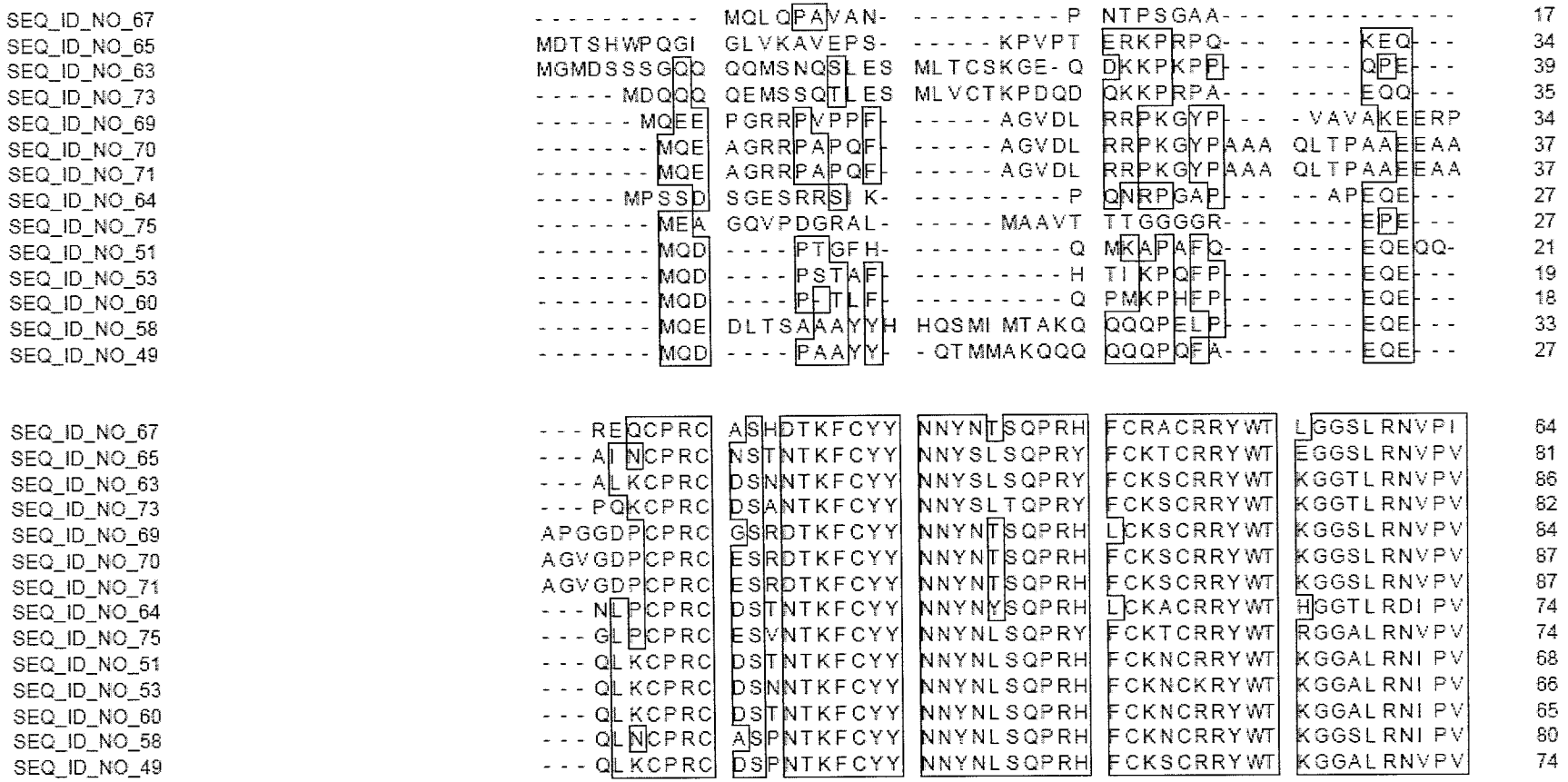

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SEQ_ID_NO_49

Figure 2 (continued)



Figure 2 (continued)

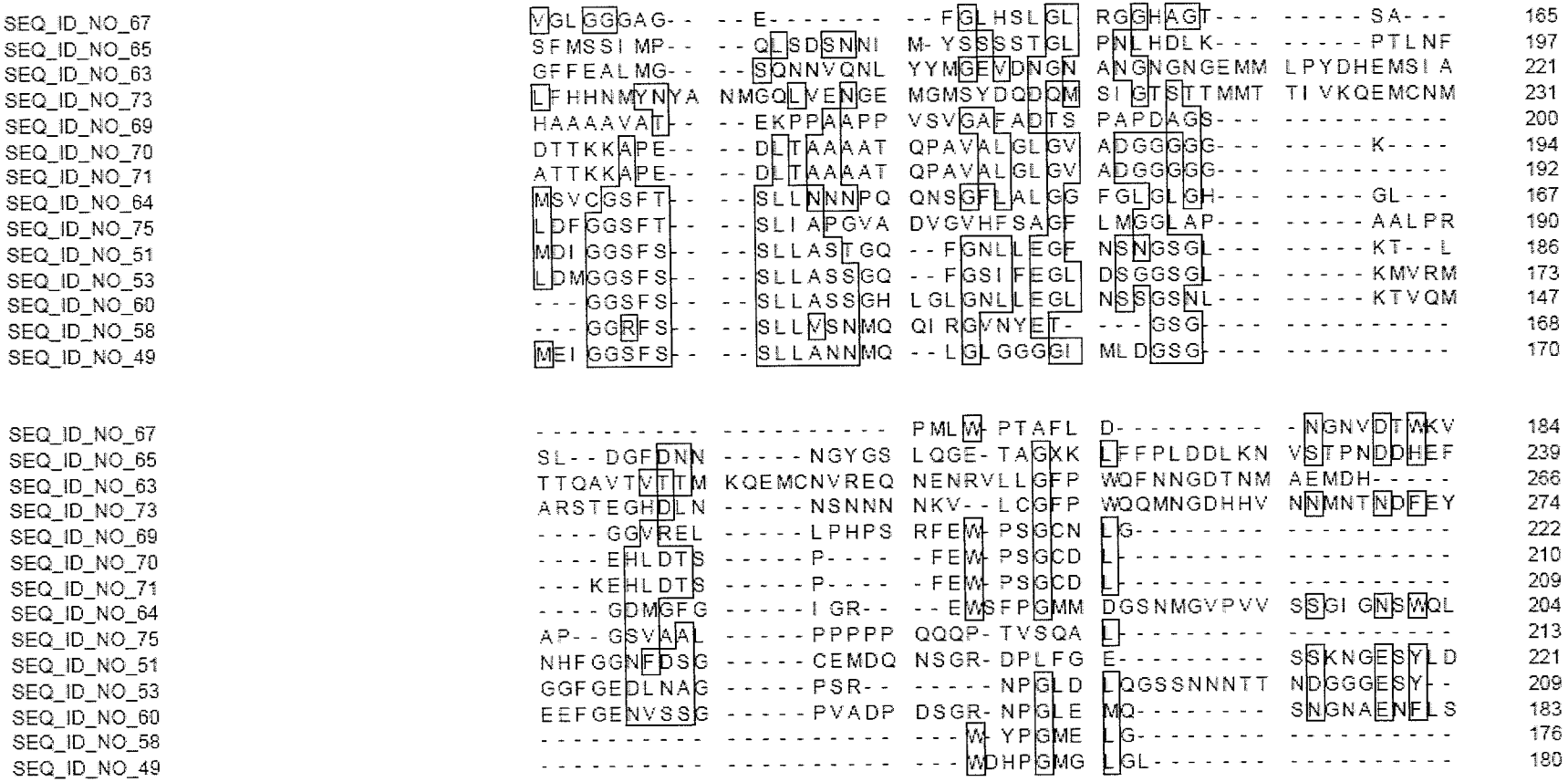


Figure 2 (continued)

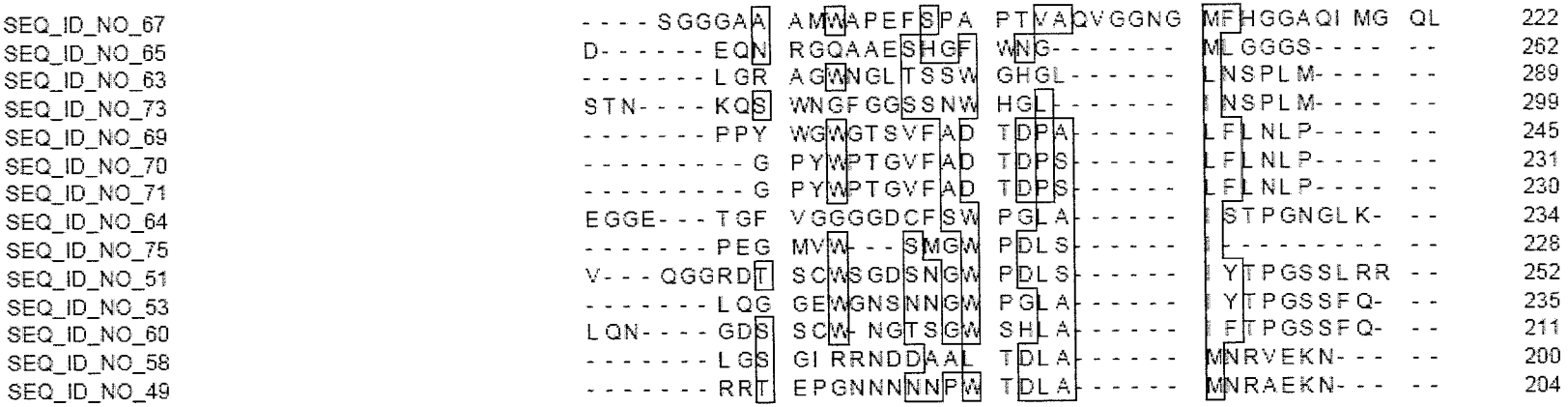


Figure 3

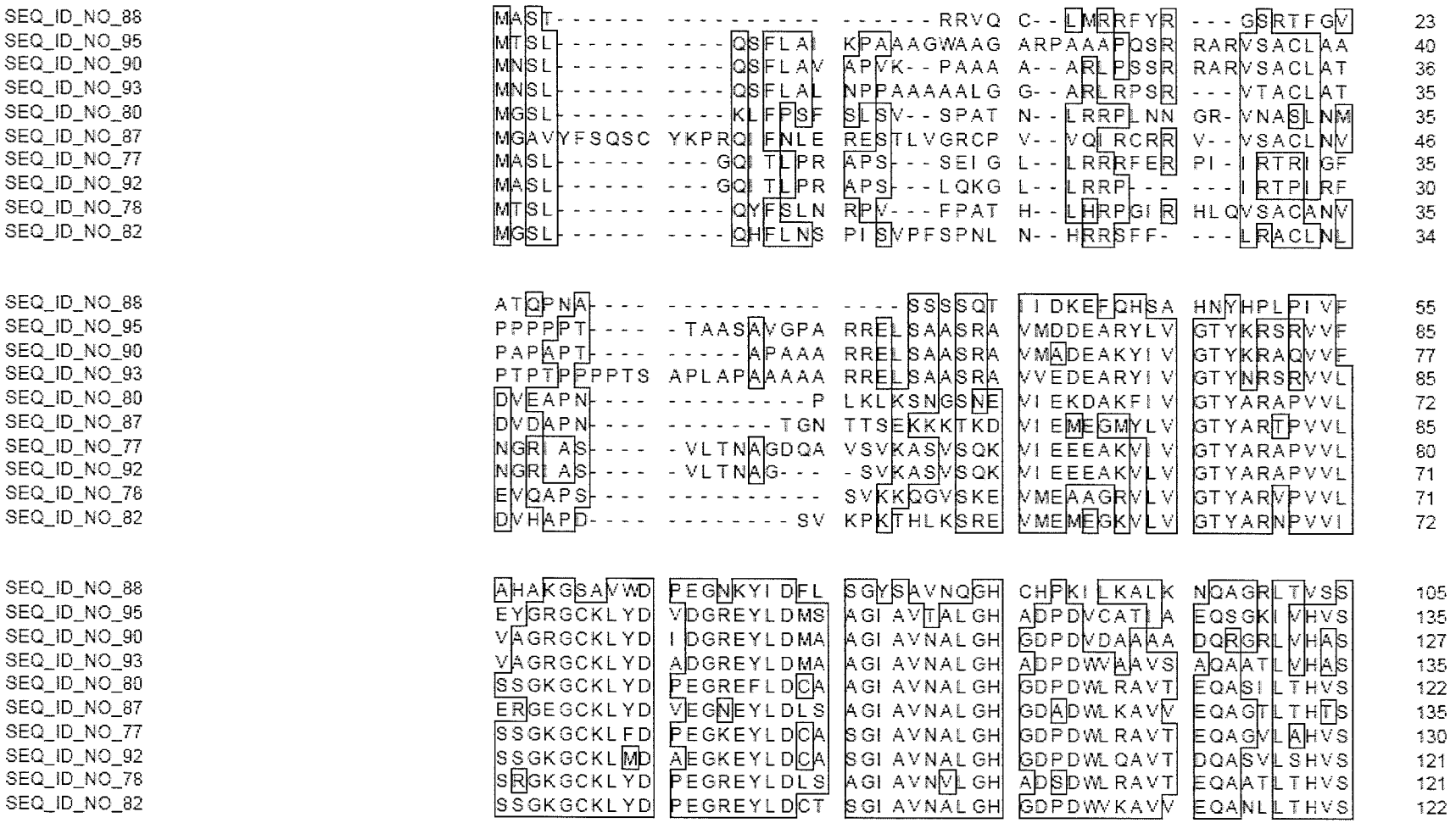

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SEQ_ID_NO_80
SEQ_ID_NO_87
SEQ_ID_NO_77
SEQ_ID_NO_92
SEQ_ID_NO_78
SEQ_ID_NO_82
MASTRRVQ C--LMRRFYR ---GSRTFGV 23
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MNSLQSFLAL NPPAAAAAALG G--ARLRPSR ---VTACLAT 35
MGSLKLFPSF SLSV--SPAT N--LRRPLNN GR-VNASLNM 35
MGAVYFSQSC YKPRQIFNLE RESTLVGRCP V--VQIRCRR V--VSACLNV 46
MASLGQITLPR APS---SEIG L--LRRRFER PI-IRTRIGF 35
MASLGQITLPR APS---LQKG L--LRRRP--- ---IRTPIRF 30
MTSLQYFSLN RPV---FPAT H--LHRPGIR HLQVSACANV 35
MGSLQHFLNS PISVPFSPNL N--HRRSFF- ---LRACLNL 34
ATQPNA---- ----------SSSSQT IIDKEFQHSA HNYHPLPIVF 55
PPPPPT---- -TAASAVGPA RRELSAASRA VMDDEARYLV GTYKRSRVVF 85
PAPAPT---- -----APAAA RRELSAASRA VMADEAKYIV GTYKRAQVVF 77
PTPTPPPPTS APLAPAAAAA RRELSAASRA VVEDEARYIV GTYNRSRVVL 85
DVEAPN---- ----------P LKLKSNGSNE VIEKDAKFIV GTYARAPVVL 72
DVDAPN---- --------TGN TTSEKKKTKD VIEMEGMYLV GTYARTPVVL 85
NGRLAS---- -VLTNAGDQA VSVKASVSQK VIEEEAKVIV GTYARAPVVL 80
NGRLAS---- -VLTNAG--- -SVKASVSQK VIEEEAKVLV GTYARAPVVL 71
EVQAPS---- ---------- SVKKQGVSKE VMEAAGRVLV GTYARVPVVL 71
DVHAPD---- --------SV KPKTHLKSRE VMEMEGKVLV GTYARNPVVI 72
AHAKGSAVWD PEGNKYIDFL SGYSAVNQGH CHPKILKALK NQAGRLTVSS 105
EYGRGCKLYD VDGREYLDMS AGIAVTALGH ADPDVCATLA EQSGKIVHVS 135
VAGRGCKLYD IDGREYLDMA AGIAVNALGH GDPDVDAAAA DQRGRLVHAS 127
VAGRGCKLYD ADGREYLDMA AGIAVNALGH ADPDWAAVS AQAATLVHAS 135
SSGKGCKLYD PEGREFLDCA AGIAVNALGH GDPDWLRAVT EQASILTHVS 122
ERGEGCKLYD VEGNEYLDLS AGIAVNALGH GDADWLKAVV EQAGTLTHTS 135
SSGKGCKLFD PEGKEYLDCA SGIAVNALGH GDPDWLRAVT EQAGVLAHVS 130
SSGKGCKLMD AEGKEYLDCA SGIAVNALGH GDPDWLQAVT DQASVLSHVS 121
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Figure 3 (continued)

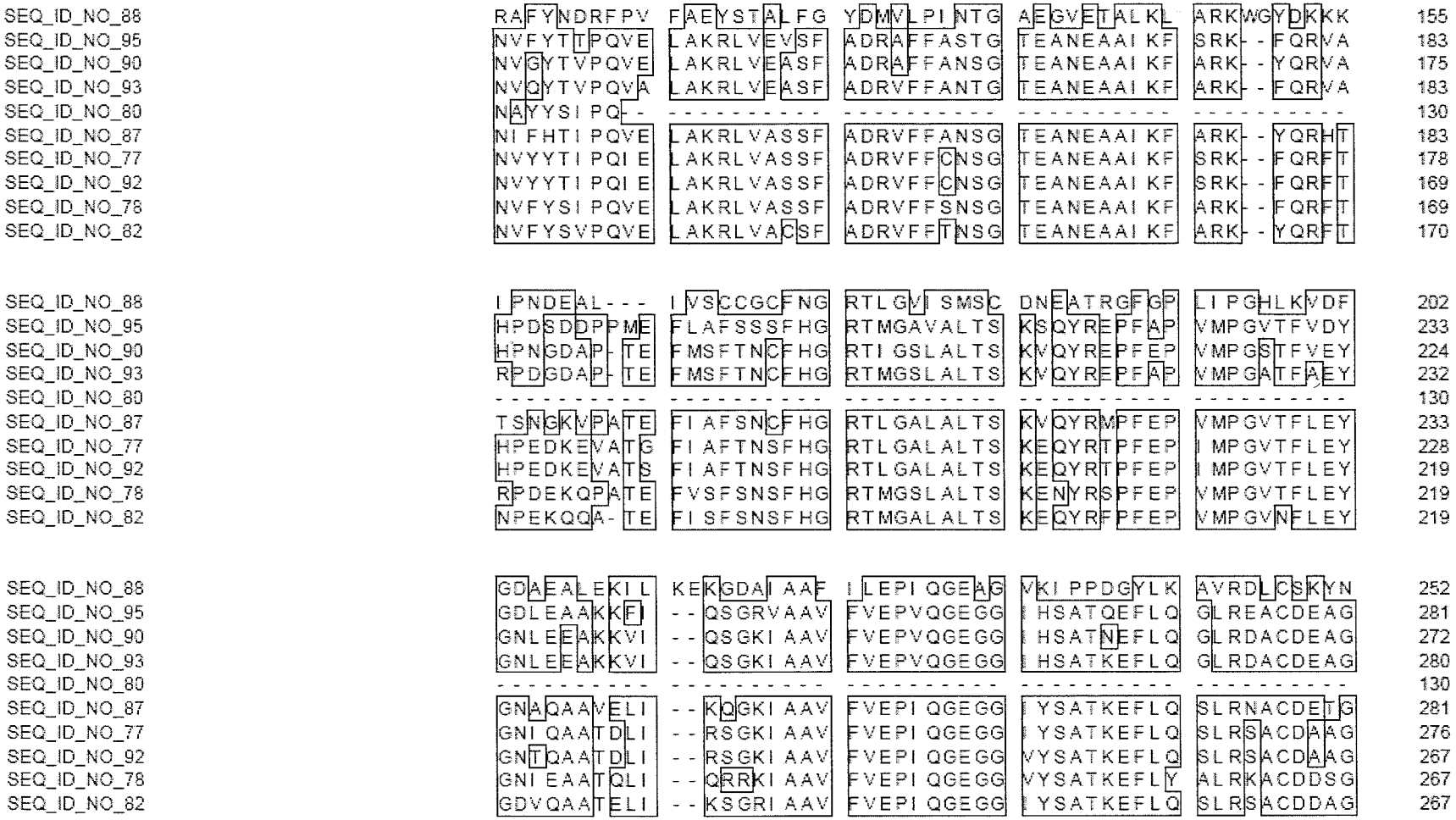


Figure 3 (continued)



Figure 3 (continued)

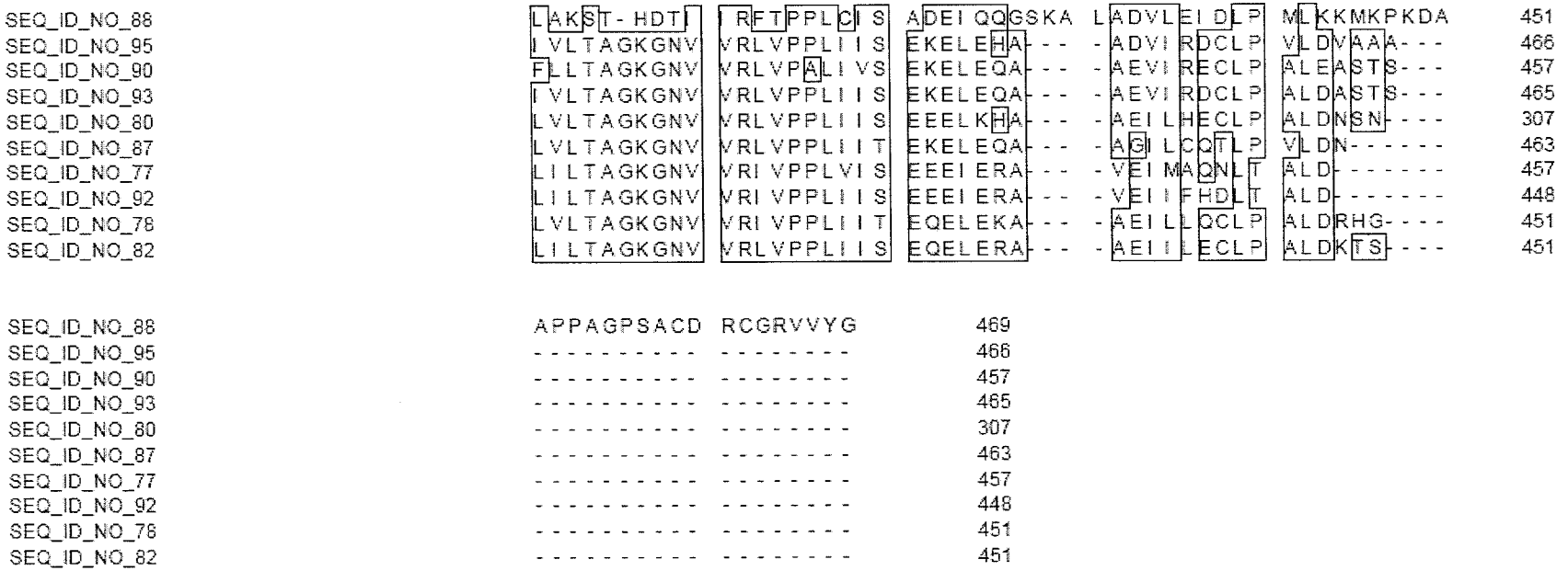


Figure 4

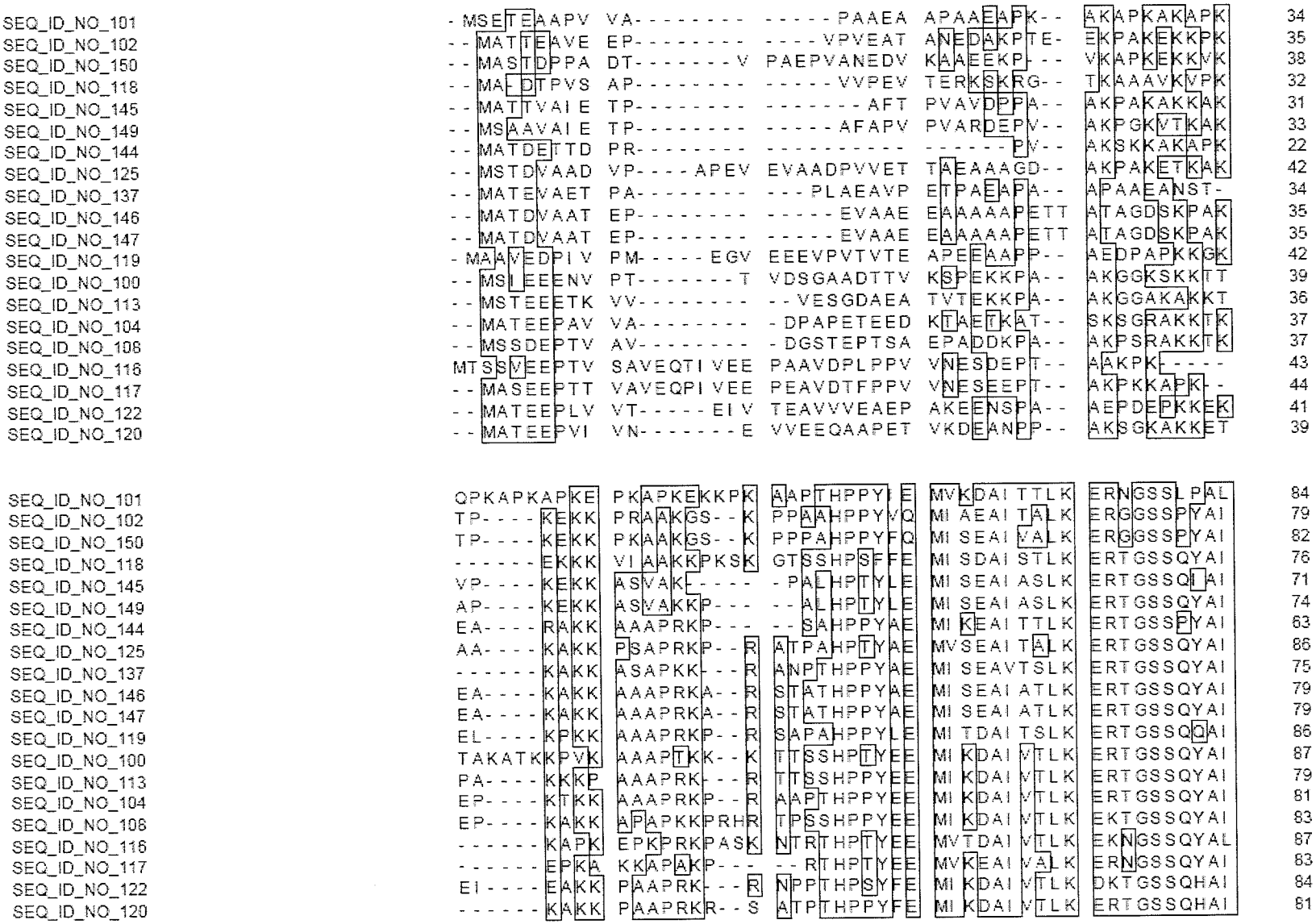

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SEQ_ID_NO_119
SEQ_ID_NO_100
SEQ_ID_NO_113
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SEQ_ID_NO_117
SEQ_ID_NO_122
SEQ_ID_NO_120

Figure 4 (continued)

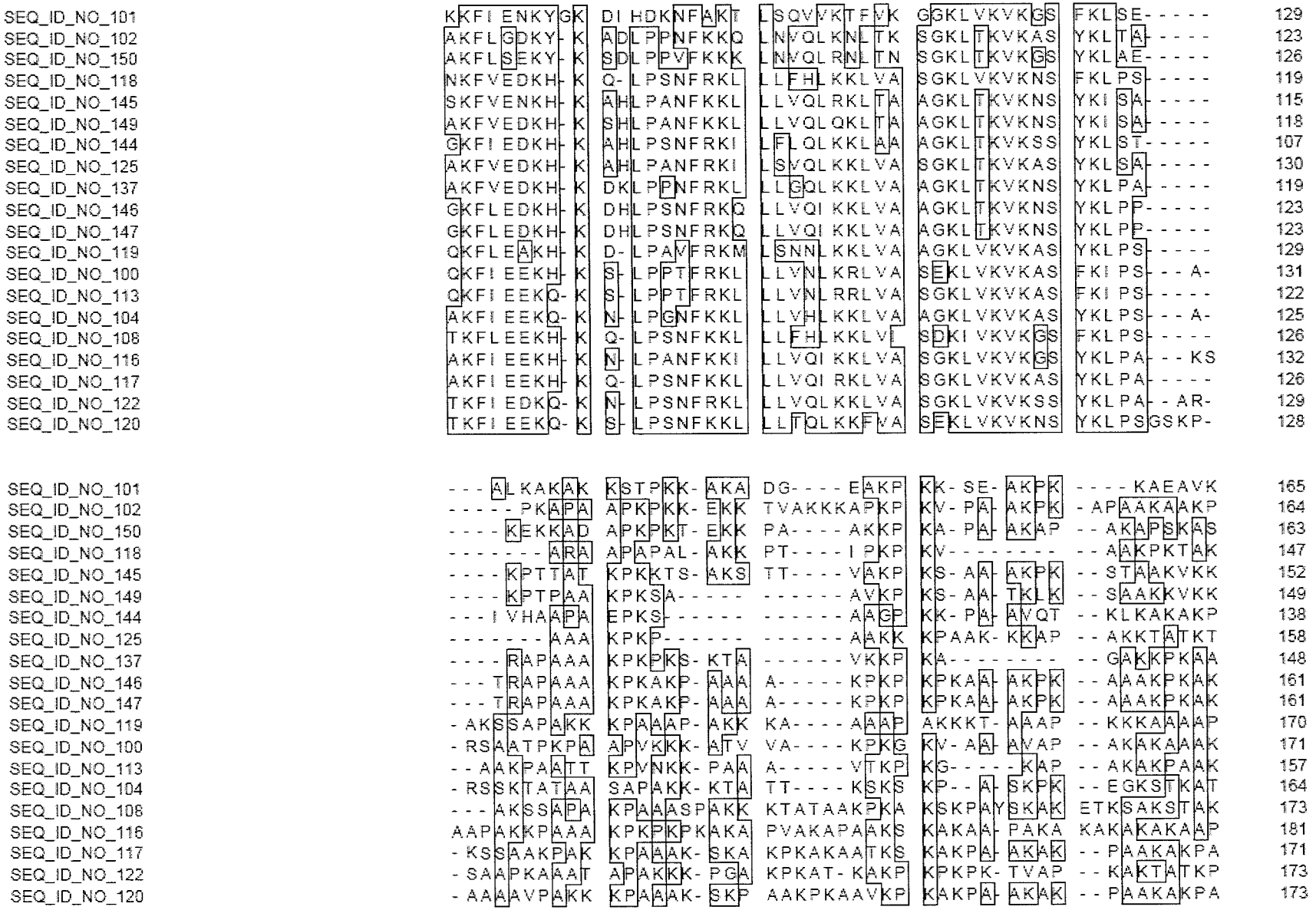


Figure 4 (continued)



Figure 4 (continued)

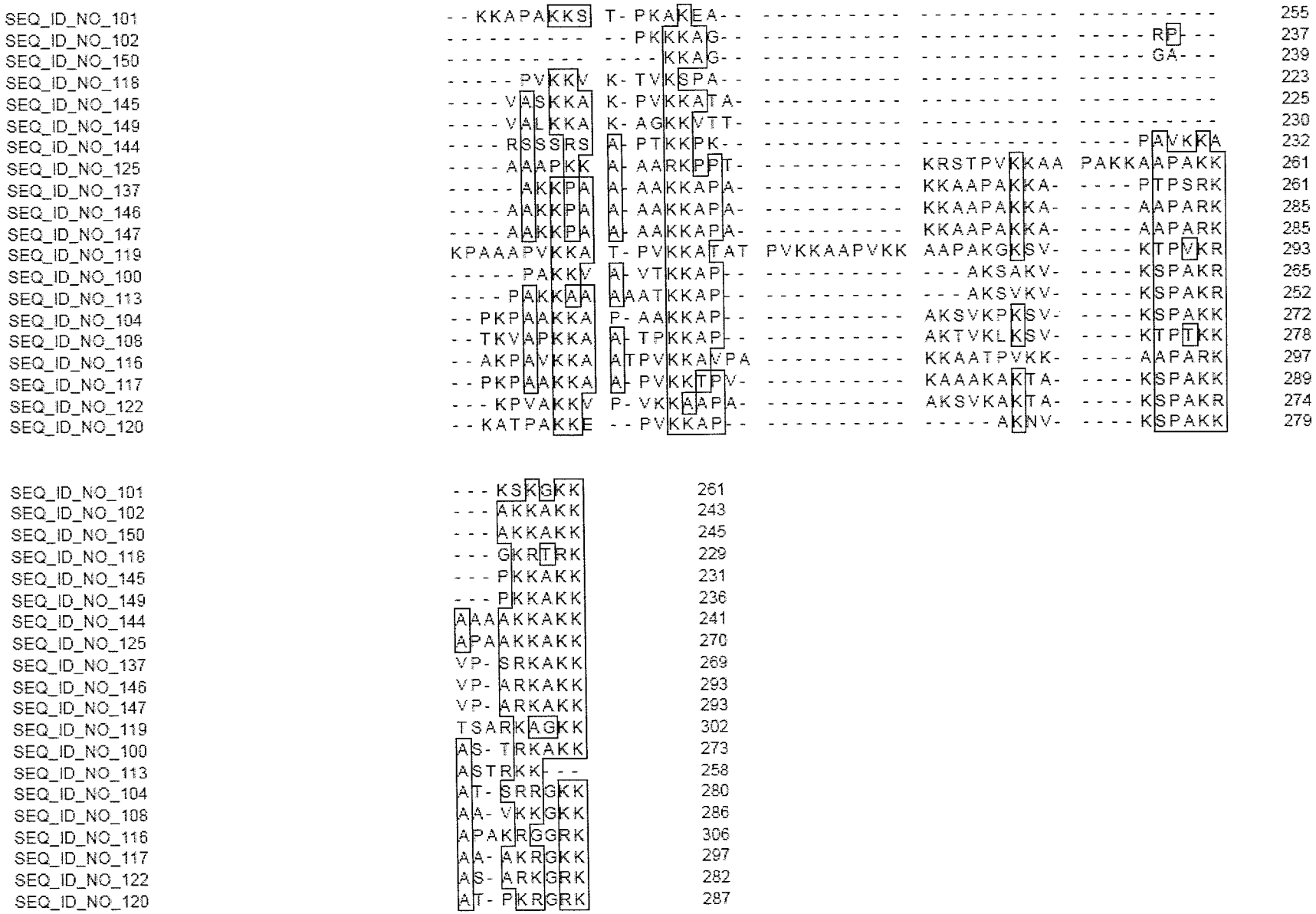


Figure 5

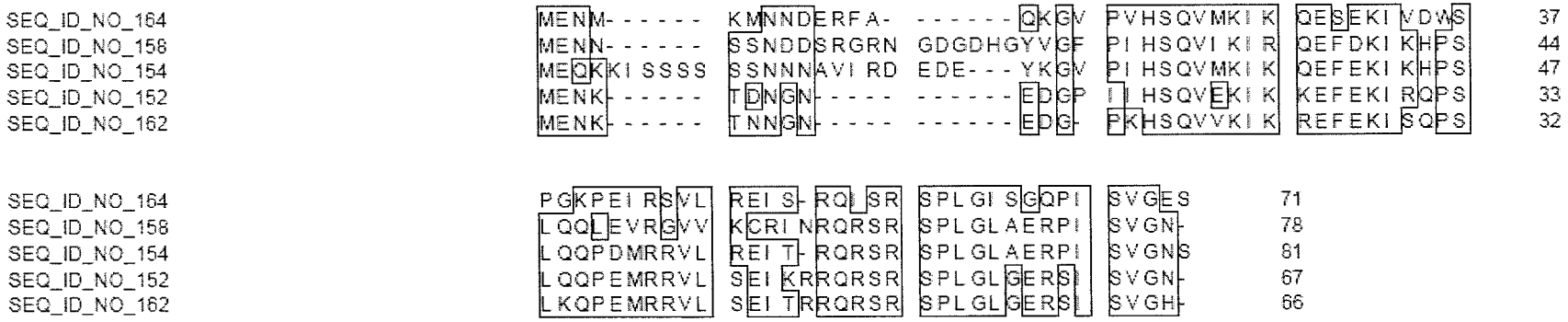

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SEQ_ID_NO_158 MENN------ SSNDDSRGRN GDGDHGYVGF PIHSQVIKIR QEFDKIKHPS 44
SEQ_ID_NO_154 MEQKKISSSS SSNNNAVIRD EDE---YKGV PIHSQVMKIK QEFEKIKHPS 47
SEQ_ID_NO_152 MENK------ TDNGN----- ------EDGP IIHSQVEKIK KEFEKIRQPS 33
SEQ_ID_NO_162 MENK------ TNNGN----- ------EDG- PKHSQVVKIK REFEKISQPS 32
SEQ_ID_NO_164 PGKPEIRSVL REIS-RQLSR SPLGISGQPI SVGES 71
SEQ_ID_NO_158 LQQLEVRGVV KCRINRQRSR SPLGLAERPI SVGN- 78
SEQ_ID_NO_154 LQQPDMRRVL REIT-RQRSR SPLGLAERPI SVGNS 81
SEQ_ID_NO_152 LQQPEMRRVL SEIKRRQRSR SPLGLGERSI SVGN- 67
SEQ_ID_NO_162 LKQPEMRRVL SEITRRQRSR SPLGLGERSI SVGH- 66

Figure 6


SEQ_ID_NO_184
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SEQ_ID_NO_177
SEQ_ID_NO_181
SEQ_ID_NO_182
SEQ_ID_NO_183
SEQ_ID_NO_170
SEQ_ID_NO_166
SEQ_ID_NO_174
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Figure 6 (continued)

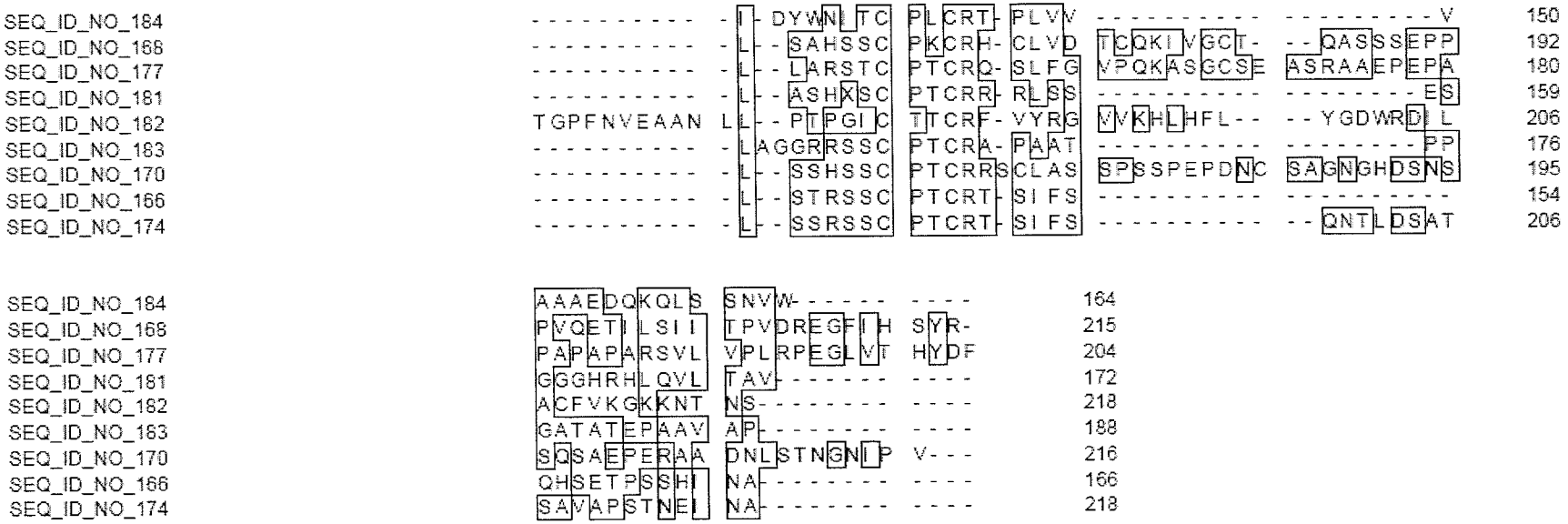


Figure 7

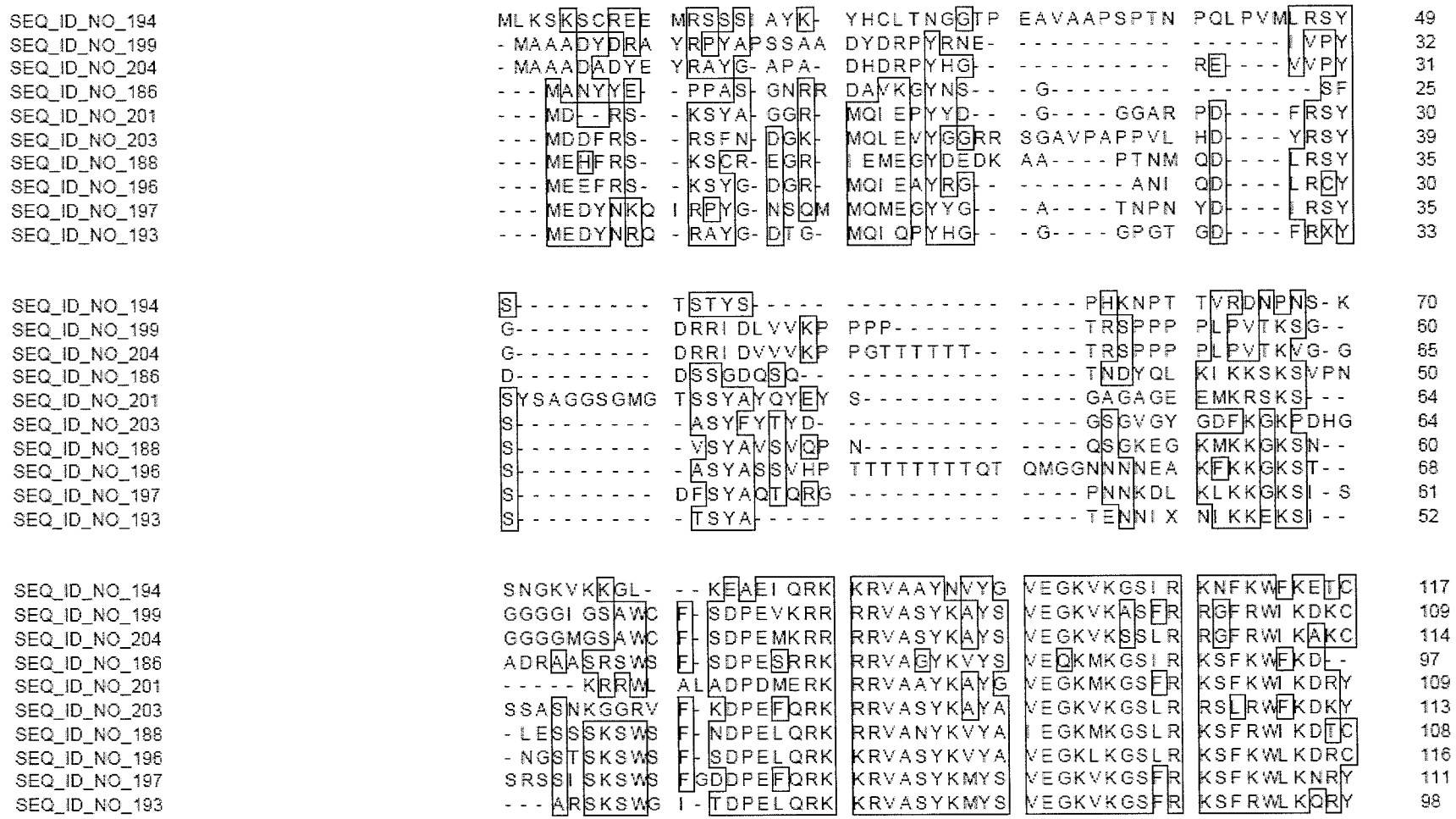

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-MAAADYDRA YRPYAPSSAA DYDRPYRNE- ---------- ------IVPY 32
-MAAADADYE YRAYG-APA- DHDRPYHG-- ---------- RE---VVPY 31
---MANYYE- -PPAS-GNRR DAVKGYNS-- -G-------- --------SF 25
---MD--RS- -KSYA-GGR- MQIEPYYD-- -G----GGAR PD----FRSY 30
---MDDFRS- -RSFN-DGK- MQLEVYGGRR SGAVPAPPVL HD----YRSY 39
---MEHFRS- -KSCR-EGR- IEMEGYDEDK AA----PTNM QD----LRSY 35
---MEEFRS- -KSYG-DGR- MQIEAYRG-- --------ANI QD----LRCY 30
---MEDYNKQ IRPYG-NSQM MQMEGYYG-- -A----TNPN YD----LRSY 35
---MEDYNRQ -RAYG-DTG- MQIQPYHG-- -G----GPGT GD----FRKY 33
SEQ_ID_NO_194
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SEQ_ID_NO_204
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SEQ_ID_NO_201
SEQ_ID_NO_203
SEQ_ID_NO_188
SEQ_ID_NO_196
SEQ_ID_NO_197
SEQ_ID_NO_193
S--------- TSTYS----- ---------- ----PHKNPT TVRDNPNS-K 70
G--------- DRRIDLVVKP PPP------- ----TRSPPP PLPVTKSG-- 60
G--------- DRRIDVVVKP PGTTTTTT-- ----TRSPPP PLPVTKVG-G 65
D--------- DSSGDQSQ-- ---------- ----TNDYQL KIKKSKSVPN 50
SYSAGGSGMG TSSYAYQYEY S--------- ----GAGAGE EMKRSKS--- 64
S--------- -ASYFYTYD- ---------- ----GSGVGY GDFKGKPDHG 64
S--------- -VSYAVSVQP N--------- ----QSGKEG KMKKGKSN-- 60
S--------- -ASYASSVHP TTTTTTTTQT QMGGNNNNEA KFKKGKST-- 68
S--------- DFSYAQTQRG ---------- ----PNNKDL KLKKGKSI-S 61
S--------- -TSYA----- ---------- ----TENNIX NIKKEKSI-- 52
SEQ_ID_NO_194
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SEQ_ID_NO_204
SEQ_ID_NO_186
SEQ_ID_NO_201
SEQ_ID_NO_203
SEQ_ID_NO_188
SEQ_ID_NO_196
SEQ_ID_NO_197
SEQ_ID_NO_193
SNGKVKKGL- --KEAEIQRK KRVAAYNVYG VEGKVKGSIR KNFKWFKETC 117
GGGGIGSAWC F-SDPEVKRR RRVASYKAYS VEGKVKASFR RGFRWIKDKC 109
GGGGMGSAWC F-SDPEMKRR RRVASYKAYS VEGKVKSSLR RGFRWIKAKC 114
ADRAASRSWS F-SDPESRRK RRVAGYKVYS VEQKMKGSIR KSFKWFKDL- 97
-----KRRWL ALADPDMERK RRVAAYKAYG VEGKMKGSFR KSFKWIKDRY 109
SSASNKGGRV F-KDPEFQRK RRVASYKAYA VEGKVKGSLR RSLRWFKDKY 113
-LESSSKSWS F-NDPELQRK RRVANYKVYA IEGKMKGSLR KSFRWIKDTC 108
-NGSTSKSWS F-SDPELQRK KRVASYKVYA VEGKLKGSLR KSFKWLKDRC 116
SRSSISKSWS FGDDPEFQRK KRVASYKMYS VEGKVKGSFR KSFKWLKNRY 111
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Figure 7 (continued)

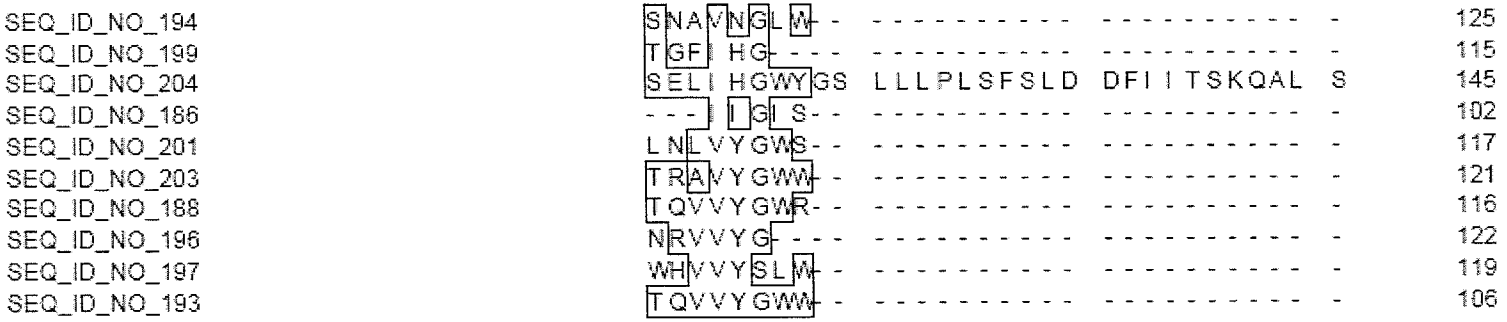


Figure 8

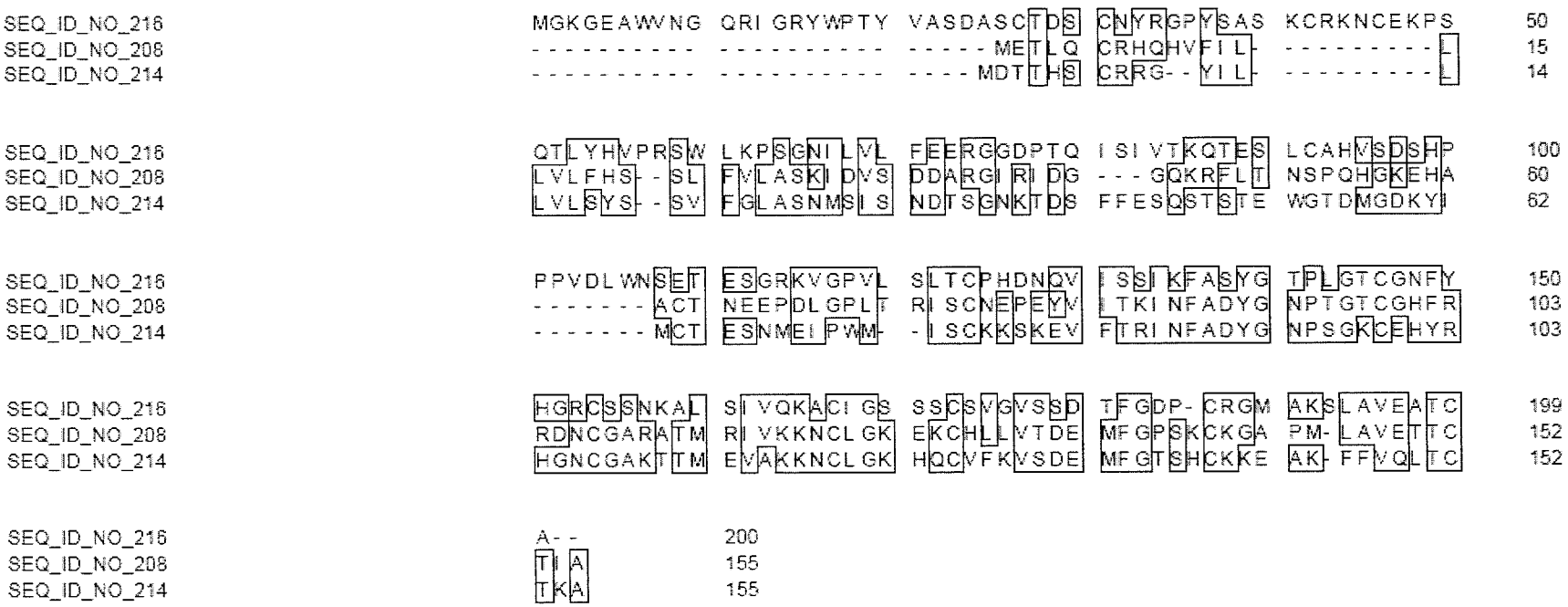

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SEQ_ID_NO_214 ---------- ---------- ----MDTTHS CRRG--YIL- ---------L 14
SEQ_ID_NO_216 QTLYHVPRSW LKPSGNILVL FEERGGDPTQ ISIVTKQTES LCAHVSDSHP 100
SEQ_ID_NO_208 LVLFHS--SL FVLASKIDVS DDARGIRIDG ---GQKRFLT NSPQHGKEHA 60
SEQ_ID_NO_214 LVLSYS--SV FGLASNMSIS NDTSGNKTDS FFESQSTSTE WGTDMGDKYI 62
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SEQ_ID_NO_214 -------MCT ESNMEIPWM- -ISCKKSKEV FTRINFADYG NPSGKCEHYR 103
SEQ_ID_NO_216 HGRCSSNKAL SIVQKACIGS SSCSVGVSSD TFGDP-CRGM AKSLAVEATC 199
SEQ_ID_NO_208 RDNCGARATM RIVKKNCLGK EKCHLLVTDE MFGPSKCKGA PM-LAVETTC 152
SEQ_ID_NO_214 HGNCGAKTTM EVAKKNCLGK HQCVFKVSDE MFGTSHCKKE AK-FFVQLTC 152
SEQ_ID_NO_216 A-- 200
SEQ_ID_NO_208 TIA 155
SEQ_ID_NO_214 TKA 155

Figure 9


SEQ_ID_NO_218
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Figure 9 (continued)

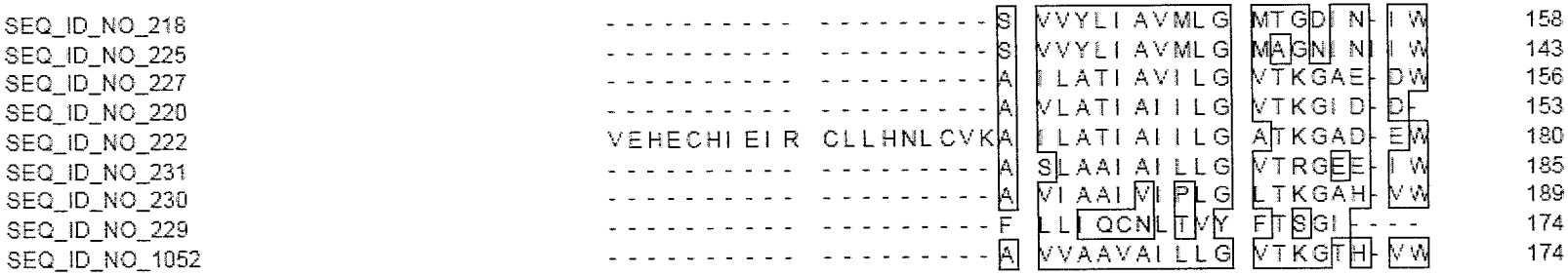


FIGURE _ Page 28 of 165

Docket Number: 2750-1699PWO1

Figure 10

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SEQ_ID_NO_244   MEYQRTNNLS LAFQFFRKAF EMCDSDPLLF NEYGVLRYRQ G-NYEEAVEN  49
SEQ_ID_NO_234   MEYMRTHSYK LADQFFMQAK AICPSDPLVY NELGVVAYHM K-EYGKAVRW  49
SEQ_ID_NO_236   MEYMRTHSYK LAEQFFMQAK TICPSDPLVY NELGVVAYNM K-EYNKAVLW  49
SEQ_ID_NO_241   MQYVRMHNFK LAEQFFTQAK SICPSDPLIH NELGVVAYNM KEEYQKAVSY  50
SEQ_ID_NO_242   MQYLRMHNFK LAEQFFTQAK SICPSDPLIY NEMGVVAYNM K-EYQKAVQW  49

SEQ_ID_NO_244   FERALDLAPK PVGSRWESLI VNLAQAFRKI GRYDEAIATF QSALLISPRN  99
SEQ_ID_NO_234   FEKTLAHIPS ALTESWEPTV VNLAHAYRKL RKDREAISYY ERALTLSTKS  99
SEQ_ID_NO_236   FEKTLKHIPS -LSQLWEPTV INLAHAYRKL KIYHEAISCY ERALALSTRS  98
SEQ_ID_NO_241   YAKALTFPTK SLSL----AF AGLAYTYHLM DDFEAAINYY HKALWLKPDD  95
SEQ_ID_NO_242   FELTLEHTSS SLNEMWEPTL VNLGHALRKL KKYQKAISYY EKALTFQTKS  99

SEQ_ID_NO_244   ASTYAALAFT YQMKSRCSEP VSLGLAIEYY HKALSLRADD AFSQHHLELA  149
SEQ_ID_NO_234   LSTYSGLAYT YHLQGNFS-- ----AAISYY HKALWLKPDD QFCTEMLNVA  143
SEQ_ID_NO_236   LSTYAGLAYT YHLQDNFT-- ----AAITCY HKALWLKPDD QFCTEMLSLA  142
SEQ_ID_NO_241   QFCTDMLTYA LESICQIT-- ---------- ---------- ---------A  114
SEQ_ID_NO_242   LSAFAGLAYT YHLMAMYH-- ----V----- HRA------- ----EVLQIL  127

SEQ_ID_NO_244   LIDQSAITIP RHQQVEWDTM FPKVEDINAV TPTFGIASSP QGGILFPTPS  199
SEQ_ID_NO_234   LMDE------ ---------- ---------- ---------- ----------  147
SEQ_ID_NO_236   LVDE------ ---------- ---------- ---------- ----------  146
SEQ_ID_NO_241   RRKP------ ---------- ---------- ---------- ----------  118
SEQ_ID_NO_242   TKEP------ ---------- ---------- ---------- ----------  131

SEQ_ID_NO_244   PHSFQGTPTF GQTPFSARVD RMDESVDMDQ SVDMDESE  237
SEQ_ID_NO_234   ---------- CQNGVDSKV- ---------- -----ELC  159
SEQ_ID_NO_236   ---------- GRRGIDPKI- ---------- -----EFR  158
SEQ_ID_NO_241   ---------- GRGLLTATGG ---------- -----VTC  131
SEQ_ID_NO_242   ---------- GR-------- ---------- --------  133
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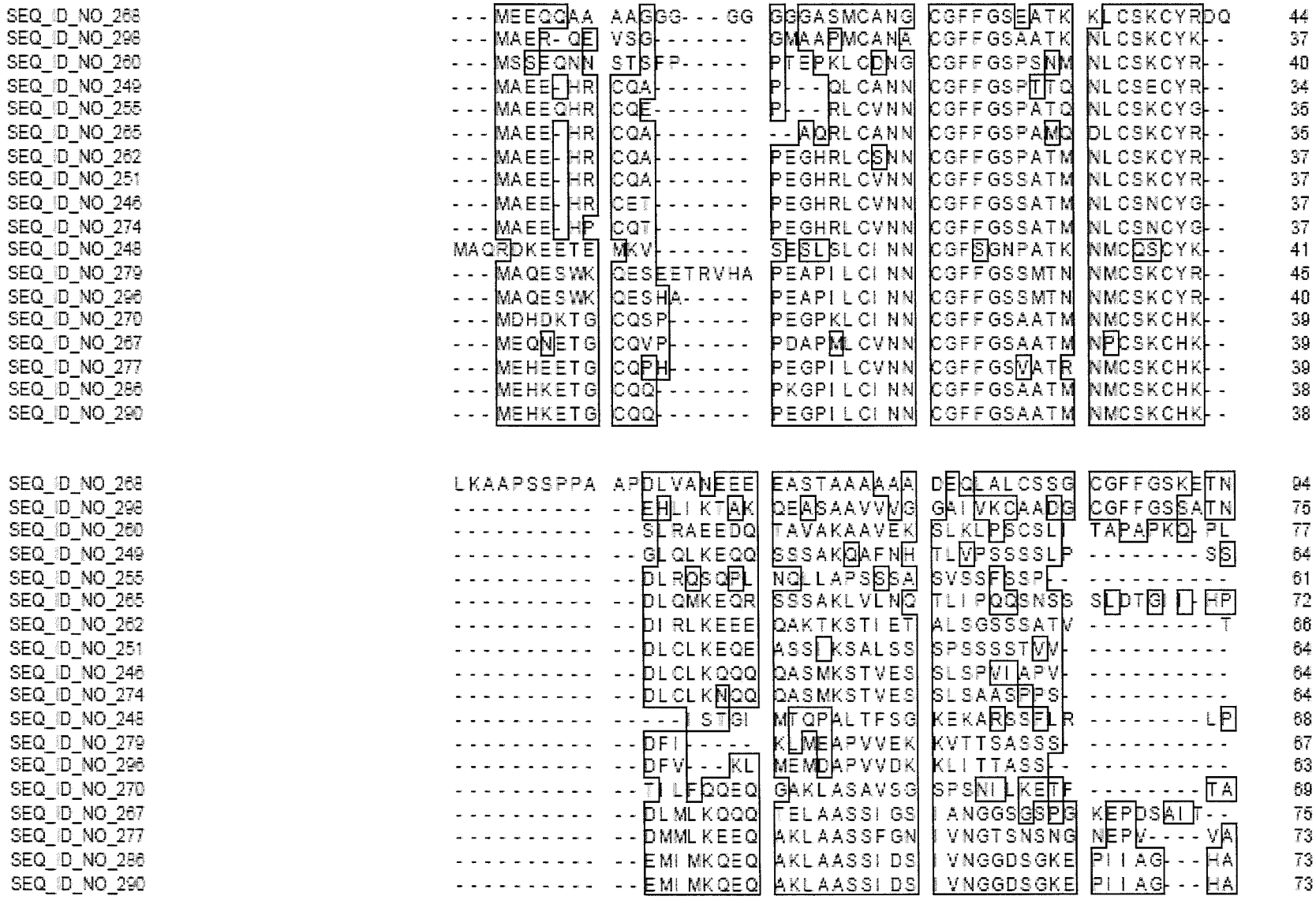

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Figure 11 (continued)

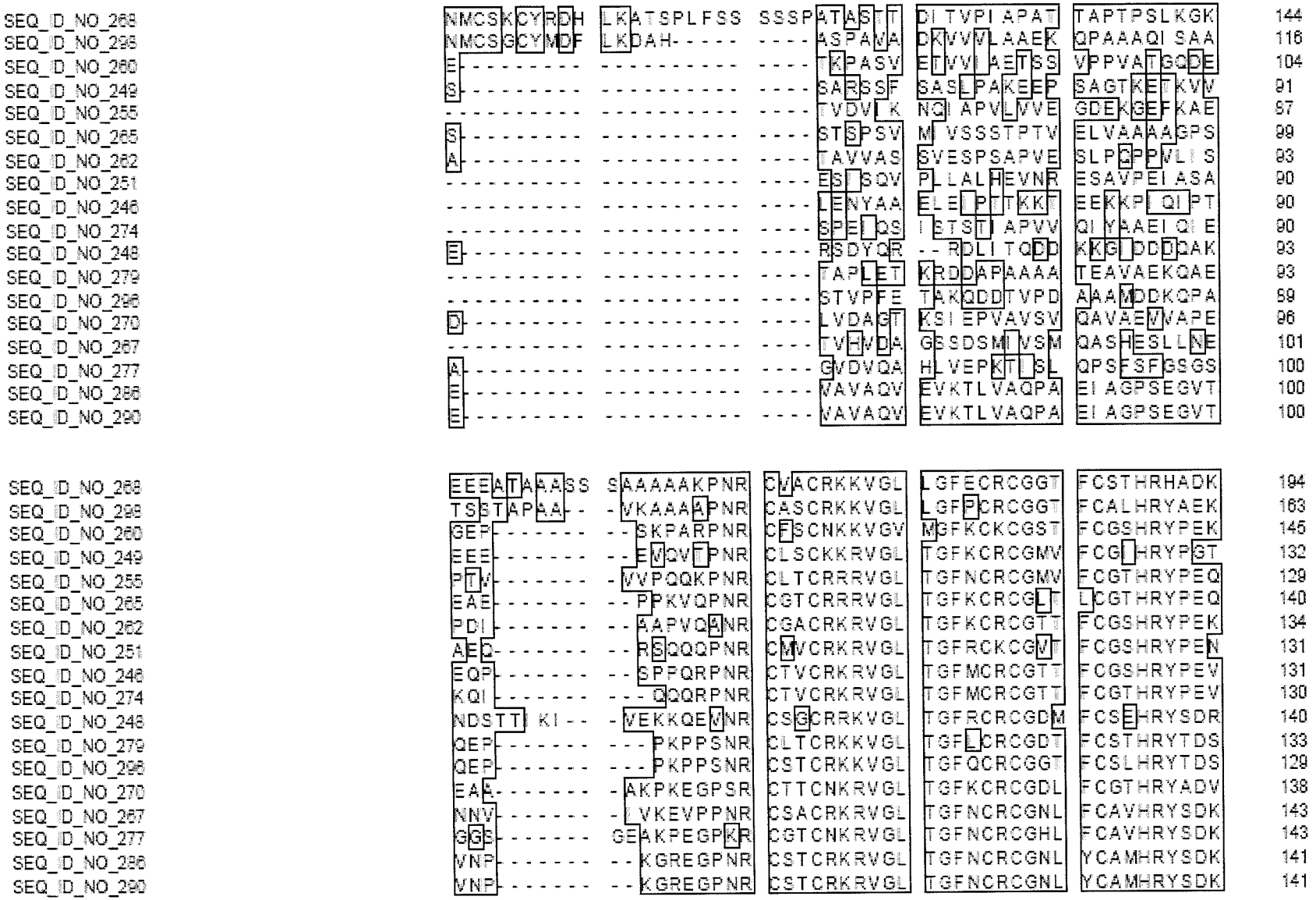


Figure 11 (continued)

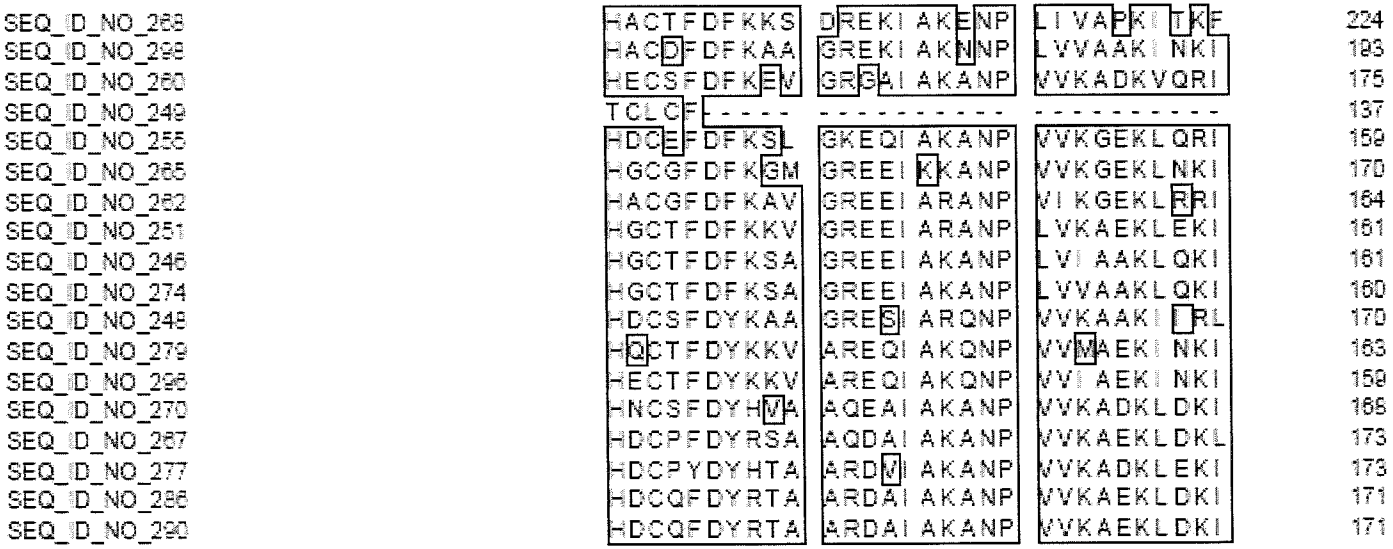


Figure 12

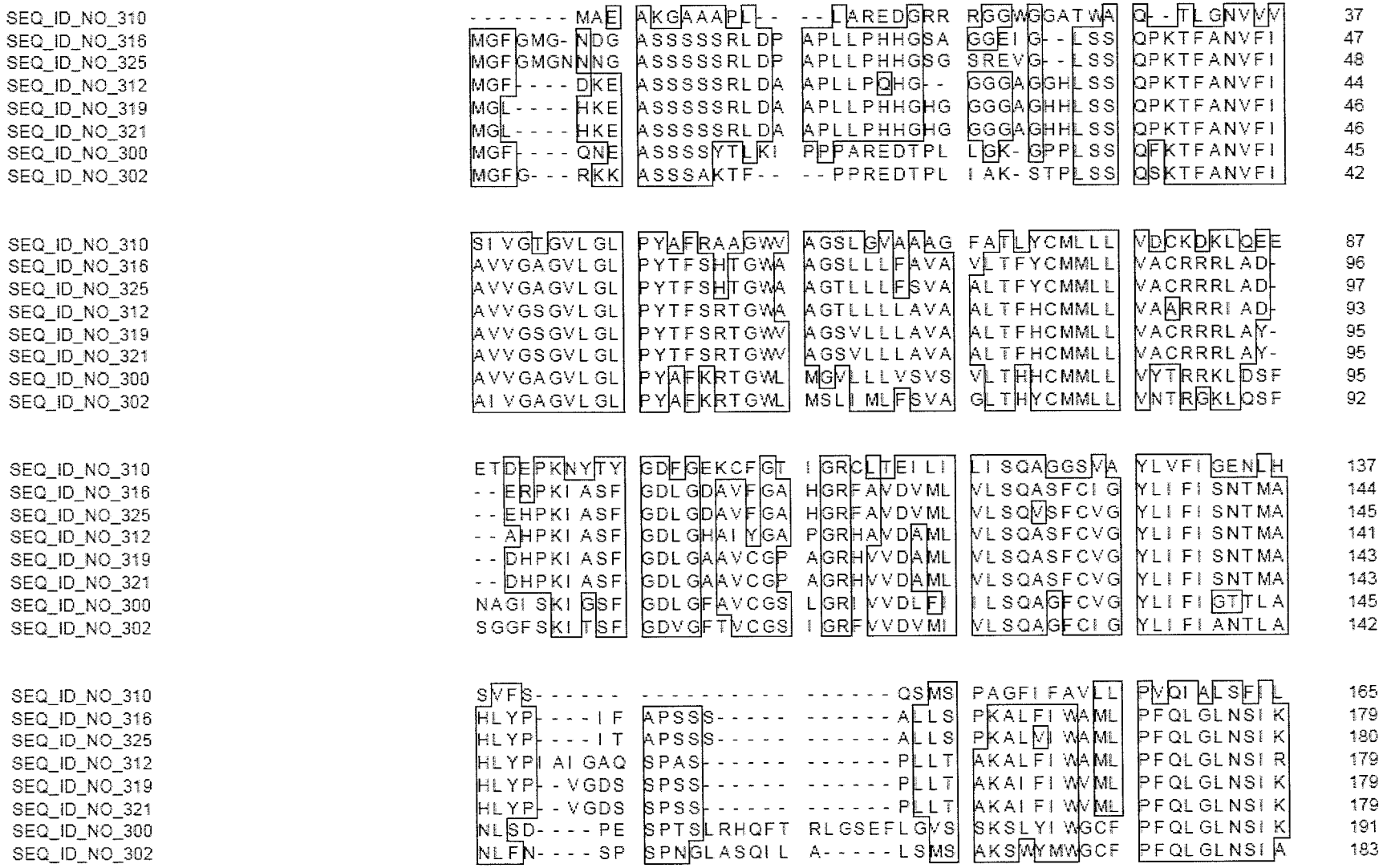

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Figure 12 (continued)

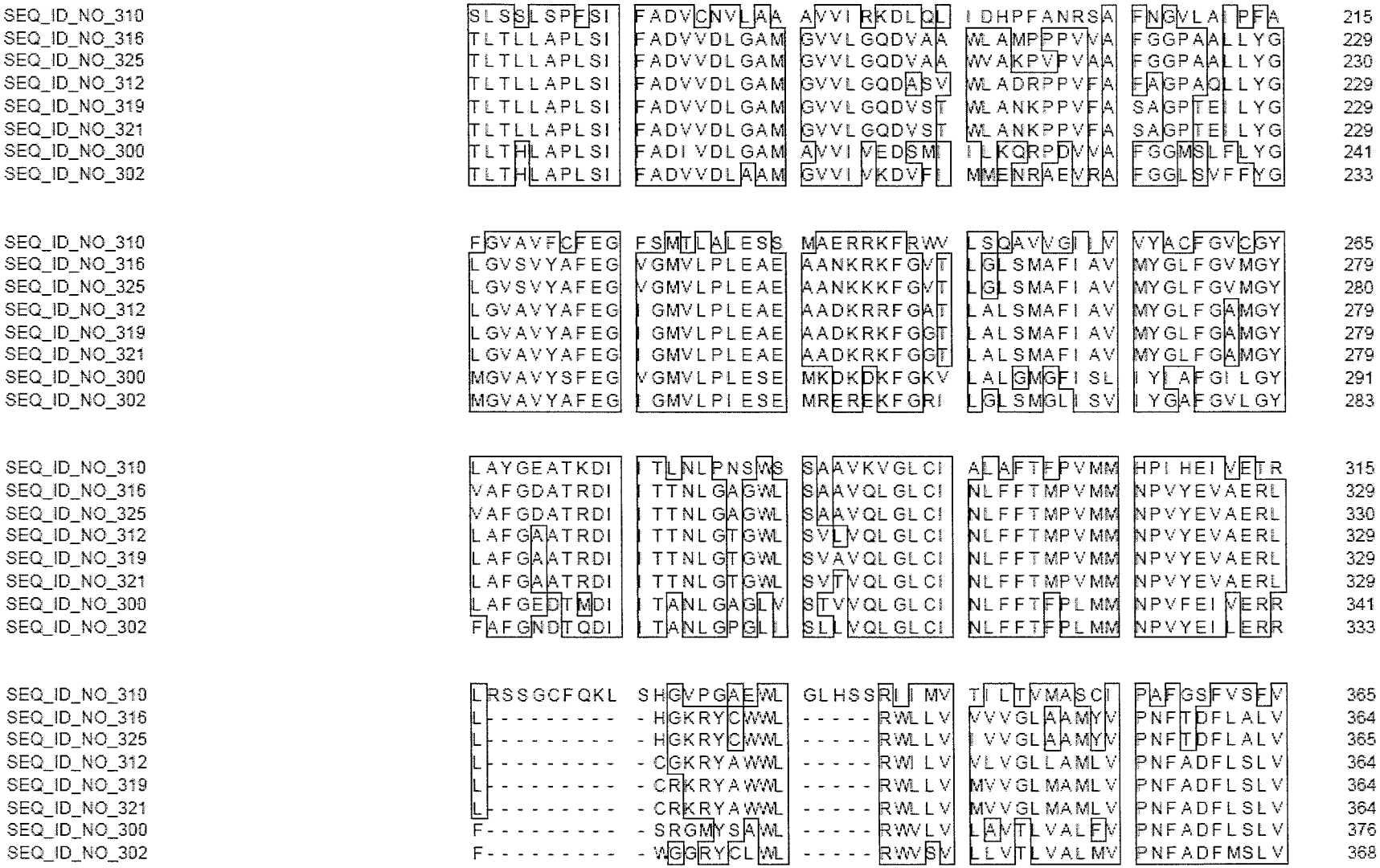


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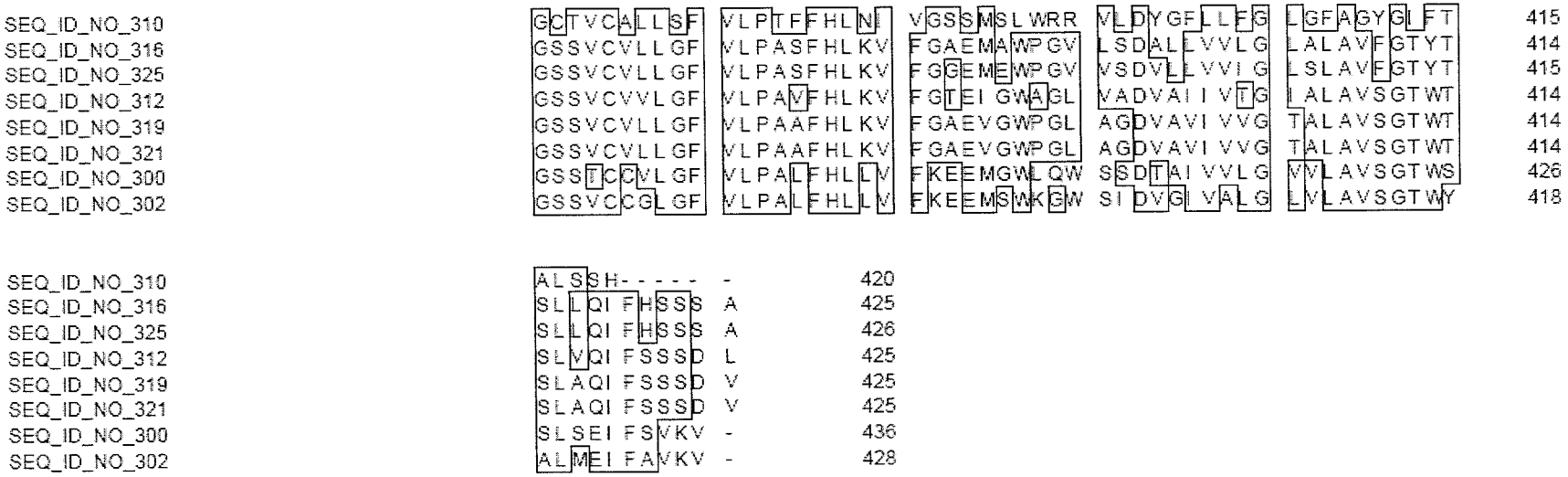


Figure 13

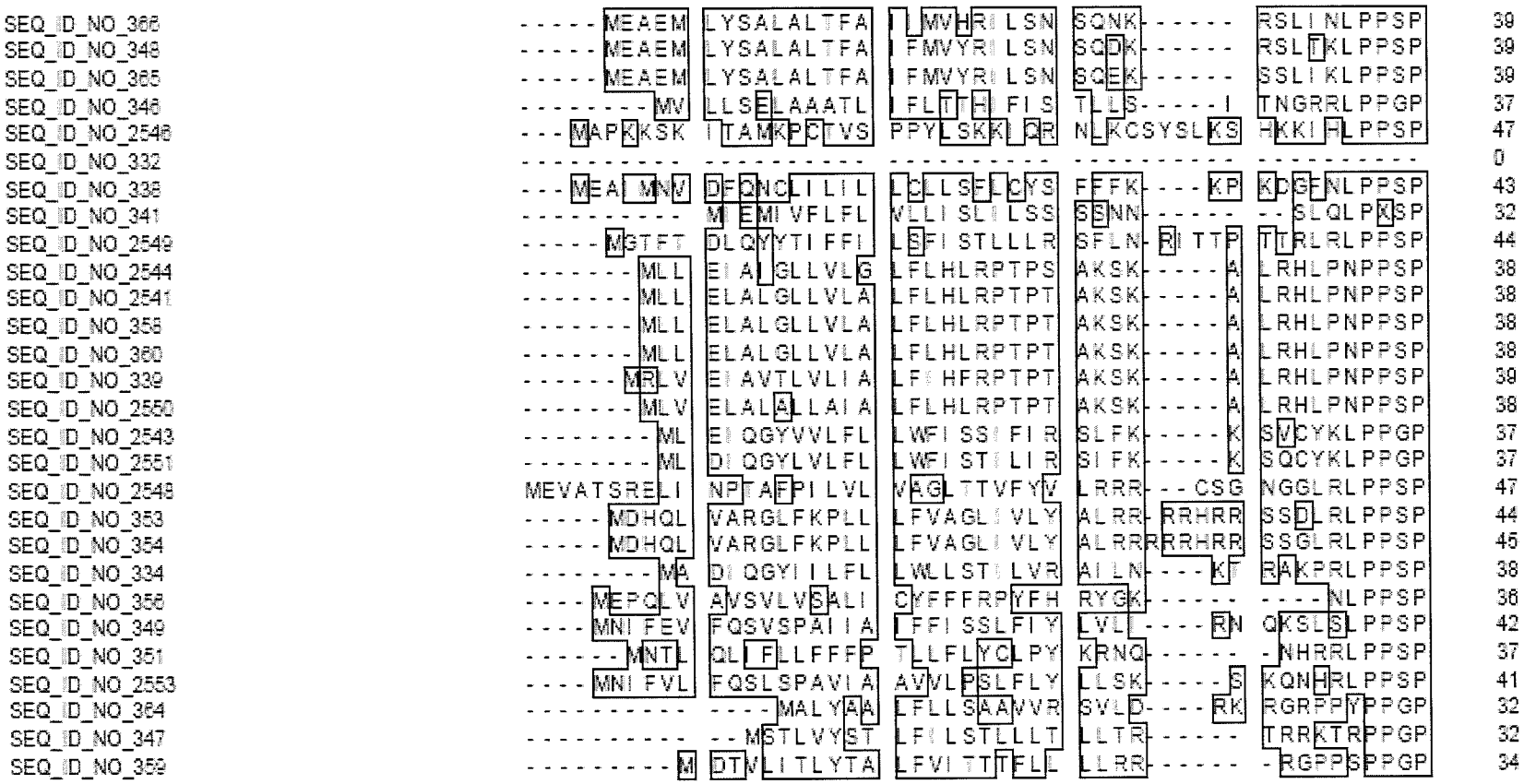

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SEQ_ID_NO_359

Figure 13 (continued)

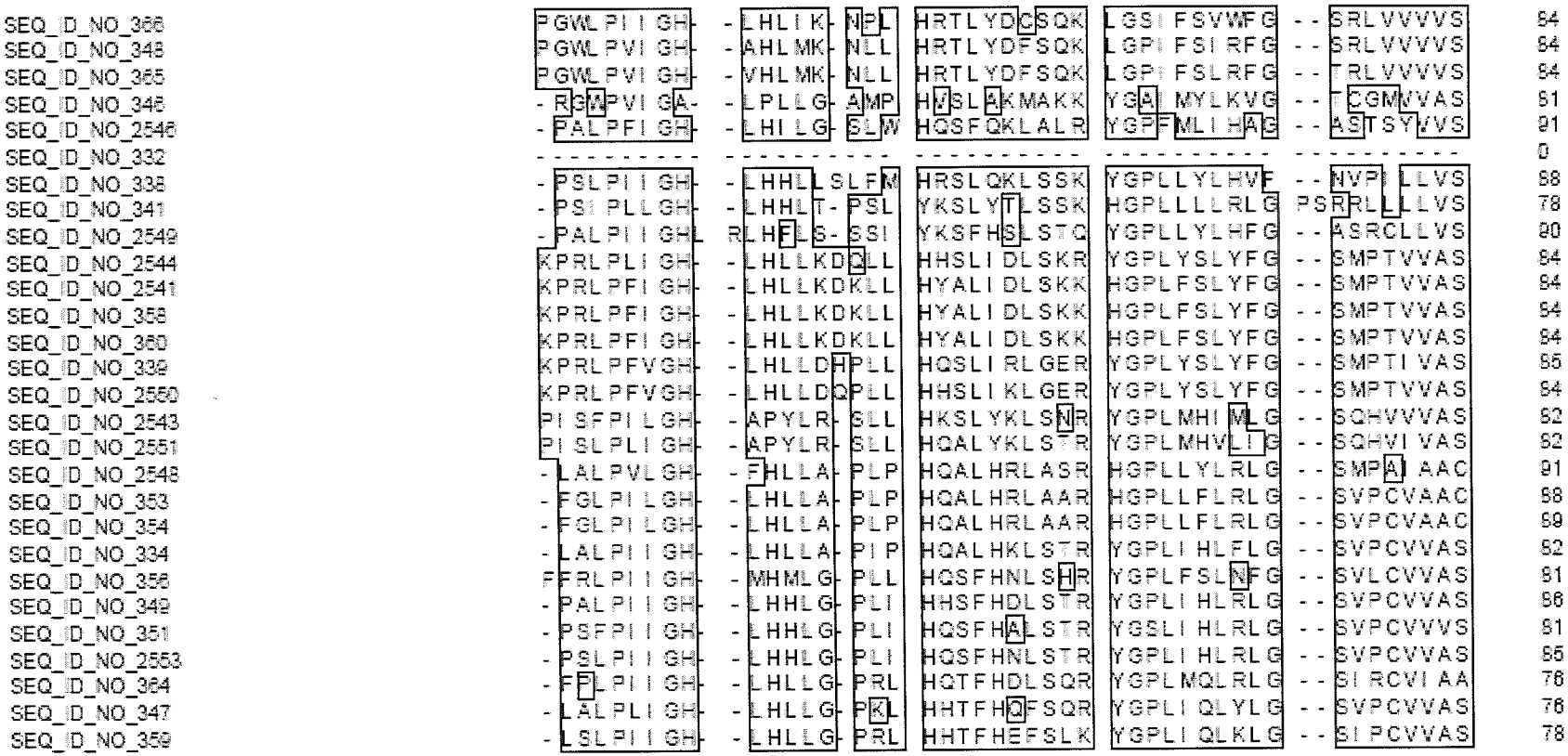


Figure 13 (continued)

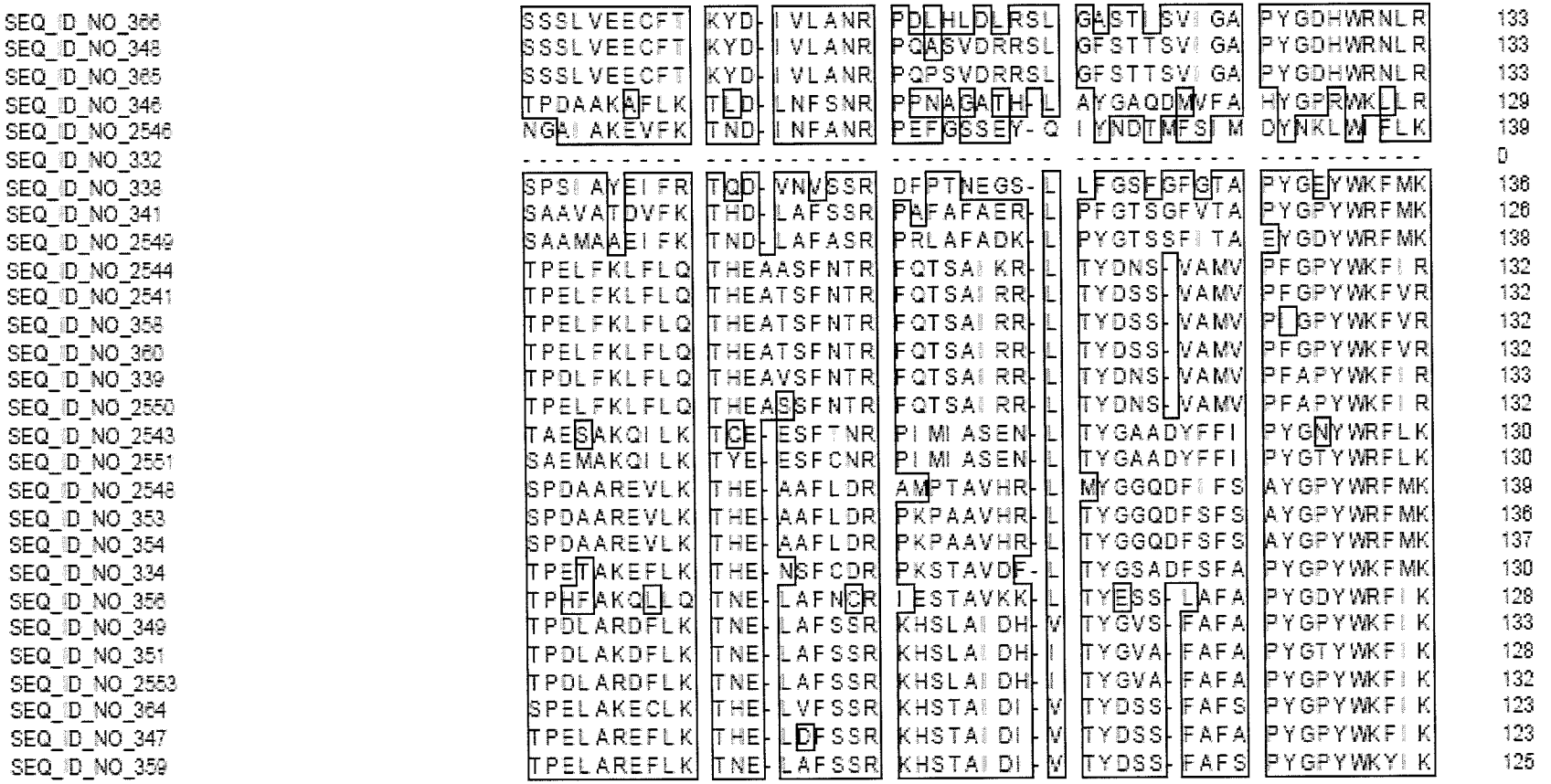


Figure 13 (continued)

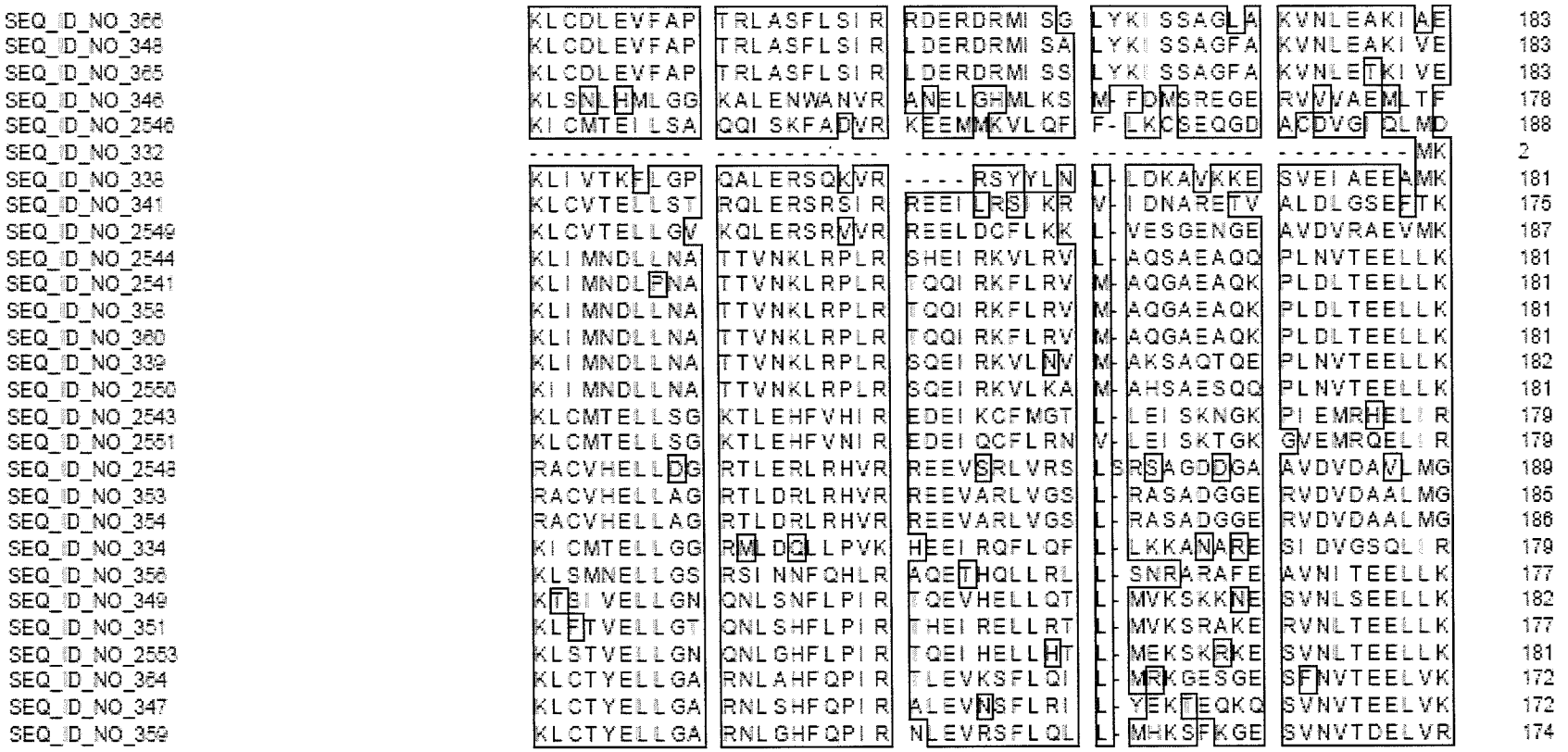


Figure 13 (continued)

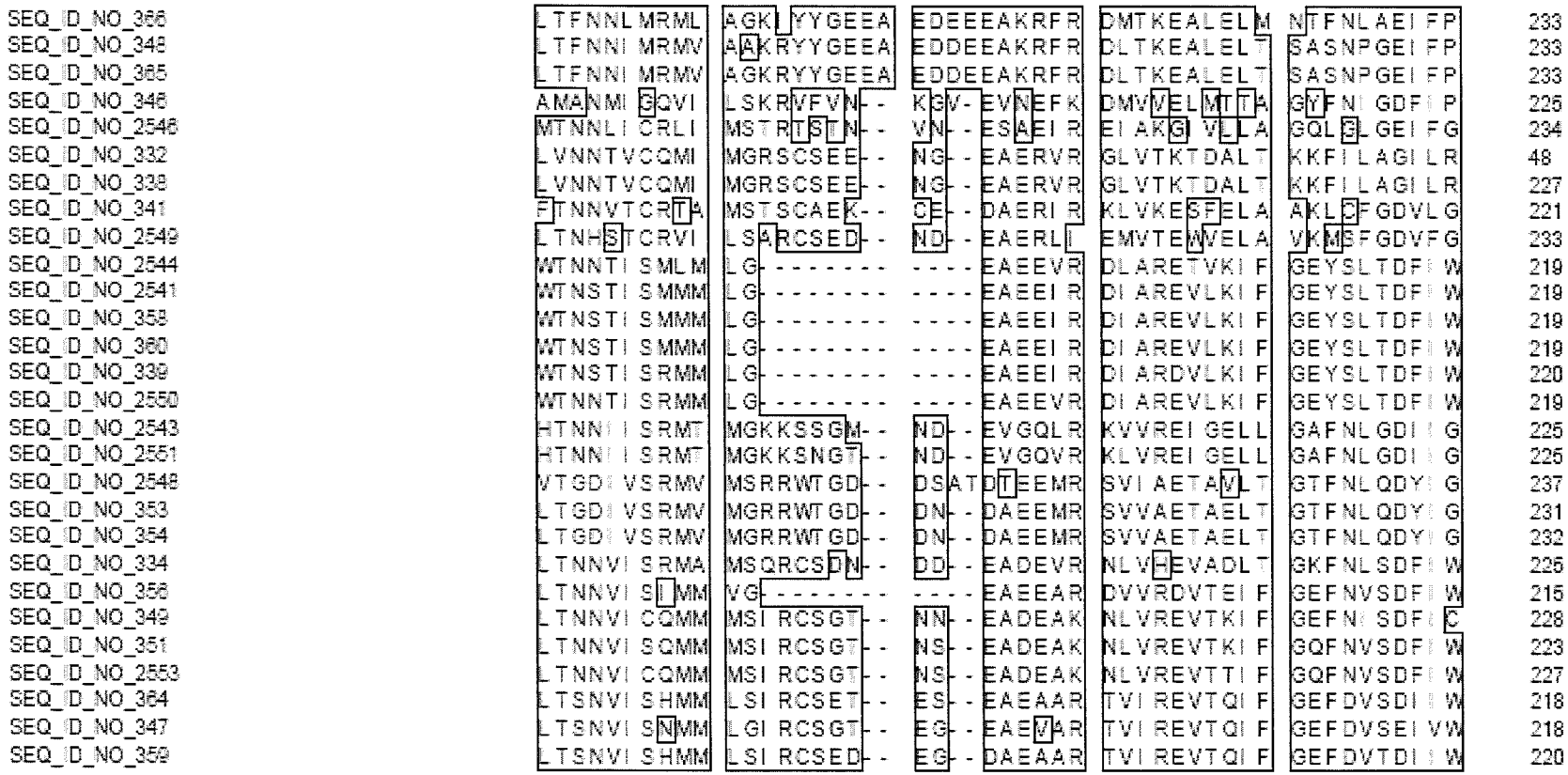


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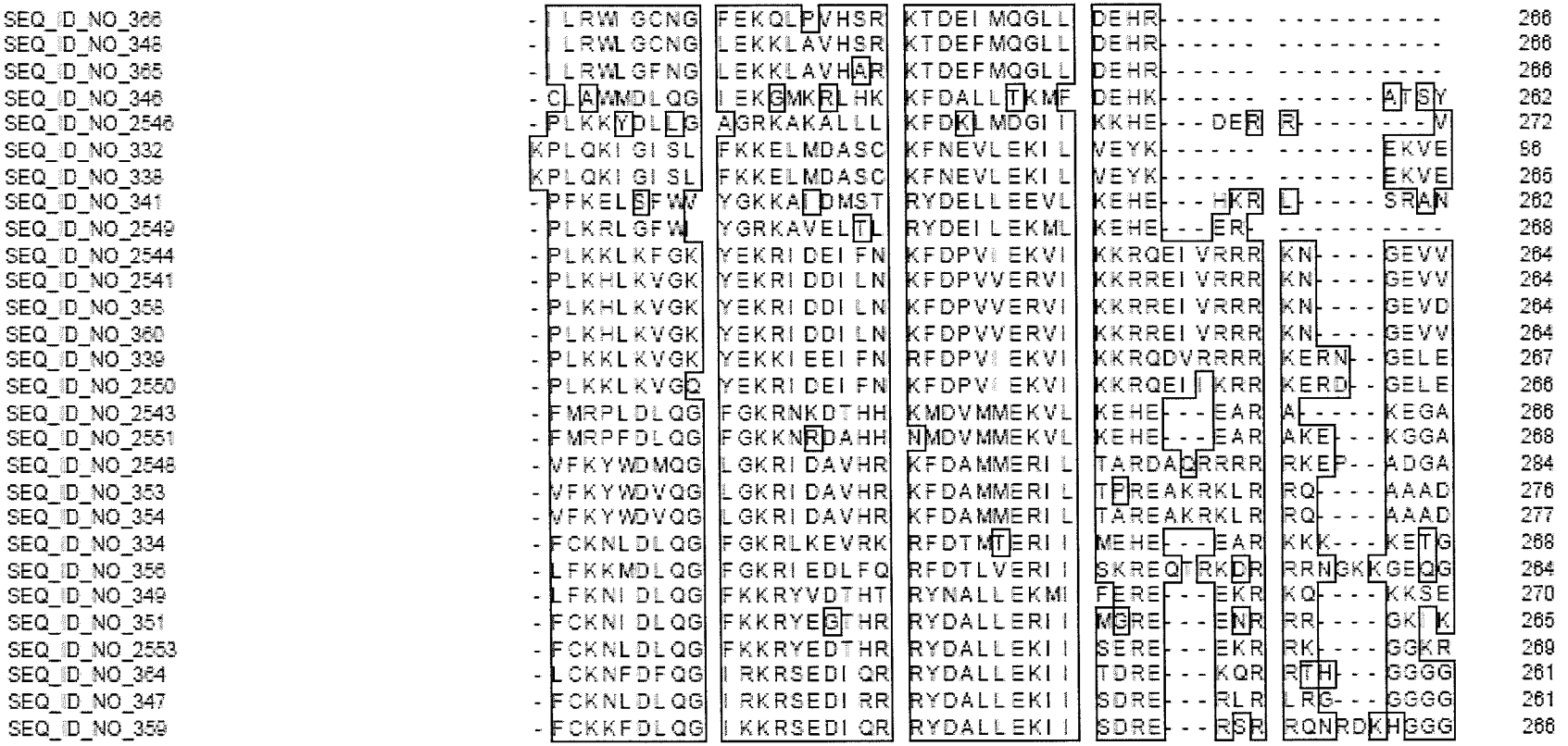


Figure 13 (continued)

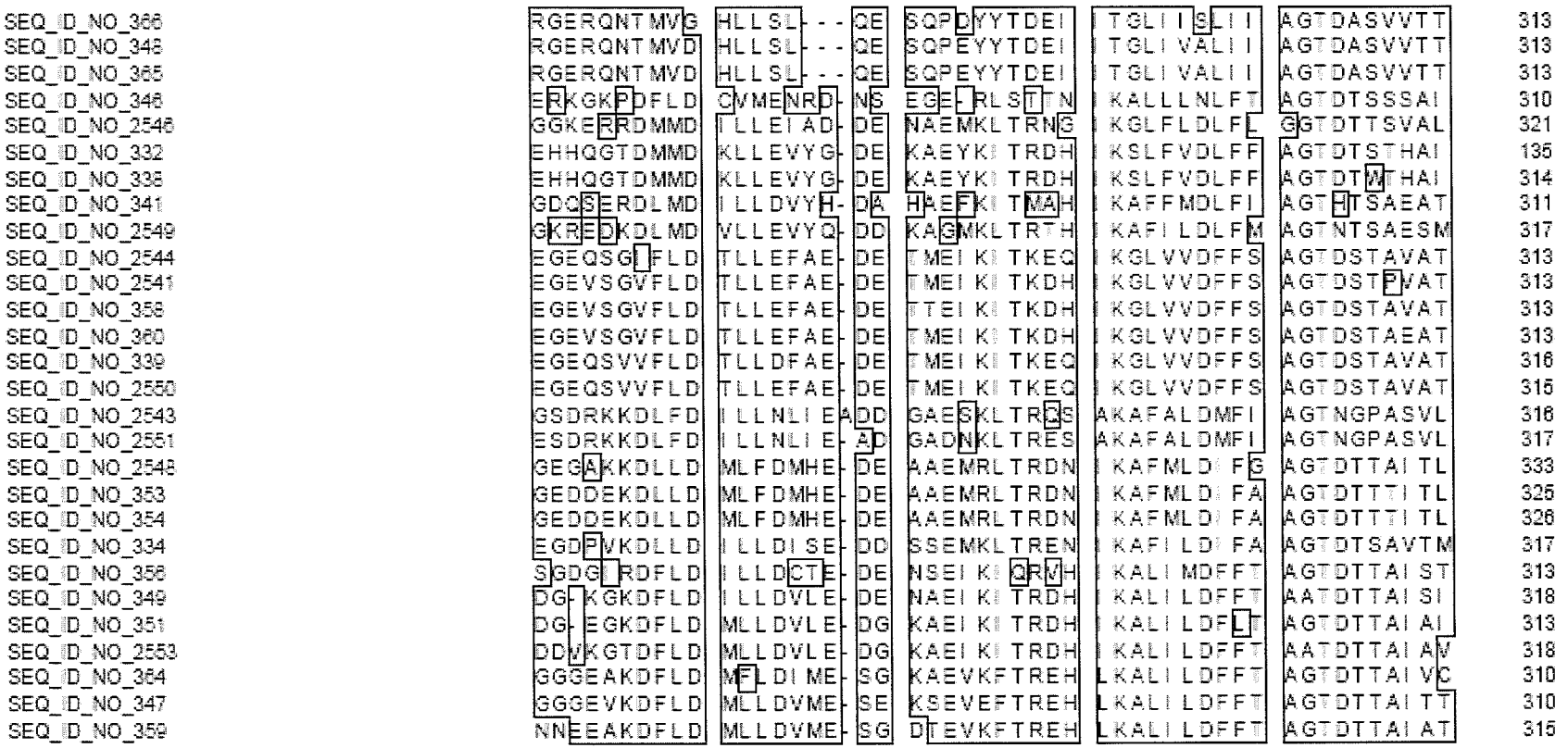


Figure 13 (continued)

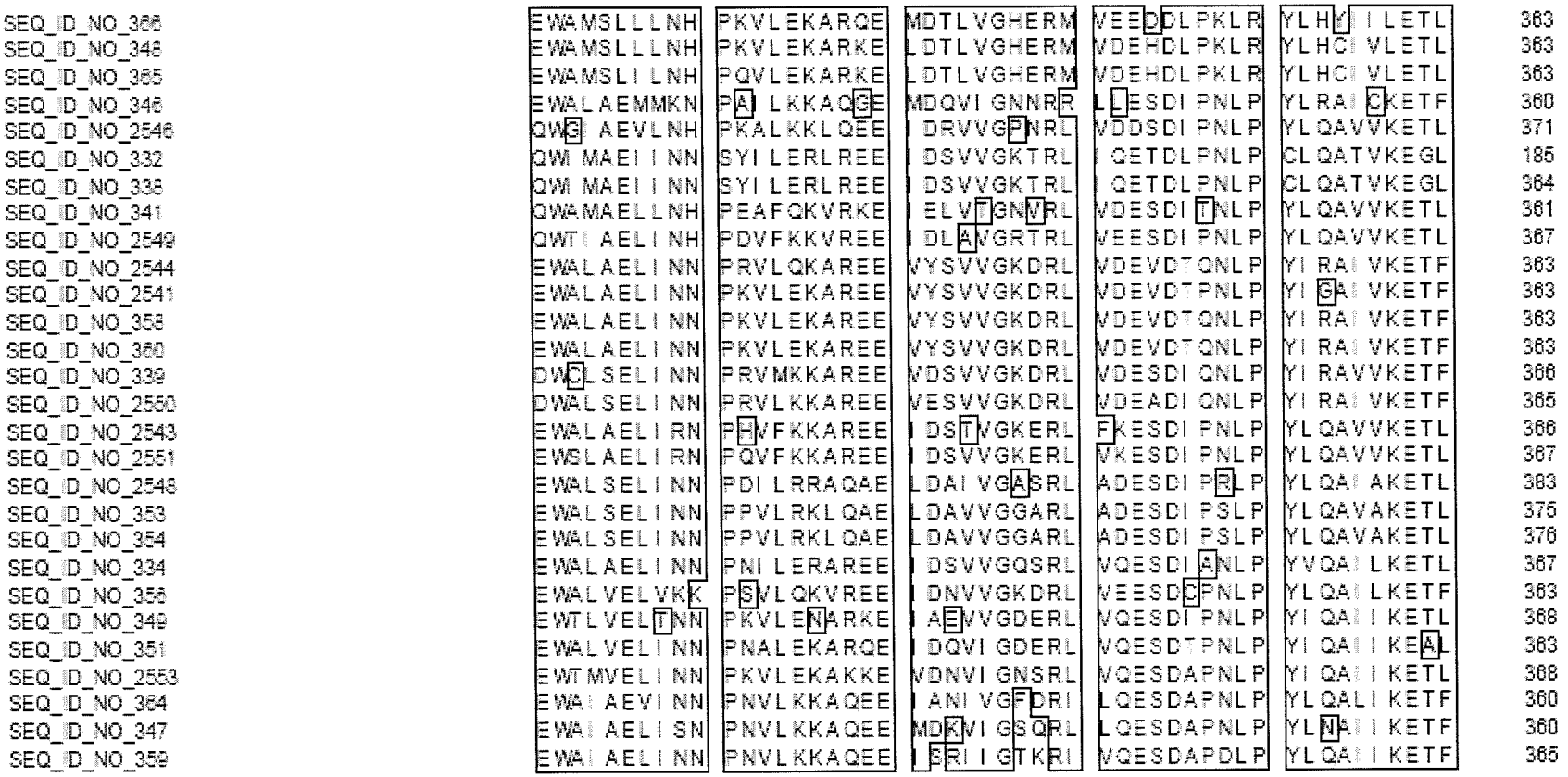


Figure 13 (continued)

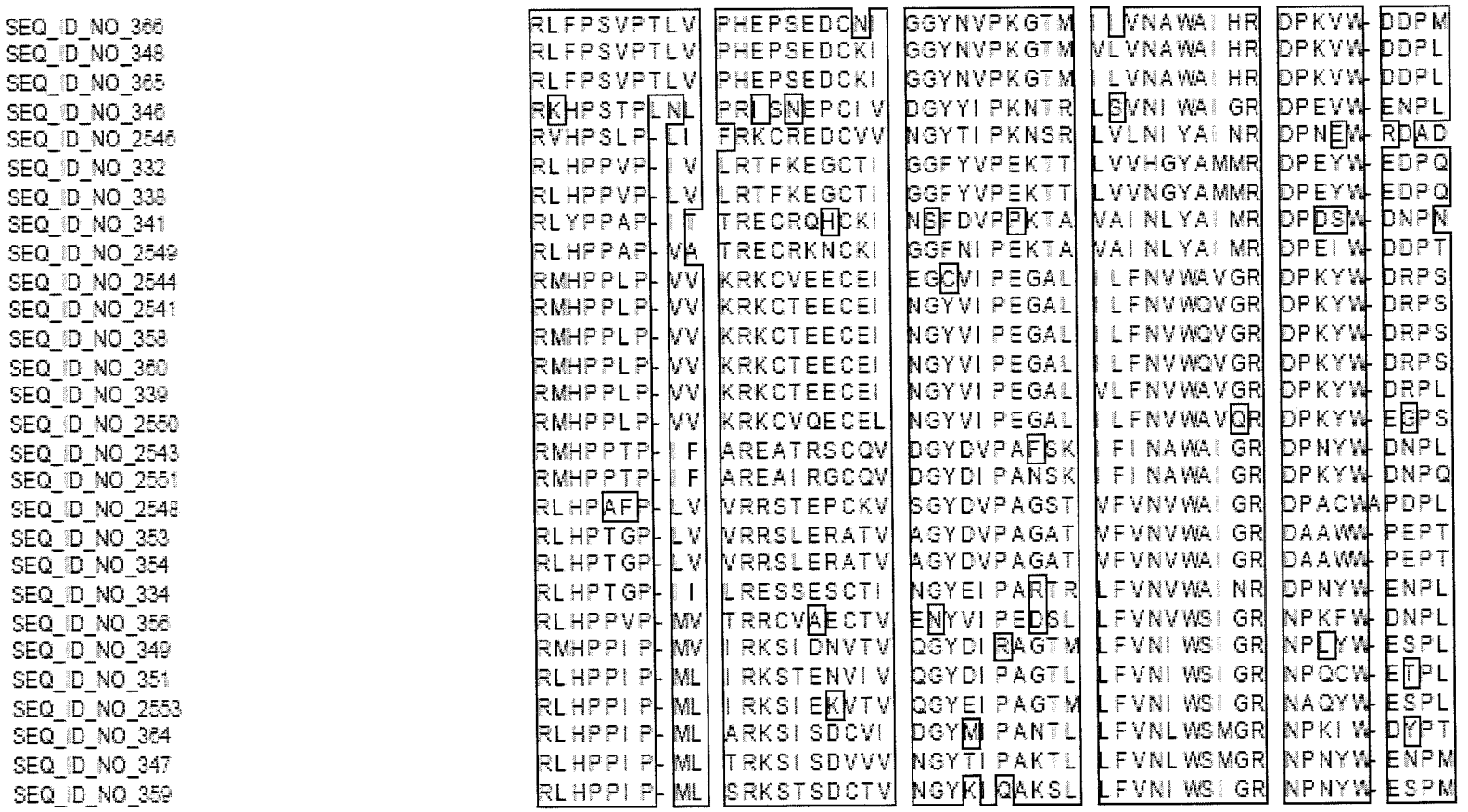


Figure 13 (continued)

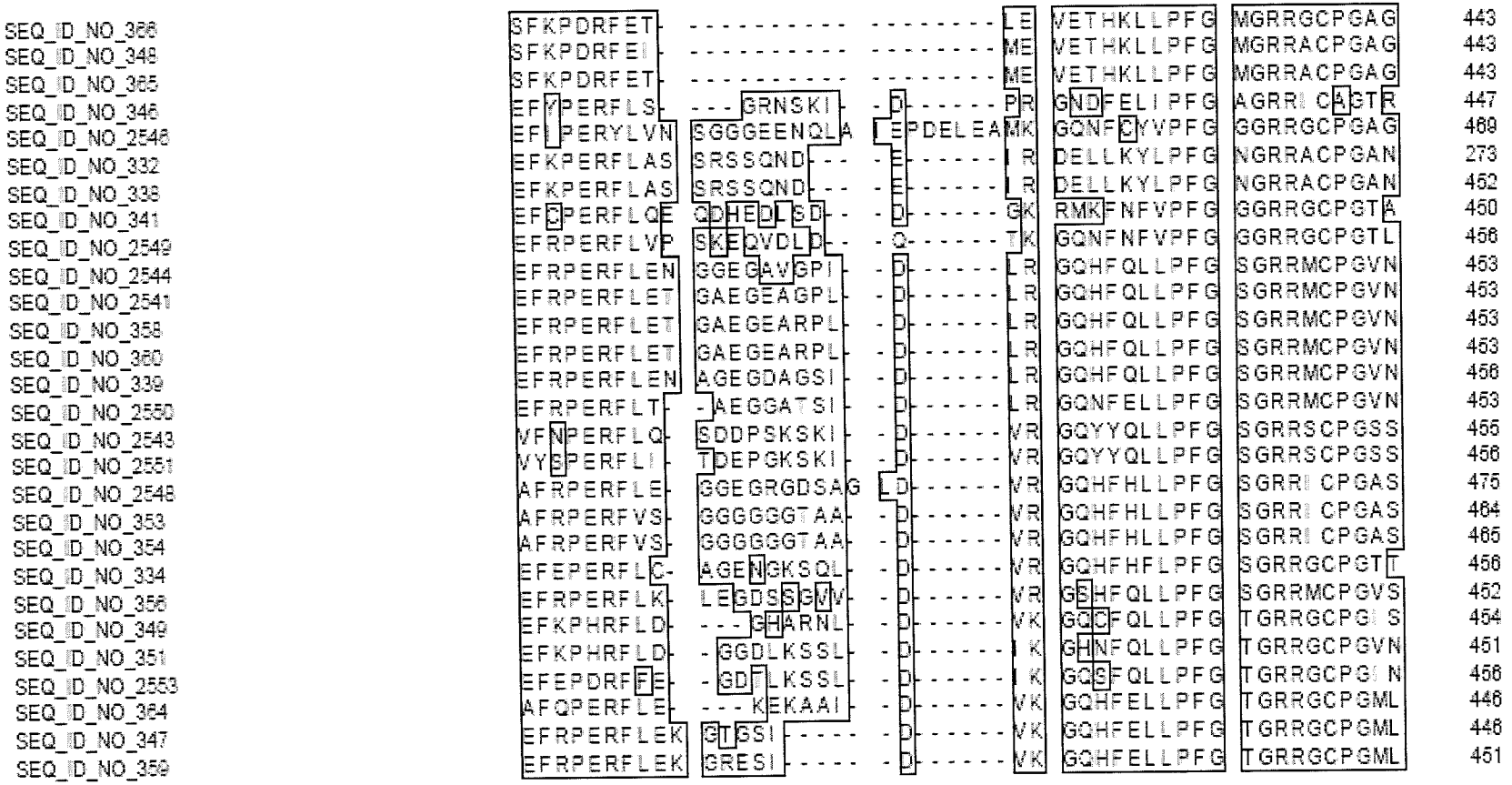


Figure 13 (continued)

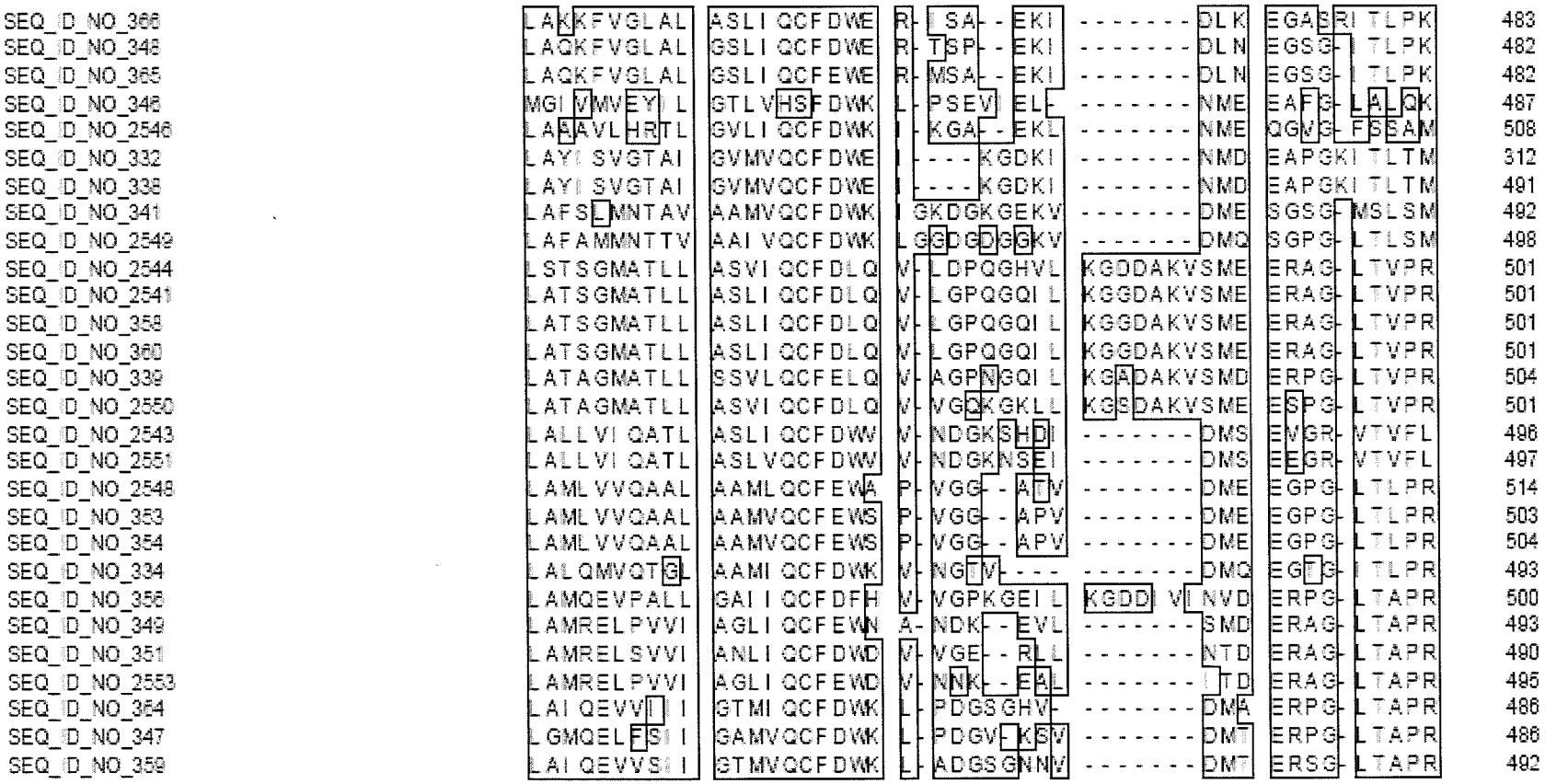


Figure 13 (continued)

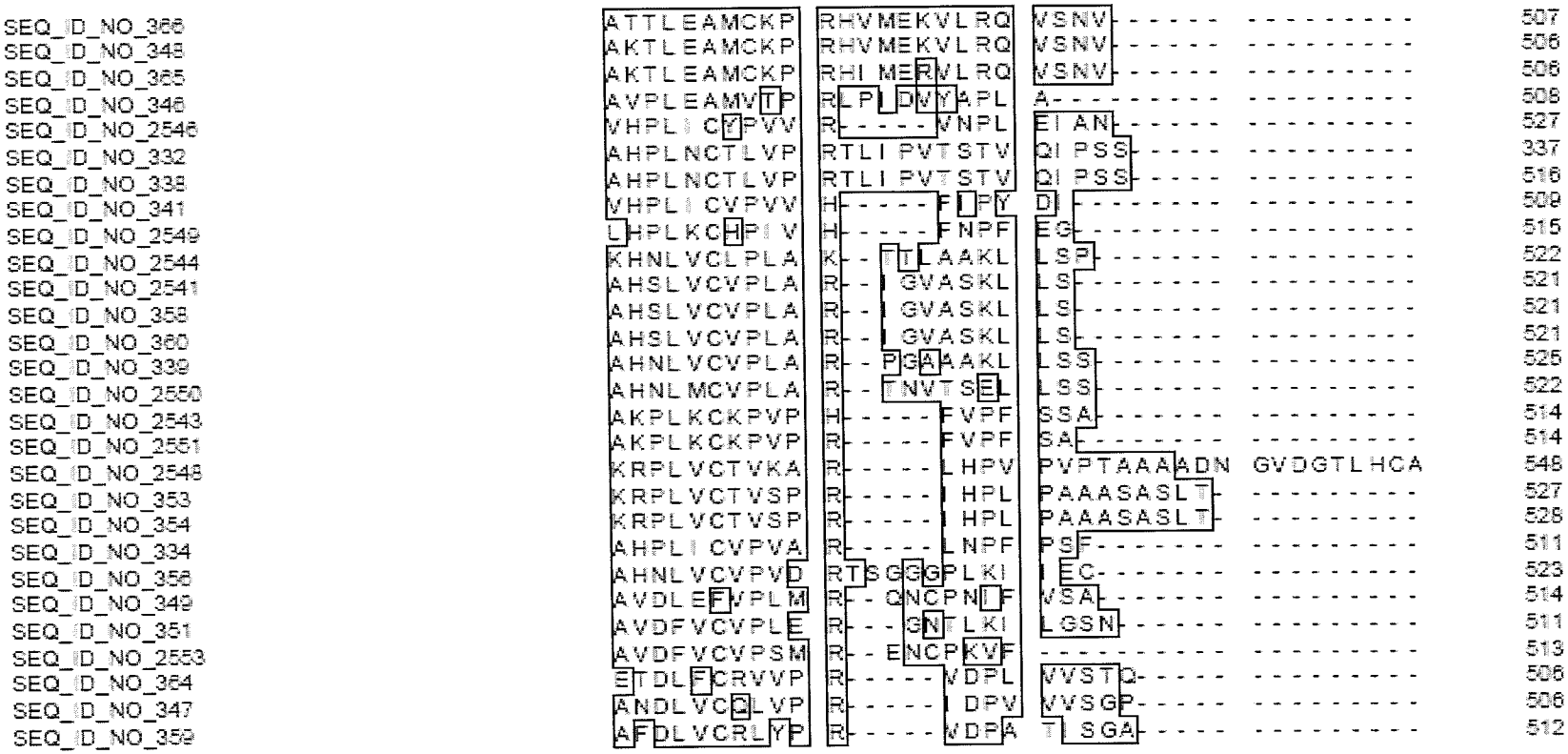


Figure 14

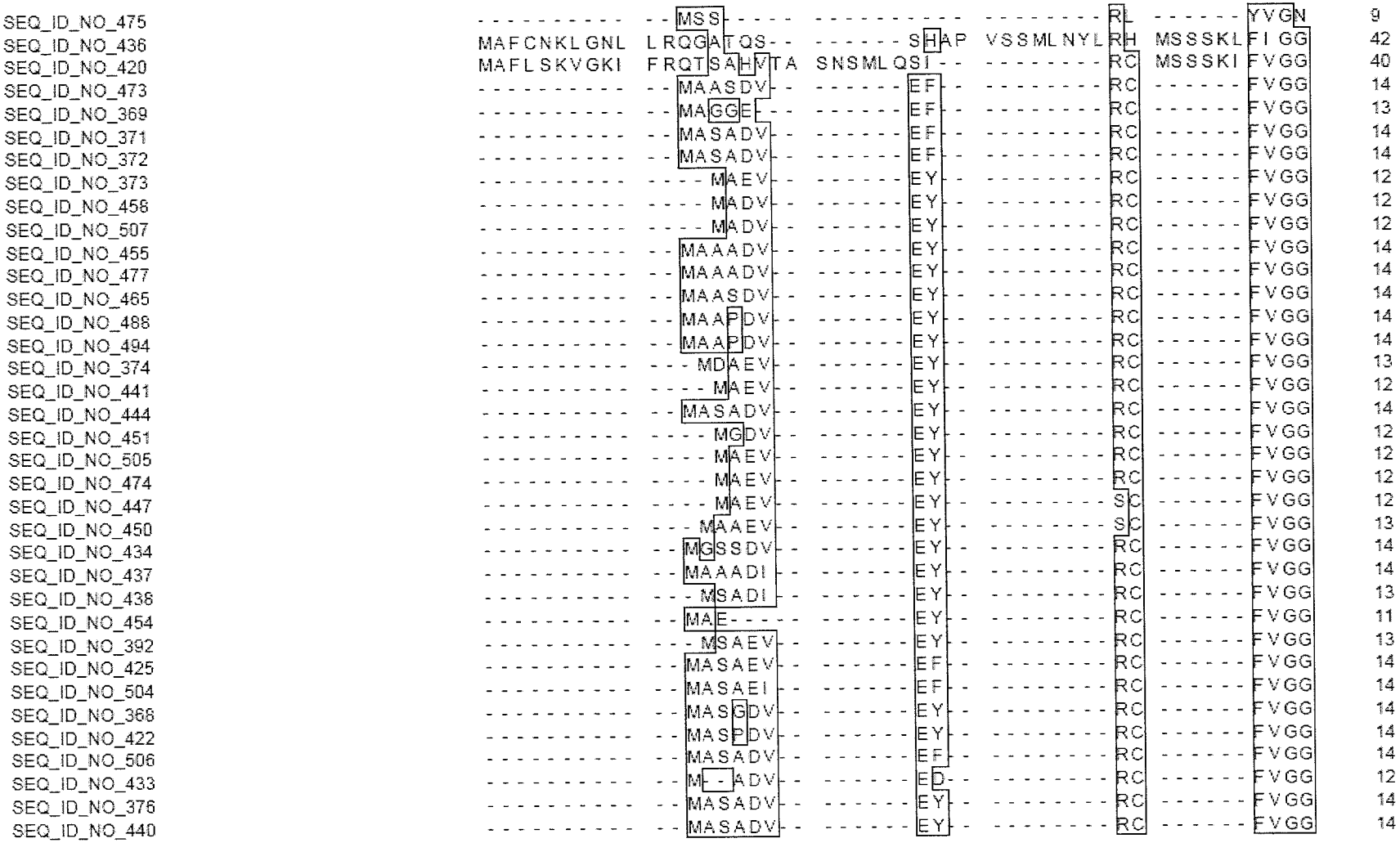

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SEQ_ID_NO_440

Figure 14 (continued)

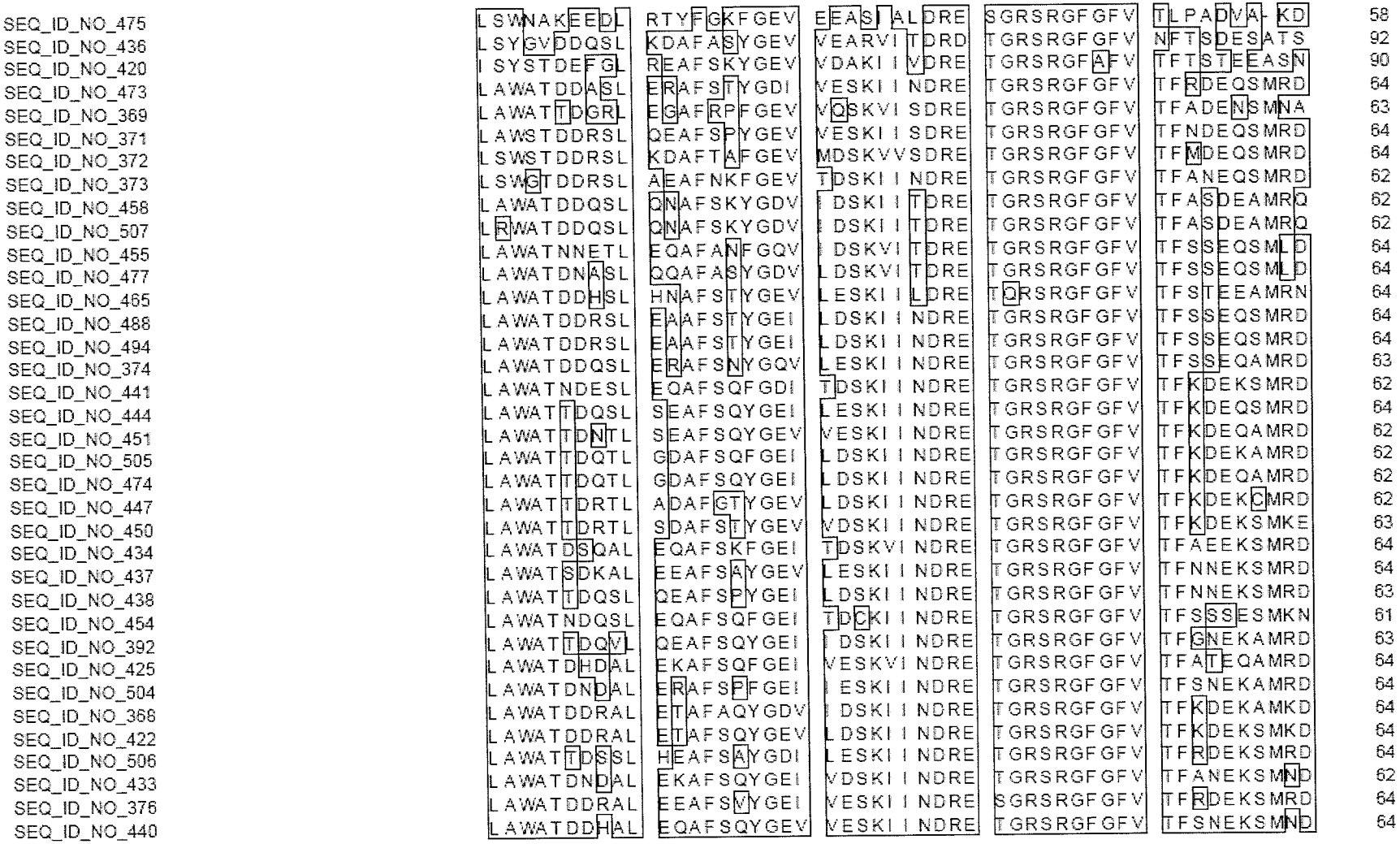


Figure 14 (continued)

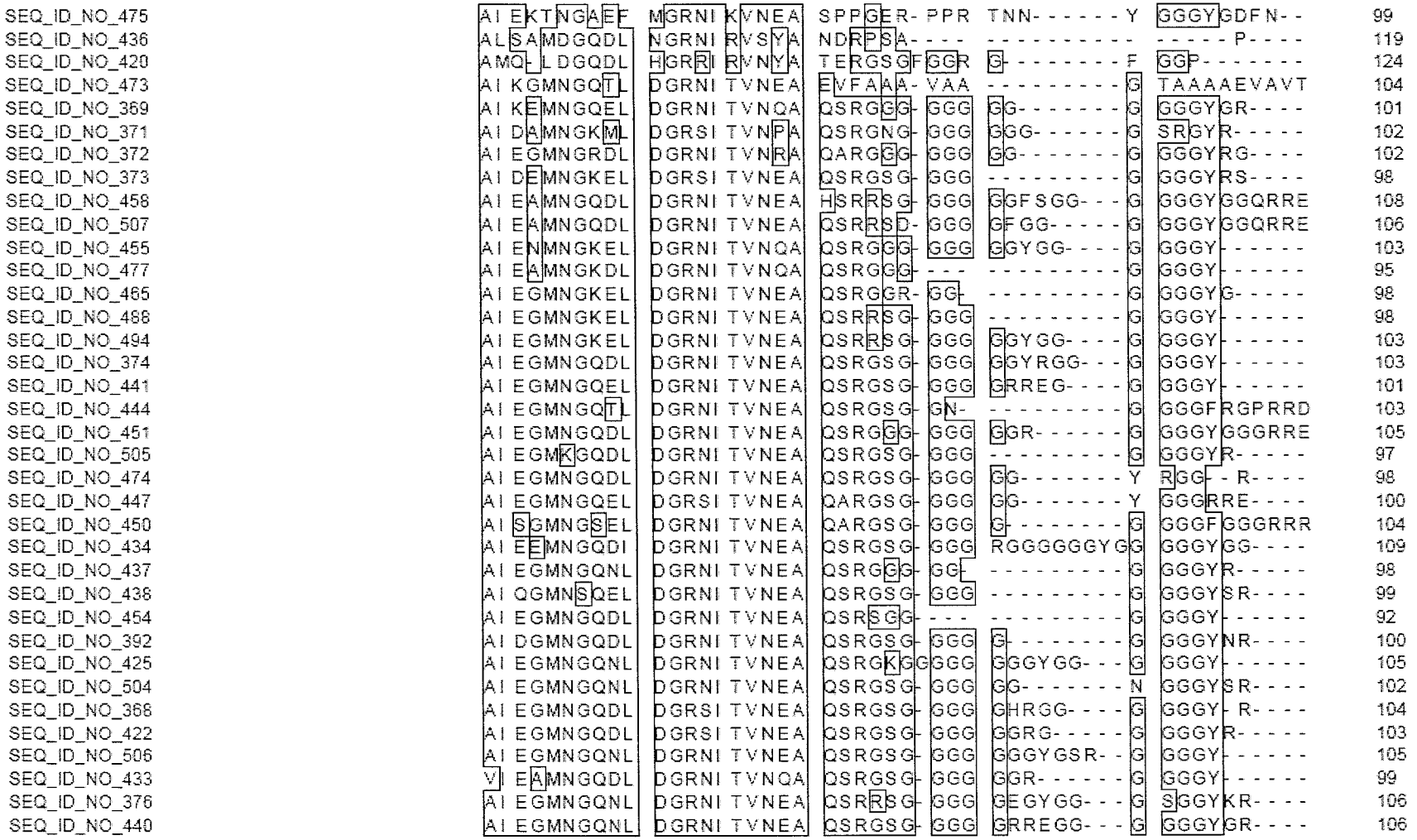
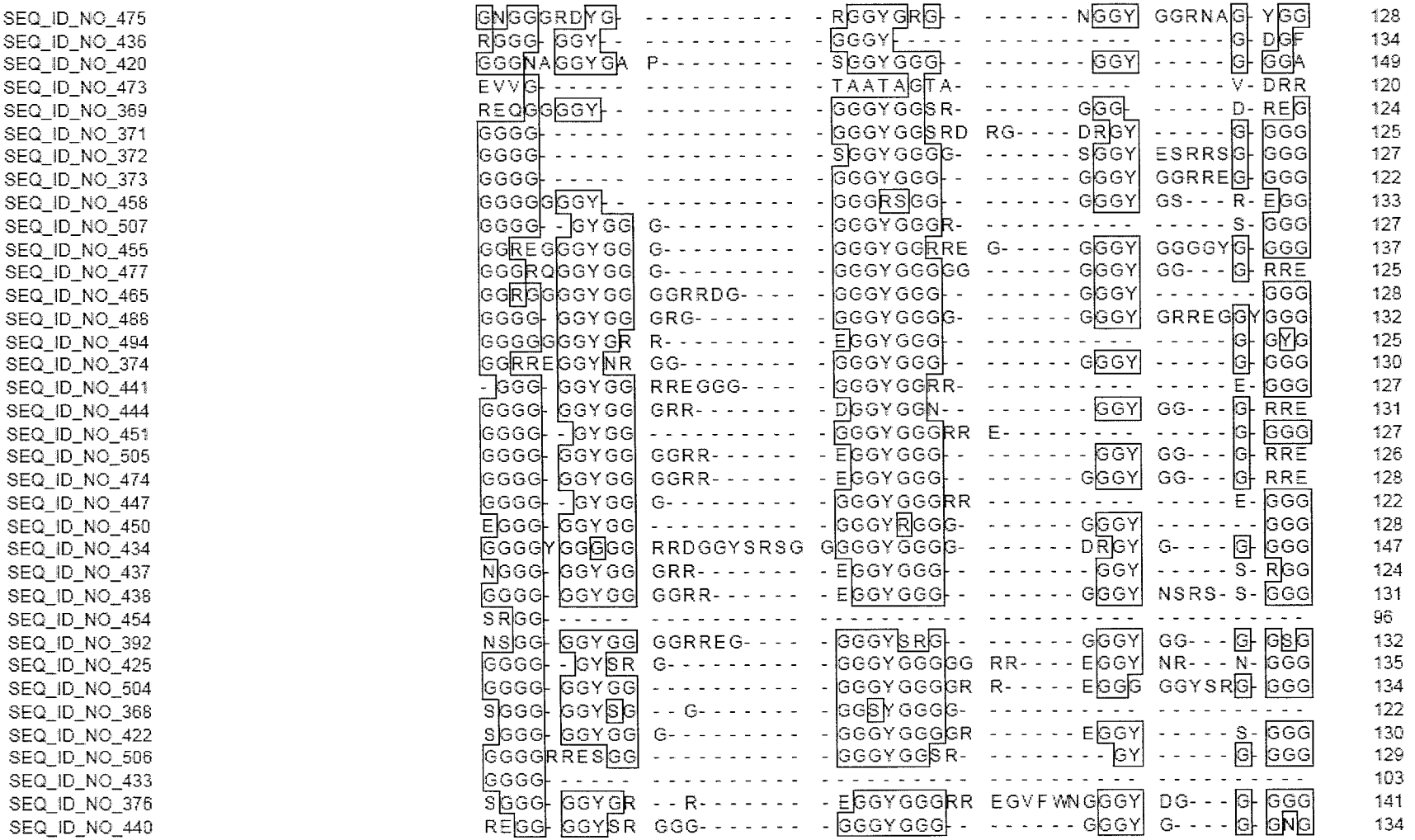


Figure 14 (continued)



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Figure 14 (continued)



Figure 14 (continued)

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SEQ_ID_NO_420   --SSWWLWRR  WLQCSRWWLR  RWLILWWKCC  WWRLWR   208
SEQ_ID_NO_473   ----SEGWAS  ----------  ----------  ------   140
SEQ_ID_NO_369   --PSSGNWRN  DRQPEY----  ----------  ------   162
SEQ_ID_NO_371   --SEGGSWRR  ----------  ----------  ------   155
SEQ_ID_NO_372   GVSDDGGWRS  ----------  ----------  ------   181
SEQ_ID_NO_373   --NSDGNWRN  ----------  ----------  ------   163
SEQ_ID_NO_458   --SGGGNWRE  ----------  ----------  ------   171
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SEQ_ID_NO_477   --DSGGNWRN  ----------  ----------  ------   158
SEQ_ID_NO_465   ---SDGNWRN  ----------  ----------  ------   156
SEQ_ID_NO_488   --DSGGNWRN  ----------  ----------  ------   163
SEQ_ID_NO_494   --DSGGNWRN  ----------  ----------  ------   153
SEQ_ID_NO_374   --NSDSDWRN  ----------  ----------  ------   168
SEQ_ID_NO_441   ----GGGGSR  W---------  ----------  ------   157
SEQ_ID_NO_444   --ASDGNWRN  ----------  ----------  ------   164
SEQ_ID_NO_451   GGSSDGNWRN  ----------  ----------  ------   178
SEQ_ID_NO_505   --GSEG----  ----------  ----------  ------   152
SEQ_ID_NO_474   --GSEGNWRN  ----------  ----------  ------   156
SEQ_ID_NO_447   --GGYGGGGR  Y---------  ----------  ------   148
SEQ_ID_NO_450   --GGYGGGDR  Y---------  ----------  ------   162
SEQ_ID_NO_434   GADSGGNWRD  ----------  ----------  ------   190
SEQ_ID_NO_437   G-ASEGNWRS  ----------  ----------  ------   165
SEQ_ID_NO_438   --ESDGNWKN  ----------  ----------  ------   164
SEQ_ID_NO_454   --DSGGNWRN  ----------  ----------  ------   107
SEQ_ID_NO_392   GESEGGSWRS  ----------  ----------  ------   170
SEQ_ID_NO_425   GGSDGGSWRN  ----------  ----------  ------   182
SEQ_ID_NO_504   GGSEGGSWRS  ----------  ----------  ------   178
SEQ_ID_NO_368   ----GGGW--  ----------  ----------  ------   148
SEQ_ID_NO_422   ----GGGW--  ----------  ----------  ------   166
SEQ_ID_NO_506   --SDGGSWRN  ----------  ----------  ------   167
SEQ_ID_NO_433   ----GG----  ----------  ----------  ------   105
SEQ_ID_NO_376   ----GG----  ----------  ----------  ------   161
SEQ_ID_NO_440   -DSDGGNWRS  ----------  ----------  ------   166
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Figure 15

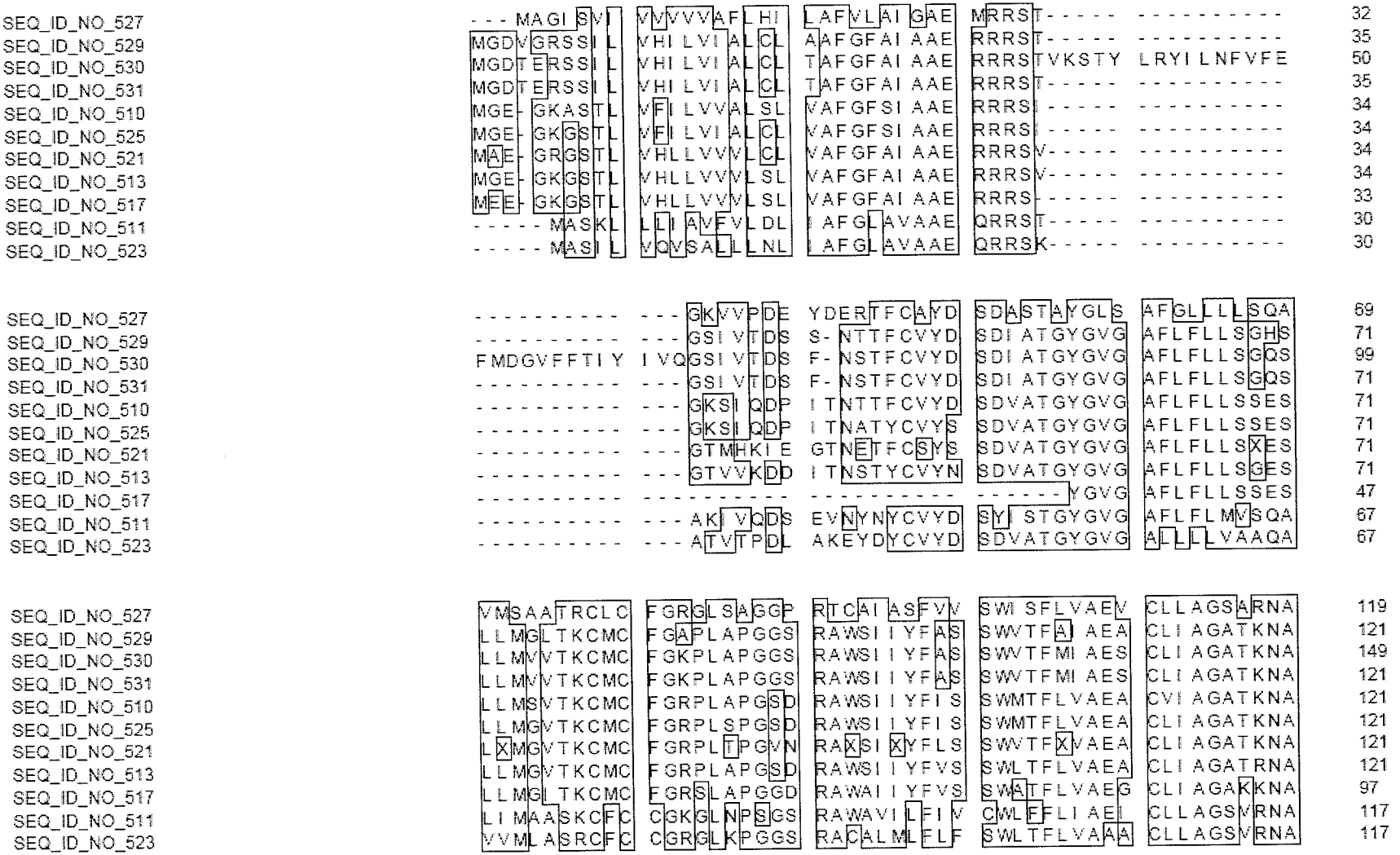

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SEQ_ID_NO_511
SEQ_ID_NO_523

Figure 15 (continued)

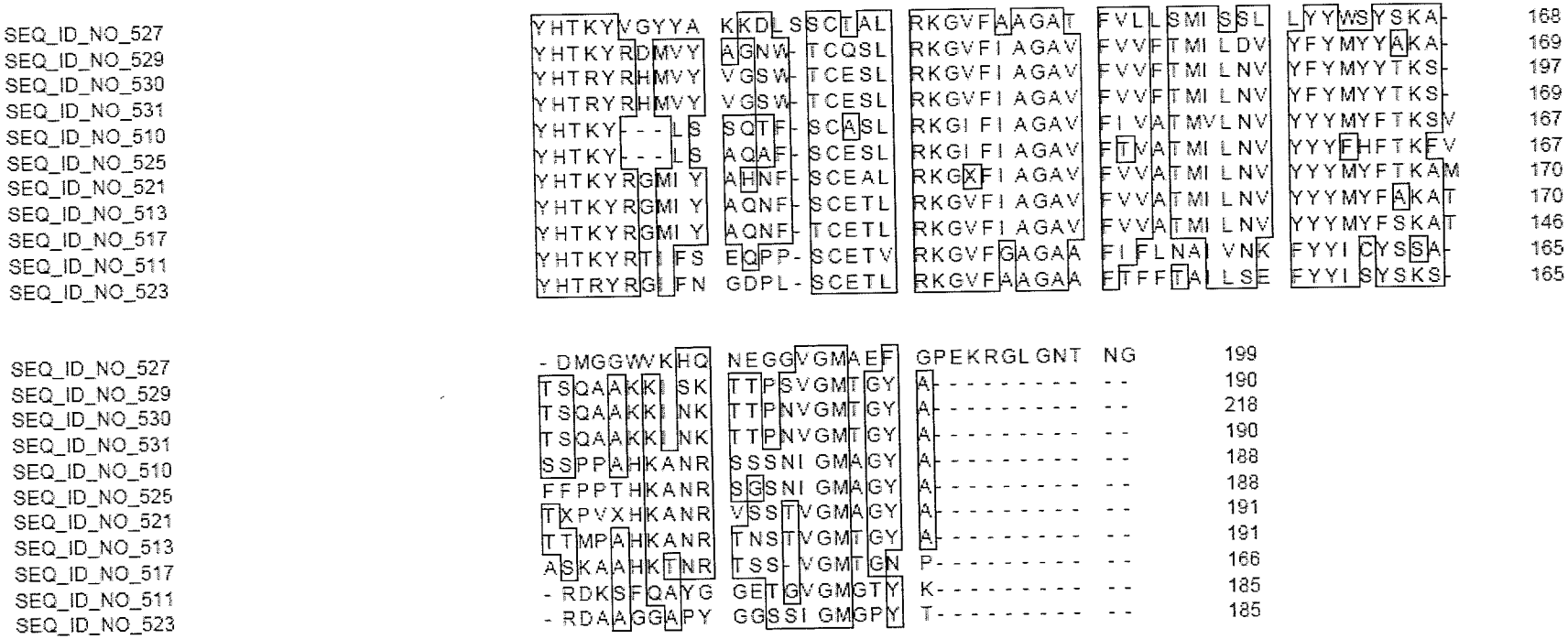


Figure 16

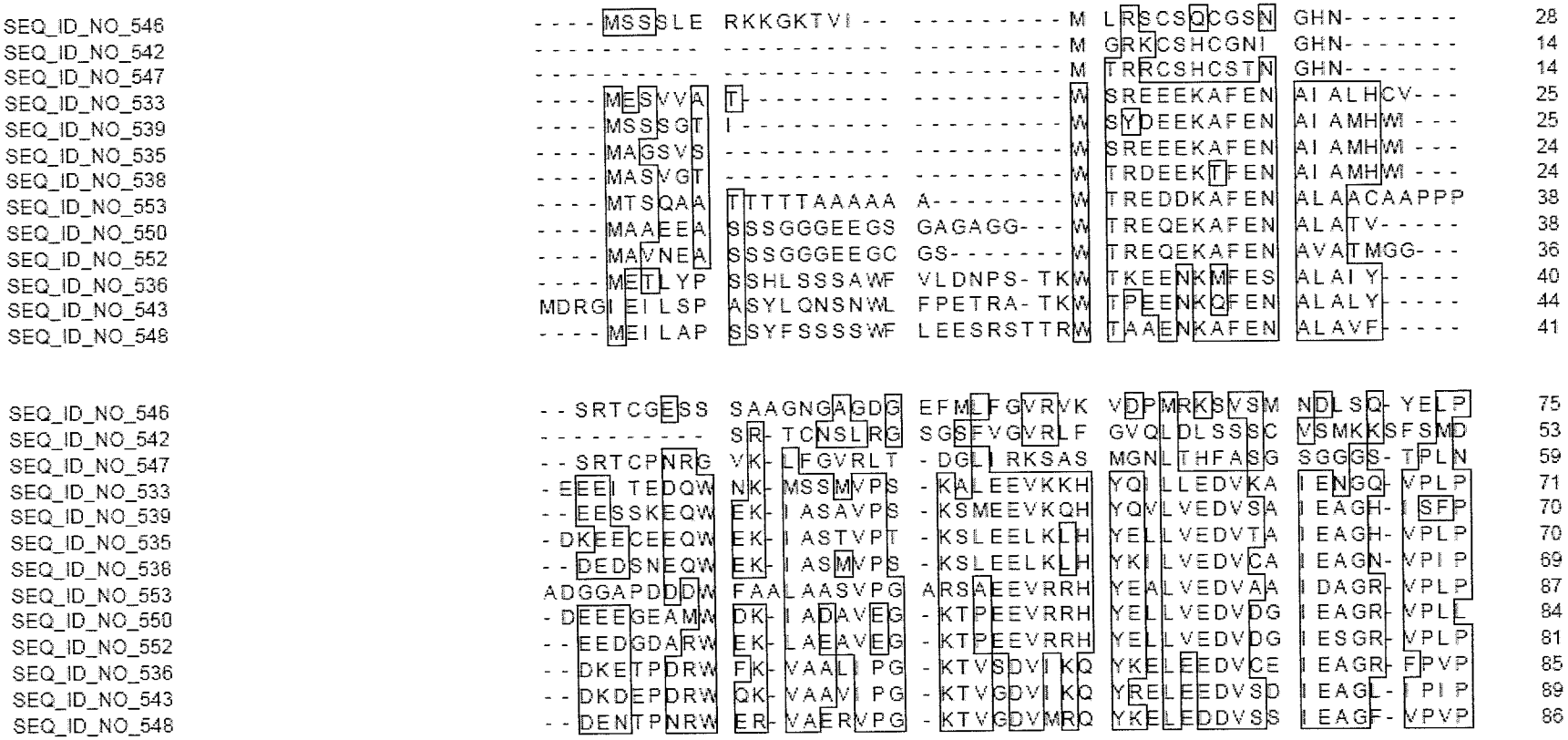

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Figure 16 (continued)

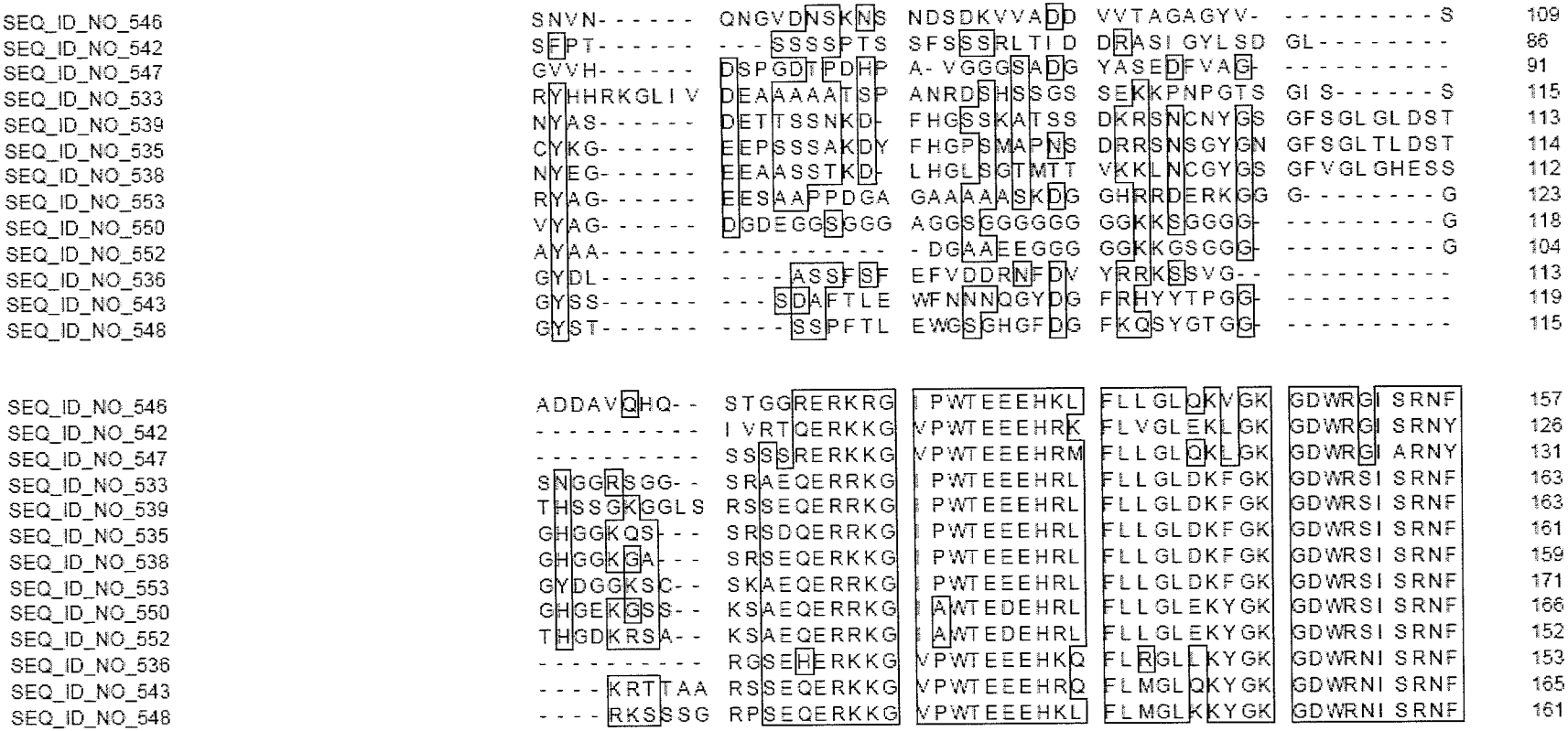


Figure 16 (continued)

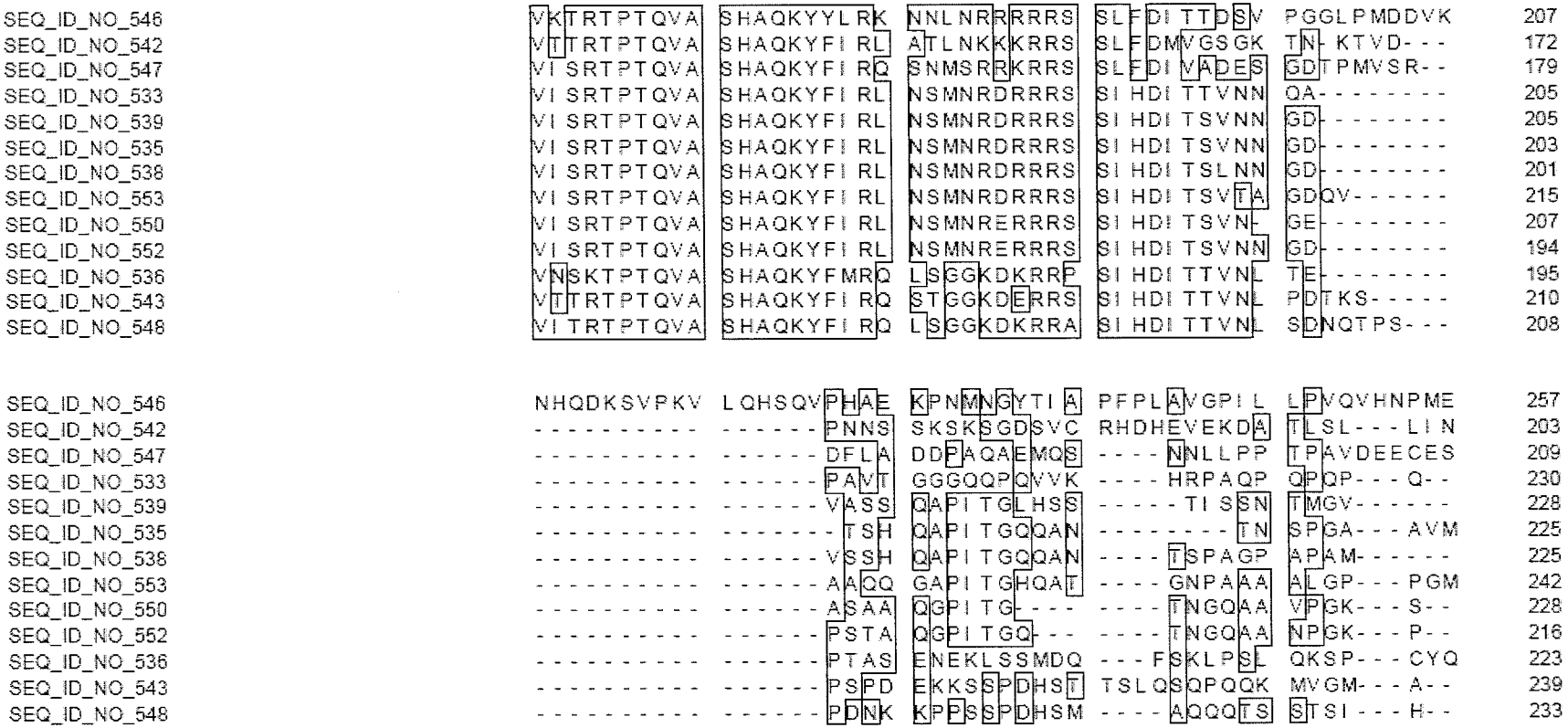


Figure 16 (continued)

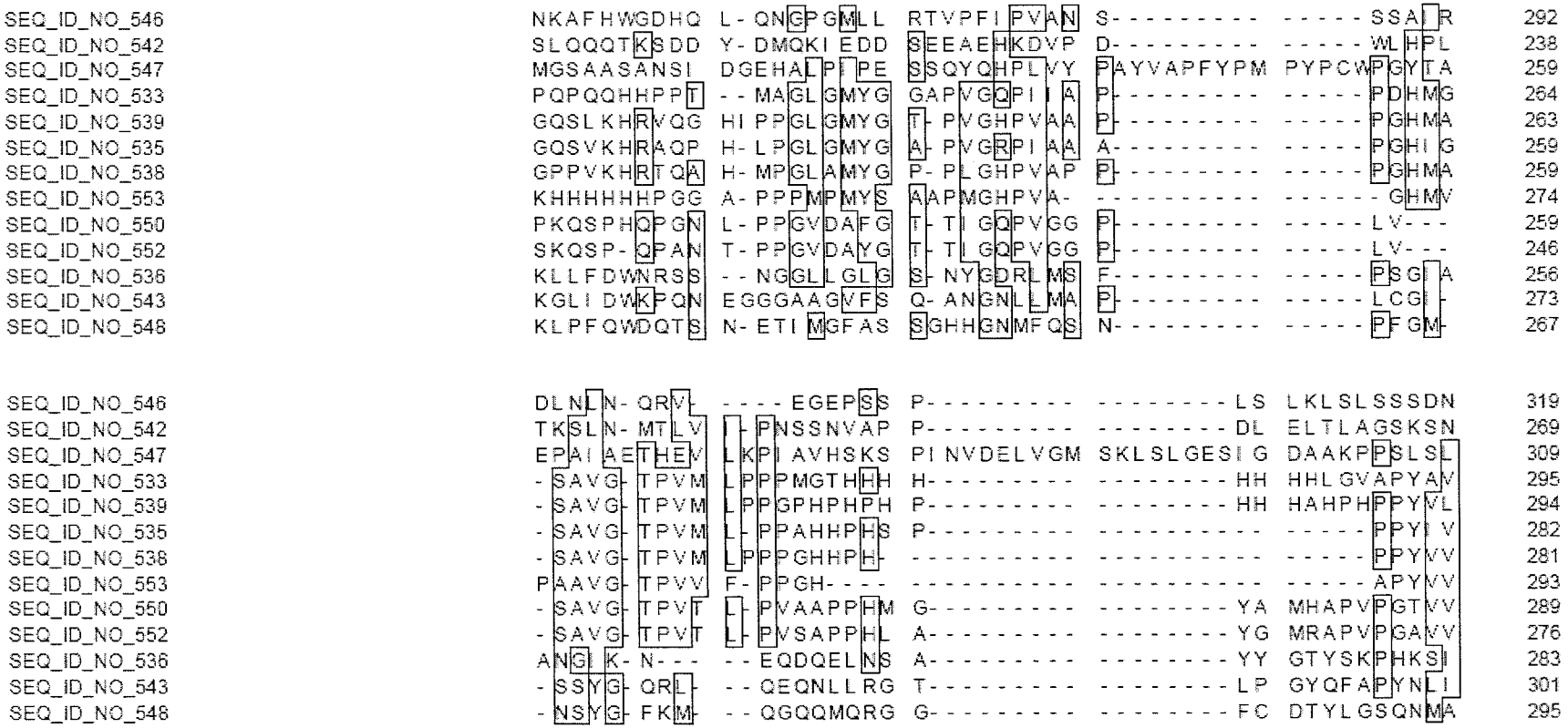


Figure 16 (continued)

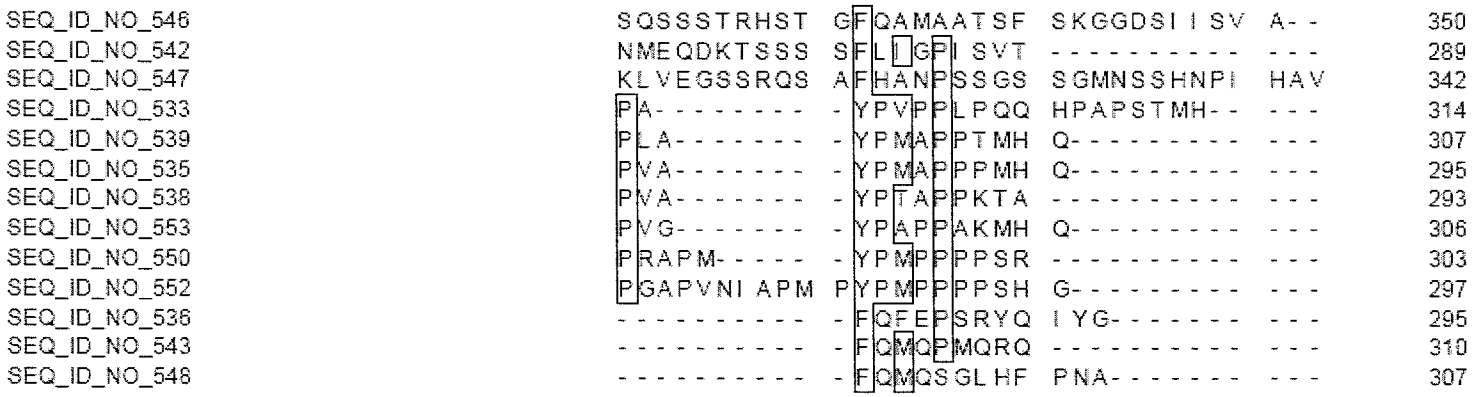
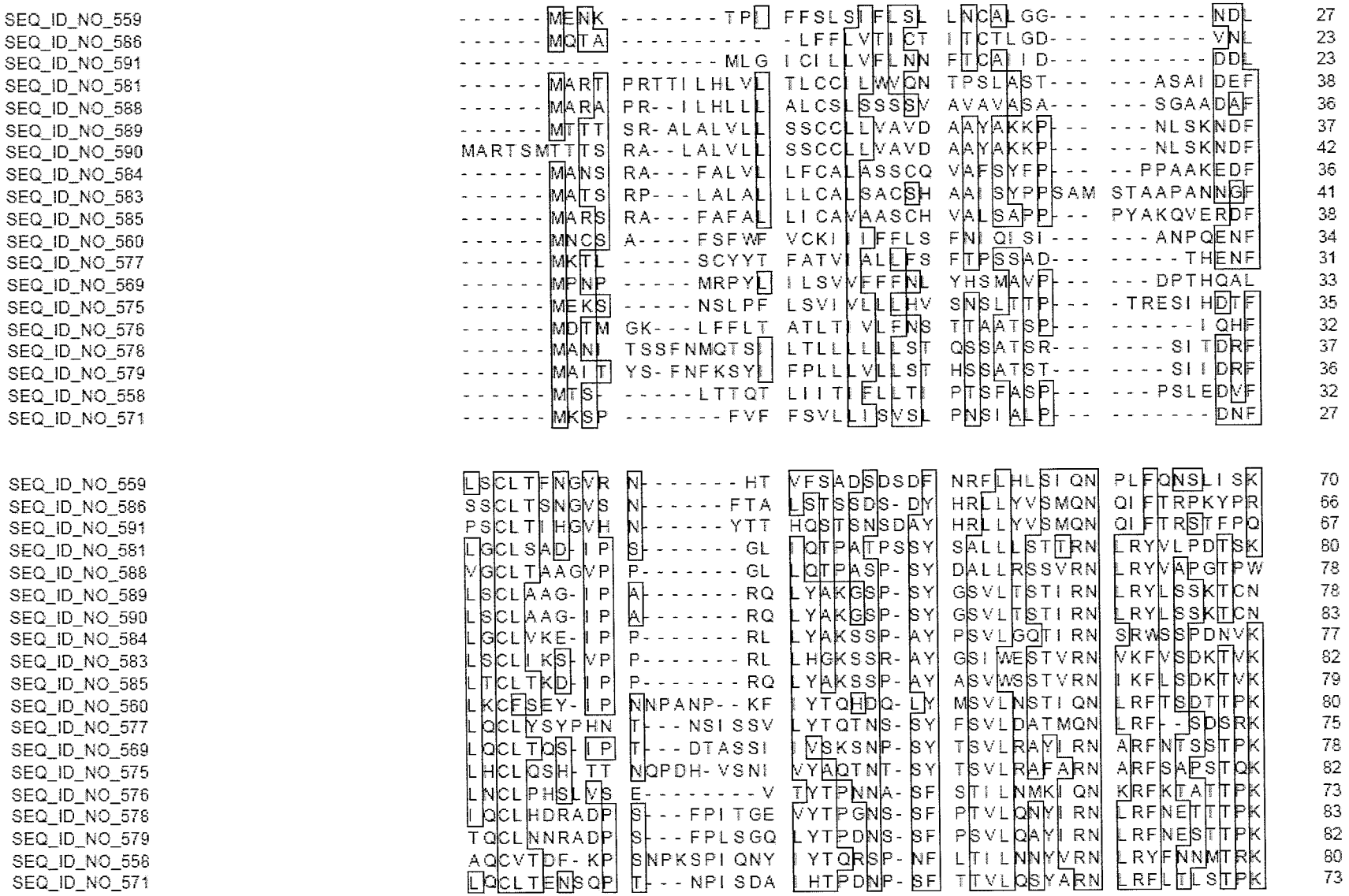


Figure 17



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Figure 17 (continued)

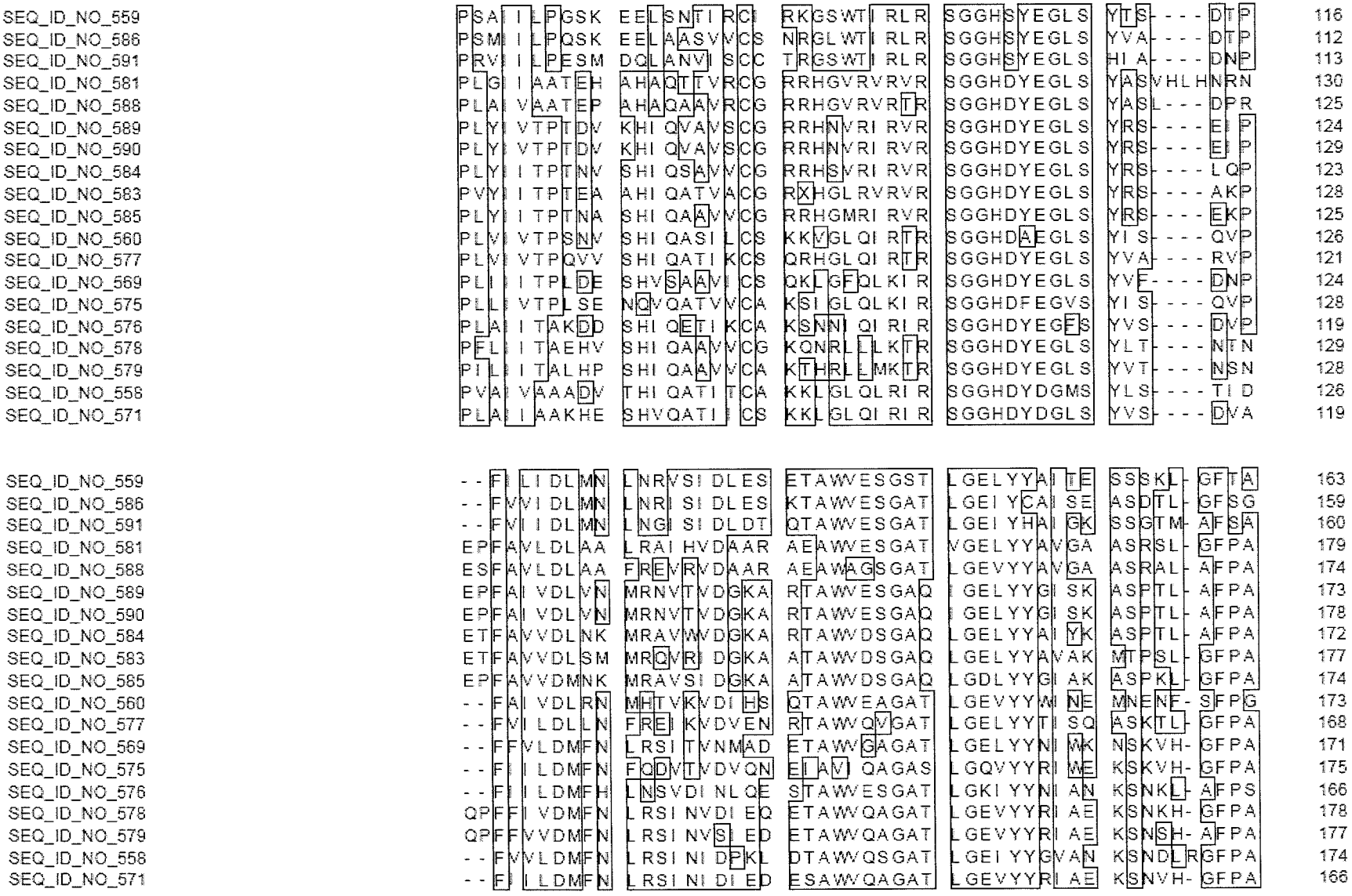


Figure 17 (continued)

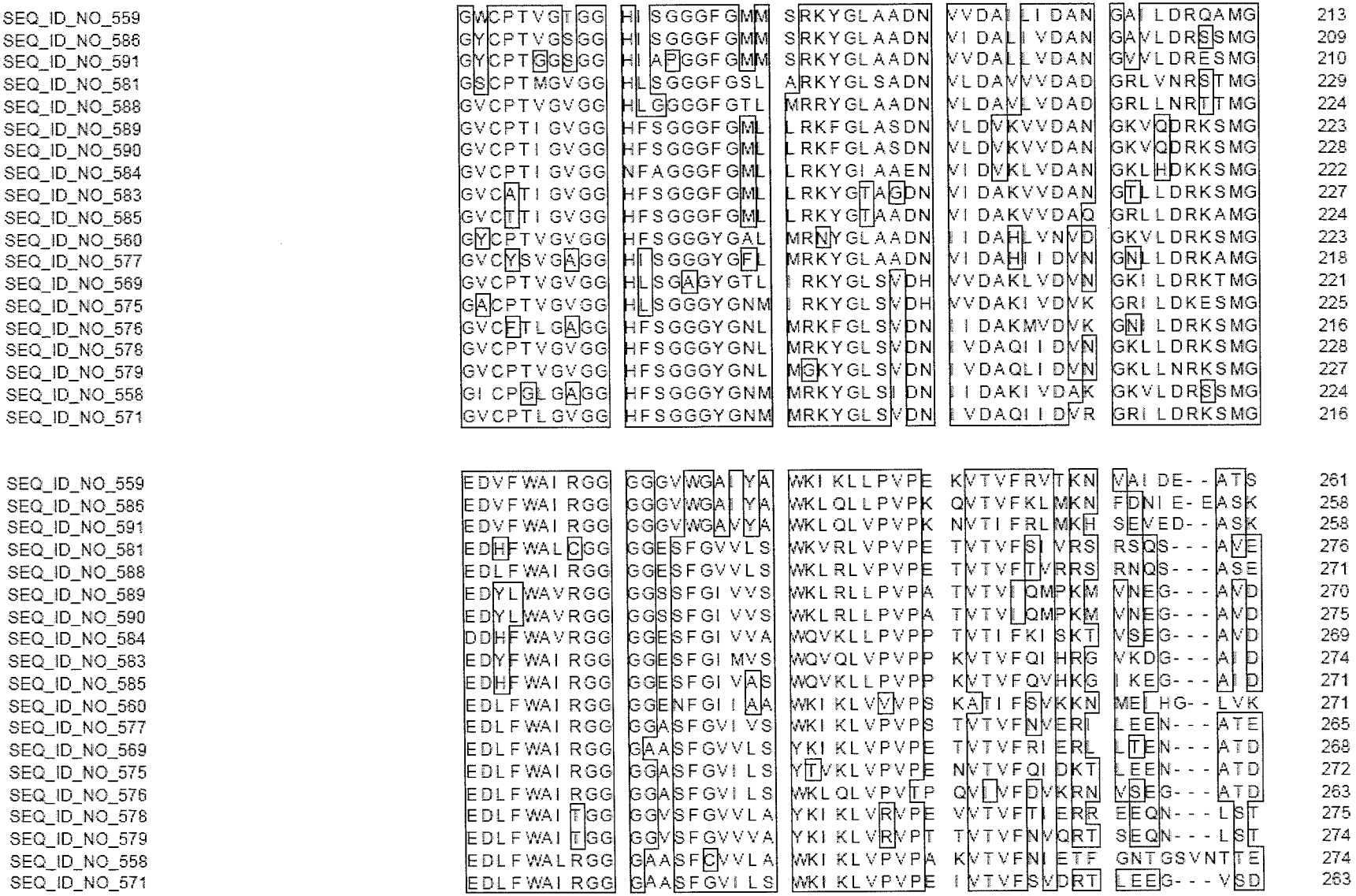


Figure 17 (continued)

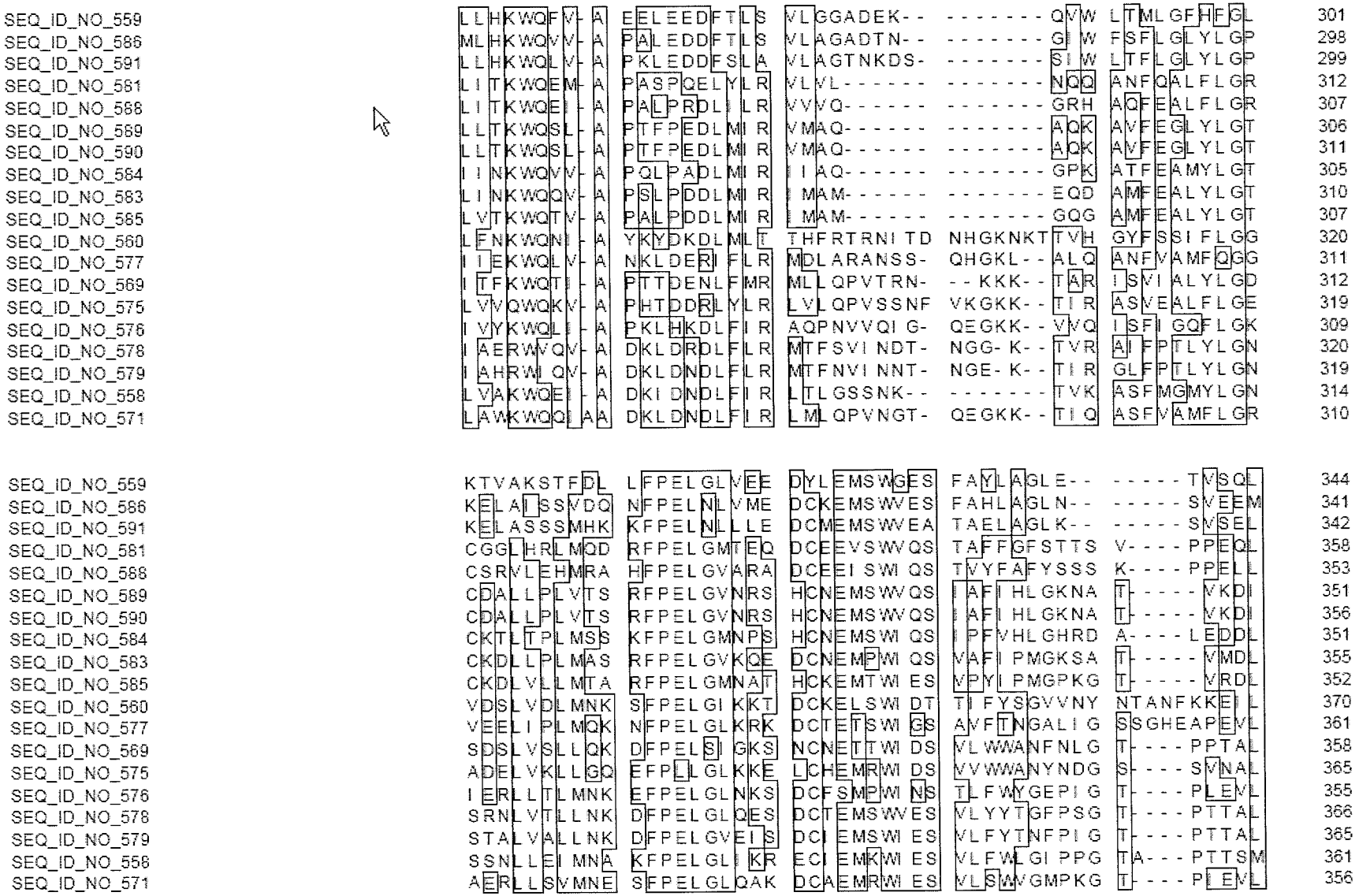


Figure 17 (continued)

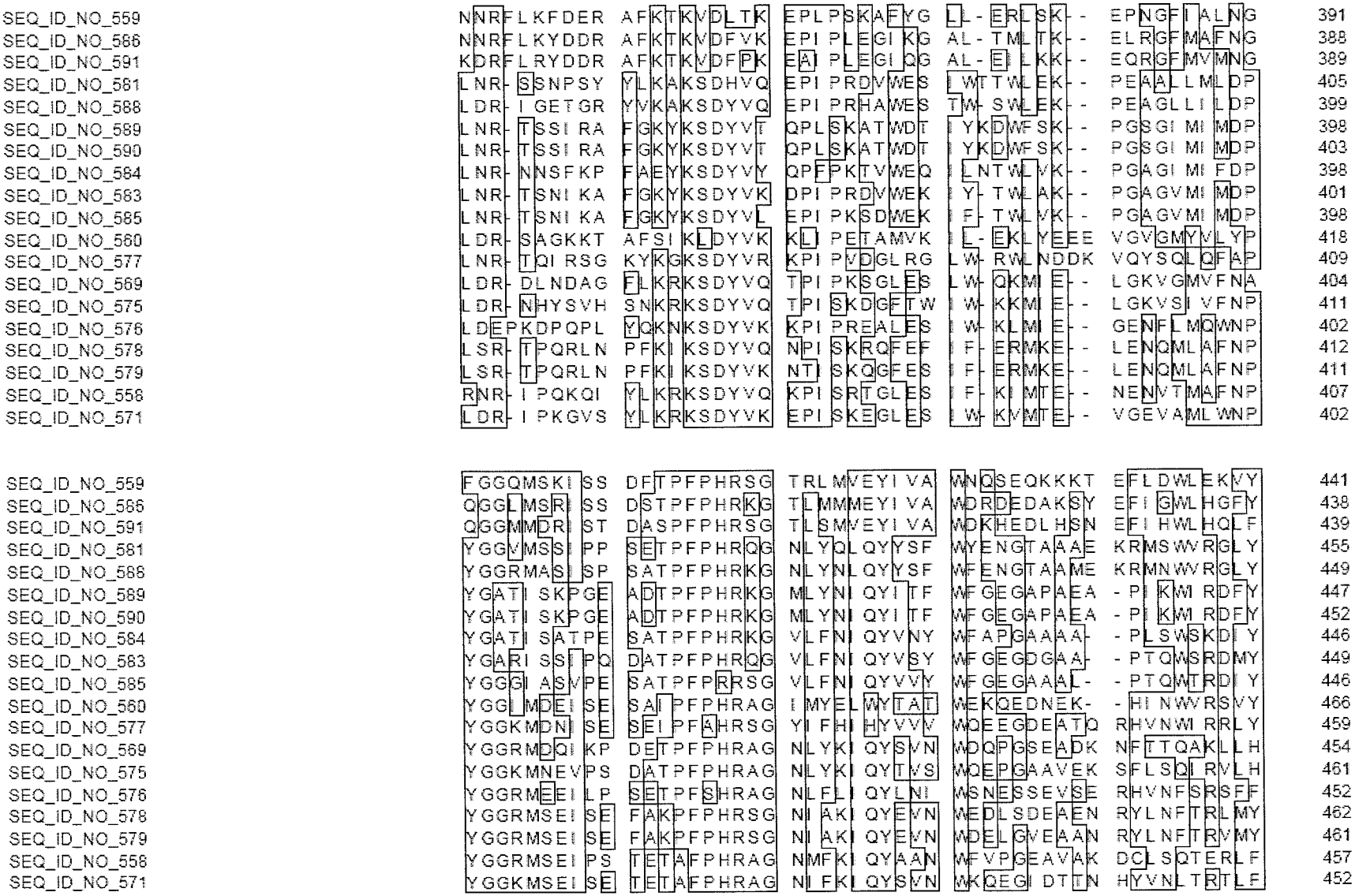


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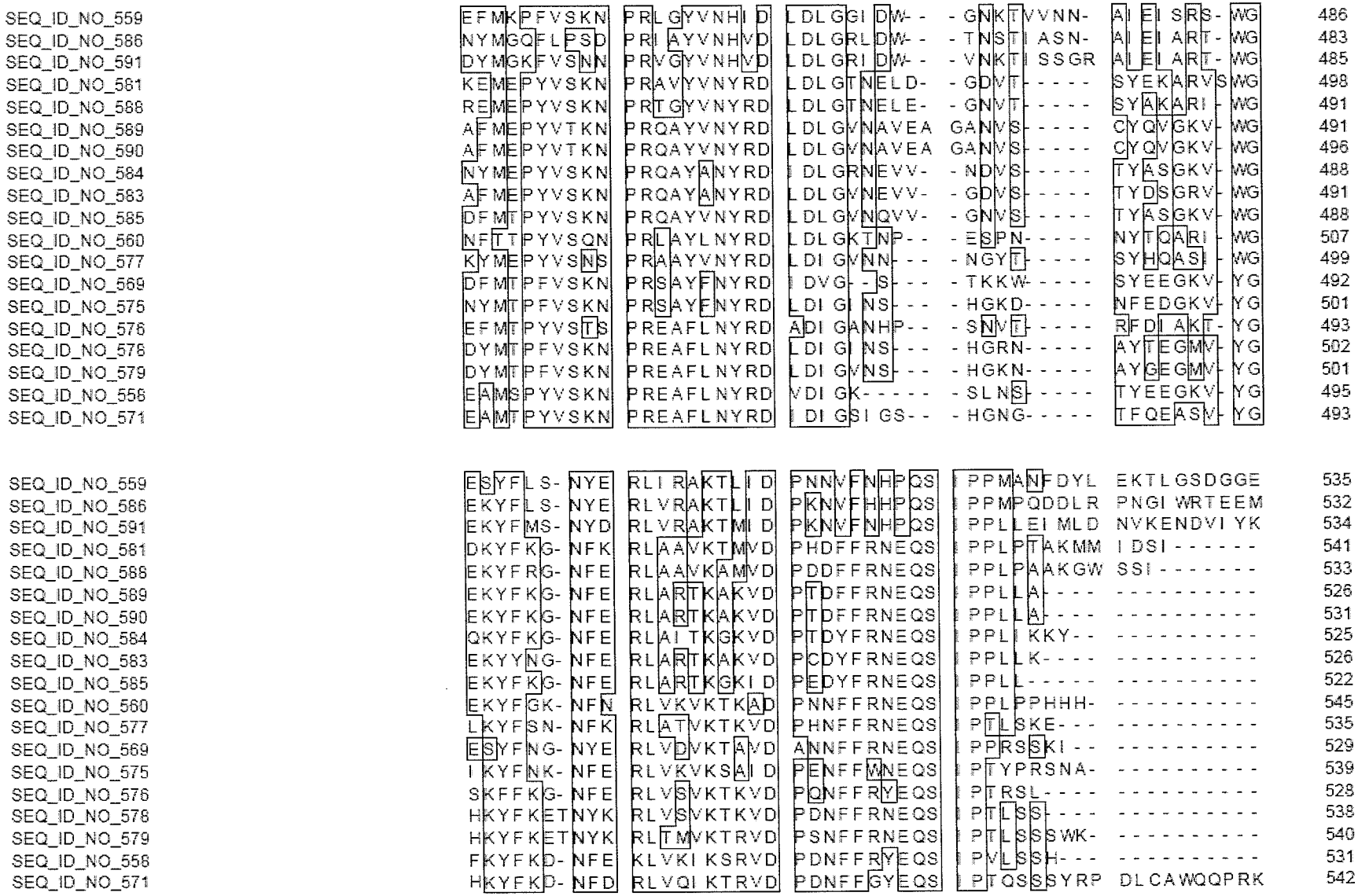


Figure 17 (continued)

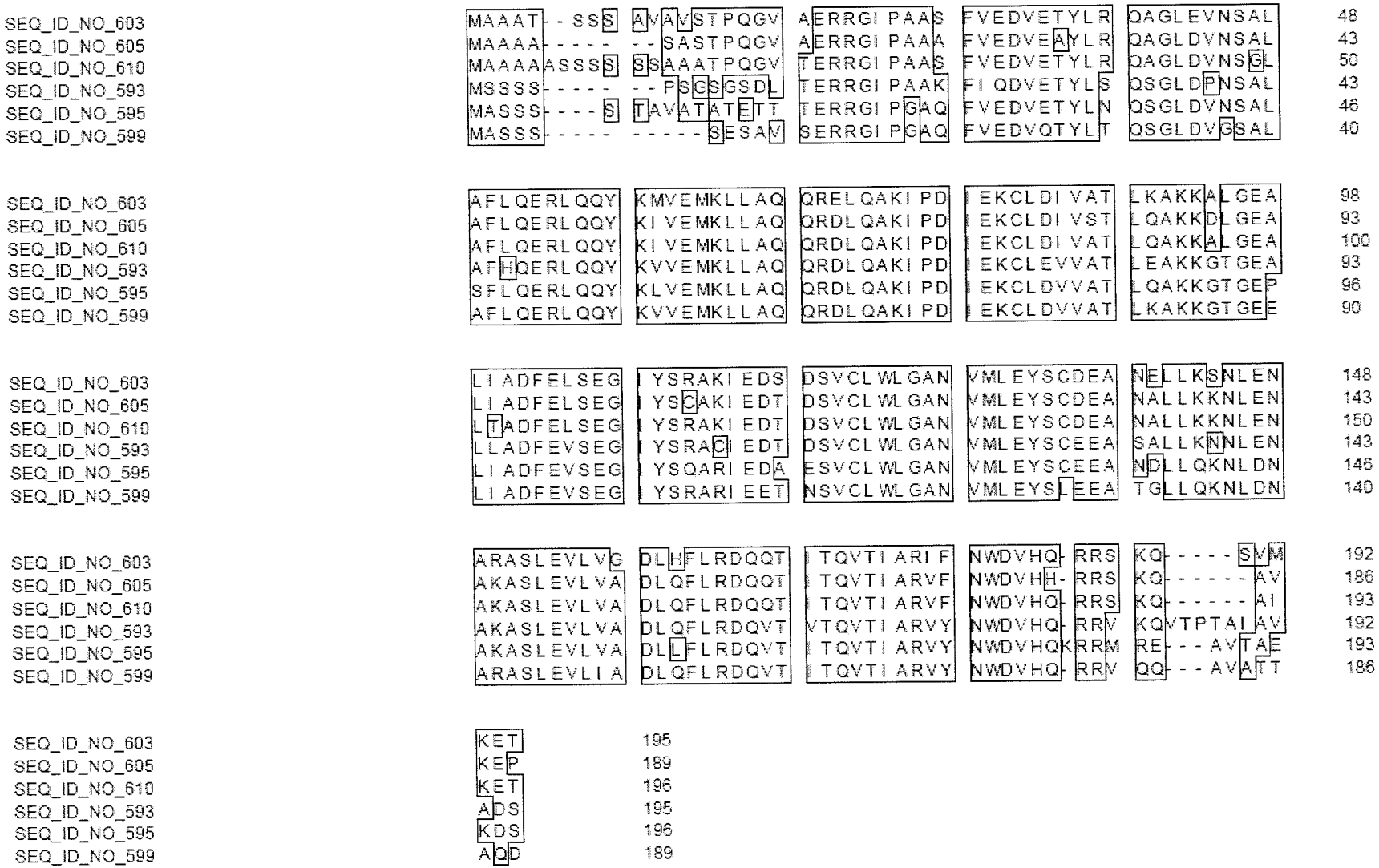
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SEQ_ID_NO_579	---------- ---------- ---------- ---------- ----------	540
SEQ_ID_NO_558	---------- ---------- ---------- ---------- ----------	531
SEQ_ID_NO_571	RTQEEYI KLG PAQQDPFKLG SALEGPKI AR LDPLALALVA LMGPVLSKTH	692

SEQ_ID_NO_559	---------- -	538
SEQ_ID_NO_586	---------- -	536
SEQ_ID_NO_591	---------- -	535
SEQ_ID_NO_581	---------- -	541
SEQ_ID_NO_588	---------- -	533
SEQ_ID_NO_589	---------- -	526
SEQ_ID_NO_590	---------- -	531
SEQ_ID_NO_584	---------- -	525
SEQ_ID_NO_583	---------- -	526
SEQ_ID_NO_585	---------- -	522
SEQ_ID_NO_560	---------- -	545
SEQ_ID_NO_577	---------- -	535
SEQ_ID_NO_569	---------- -	529
SEQ_ID_NO_575	---------- -	539
SEQ_ID_NO_576	---------- -	528
SEQ_ID_NO_578	---------- -	538
SEQ_ID_NO_579	---------- -	540
SEQ_ID_NO_558	---------- -	531
SEQ_ID_NO_571	QRSLKKKI SL M	703

Figure 18


SEQ_ID_NO_603
SEQ_ID_NO_605
SEQ_ID_NO_610
SEQ_ID_NO_593
SEQ_ID_NO_595
SEQ_ID_NO_599
MAAAT--SSS AVAVSTPQGV AERRGIPAAS FVEDVETYLR QAGLEVNSAL 48
MAAAA----- --SASTPQGV AERRGIPAAA FVEDVEAYLR QAGLDVNSAL 43
MAAAAASSSS SSAAATPQGV TERRGIPAAS FVEDVETYLR QAGLDVNSGL 50
MSSSS----- --PSGSGSDL TERRGIPAAK FIQDVETYLS QSGLDPNSAL 43
MASSS----S TAVATATETT TERRGIPGAQ FVEDVETYLN QSGLDVNSAL 46
MASSS----- -----SESAV SERRGIPGAQ FVEDVQTYLT QSGLDVGSAL 40
SEQ_ID_NO_603
SEQ_ID_NO_605
SEQ_ID_NO_610
SEQ_ID_NO_593
SEQ_ID_NO_595
SEQ_ID_NO_599
AFLQERLQQY KMVEMKLLAQ QRELQAKIPD IEKCLDIVAT LKAKKALGEA 98
AFLQERLQQY KIVEMKLLAQ QRDLQAKIPD IEKCLDIVST LQAKKDLGEA 93
AFLQERLQQY KIVEMKLLAQ QRDLQAKIPD IEKCLDIVAT LQAKKALGEA 100
AFHQERLQQY KVVEMKLLAQ QRDLQAKIPD IEKCLEVVAT LEAKKGTGEA 93
SFLQERLQQY KLVEMKLLAQ QRDLQAKIPD IEKCLDVVAT LQAKKGTGEP 96
AFLQERLQQY KVVEMKLLAQ QRDLQAKIPD IEKCLDVVAT LKAKKGTGEE 90
SEQ_ID_NO_603
SEQ_ID_NO_605
SEQ_ID_NO_610
SEQ_ID_NO_593
SEQ_ID_NO_595
SEQ_ID_NO_599
LIADFELSEG IYSRAKIEDS DSVCLWLGAN VMLEYSCDEA NELLKSNLEN 148
LIADFELSEG IYSCAKIEDT DSVCLWLGAN VMLEYSCDEA NALLKKNLEN 143
LTADFELSEG IYSRAKIEDT DSVCLWLGAN VMLEYSCDEA NALLKKNLEN 150
LLADFEVSEG IYSRACIEDT DSVCLWLGAN VMLEYSCEEA SALLKNNLEN 143
LIADFEVSEG IYSQARIEDA ESVCLWLGAN VMLEYSCEEA NDLLQKNLDN 146
LIADFEVSEG IYSRARIEET NSVCLWLGAN VMLEYSLEEA TGLLQKNLDN 140
SEQ_ID_NO_603
SEQ_ID_NO_605
SEQ_ID_NO_610
SEQ_ID_NO_593
SEQ_ID_NO_595
SEQ_ID_NO_599
ARASLEVLVG DLHFLRDQQT ITQVTIARIF NWDVHQ-RRS KQ----SVM 192
AKASLEVLVA DLQFLRDQQT ITQVTIARVF NWDVHH-RRS KQ-----AV 186
AKASLEVLVA DLQFLRDQQT ITQVTIARVF NWDVHQ-RRS KQ-----AI 193
AKASLEVLVA DLQFLRDQVT VTQVTIARVY NWDVHQ-RRV KQVTPTAIAV 192
AKASLEVLVA DLLFLRDQVT ITQVTIARVY NWDVHQKRRM RE--AVTAE 193
ARASLEVLIA DLQFLRDQVT ITQVTIARVY NWDVHQ-RRV QQ--AVATT 186
SEQ_ID_NO_603
SEQ_ID_NO_605
SEQ_ID_NO_610
SEQ_ID_NO_593
SEQ_ID_NO_595
SEQ_ID_NO_599
KET 195
KEP 189
KET 196
ADS 195
KDS 196
AQD 189

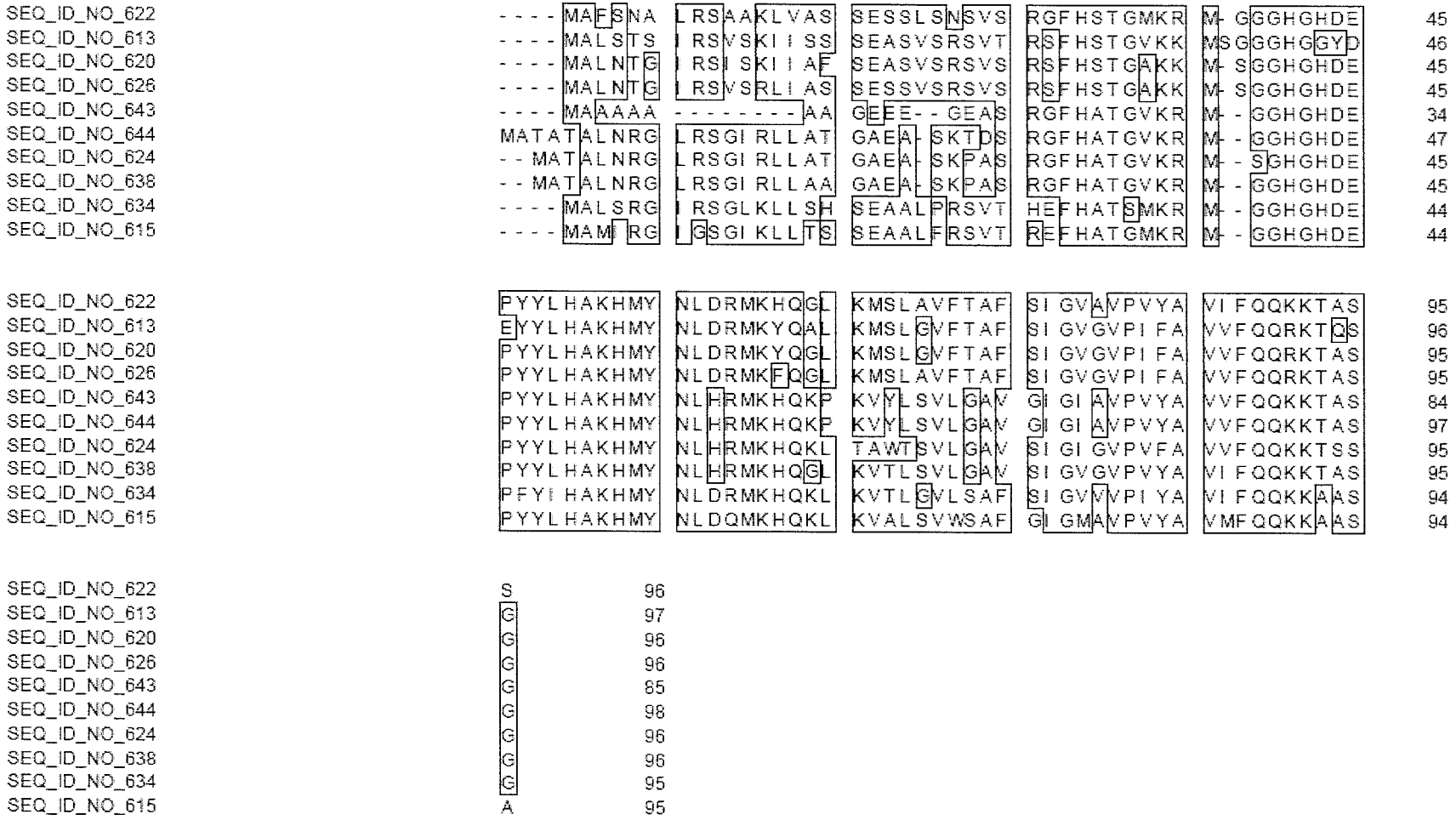

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SEQ_ID_NO_613 ----MALSTS IRSVSKIISS SEASVSRSVT RSFHSTGVKK MSGGGHGGYD 46
SEQ_ID_NO_620 ----MALNTG IRSISKIIAF SEASVSRSVS RSFHSTGAKK M-SGGGHGHDE 45
SEQ_ID_NO_626 ----MALNTG IRSVSRLIAS SESSVSRSVS RSFHSTGAKK M-SGGGHGHDE 45
SEQ_ID_NO_643 ----MAAAAA ---------AA GEEE--GEAS RGFHATGVKR M--GGHGHDE 34
SEQ_ID_NO_644 MATATALNRG LRSGIRLLAT GAEA-SKTDS RGFHATGVKR M--GGHGHDE 47
SEQ_ID_NO_624 --MATALNRG LRSGIRLLAT GAEA-SKPAS RGFHATGVKR M--SGHGHDE 45
SEQ_ID_NO_638 --MATALNRG LRSGIRLLAA GAEA-SKPAS RGFHATGVKR M--GGHGHDE 45
SEQ_ID_NO_634 ----MALSRG IRSGLKLLSH SEAALPRSVT HEFHATSMKR M--GGHGHDE 44
SEQ_ID_NO_615 ----MAMIRG LGSGIKLLTS SEAALFRSVT REFHATGMKR M--GGHGHDE 44
SEQ_ID_NO_622 PYYLHAKHMY NLDRMKHQGL KMSLAVFTAF SIGVAVPVYA VIFQQKKTAS 95
SEQ_ID_NO_613 EYYLHAKHMY NLDRMKYQAL KMSLGVFTAF SIGVGVPIFA VVFQQRKTQS 96
SEQ_ID_NO_620 PYYLHAKHMY NLDRMKYQGL KMSLGVFTAF SIGVGVPIFA VVFQQRKTAS 95
SEQ_ID_NO_626 PYYLHAKHMY NLDRMKFQGL KMSLAVFTAF SIGVGVPIFA VVFQQRKTAS 95
SEQ_ID_NO_643 PYYLHAKHMY NLHRMKHQKP KVYLSVLGAV GIGIAVPVYA VVFQQKKTAS 84
SEQ_ID_NO_644 PYYLHAKHMY NLHRMKHQKP KVYLSVLGAV GIGIAVPVYA VVFQQKKTAS 97
SEQ_ID_NO_624 PYYLHAKHMY NLHRMKHQKL TAWTSVLGAV SIGIGVPVFA VVFQQKKTSS 95
SEQ_ID_NO_638 PYYLHAKHMY NLHRMKHQGL KVTLSVLGAV SIGVGVPVYA VIFQQKKTAS 95
SEQ_ID_NO_634 PFYIHAKHMY NLDRMKHQKL KVTLGVLSAF SIGVVVPIYA VIFQQKKAAS 94
SEQ_ID_NO_615 PYYLHAKHMY NLDQMKHQKL KVALSVWSAF GIGMAVPVYA VMFQQKKAAS 94
SEQ_ID_NO_622 S 96
SEQ_ID_NO_613 G 97
SEQ_ID_NO_620 G 96
SEQ_ID_NO_626 G 96
SEQ_ID_NO_643 G 85
SEQ_ID_NO_644 G 98
SEQ_ID_NO_624 G 96
SEQ_ID_NO_638 G 96
SEQ_ID_NO_634 G 95
SEQ_ID_NO_615 A 95

Figure 20

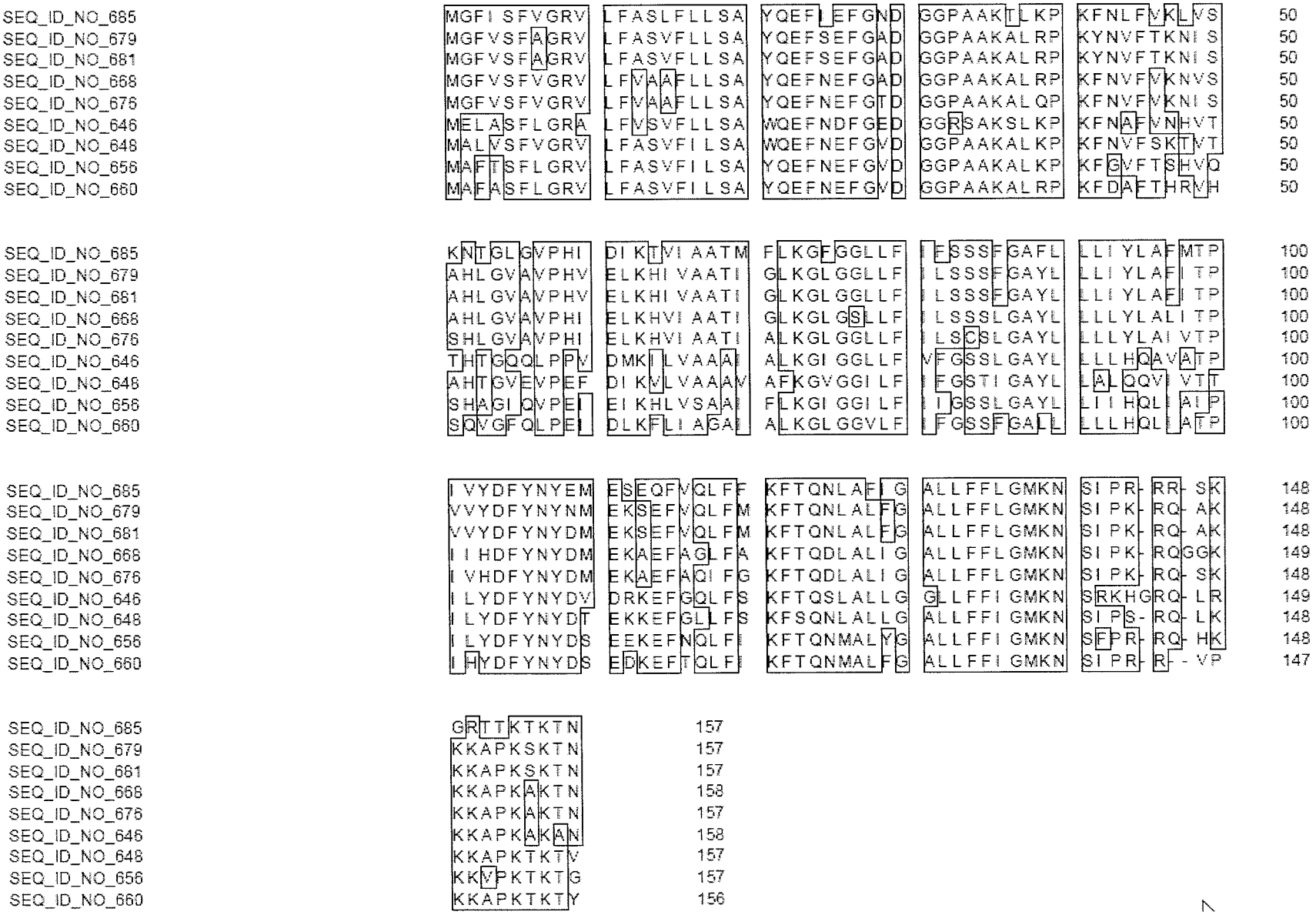

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SEQ_ID_NO_668
SEQ_ID_NO_676
SEQ_ID_NO_646
SEQ_ID_NO_648
SEQ_ID_NO_656
SEQ_ID_NO_660
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MGFVSFAGRV LFASVFLLSA YQEFSEFGAD GGPAAKALRP KYNVFTKNIS 50
MGFVSFAGRV LFASVFLLSA YQEFSEFGAD GGPAAKALRP KYNVFTKNIS 50
MGFVSFVGRV LFVAAFLLSA YQEFNEFGAD GGPAAKALRP KFNVFVKNVS 50
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MELASFLGRA LFVSVFLLSA WQEFNDFGED GGRSAKSLKP KFNAFVNHVT 50
MALVSFVGRV LFASVFILSA WQEFNEFGVD GGPAAKALKP KFNVFSKTVT 50
MAFTSFLGRV LFASVFILSA YQEFNEFGVD GGPAAKALKP KFGVFTSHVQ 50
MAFASFLGRV LFASVFILSA YQEFNEFGVD GGPAAKALRP KFDAFTHRVH 50
SEQ_ID_NO_685
SEQ_ID_NO_679
SEQ_ID_NO_681
SEQ_ID_NO_668
SEQ_ID_NO_676
SEQ_ID_NO_646
SEQ_ID_NO_648
SEQ_ID_NO_656
SEQ_ID_NO_660
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AHLGVAVPHV ELKHIVAATI GLKGLGGLLF ILSSSFGAYL LLIYLAFITP 100
AHLGVAVPHV ELKHIVAATI GLKGLGGLLF ILSSSFGAYL LLIYLAFITP 100
AHLGVAVPHI ELKHVIAATI GLKGLGGSLF ILSSSLGAYL LLLYLALITP 100
SHLGVAVPHI ELKHVIAATI ALKGLGGLLF ILSCSLGAYL LLLYLAIVTP 100
THTGQQLPPV DMKILVAAAI ALKGIGGLLF VFGSSLGAYL LLLHQAVATP 100
AHTGVEVPEF DIKVLVAAAV AFKGVGGILF IFGSTIGAYL LALQQVIVTT 100
SHAGIQVPEI EIKHLVSAAI FLKGIGGILF IIGSSLGAYL LIIHQLIAIP 100
SQVGFQLPEI DLKFLIAGAI ALKGLGGVLF IFGSSFGALL LLLHQLIATP 100
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SEQ_ID_NO_681
SEQ_ID_NO_668
SEQ_ID_NO_676
SEQ_ID_NO_646
SEQ_ID_NO_648
SEQ_ID_NO_656
SEQ_ID_NO_660
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VVYDFYNYNM EKSEFVQLFM KFTQNLALFG ALLFFLGMKN SIPK-RQ-AK 148
VVYDFYNYDM EKSEFVQLFM KFTQNLALFG ALLFFLGMKN SIPK-RQ-AK 148
IIHDFYNYDM EKAEFAGLFA KFTQDLALIG ALLFFLGMKN SIPK-RQGGK 149
IVHDFYNYDM EKAEFAQIFG KFTQDLALIG ALLFFLGMKN SIPK-RQ-SK 148
ILYDFYNYDV DRKEFGQLFS KFTQSLALLG GLLFFIGMKN SRKHGRQ-LR 149
ILYDFYNYDT EKKEFGLLFS KFSQNLALLG ALLFFIGMKN SIPS-RQ-LK 148
ILYDFYNYDS EEKEFNQLFI KFTQNMALYG ALLFFIGMKN SFPR-RQ-HK 148
IHYDFYNYDS EDKEFTQLFI KFTQNMALFG ALLFFIGMKN SIPR-R--VP 147
SEQ_ID_NO_685
SEQ_ID_NO_679
SEQ_ID_NO_681
SEQ_ID_NO_668
SEQ_ID_NO_676
SEQ_ID_NO_646
SEQ_ID_NO_648
SEQ_ID_NO_656
SEQ_ID_NO_660
GRTTKTKTN 157
KKAPKSKTN 157
KKAPKSKTN 157
KKAPKAKTN 158
KKAPKAKTN 157
KKAPKAKAN 158
KKAPKTKTV 157
KKVPKTKTG 157
KKAPKTKTY 156

FIGURE _ Page 71 of 165

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Figure 21

```
SEQ_ID_NO_708   MDEIMNKMGS  YWLGQRANKE  MSSAGDDIES  LSTSVGDGAK  WLVNKLKGKM   50
SEQ_ID_NO_728   MDQIFNKVGS  YWLGQKANKE  FNSVGDDINS  MGSSIGDGTK  WLVNKLKGKM   50
SEQ_ID_NO_718   MDQILNKVGS  YWINKRANKE  ISSVGDDLNS  LSSSIEGGAK  WLVNKLKGKM   50
SEQ_ID_NO_687   MDQIFNKVGS  YWLGQKANKQ  FDSVGNDLNS  VSTSIEGGTK  WLVNKIKGKM   50
SEQ_ID_NO_699   MDQVFXKVGS  YWLGQKANKQ  FDSVGKDVSS  LSTSIEGGTK  WLVNKFKGTM   50
SEQ_ID_NO_689   MDQILNKVGS  YWLGQKANKE  IDSVGDDLNS  LSTSIEGGAK  WLVNKIKGKM   50
SEQ_ID_NO_691   MDAVLNKVGS  YWLGQKASKE  FNSVGDDINS  LSTSIEGGTK  WLVNKLKGKM   50
SEQ_ID_NO_703   MDQIFNKVGS  YWFNQKASSQ  LNSVGDDINS  MTNSIXGGTK  WLVNKIKGKM   50
SEQ_ID_NO_706   MDQVFNKVGS  YWFNQKASKE  LNSVGDEINS  LSNSIEGGTK  WLVNKVKGKM   50
SEQ_ID_NO_721   MDQIMGKVGG  YWFKQNAGKE  INNIGDDINS  ISSSIGDGAK  WMVNKIKGKM   50
SEQ_ID_NO_712   MDQVLNKVGS  YWFSKRASKE  IDSIGDDLNS  VSSSIGGGAK  WMVNKIKGKL   50
SEQ_ID_NO_724   MDQVLNKVGS  YWFSKRASKE  IDSIGDDISS  ISTSIGTGAK  WMVNKIKGKM   50

SEQ_ID_NO_708   QKPLAELLQE  HDLPAGLFPR  EATNYEFEPE  TRRLTVHIPA  VCEVGYRDGS  100
SEQ_ID_NO_728   QKPLPELLKD  YDLAVGIFPR  DATHYEFDER  QGKLTVYVPQ  ICEVGYKDSS  100
SEQ_ID_NO_718   QKSLPELLRE  YDMPIGLFPQ  DATHYEFNEE  TGKLTVFIPS  ICEVGYRDSS  100
SEQ_ID_NO_687   QKPLPELLKE  YDLPIGIFPG  DATNYEFDEE  TKKLTVLIPS  ICEVGYKDSS  100
SEQ_ID_NO_699   QKPLAELLKD  YDLPVGIFPR  DATNYEFDEQ  TKKLTVLIPS  VCEVGYKDSS  100
SEQ_ID_NO_689   QKPLPELLRE  YNLPIGIFPR  DATNYEFNEE  TGKLTVFIPA  ICEVGYKDSS  100
SEQ_ID_NO_691   QKPLPDLLKE  YDLPIGIFPR  DATNYEFNEE  TRKLTVFIPS  ICEVGYKDSS  100
SEQ_ID_NO_703   QKALPELLKE  YDLPIGIFPR  DATNYEFNEE  TGKLVVYIPQ  VCEVGYKDSS  100
SEQ_ID_NO_706   QKPLPELLKE  YDLPIGIFPR  DATNYEFNEE  TGKLEVFIPQ  VCEVGYKDSS  100
SEQ_ID_NO_721   QKPLPEFLKE  YDLPVGLFPQ  DATNYEFNEE  TKKLTVYISS  VCEVGYKDSS  100
SEQ_ID_NO_712   QKALPDLLKE  YDMPAGLFPR  DTTNYEFNEE  TKKLTVYIPS  ACDVGYKDSS  100
SEQ_ID_NO_724   QKALPDLLKE  YDMPAGLFPR  DATNYEFNEE  TKKLTVYIPS  ACDVGYKDSS  100

SEQ_ID_NO_708   ELRFDTTVTG  TLDKGSLTGV  EGLKAKVLVW  ARVTAVKADA  AKVYFAVGIK  150
SEQ_ID_NO_728   VLRFFATVTG  YLEKGKLADI  EGLKTKIIIW  VKVTAITSEG  SKLHFTAGVK  150
SEQ_ID_NO_718   VLRFLNIVTG  YLEKGKLVDI  EGIKTKVLIW  SKVTRISTEG  SKIHFTIGVK  150
SEQ_ID_NO_687   VLKFTTTVTG  HLEKGKLTDV  EGIKTKVMIW  VKVTSISTDA  SKVYFTAGMK  150
SEQ_ID_NO_699   VLKFTTTVTG  RLEKGKLGDL  EGMKTKVMIW  VKVTSISADS  SKVYFTAGVK  150
SEQ_ID_NO_689   F-----CASS  PL--------  ----------  ----------  ----------  107
SEQ_ID_NO_691   VVRFLTTVTG  YLEKGKIADI  EGMKTKVMIW  VKVTCIASTG  SKLNFTAGMK  150
SEQ_ID_NO_703   VLRFXTTVTG  YLEKGKLADI  EGMKTKVLIW  VKVTTILSXG  XKXYVTAGKK  150
SEQ_ID_NO_706   VLRFFTTVTG  YLEKGKLADI  EGMKTKVIIW  VKVTTIFSEG  SKLYVTAGMK  150
SEQ_ID_NO_721   VLRFSTTVTG  YLENGKLSEV  EGLKTKILIW  TKVTAVRTEA  TKVHFAAGMN  150
SEQ_ID_NO_712   VVRFFTCVTG  YLEKGKLSDI  EGMKTKVLVW  TKVTSIKTEG  SKVHFTAGMK  150
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Figure 21 (continued)

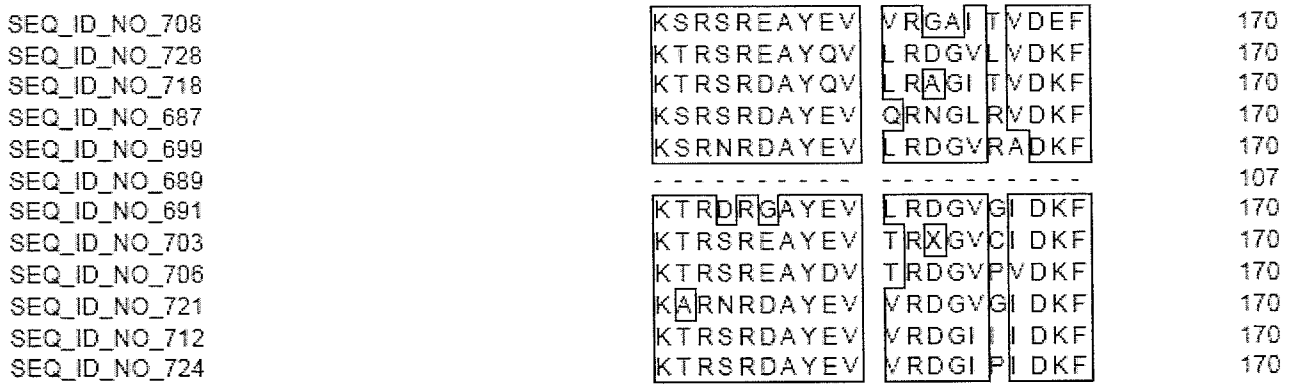


Figure 22

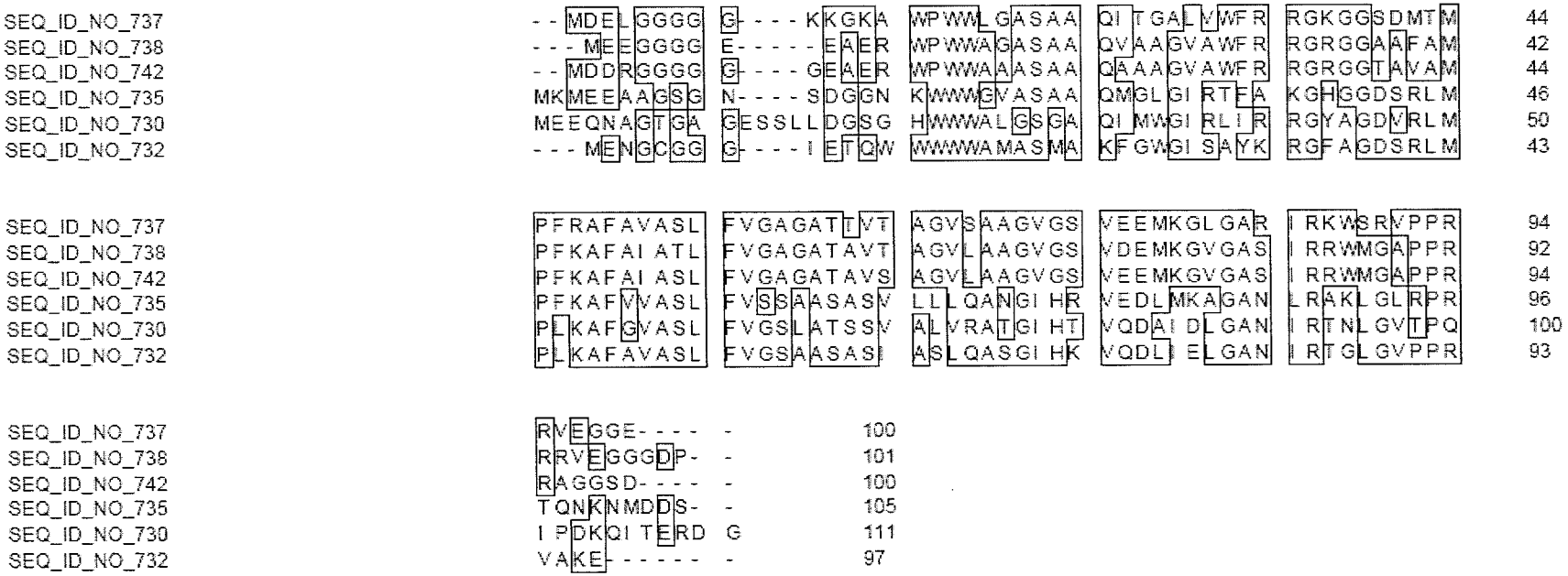

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SEQ_ID_NO_742
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SEQ_ID_NO_730
SEQ_ID_NO_732
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---MEEGGGG E-----EAER WPWWAGASAA QVAAGVAWFR RGRGGAAFAM 42
--MDDRGGGG G----GEAER WPWWAAASAA QAAAGVAWFR RGRGGTAVAM 44
MKMEEAAGSG N----SDGGN KWWWGVASAA QMGLGIRTFA KGHGGDSRLM 46
MEEQNAGTGA GESSLLDGSG HWWWALGSGA QIMWGIRLIR RGYAGDVRLM 50
---MENGCGG G----IETQW WWWWAMASMA KFGWGISAYK RGFAGDSRLM 43
SEQ_ID_NO_737
SEQ_ID_NO_738
SEQ_ID_NO_742
SEQ_ID_NO_735
SEQ_ID_NO_730
SEQ_ID_NO_732
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PFKAFAIATL FVGAGATAVT AGVLAAGVGS VDEMKGVGAS IRRWMGAPPR 92
PFKAFAIASL FVGAGATAVS AGVLAAGVGS VEEMKGVGAS IRRWMGAPPR 94
PFKAFVVASL FVSSAASASV LLLQANGIHR VEDLMKAGAN LRAKLGLRPR 96
PLKAFGVASL FVGSLATSSV ALVRATGIHT VQDAIDLGAN IRTNLGVTPQ 100
PLKAFAVASL FVGSAASASI ASLQASGIHK VQDLIELGAN IRTGLGVPPR 93
SEQ_ID_NO_737
SEQ_ID_NO_738
SEQ_ID_NO_742
SEQ_ID_NO_735
SEQ_ID_NO_730
SEQ_ID_NO_732
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RAGGSD---- - 100
TQNKNMDDS- - 105
IPDKQITERD G 111
VAKE------ - 97

Figure 23

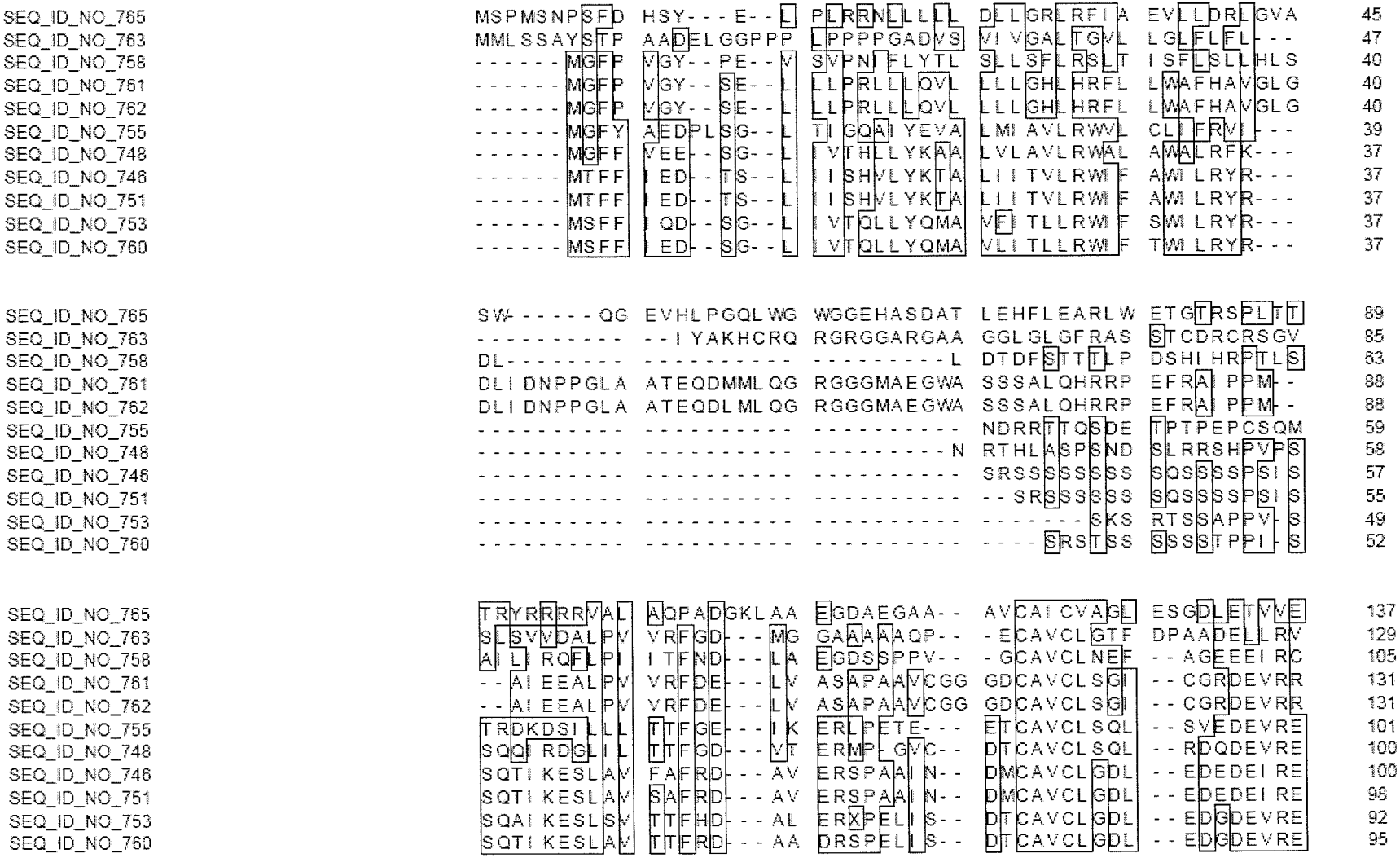

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SEQ_ID_NO_760

Figure 23 (continued)

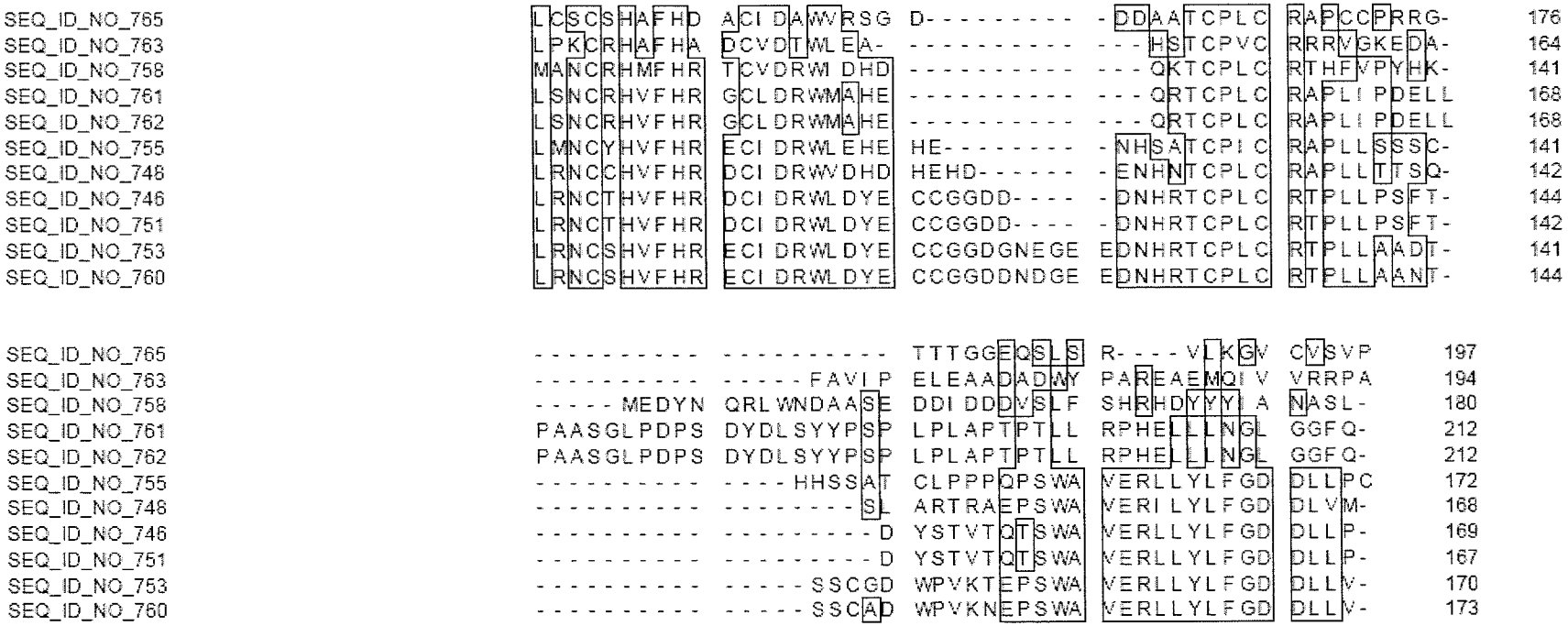


Figure 24

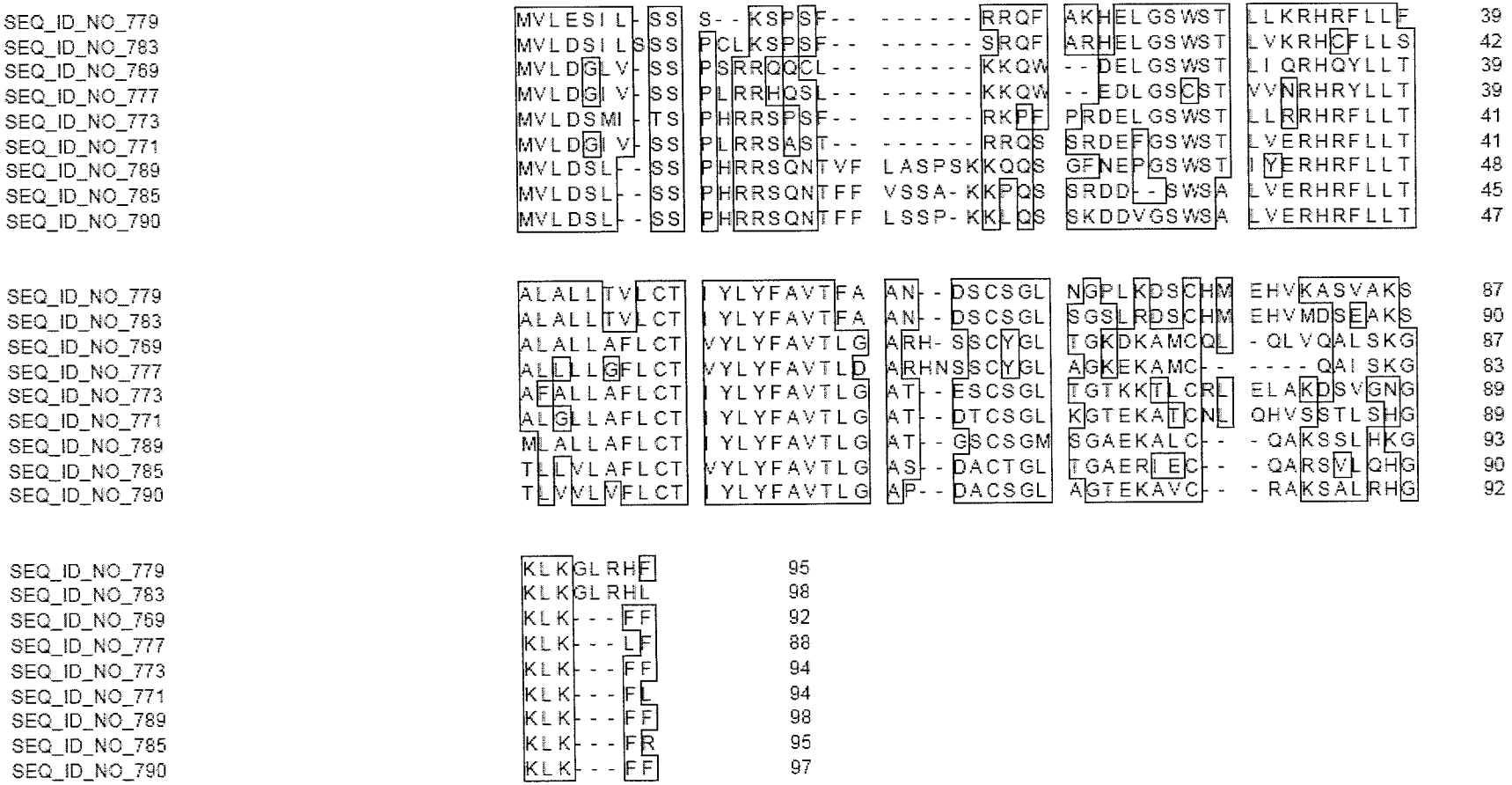

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SEQ_ID_NO_771
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SEQ_ID_NO_785
SEQ_ID_NO_790
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MVLDSILSSS PCLKSPSF-- ------SRQF ARHELGSWST LVKRHCFLLS 42
MVLDGLV-SS PSRRQQCL-- ------KKQW --DELGSWST LIQRHQYLLT 39
MVLDGIV-SS PLRRHQSL-- ------KKQW --EDLGSCST VVNRHRYLLT 39
MVLDSMI-TS PHRRSPSF-- ------RKPF PRDELGSWST LLRRHRFLLT 41
MVLDGIV-SS PLRRSAST-- ------RRQS SRDEFGSWST LVERHRFLLT 41
MVLDSLF-SS PHRRSQNTVF LASPSKKQQS GFNEPGSWST IYERHRFLLT 48
MVLDSL--SS PHRRSQNTFF VSSA-KKPQS SRDD--SWSA LVERHRFLLT 45
MVLDSL--SS PHRRSQNTFF LSSP-KKLQS SKDDVGSWSA LVERHRFLLT 47
ALALLTVLCT IYLYFAVTFA AN--DSCSGL NGPLKDSCHM EHVKASVAKS 87
ALALLTVLCT IYLYFAVTFA AN--DSCSGL SGSLRDSCHM EHVMDSEAKS 90
ALALLAFLCT VYLYFAVTLG ARH-SSCYGL TGKDKAMCQL -QLVQALSKG 87
ALLLLGFLCT VYLYFAVTLD ARHNSSCYGL AGKEKAMC-- ----QAISKG 83
AFALLAFLCT IYLYFAVTLG AT--ESCSGL TGTKKTLCRL ELAKDSVGNG 89
ALGLLAFLCT IYLYFAVTLG AT--DTCSGL KGTEKATCNL QHVSSTLSHG 89
MLALLAFLCT IYLYFAVTLG AT--GSCSGM SGAEKALC-- -QAKSSLHKG 93
TLLVLAFLCT VYLYFAVTLG AS--DACTGL TGAERIEC-- -QARSVLQHG 90
TLVVLVFLCT IYLYFAVTLG AP--DACSGL AGTEKAVC-- -RAKSALRHG 92
KLKGLRHF 95
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KLK---FF 98
KLK---FR 95
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Figure 25

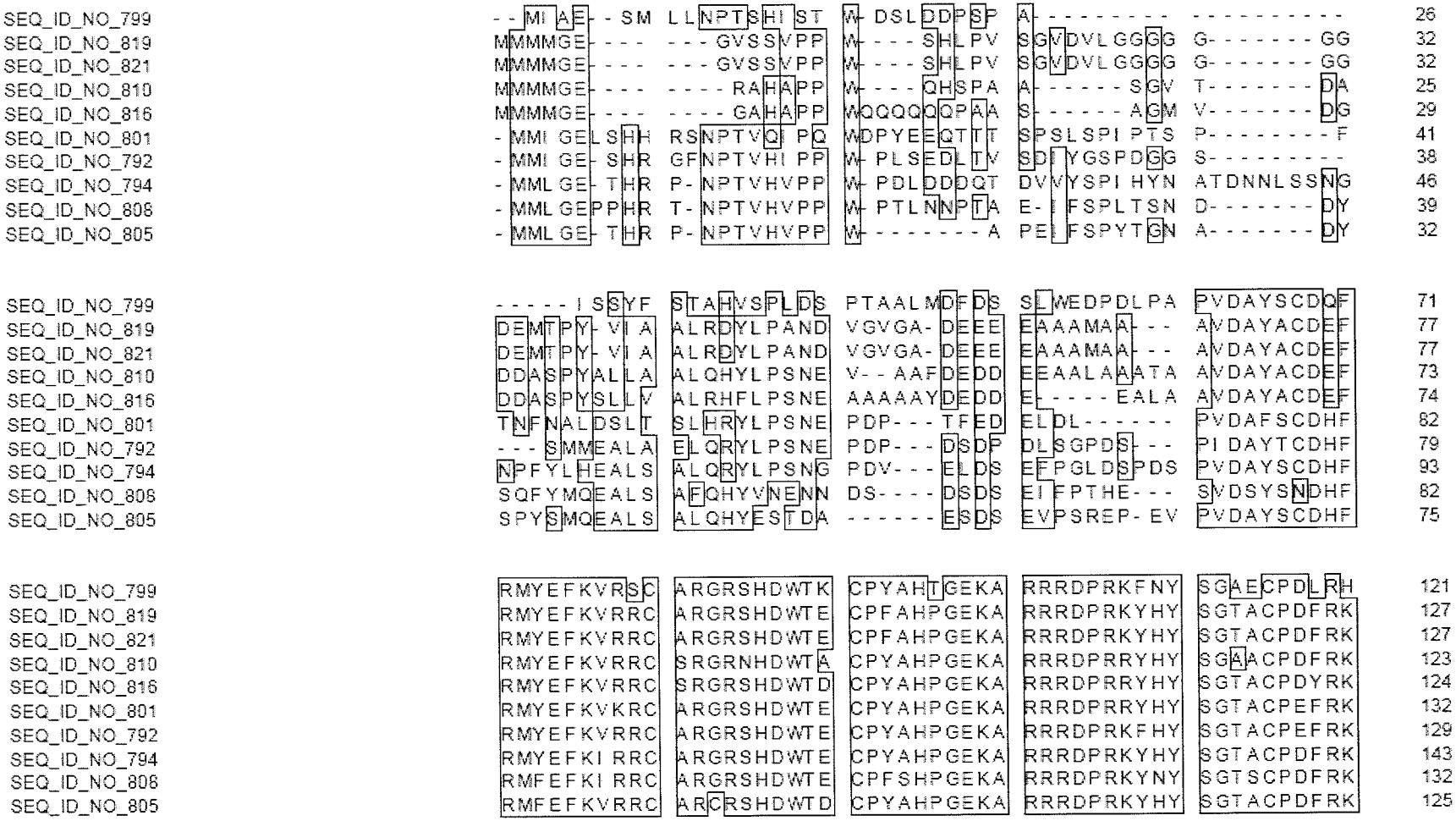

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Figure 25 (continued)



Figure 25 (continued)

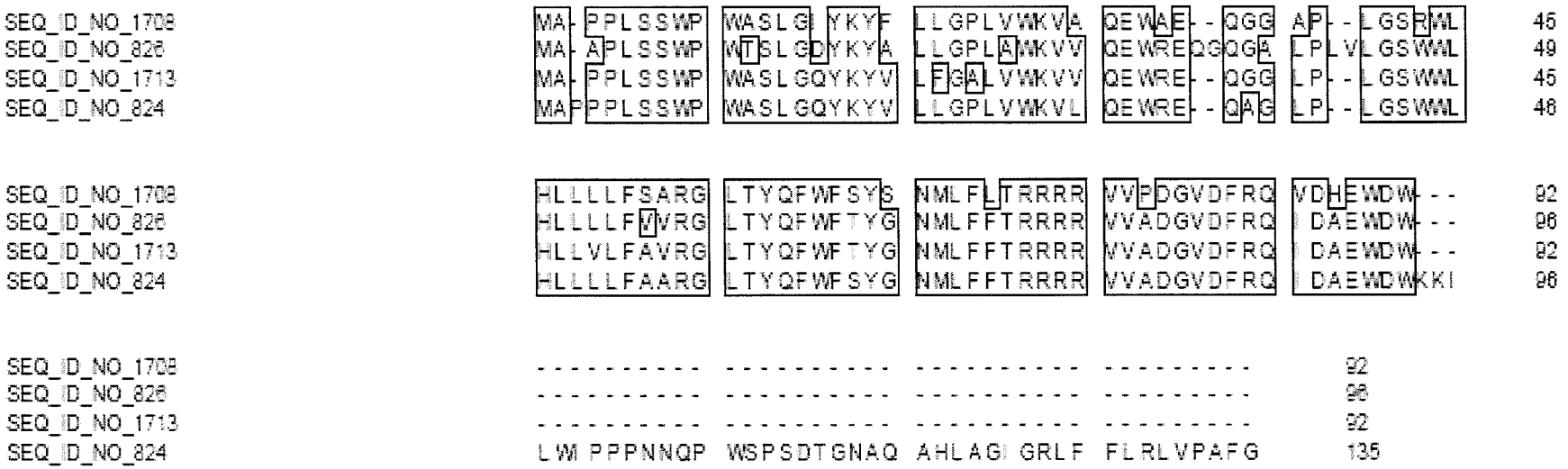


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Figure 25 (continued)

SEQ_ID_NO_799	- - - - - -	307
SEQ_ID_NO_819	- - - - - -	386
SEQ_ID_NO_821	- - - - - -	386
SEQ_ID_NO_810	- - - - - -	391
SEQ_ID_NO_816	- - - - - -	398
SEQ_ID_NO_801	- - - - - -	389
SEQ_ID_NO_792	- - - - - -	359
SEQ_ID_NO_794	L F I K Y F	392
SEQ_ID_NO_808	- - - - - -	381
SEQ_ID_NO_805	- - - - - -	353

Figure 26


SEQ_ID_NO_1708
SEQ_ID_NO_826
SEQ_ID_NO_1713
SEQ_ID_NO_824
MA-PPLSSWP WASLGLYKYF LLGPLVWKVA QEWAE--QGG AP--LGSPWL 46
MA-APLSSWP WTSLGDYKYA LLGPLAWKVV QEWREQGQGA LPLVLGSWWL 49
MA-PPLSSWP WASLGQYKYV LFGALVWKVV QEWRE--QGG LP--LGSWWL 45
MAPPPLSSWP WASLGQYKYV LLGPLVWKVL QEWRE--QAG LP--LGSWWL 48
HLLLLFSARG LTYQFWFSYS NMLFLLTRRRR VVPDGVDFRQ VDHEWDW--- 92
HLLLLFVVRG LTYQFWFTYG NMLFFTRRRR VVADGVDFRQ IDAEWDW--- 96
HLLVLFAVRG LTYQFWFTYG NMLFFTRRRR VVADGVDFRQ IDAEWDW--- 92
HLLLLFAARG LTYQFWFSYG NMLFFTRRRR VVADGVDFRQ IDAEWDWKKI 96
---------- ---------- ---------- ---------- 92
---------- ---------- ---------- ---------- 96
---------- ---------- ---------- ---------- 92
LWIPPPNNQP WSPSDTGNAQ AHLAGIGRLF FLRLVPAFG 135

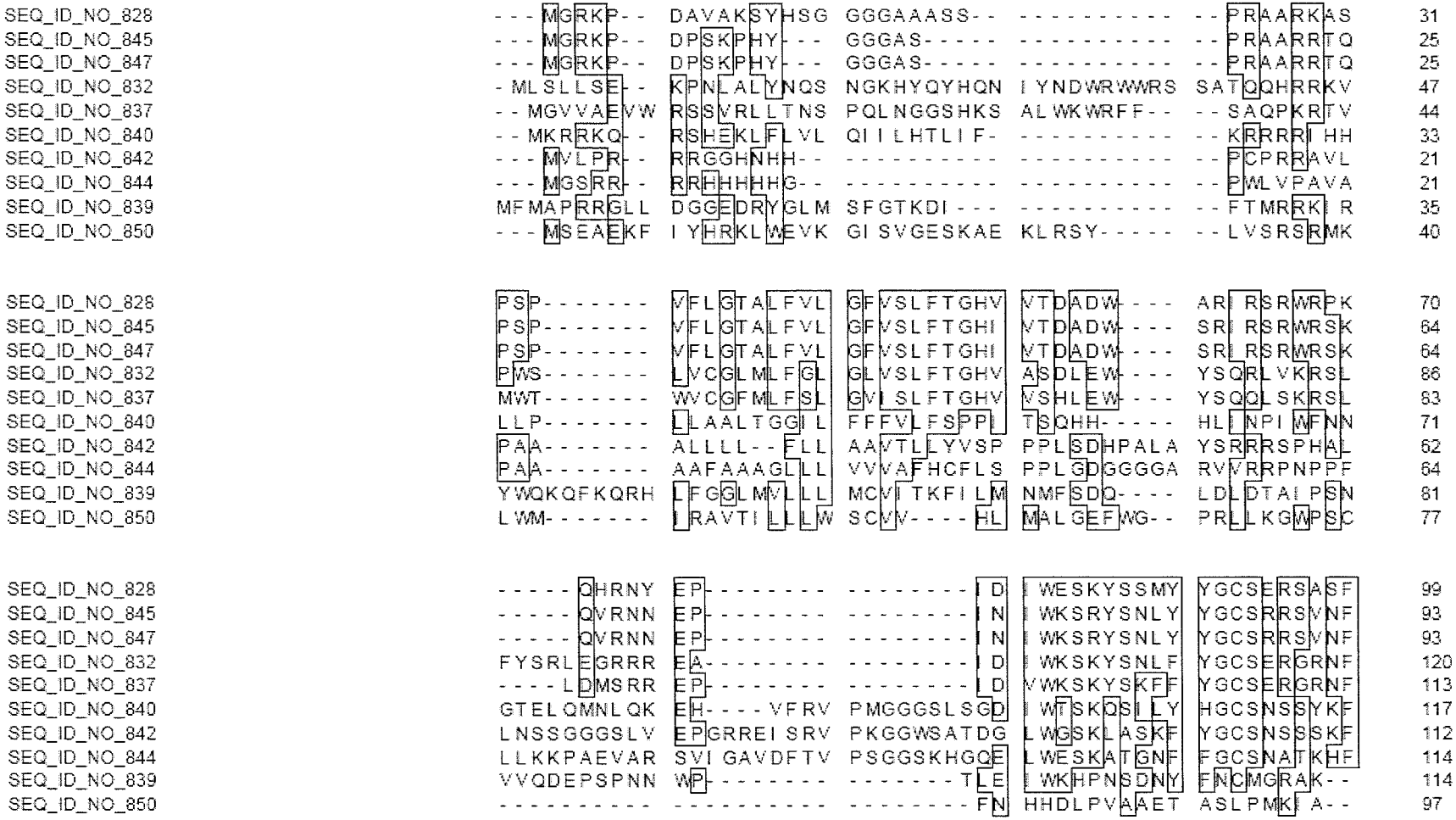

SEQ_ID_NO_828
SEQ_ID_NO_845
SEQ_ID_NO_847
SEQ_ID_NO_832
SEQ_ID_NO_837
SEQ_ID_NO_840
SEQ_ID_NO_842
SEQ_ID_NO_844
SEQ_ID_NO_839
SEQ_ID_NO_850

Figure 27 (continued)

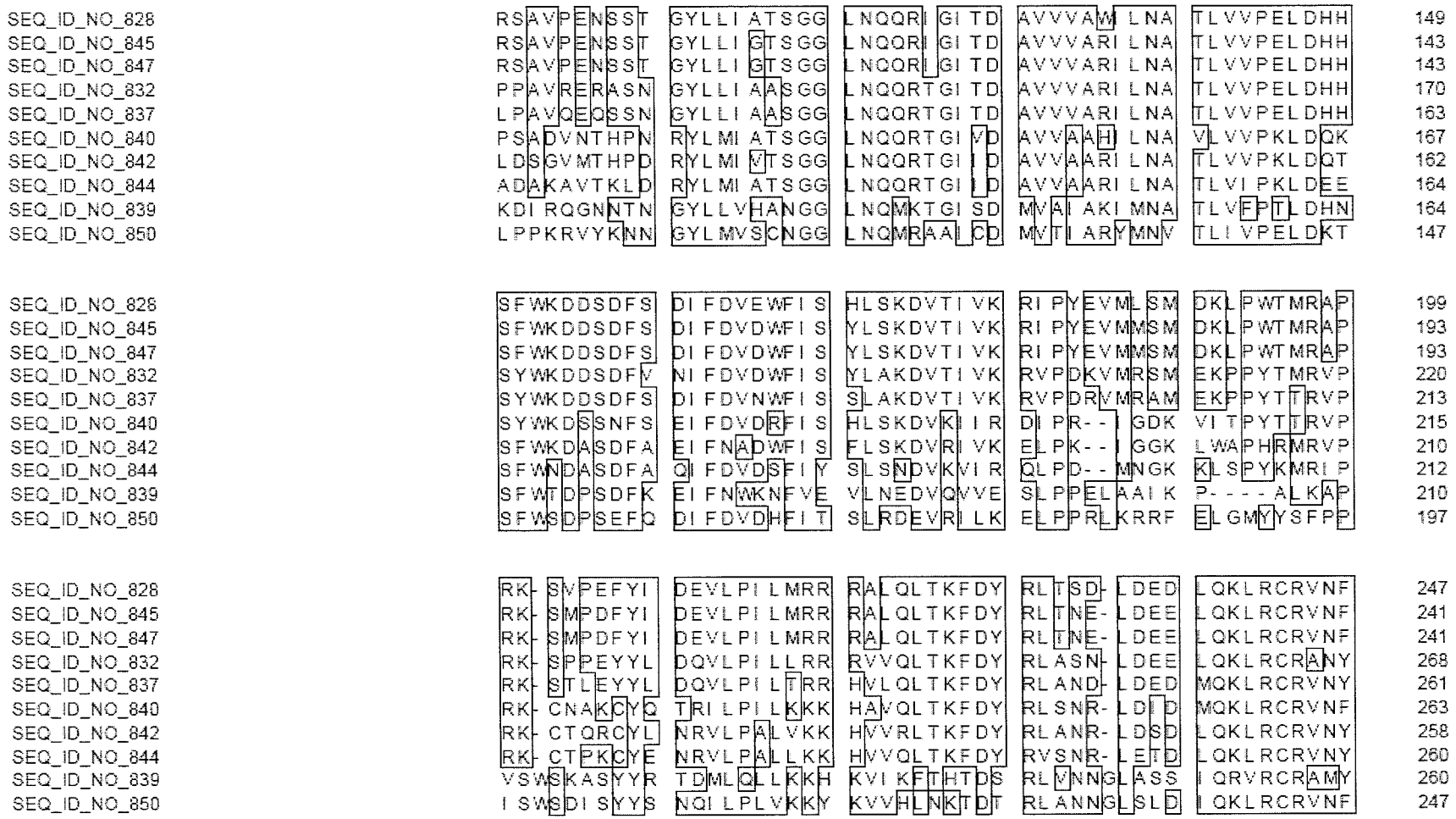


Figure 27 (continued)



Figure 27 (continued)

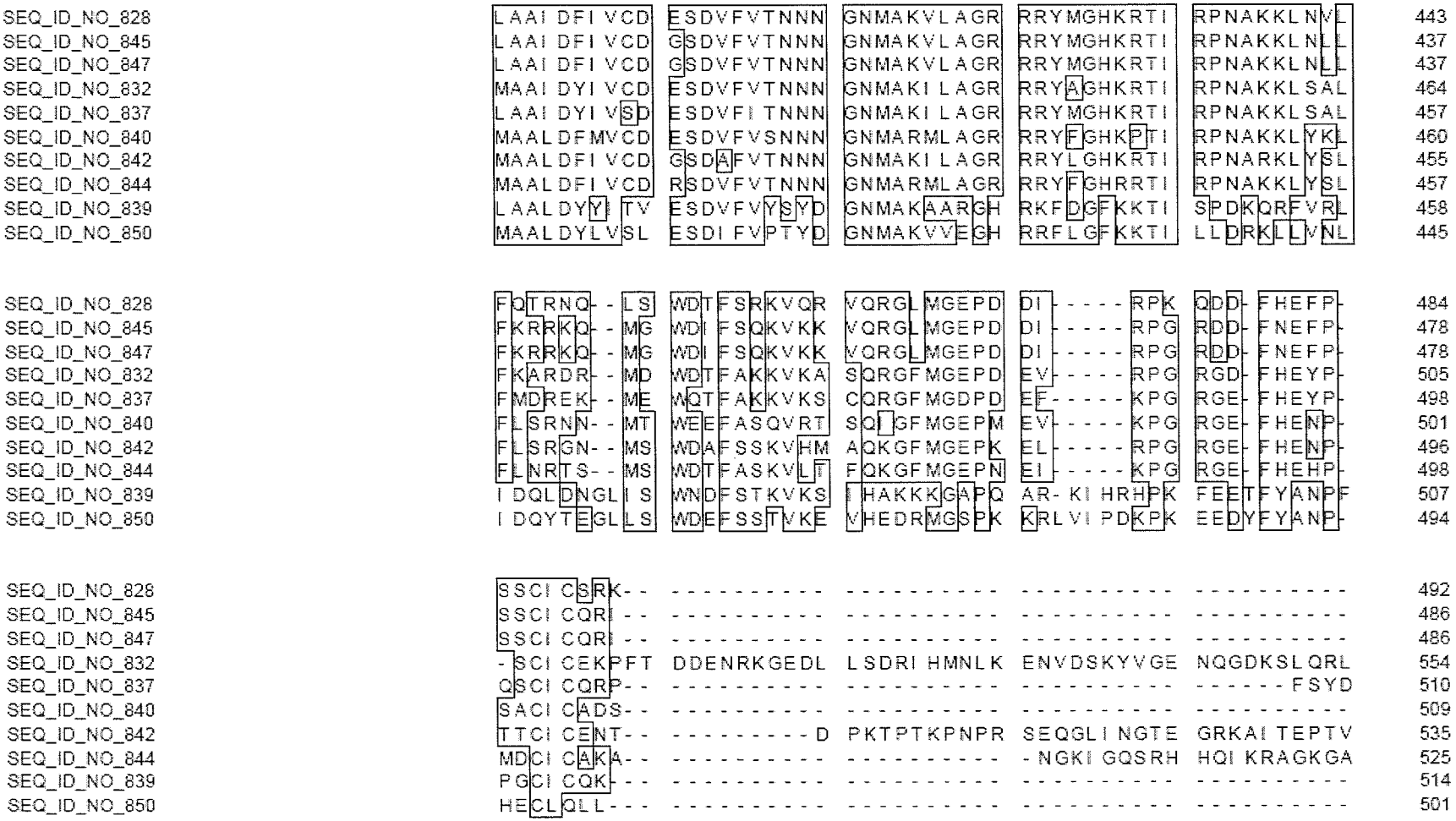


Figure 27 (continued)

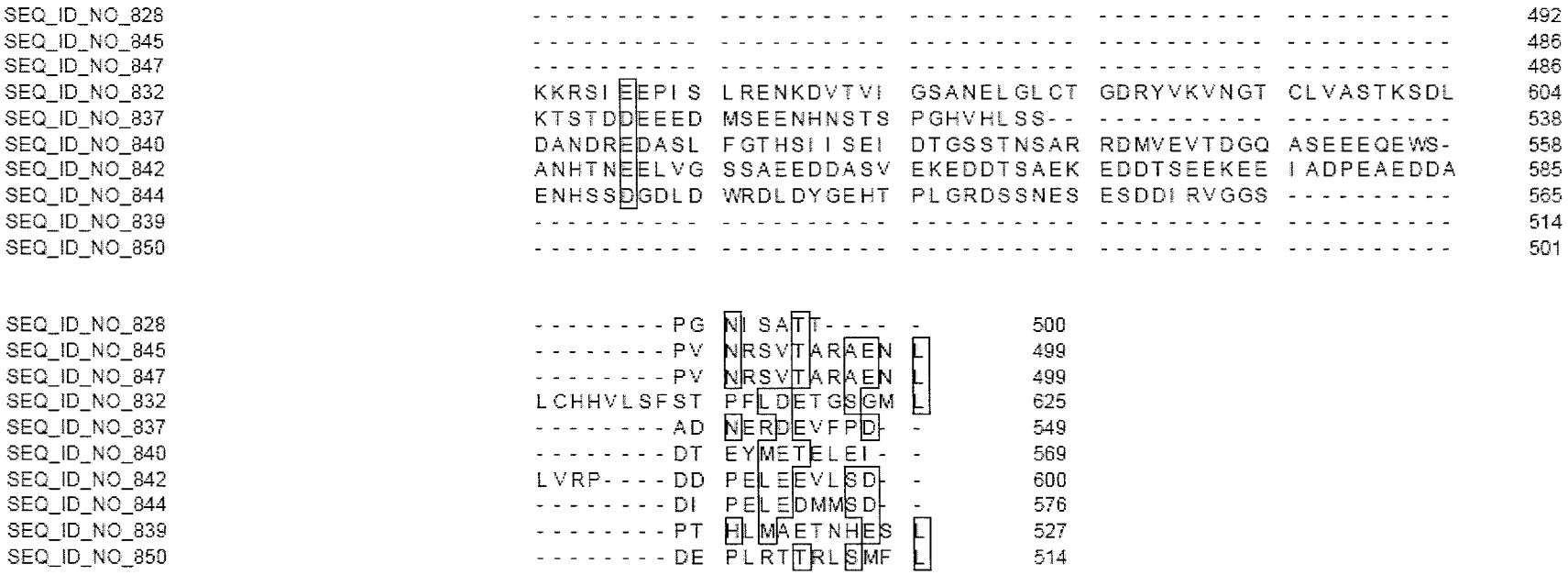


Figure 28


SEQ_ID_NO_876
SEQ_ID_NO_855
SEQ_ID_NO_862
SEQ_ID_NO_858
SEQ_ID_NO_856
SEQ_ID_NO_885
SEQ_ID_NO_868
SEQ_ID_NO_886
SEQ_ID_NO_870
SEQ_ID_NO_878
39
35
33
35
35
49
37
42
37
37
SEQ_ID_NO_876
SEQ_ID_NO_855
SEQ_ID_NO_862
SEQ_ID_NO_858
SEQ_ID_NO_856
SEQ_ID_NO_885
SEQ_ID_NO_868
SEQ_ID_NO_886
SEQ_ID_NO_870
SEQ_ID_NO_878
81
77
75
77
77
98
80
85
80
80
SEQ_ID_NO_876
SEQ_ID_NO_855
SEQ_ID_NO_862
SEQ_ID_NO_858
SEQ_ID_NO_856
SEQ_ID_NO_885
SEQ_ID_NO_868
SEQ_ID_NO_886
SEQ_ID_NO_870
SEQ_ID_NO_878
101
97
96
98
98
117
109
120
107
105

Figure 29

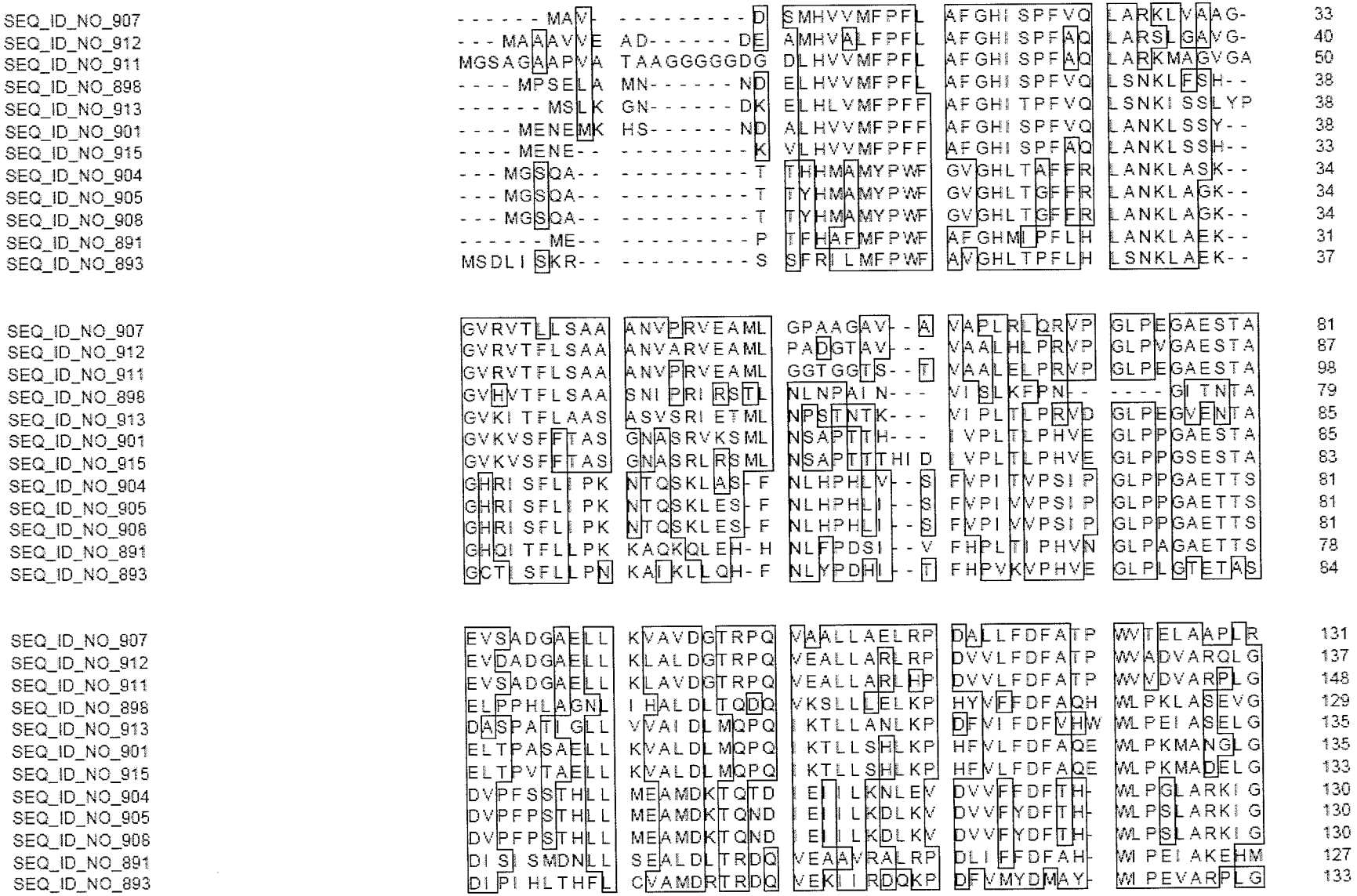

SEQ_ID_NO_907
SEQ_ID_NO_912
SEQ_ID_NO_911
SEQ_ID_NO_898
SEQ_ID_NO_913
SEQ_ID_NO_901
SEQ_ID_NO_915
SEQ_ID_NO_904
SEQ_ID_NO_905
SEQ_ID_NO_908
SEQ_ID_NO_891
SEQ_ID_NO_893
33
40
50
38
38
38
33
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34
34
31
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81
87
98
79
85
85
83
81
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137
148
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135
135
133
130
130
130
127
133

Figure 29 (continued)



Figure 29 (continued)

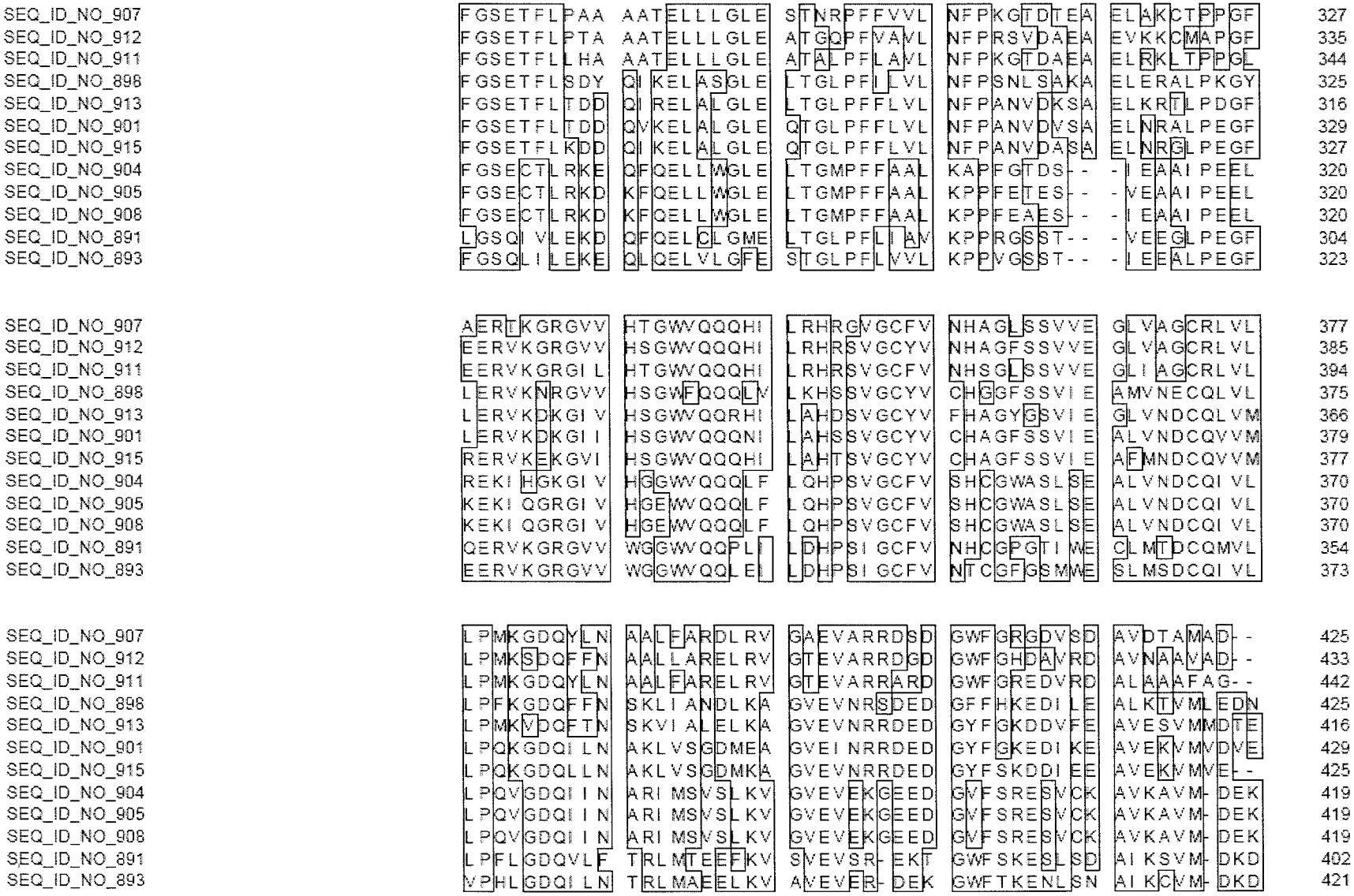


Figure 29 (continued)

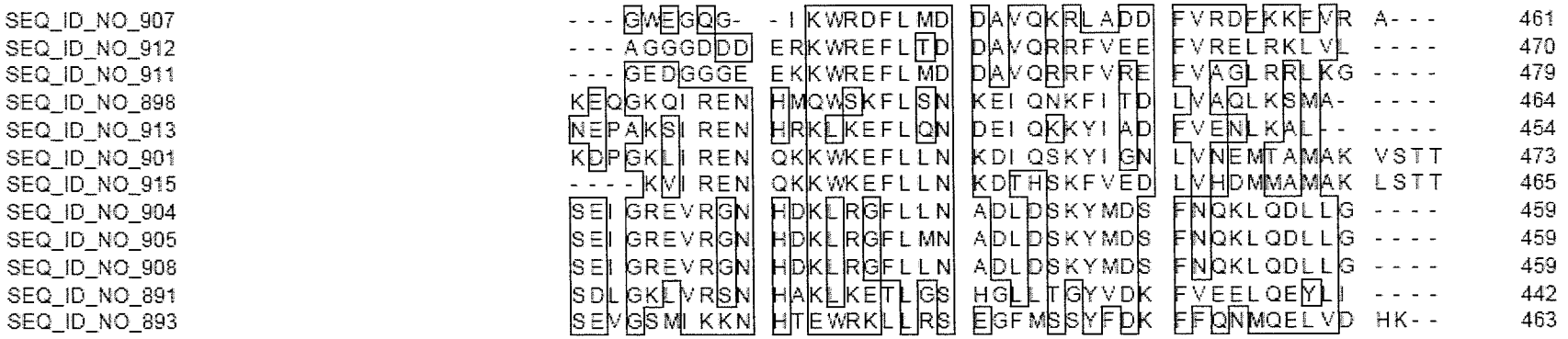


Figure 30

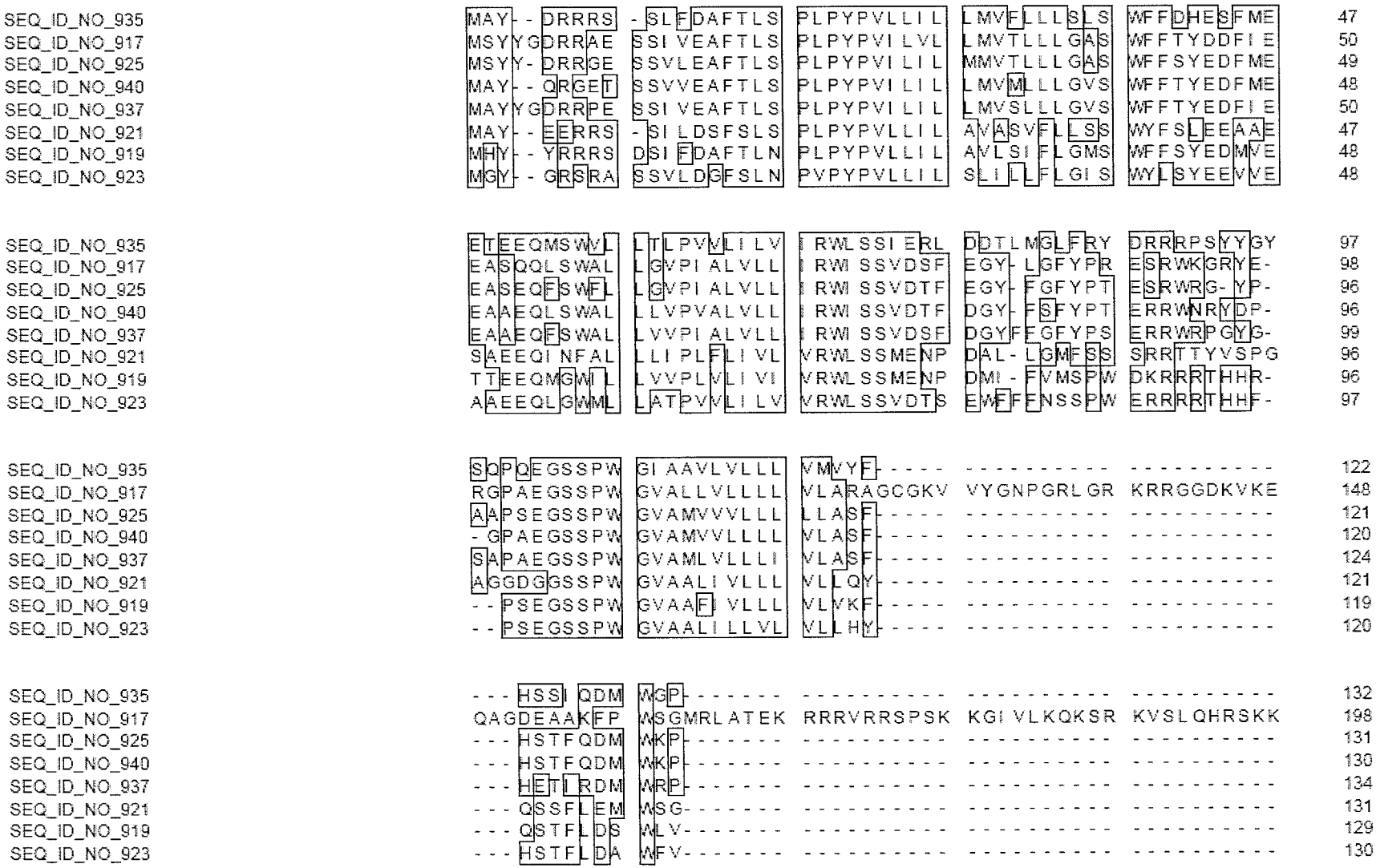

SEQ_ID_NO_935
SEQ_ID_NO_917
SEQ_ID_NO_925
SEQ_ID_NO_940
SEQ_ID_NO_937
SEQ_ID_NO_921
SEQ_ID_NO_919
SEQ_ID_NO_923
MAY--DRRRS-SLFDAFTLS PLPYPVLLIL LMVFLLLSLS WFFDHESFME 47
MSYYGDRRAE SSIVEAFTLS PLPYPVILVL LMVTLLLGAS WFFTYDDFIE 50
MSYY-DRRGE SSVLEAFTLS PLPYPVILIL MMVTLLLGAS WFFSYEDFME 49
MAY--QRGET SSVVEAFTLS PLPYPVILIL LMVMLLLGVS WFFTYEDFME 48
MAYYGDRRPE SSIVEAFTLS PLPYPVILIL LMVSLLLGVS WFFTYEDFIE 50
MAY--EERRS-SILDSFSLS PLPYPVLLIL AVASVFLLSS WYFSLEEAAE 47
MHY--YRRRS DSIFDAFTLN PLPYPVLLIL AVLSIFLGMS WFFSYEDMVE 48
MGY--GRSRA SSVLDGFSLN PVPYPVLLIL SLILLFLGIS WYLSYEEVVE 48
ETEEQMSWVL LTLPVVLILV IRWLSSIERL DDTLMGLFRY DRRRPSYYGY 97
EASQQLSWAL LGVPIALVLL IRWISSVDSF EGY-LGFYPR ESRWKGRYE- 98
EASEQFSWFL LGVPIALVLL IRWISSVDTF EGY-FGFYPT ESRWRG-YP- 96
EAAEQLSWAL LLVPVALVLL IRWISSVDTF DGY-FSFYPT ERRWNRYDP- 96
EAAEQFSWAL LVVPIALVLL IRWISSVDSF DGYFFGFYPS ERRWRPGYG- 99
SAEEQINFAL LLIPLFLIVL VRWLSSMENP DAL-LGMFSS SRRTTYVSPG 96
TTEEQMGWIL LVVPLVLIVI VRWLSSMENP DMI-FVMSPW DKRRRTHHR- 96
AAEEQLGWML LATPVVLILV VRWLSSVDTS EWFFFNSSPW ERRRRTHHF- 97
SQPQEGSSPW GIAAVLVLLL VMVYF----- ---------- ---------- 122
RGPAEGSSPW GVALLVLLLL VLARAGCGKV VYGNPGRLGR KRRGGDKVKE 148
APSEGSSPW GVAMVVVLLL LLASF----- ---------- ---------- 121
-GPAEGSSPW GVAMVVLLLL VLASF----- ---------- ---------- 120
SAPAEGSSPW GVAMLVLLLI VLASF----- ---------- ---------- 124
AGGDGGSSPW GVAALIVLLL VLLQY----- ---------- ---------- 121
--PSEGSSPW GVAAFIVLLL VLVKF----- ---------- ---------- 119
--PSEGSSPW GVAALILLVL VLLHY----- ---------- ---------- 120
---HSSIQDM WGP------ ---------- ---------- ---------- 132
QAGDEAAKFP WSGMRLATEK RRRVRRSPSK KGIVLKQKSR KVSLQHRSKK 198
---HSTFQDM WKP------ ---------- ---------- ---------- 131
---HSTFQDM WKP------ ---------- ---------- ---------- 130
---HETLRDM WRP------ ---------- ---------- ---------- 134
---QSSFLEM WSG------ ---------- ---------- ---------- 131
---QSTFLDS WLV------ ---------- ---------- ---------- 129
---HSTFLDA WFV------ ---------- ---------- ---------- 130

Figure 30 (continued)

SEQ_ID_NO_935	- - -	132
SEQ_ID_NO_917	L K A	201
SEQ_ID_NO_925	- - -	131
SEQ_ID_NO_940	- - -	130
SEQ_ID_NO_937	- - -	134
SEQ_ID_NO_921	- - -	131
SEQ_ID_NO_919	- - -	129
SEQ_ID_NO_923	- - -	130

Figure 31

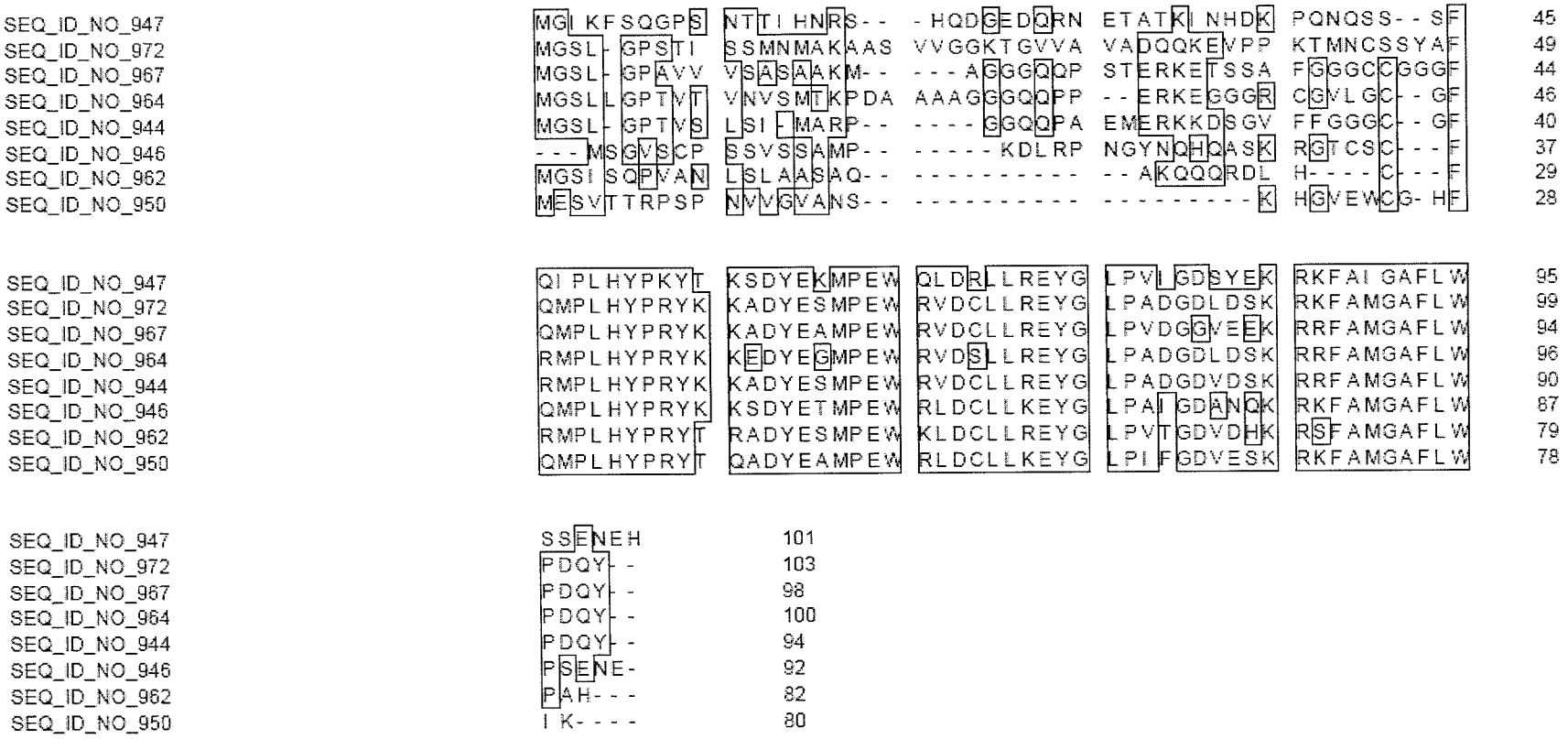

SEQ_ID_NO_947
SEQ_ID_NO_972
SEQ_ID_NO_967
SEQ_ID_NO_964
SEQ_ID_NO_944
SEQ_ID_NO_946
SEQ_ID_NO_962
SEQ_ID_NO_950
MGIKFSQGPS NTTIHNRS-- -HQDGEDQRN ETATKLNHDK PQNQSS--SF 45
MGSL-GPSTI SSMNMAKAAS VVGGKTGVVA VADQQKEVPP KTMNCSSYAF 49
MGSL-GPAVV VSASAAAKM- ---AGGGQQP STERKETSSA FGGGCCGGGF 44
MGSLLGPTVT VNVSMTKPDA AAAGGGQQPP --ERKEGGGR CGVLGC--GF 46
MGSL-GPTVS LSI-MARP-- ----GGQQPA EMERKKDSGV FFGGGC--GF 40
---MSGVSCP SSVSSAMP-- -----KDLRP NGYNQHQASK RGTCSC---F 37
MGSISQPVAN LSLAASAQ-- ---------- --AKQQQRDL H----C---F 29
MESVTTRPSP NVVGVANS-- ---------- ---------K HGVEWCG-HF 28
QIPLHYPKYT KSDYEKMPEW QLDRLLREYG LPVIGDSYEK RKFAIGAFLW 95
QMPLHYPRYK KADYESMPEW RVDCLLREYG LPADGDLDSK RKFAMGAFLW 99
QMPLHYPRYK KADYEAMPEW RVDCLLREYG LPVDGGVEEK RRFAMGAFLW 94
RMPLHYPRYK KEDYEGMPEW RVDSLLREYG LPADGDLDSK RRFAMGAFLW 96
RMPLHYPRYK KADYESMPEW RVDCLLREYG LPADGDVDSK RRFAMGAFLW 90
QMPLHYPRYK KSDYETMPEW RLDCLLKEYG LPAIGDANQK RKFAMGAFLW 87
RMPLHYPRYT RADYESMPEW KLDCLLREYG LPVTGDVDHK RSFAMGAFLW 79
QMPLHYPRYT QADYEAMPEW RLDCLLKEYG LPIFGDVESK RKFAMGAFLW 78
SSENEH 101
PDQY-- 103
PDQY-- 98
PDQY-- 100
PDQY-- 94
PSENE- 92
PAH--- 82
IK---- 80

Figure 32

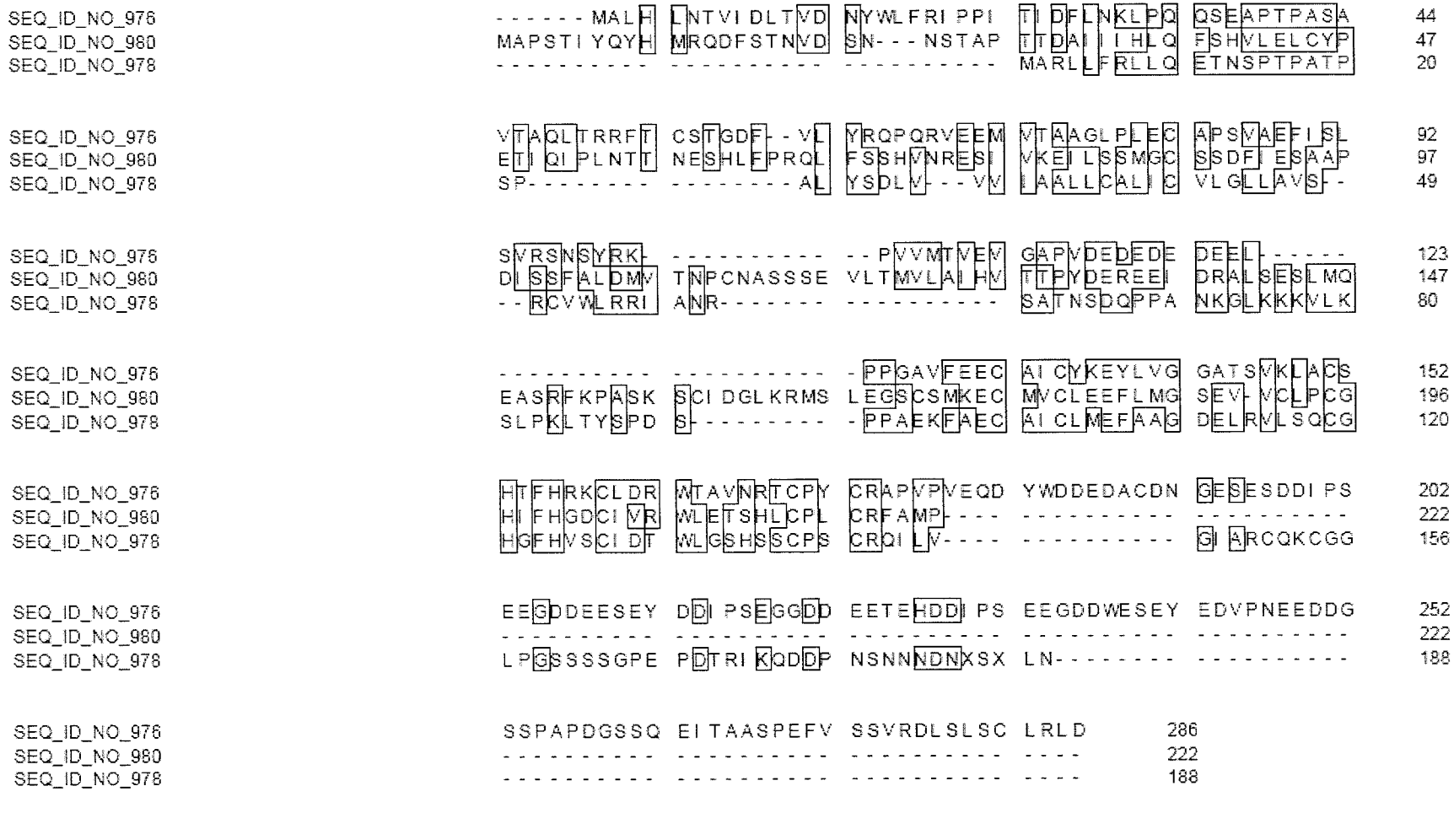

SEQ_ID_NO_976
SEQ_ID_NO_980
SEQ_ID_NO_978
MALHLNTVIDLTVDNYWLFRIPPITIDFLNKLPQQSEAPTPASA 44
MAPSTIYQYHMRQDFSTNVDSN---NSTAPTTDAIIIHLQFSHVLELCYP 47
MARLLFRLLQETNSPTPATP 20
SEQ_ID_NO_976
SEQ_ID_NO_980
SEQ_ID_NO_978
VTAQLTRRFTCSTGDF--VLYRQPQRVEEMVTAAGLPLECAPSVAEFISL 92
ETIQIPLNTTNESHLFPRQLFSSHVNRESIVKEILSSMGCSSDFIESAAP 97
SP--------------------ALYSDLV---VVIAALLCALICVLGLLAVS-- 49
SEQ_ID_NO_976
SEQ_ID_NO_980
SEQ_ID_NO_978
SVRSNSYRK--PVVMTVEVGAPVDEDEDEDEEL------ 123
DISSFALDMVTNPCNASSSEVLTMVLAIHVTTPYDEREEIDRALSESLMQ 147
--RCVWLRRIANR-------SATNSDQPPANKGLKKKVLK 80
SEQ_ID_NO_976
SEQ_ID_NO_980
SEQ_ID_NO_978
PPGAVFEECAICYKEYLVGGATSVKLACS 152
EASRFKPASKSCIDGLKRMSLEGSCSMKECMVCLEEFLMGSEV-VCLPCG 196
SLPKLTYSPDS---------PPAEKFAECAICLMEFAAGDELRVLSQCG 120
SEQ_ID_NO_976
SEQ_ID_NO_980
SEQ_ID_NO_978
HTFHRKCLDRWTAVNRTCPYCRAPVPVEQDYWDDEDACDNGESESDDIPS 202
HIFHGDCIVRWLETSHLCPLCRFAMP------ 222
HGFHVSCIDTWLGSHSSCPSCRQILV---- 156
SEQ_ID_NO_976
SEQ_ID_NO_980
SEQ_ID_NO_978
EEGDDEESEYDDIPSEGGDDEETEHDDIPSEEGDDWESEYEDVPNEEDDG 252
LPGSSSSGPEPDTRIKQDDPNSNNNDNXSXLN-------- 222 188
SEQ_ID_NO_976
SEQ_ID_NO_980
SEQ_ID_NO_978
SSPAPDGSSQEITAASPEFVSSVRDLSLSCLRLD 286
222
188

Figure 33

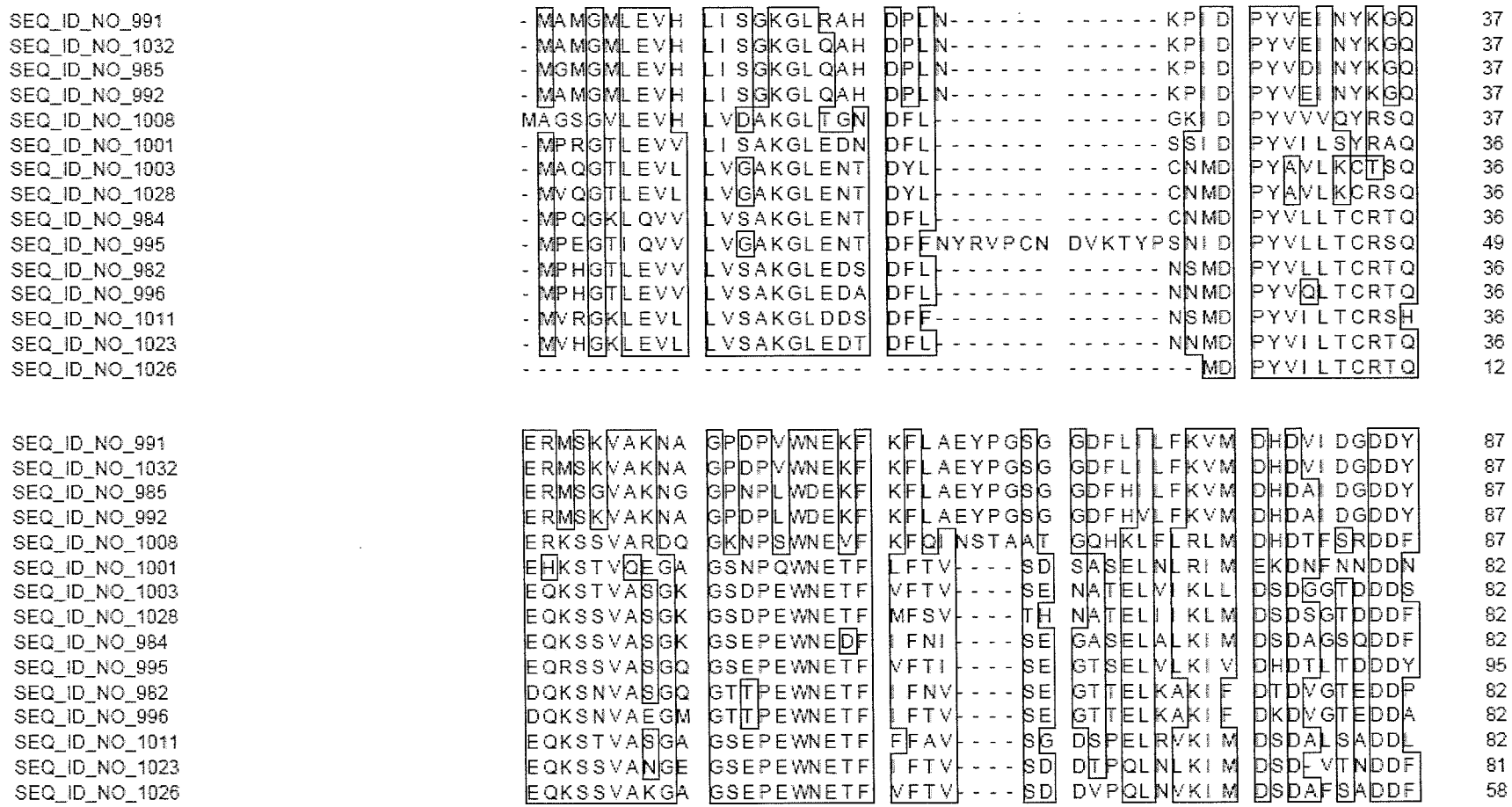

SEQ_ID_NO_991
SEQ_ID_NO_1032
SEQ_ID_NO_985
SEQ_ID_NO_992
SEQ_ID_NO_1008
SEQ_ID_NO_1001
SEQ_ID_NO_1003
SEQ_ID_NO_1028
SEQ_ID_NO_984
SEQ_ID_NO_995
SEQ_ID_NO_962
SEQ_ID_NO_996
SEQ_ID_NO_1011
SEQ_ID_NO_1023
SEQ_ID_NO_1026

Figure 33 (continued)

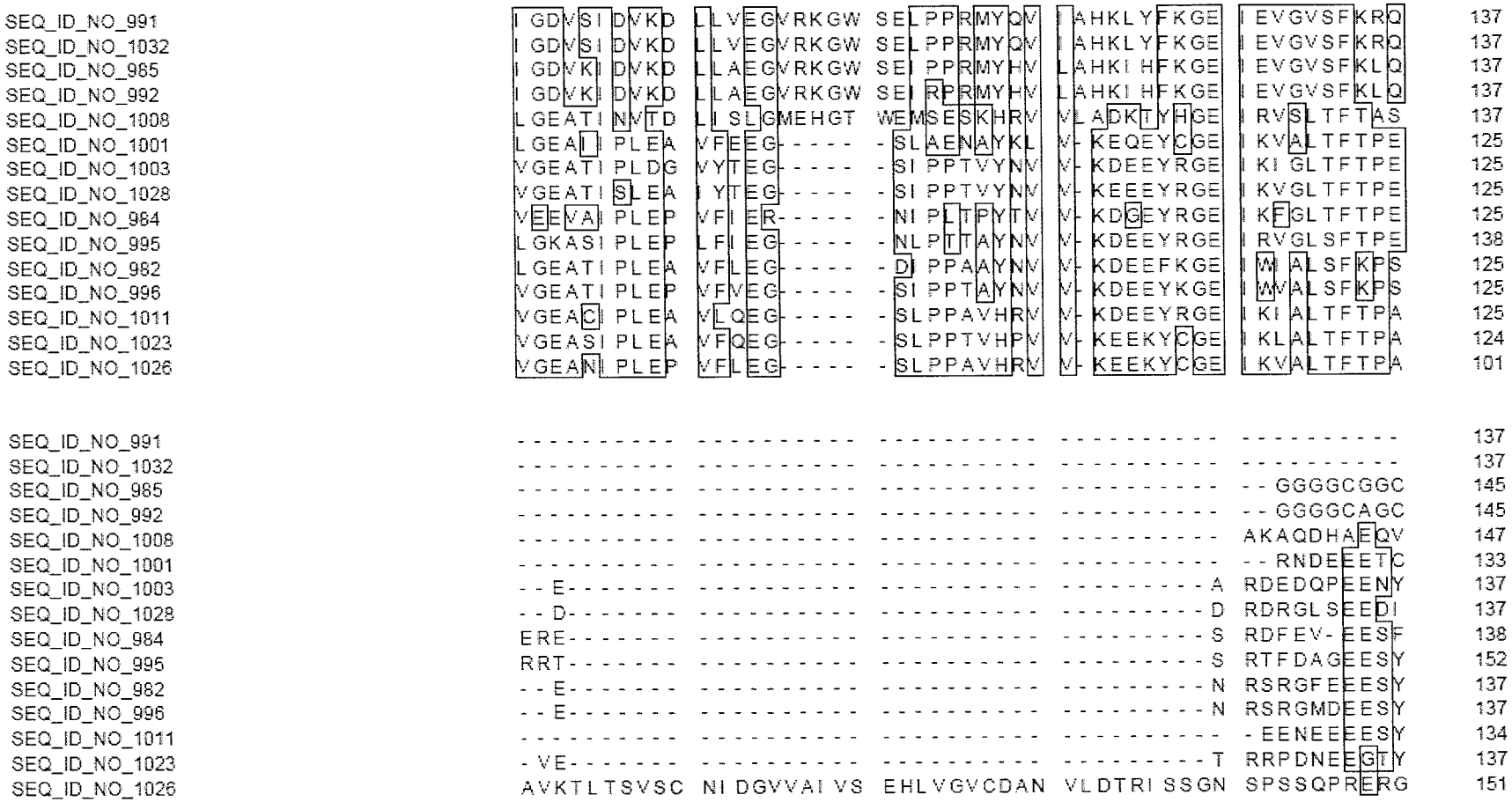


Figure 33 (continued)

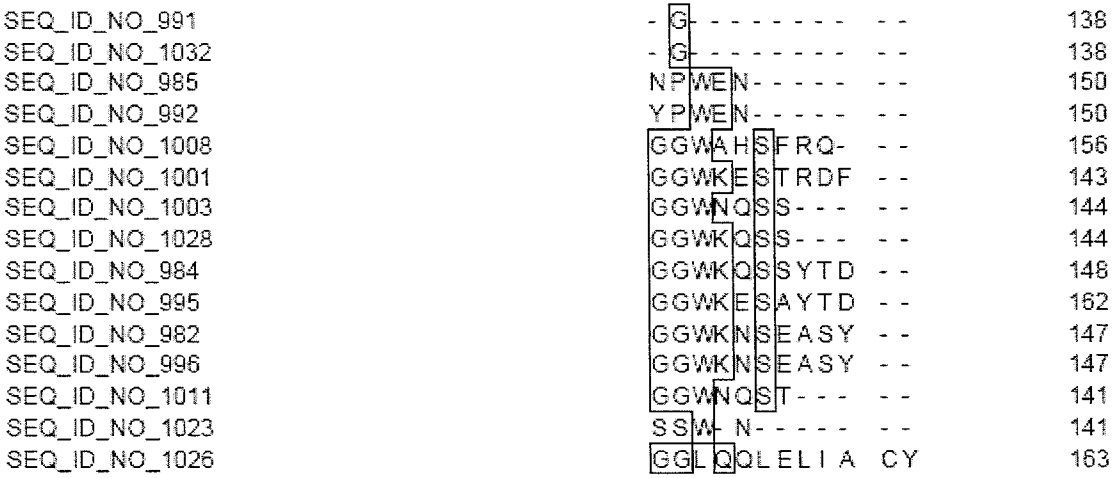


Figure 34


SEQ_ID_NO_1058
SEQ_ID_NO_1077
SEQ_ID_NO_1078
SEQ_ID_NO_1075
SEQ_ID_NO_1095
SEQ_ID_NO_1055
SEQ_ID_NO_1080
SEQ_ID_NO_1086
SEQ_ID_NO_1085
SEQ_ID_NO_1097
SEQ_ID_NO_1054
SEQ_ID_NO_1088
SEQ_ID_NO_1068
SEQ_ID_NO_1072
SEQ_ID_NO_1057
SEQ_ID_NO_1061
SEQ_ID_NO_1076
SEQ_ID_NO_1092
SEQ_ID_NO_1074
SEQ_ID_NO_1083

Figure 34 (continued)

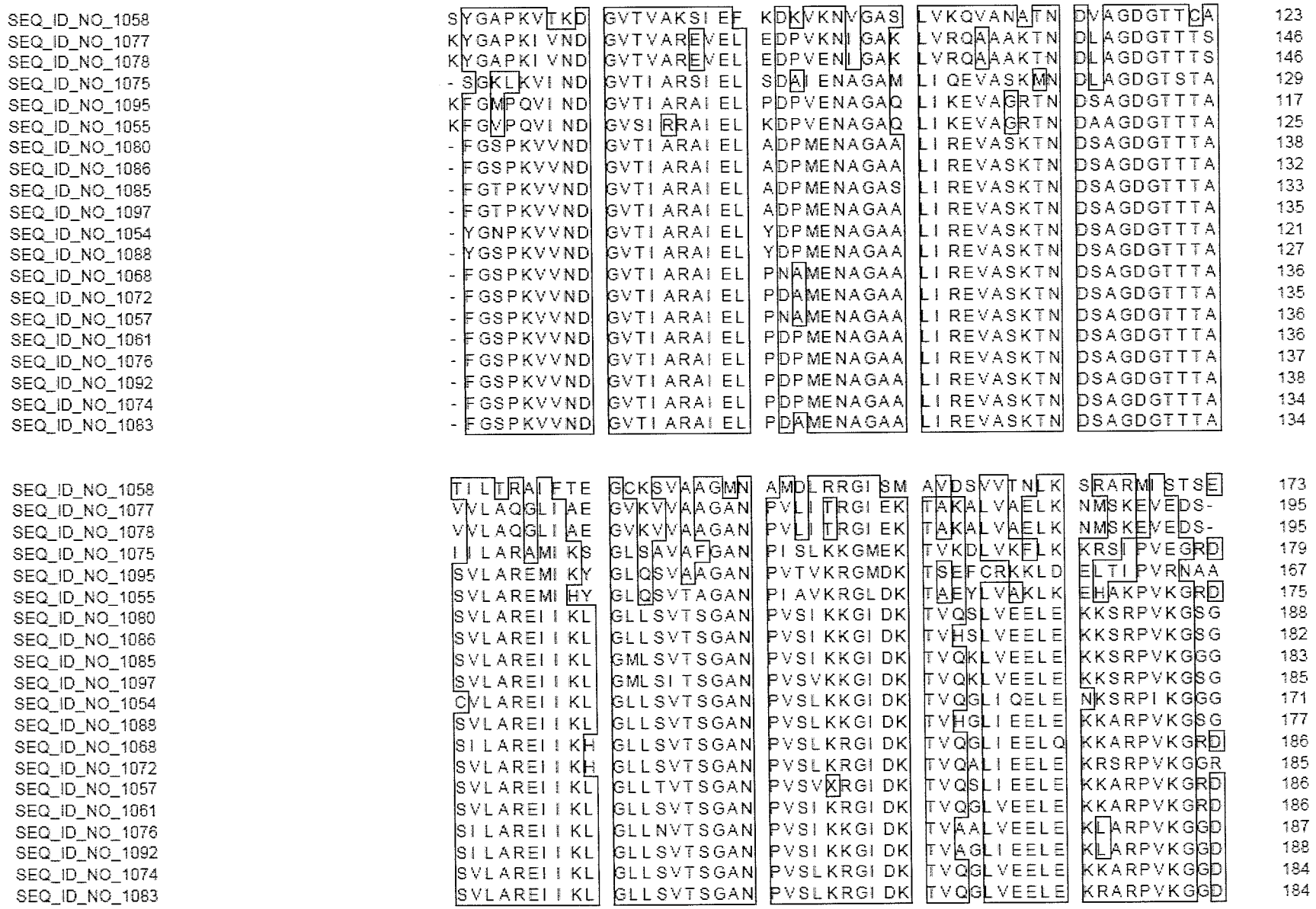


Figure 34 (continued)

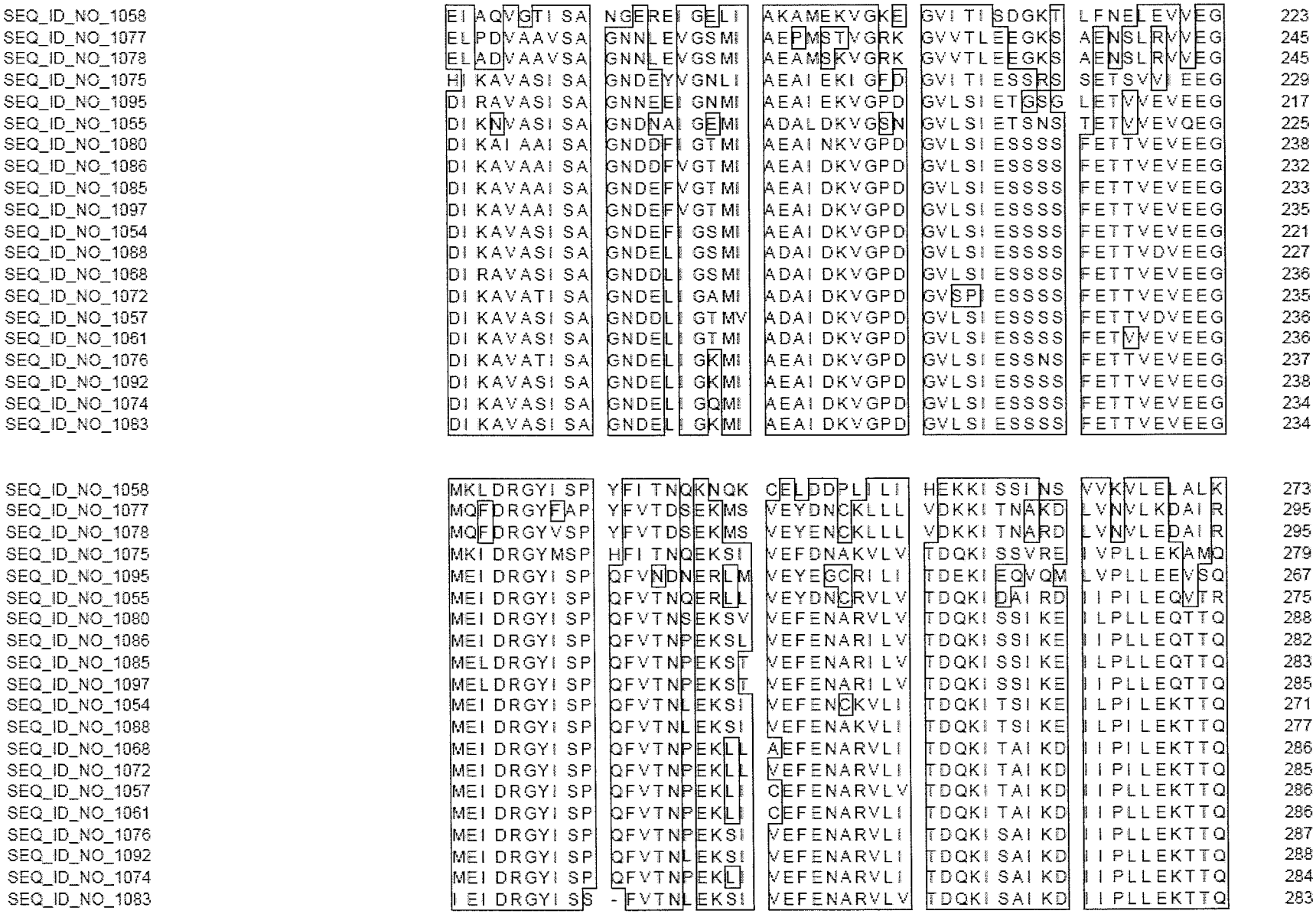


Figure 34 (continued)



Figure 34 (continued)

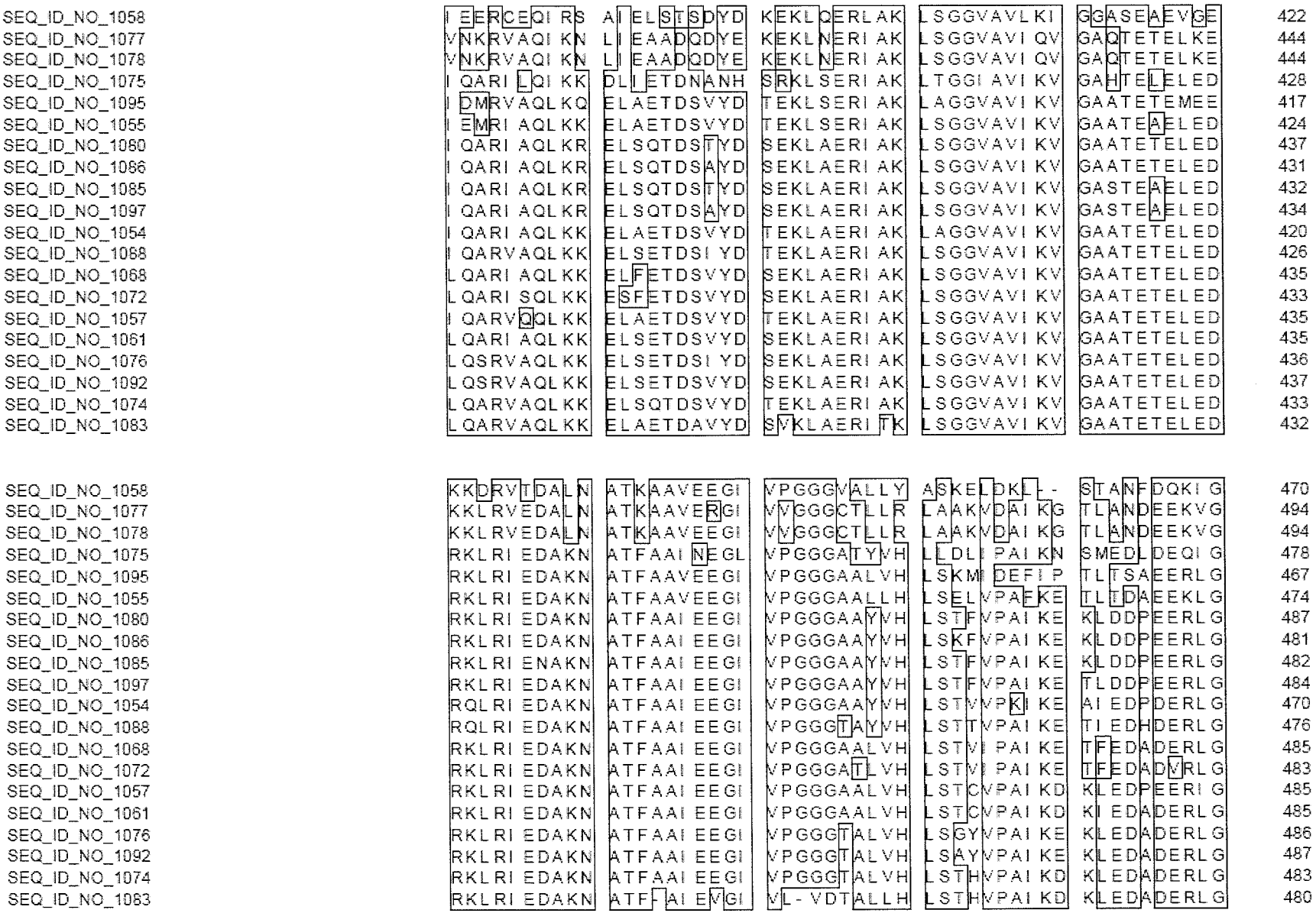


Figure 34 (continued)



Figure 34 (continued)

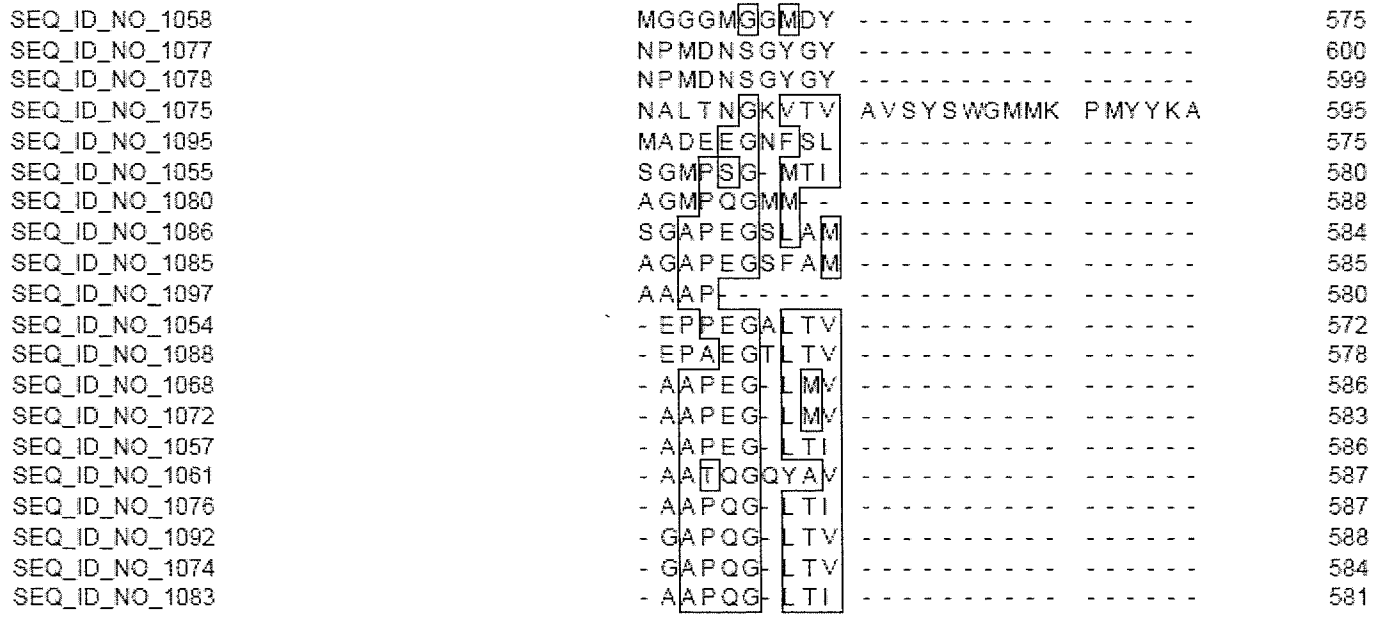


Figure 35

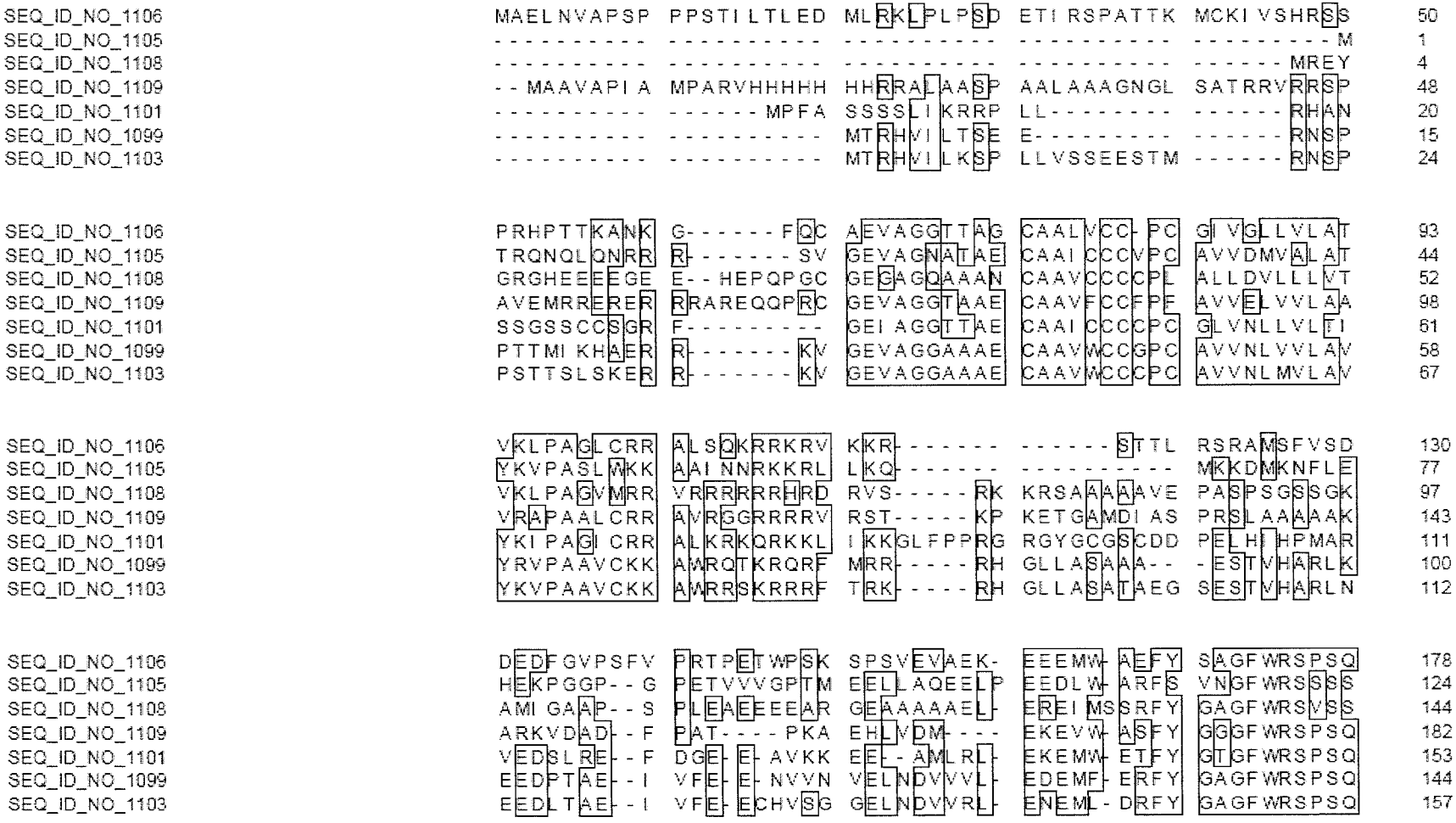

SEQ_ID_NO_1106 MAELNVAPSP PPSTILTLED MLRKLPLPSD ETIRSPATTK MCKIVSHRSS 50
SEQ_ID_NO_1105 ---------- ---------- ---------- ---------- ---------M 1
SEQ_ID_NO_1108 ---------- ---------- ---------- ---------- ------MREY 4
SEQ_ID_NO_1109 --MAAVAPIA MPARVHHHHH HHRRALAASP AALAAAGNGL SATRRVRRSP 48
SEQ_ID_NO_1101 ---------- ------MPFA SSSSLIKRRP LL-------- ------RHAN 20
SEQ_ID_NO_1099 ---------- ---------- MTRHVILTSE E--------- ------RNSP 15
SEQ_ID_NO_1103 ---------- ---------- MTRHVILKSP LLVSSEESTM ------RNSP 24
SEQ_ID_NO_1106 PRHPTTKANK G------FQC AEVAGGTTAG CAALVCC-PC GIVGLLVLAT 93
SEQ_ID_NO_1105 TRQNQLQNRR R------SV GEVAGNATAE CAAICCCVPC AVVDMVALAT 44
SEQ_ID_NO_1108 GRGHEEEEGE E--HEPQPGC GEGAGQAAAN CAAVCCCCPL ALLDVLLLVT 52
SEQ_ID_NO_1109 AVEMRREREK RRAREQQPRC GEVAGGTAAE CAAVFCCFPF AVVELVVLAA 98
SEQ_ID_NO_1101 SSGSSCCSGR F--------- GEIAGGTTAE CAAICCCCPC GLVNLLVLFI 61
SEQ_ID_NO_1099 PTTMIKHAER R------KV GEVAGGAAAE CAAVWCCGPC AVVNLVVLAV 58
SEQ_ID_NO_1103 PSTTSLSKER R------KV GEVAGGAAAE CAAVWCCCPC AVVNLMVLAV 67
SEQ_ID_NO_1106 VKLPAGLCRR ALSQKRRKRV KKR------ ------STTL RSRAMSFVSD 130
SEQ_ID_NO_1105 YKVPASLWKK AAINNRKKRL LKQ------ ---------- MKKDMKNFLE 77
SEQ_ID_NO_1108 VKLPAGVMRR VRRRRRRHRD RVS-----RK KRSAAAAAVE PASPSGSSGK 97
SEQ_ID_NO_1109 VRAPAALCRR AVRGGRRRRV RST-----KP KETGAMDIAS PRSLAAAAAK 143
SEQ_ID_NO_1101 YKIPAGICRR ALKRKQRKKL IKKGLFPPRG RGYGCGSCDD PELHIHPMAR 111
SEQ_ID_NO_1099 YRVPAAVCKK AWRQTKRQRF MRR-----RH GLLASAAA-- -ESTVHARLK 100
SEQ_ID_NO_1103 YKVPAAVCKK AWRRSKRRRF TRK-----RH GLLASATAEG SESTVHARLN 112
SEQ_ID_NO_1106 DEDFGVPSFV PRTPETWPSK SPSVEVAEK- EEEMW-AEFY SAGFWRSPSQ 178
SEQ_ID_NO_1105 HEKPGGP--G PETVVVGPTM EELLAQEELP EEDLW-ARFS VNGFWRSSSS 124
SEQ_ID_NO_1108 AMIGAAP--S PLEAEEEEAR GEAAAAAAEL- ERREIMSSRFY GAGFWRSVSS 144
SEQ_ID_NO_1109 ARKVDAD--F PAT----PKA EHLVDM---- EKEVW-ASFY GGGFWRSPSQ 182
SEQ_ID_NO_1101 VEDSLRE--F DGE-E-AVKK EEL--AMLRL- EKEMW-ETFY GTGFWRSPSQ 153
SEQ_ID_NO_1099 EEDPTAE--I VFE-E-NVVN VELNDVVVL- EDEMF-ERFY GAGFWRSPSQ 144
SEQ_ID_NO_1103 EEDLTAE--I VFE-ECHVSG GELNDVVRL- ENEML-DRFY GAGFWRSPSQ 157

Figure 35 (continued)

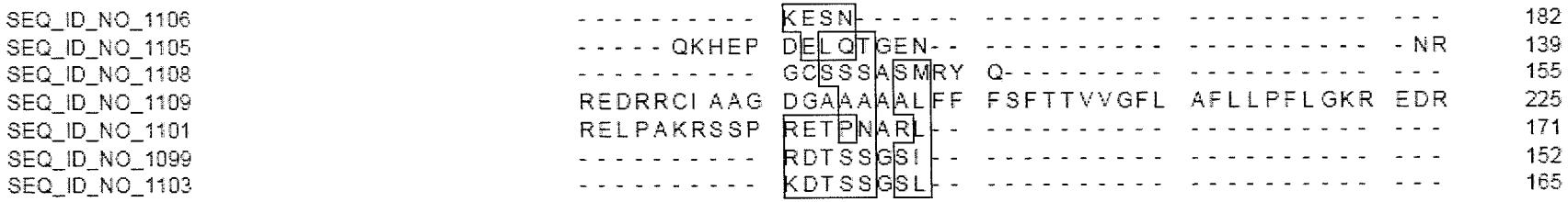


Figure 36

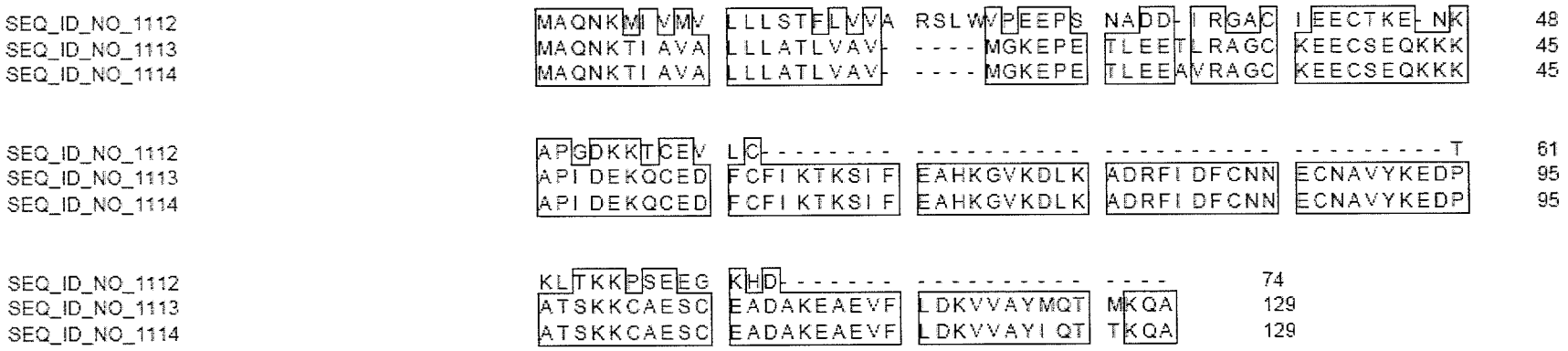

SEQ_ID_NO_1112
SEQ_ID_NO_1113
SEQ_ID_NO_1114
MAQNKMIVMV LLLSTFLVVA RSLWVPEEPS NADD-IRGAC IEECTKE-NK 48
MAQNKTIAVA LLLATLVAV- ----MGKEPE TLEETLRAGC KEECSEQKKK 45
MAQNKTIAVA LLLATLVAV- ----MGKEPE TLEEAVRAGC KEECSEQKKK 45
APGDKKTCEV LC---------- ---------- ---------- ---------T 61
APIDEKQCED FCFIKTKSIF EAHKGVKDLK ADRFIDFCNN ECNAVYKEDP 95
APIDEKQCED FCFIKTKSIF EAHKGVKDLK ADRFIDFCNN ECNAVYKEDP 95
KLTKKPSEEG KHD------- ---------- ---- 74
ATSKKCAESC EADAKEAEVF LDKVVAYMQT MKQA 129
ATSKKCAESC EADAKEAEVF LDKVVAYIQT TKQA 129

Figure 37

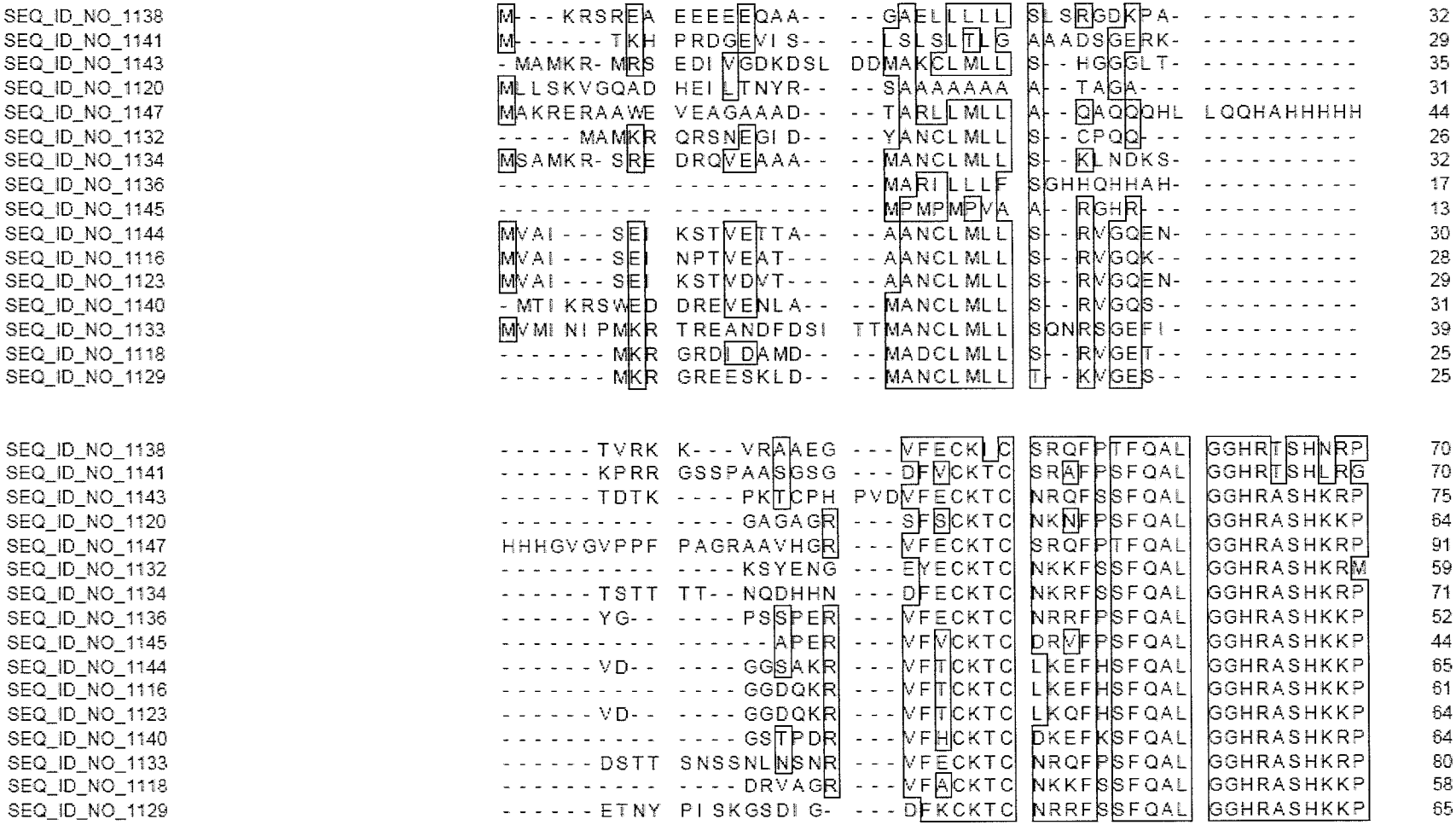

SEQ_ID_NO_1138
SEQ_ID_NO_1141
SEQ_ID_NO_1143
SEQ_ID_NO_1120
SEQ_ID_NO_1147
SEQ_ID_NO_1132
SEQ_ID_NO_1134
SEQ_ID_NO_1136
SEQ_ID_NO_1145
SEQ_ID_NO_1144
SEQ_ID_NO_1116
SEQ_ID_NO_1123
SEQ_ID_NO_1140
SEQ_ID_NO_1133
SEQ_ID_NO_1118
SEQ_ID_NO_1129
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Figure 37 (continued)

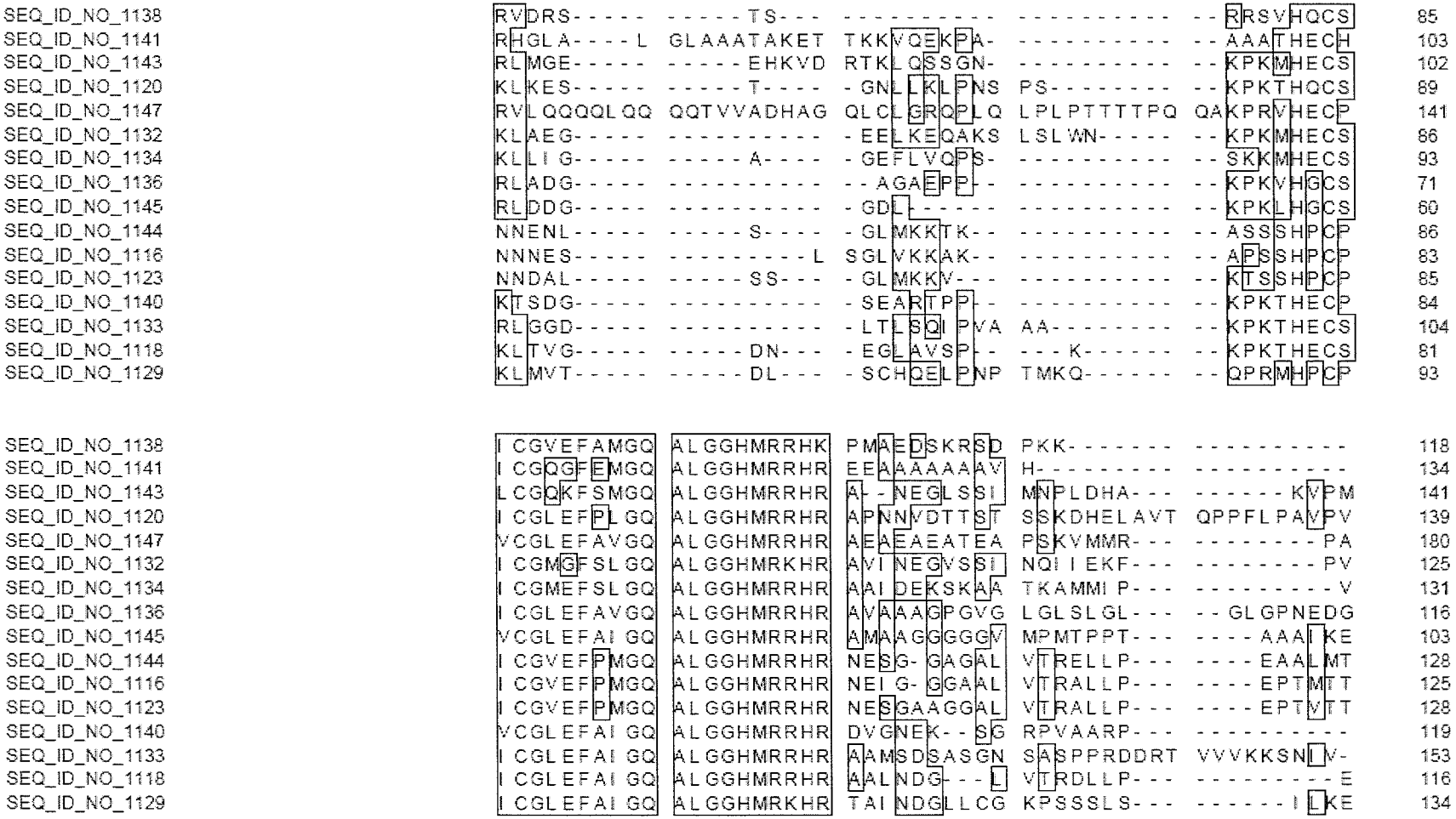


Figure 37 (continued)

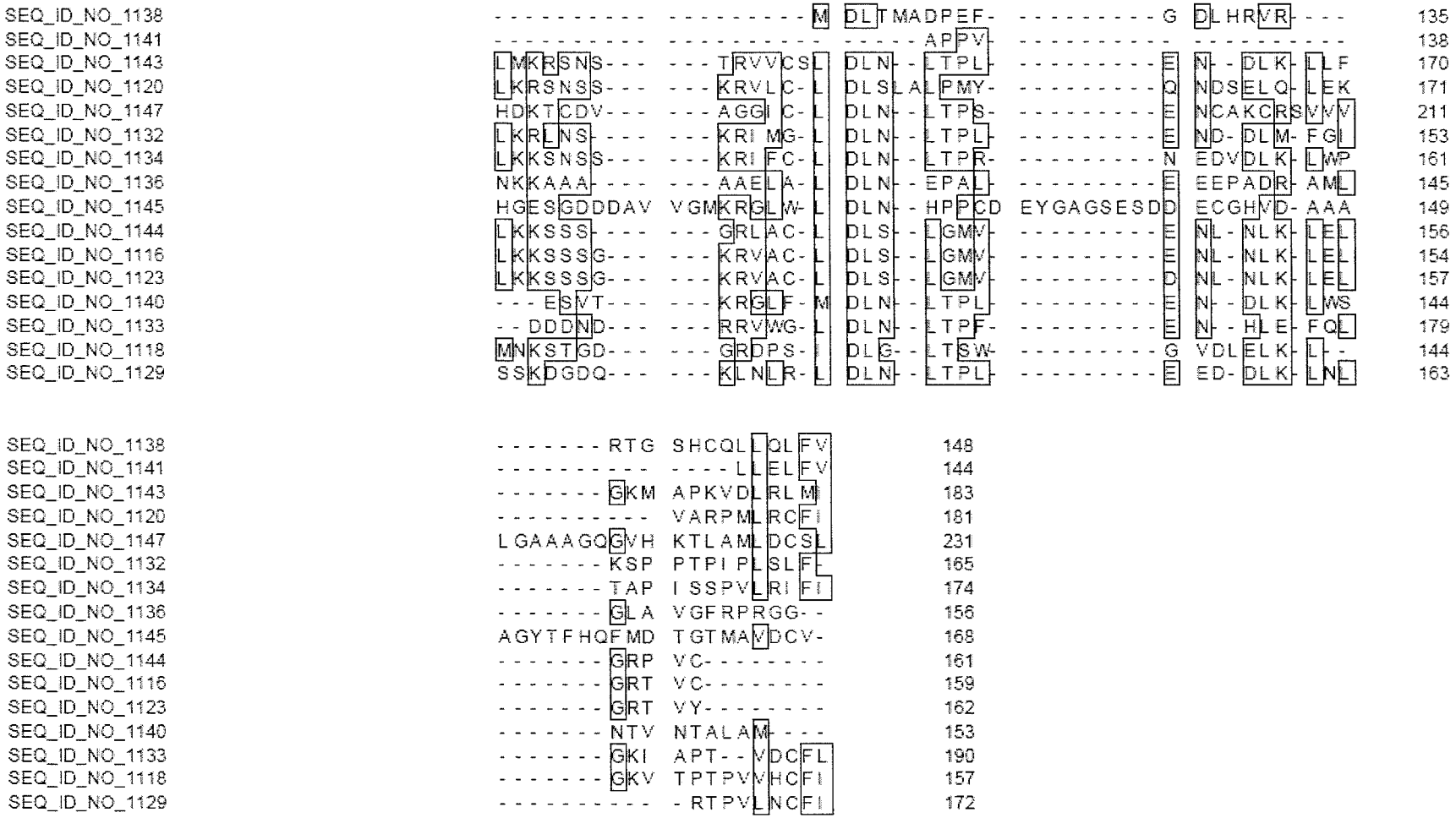
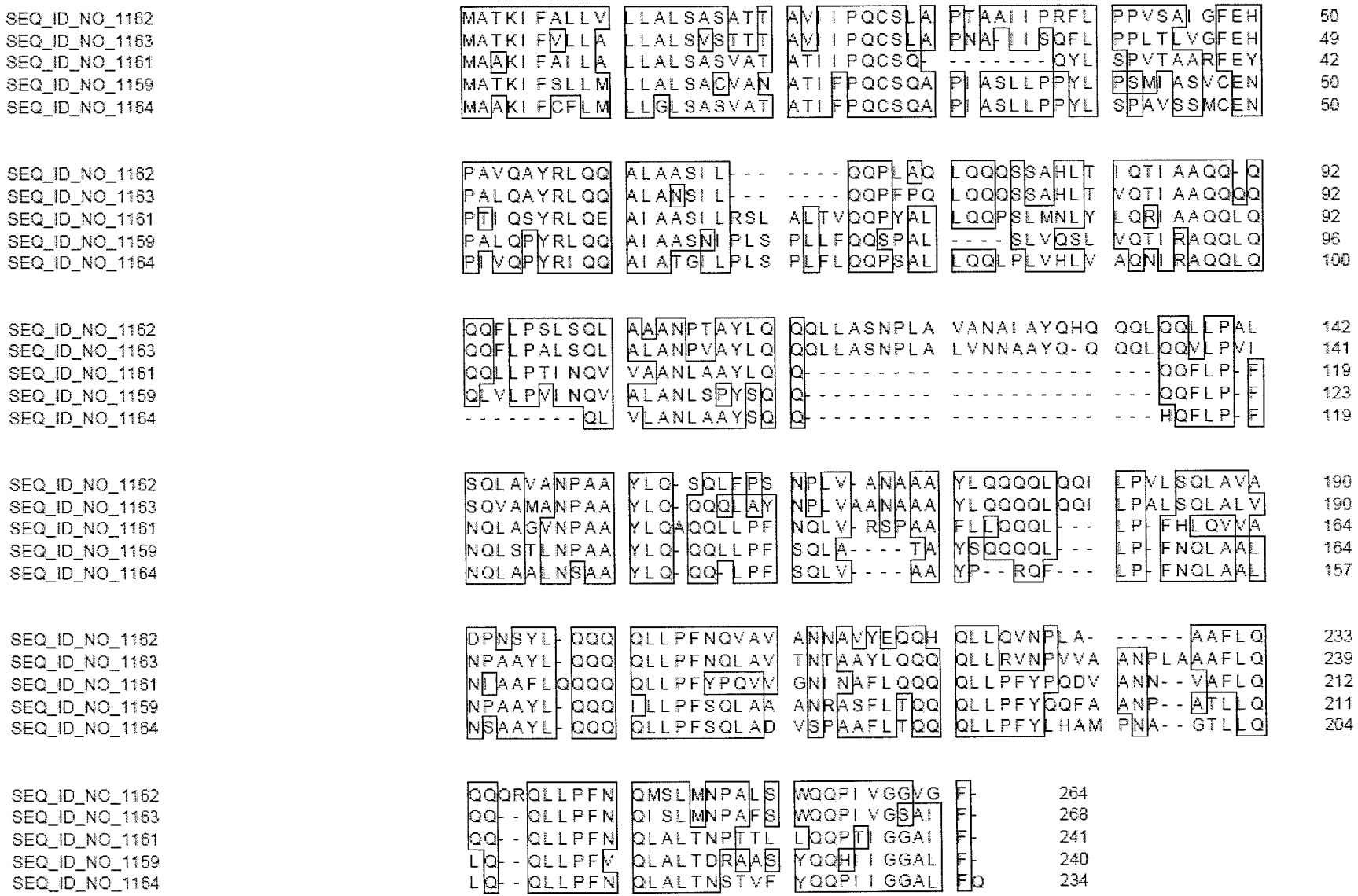


Figure 38


SEQ_ID_NO_1162
SEQ_ID_NO_1163
SEQ_ID_NO_1161
SEQ_ID_NO_1159
SEQ_ID_NO_1164
MATKIFALLVLLALSASATTAVIIPQCSLAPTAAIIPRFLPPVSAIGFEH 50
MATKIFVLLALLALSVSTTTAVIIPQCSLAPNAFIISQFLPPLTLVGFEH 49
MAAKIFAILALLALSASVATATIIPQCSQ-------QYLSPVTAARFEY 42
MATKIFSLLMLLALSACVANATIFPQCSQAPIASLLPPYLPSMIASVCEN 50
MAAKIFCFLMLLGLSASVATATIFPQCSQAPIASLLPPYLSPAVSSMCEN 50
SEQ_ID_NO_1162
SEQ_ID_NO_1163
SEQ_ID_NO_1161
SEQ_ID_NO_1159
SEQ_ID_NO_1164
PAVQAYRLQQALAASIL----QQPLAQLQQQSSAHLTIQTIAAQQ-Q 92
PALQAYRLQQALANSIL----QQPFPQLQQQSSAHLTVQTIAAQQQQ 92
PTIQSYRLQEAIAASILRSLALTVQQPYALLQQPSLMNLYLQRIAAQQLQ 92
PALQPYRLQQAIAASNIPLSPLLFQQSPAL----SLVQSLVQTIRAQQLQ 96
PIVQPYRIQQAIATGLLPLSPLFLQQPSALLQQLPLVHLVAQNIRAQQLQ 100
SEQ_ID_NO_1162
SEQ_ID_NO_1163
SEQ_ID_NO_1161
SEQ_ID_NO_1159
SEQ_ID_NO_1164
QQFLPSLSQLAAANPTAYLQQQLLASNPLAVANAIAYQHQQQLQQLLPAL 142
QQFLPALSQLALANPVAYLQQQLLASNPLALVNNAAYQ-QQQLQQVLPVI 141
QQLLPTINQVVAANLAAYLQQ---------------------QQFLP-F 119
QLVLPVINQVALANLSPYSQQ---------------------QQFLP-F 123
--------QLVLANLAAYSQQ---------------------HQFLP-F 119
SEQ_ID_NO_1162
SEQ_ID_NO_1163
SEQ_ID_NO_1161
SEQ_ID_NO_1159
SEQ_ID_NO_1164
SQLAVANPAAYLQ-SQLFPSNPLV-ANAAAYLQQQQLQQILPVLSQLAVA 190
SQVAMANPAAYLQ-QQQLAAYNPLVAANAAAYLQQQQLQQILPALSQLALV 190
NQLAGVNPAAYLQAQQLLPFNQLV-RSPAAFLLQQQL---LP-FHLQVVA 164
NQLSTLNPAAYLQ-QQLLPFSQLA----TAYSQQQQL---LP-FNQLAAL 164
NQLAALNSAAYLQ-QQ-LPFSQLV---AAYP--RQF---LP-FNQLAAL 157
SEQ_ID_NO_1162
SEQ_ID_NO_1163
SEQ_ID_NO_1161
SEQ_ID_NO_1159
SEQ_ID_NO_1164
DPNSYL-QQQQLLPFNQVAVANNAVYEQQHQLLQVNPLA-----AAFLQ 233
NPAAYL-QQQQLLPFNQLAVTNTAAYLQQQQLLRVNPVVAANPLAAAFLQ 239
NIAAFLQQQQQLLPFYPQVVGNINAFLQQQQLLPFYPQDVANN--VAFLQ 212
NPAAYL-QQQILLPFSQLAAANRASFLTQQQLLPFYQQFAANP--ATLLQ 211
NSAAYL-QQQQLLPFSQLADVSPAAFLTQQQLLPFYLHAMPNA--GTLLQ 204
SEQ_ID_NO_1162
SEQ_ID_NO_1163
SEQ_ID_NO_1161
SEQ_ID_NO_1159
SEQ_ID_NO_1164
QQQRQLLPFNQMSLMNPALSWQQPIVGGVGF- 264
QQ--QLLPFNQISLMNPAFSWQQPIVGSAIF- 268
QQ--QLLPFNQLALTNPTTLLQQPTIGGAIF- 241
LQ--QLLPFVQLALTDRAASYQQHIIGGALF- 240
LQ--QLLPFNQLALTNSTVFYQQPIIGGALFQ 234

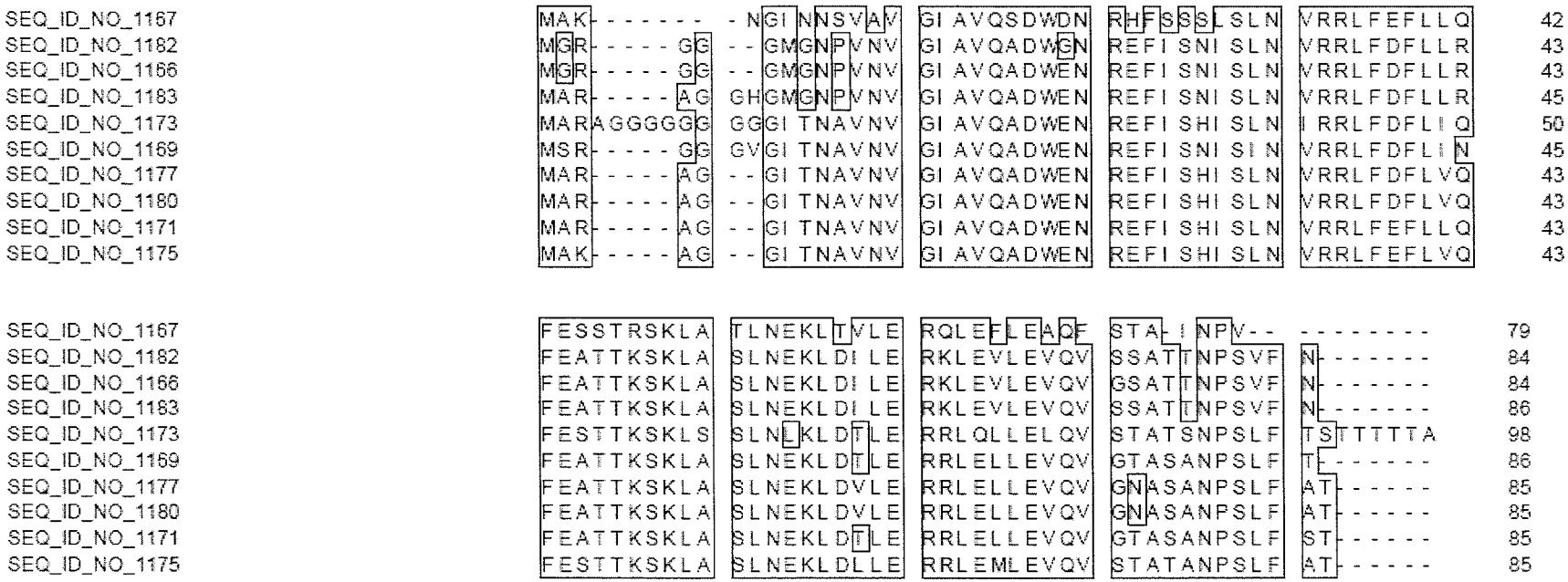
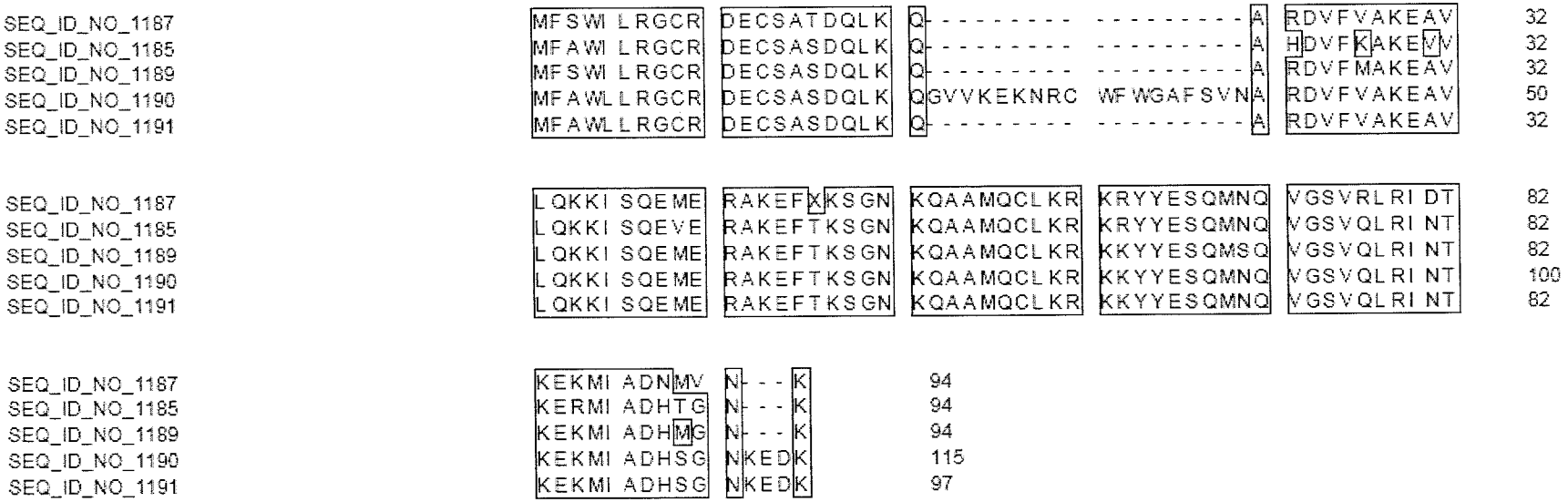
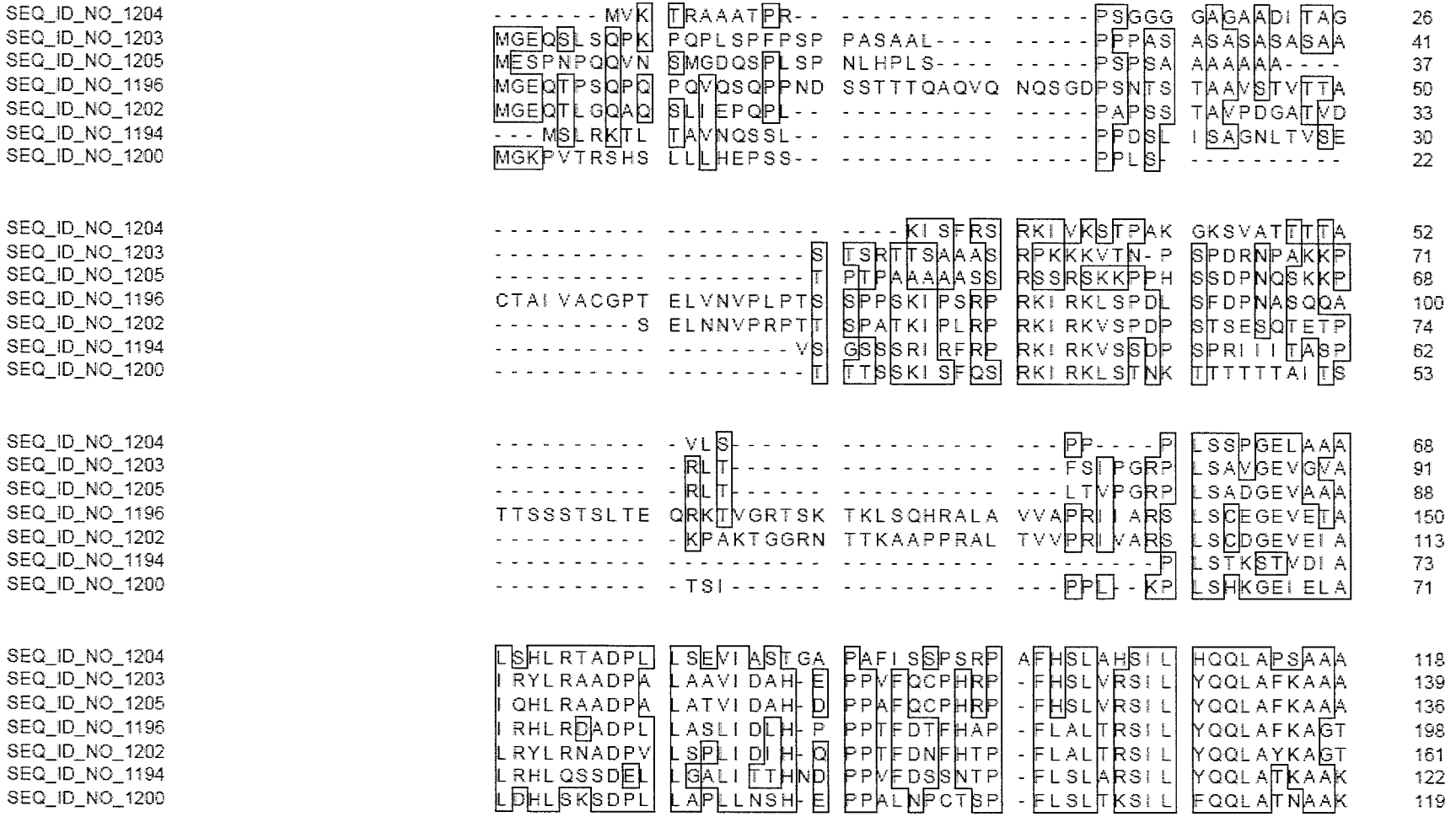

SEQ_ID_NO_1167 MAK------ -NGINNSVAV GIAVQSDWDN RHFSSSLSLN VRRLFEFLLQ 42
SEQ_ID_NO_1182 MGR----GG --GMGNPVNV GIAVQADWGN REFISNISLN VRRLFDFLLR 43
SEQ_ID_NO_1166 MGR----GG --GMGNPVNV GIAVQADWEN REFISNISLN VRRLFDFLLR 43
SEQ_ID_NO_1183 MAR----AG GHGMGNPVNV GIAVQADWEN REFISNISLN VRRLFDFLLR 45
SEQ_ID_NO_1173 MARAGGGGGG GGGITNAVNV GIAVQADWEN REFISHISLN IRRLFDFLIQ 50
SEQ_ID_NO_1169 MSR----GG GVGITNAVNV GIAVQADWEN REFISNISIN VRRLFDFLIN 45
SEQ_ID_NO_1177 MAR----AG --GITNAVNV GIAVQADWEN REFISHISLN VRRLFDFLVQ 43
SEQ_ID_NO_1180 MAR----AG --GITNAVNV GIAVQADWEN REFISHISLN VRRLFDFLVQ 43
SEQ_ID_NO_1171 MAR----AG --GITNAVNV GIAVQADWEN REFISHISLN VRRLFEFLLQ 43
SEQ_ID_NO_1175 MAK----AG --GITNAVNV GIAVQADWEN REFISHISLN VRRLFEFLVQ 43
SEQ_ID_NO_1167 FESSTRSKLA TLNEKLTVLE RQLEFLEAQF STA-INPV-- -------- 79
SEQ_ID_NO_1182 FEATTKSKLA SLNEKLDILE RKLEVLEVQV SSATTNPSVF N------- 84
SEQ_ID_NO_1166 FEATTKSKLA SLNEKLDILE RKLEVLEVQV GSATTNPSVF N------- 84
SEQ_ID_NO_1183 FEATTKSKLA SLNEKLDILE RKLEVLEVQV SSATTNPSVF N------- 86
SEQ_ID_NO_1173 FESTTKSKLS SLNLKLDTLE RRLQLLELQV STATSNPSLF TSTTTTTA 98
SEQ_ID_NO_1169 FEATTKSKLA SLNEKLDTLE RRLELLEVQV GTASANPSLF T------- 86
SEQ_ID_NO_1177 FEATTKSKLA SLNEKLDVLE RRLELLEVQV GNASANPSLF AT------ 85
SEQ_ID_NO_1180 FEATTKSKLA SLNEKLDVLE RRLELLEVQV GNASANPSLF AT------ 85
SEQ_ID_NO_1171 FEATTKSKLA SLNEKLDTLE RRLELLEVQV GTASANPSLF ST------ 85
SEQ_ID_NO_1175 FESTTKSKLA SLNEKLDLLE RRLEMLEVQV STATANPSLF AT------ 85

Figure 40


SEQ_ID_NO_1187
SEQ_ID_NO_1185
SEQ_ID_NO_1189
SEQ_ID_NO_1190
SEQ_ID_NO_1191
MFSWILRGCR DECSATDQLK Q--------- ---------A RDVFVAKEAV 32
MFAWILRGCR DECSASDQLK Q--------- ---------A HDVFKAKEVV 32
MFSWILRGCR DECSASDQLK Q--------- ---------A RDVFMAKEAV 32
MFAWLLRGCR DECSASDQLK QGVVKEKNRC WFWGAFSVNA RDVFVAKEAV 50
MFAWLLRGCR DECSASDQLK Q--------- ---------A RDVFVAKEAV 32
SEQ_ID_NO_1187
SEQ_ID_NO_1185
SEQ_ID_NO_1189
SEQ_ID_NO_1190
SEQ_ID_NO_1191
LQKKISQEME RAKEFXKSGN KQAAMQCLKR KRYYESQMNQ VGSVRLRIDT 82
LQKKISQEVE RAKEFTKSGN KQAAMQCLKR KRYYESQMNQ VGSVQLRINT 82
LQKKISQEME RAKEFTKSGN KQAAMQCLKR KKYYESQMSQ VGSVQLRINT 82
LQKKISQEME RAKEFTKSGN KQAAMQCLKR KKYYESQMNQ VGSVQLRINT 100
LQKKISQEME RAKEFTKSGN KQAAMQCLKR KKYYESQMNQ VGSVQLRINT 82
SEQ_ID_NO_1187
SEQ_ID_NO_1185
SEQ_ID_NO_1189
SEQ_ID_NO_1190
SEQ_ID_NO_1191
KEKMIADNMV N---K 94
KERMIADHTG N---K 94
KEKMIADHMG N---K 94
KEKMIADHSG NKEDK 115
KEKMIADHSG NKEDK 97


SEQ_ID_NO_1204
SEQ_ID_NO_1203
SEQ_ID_NO_1205
SEQ_ID_NO_1196
SEQ_ID_NO_1202
SEQ_ID_NO_1194
SEQ_ID_NO_1200
26
41
37
50
33
30
22
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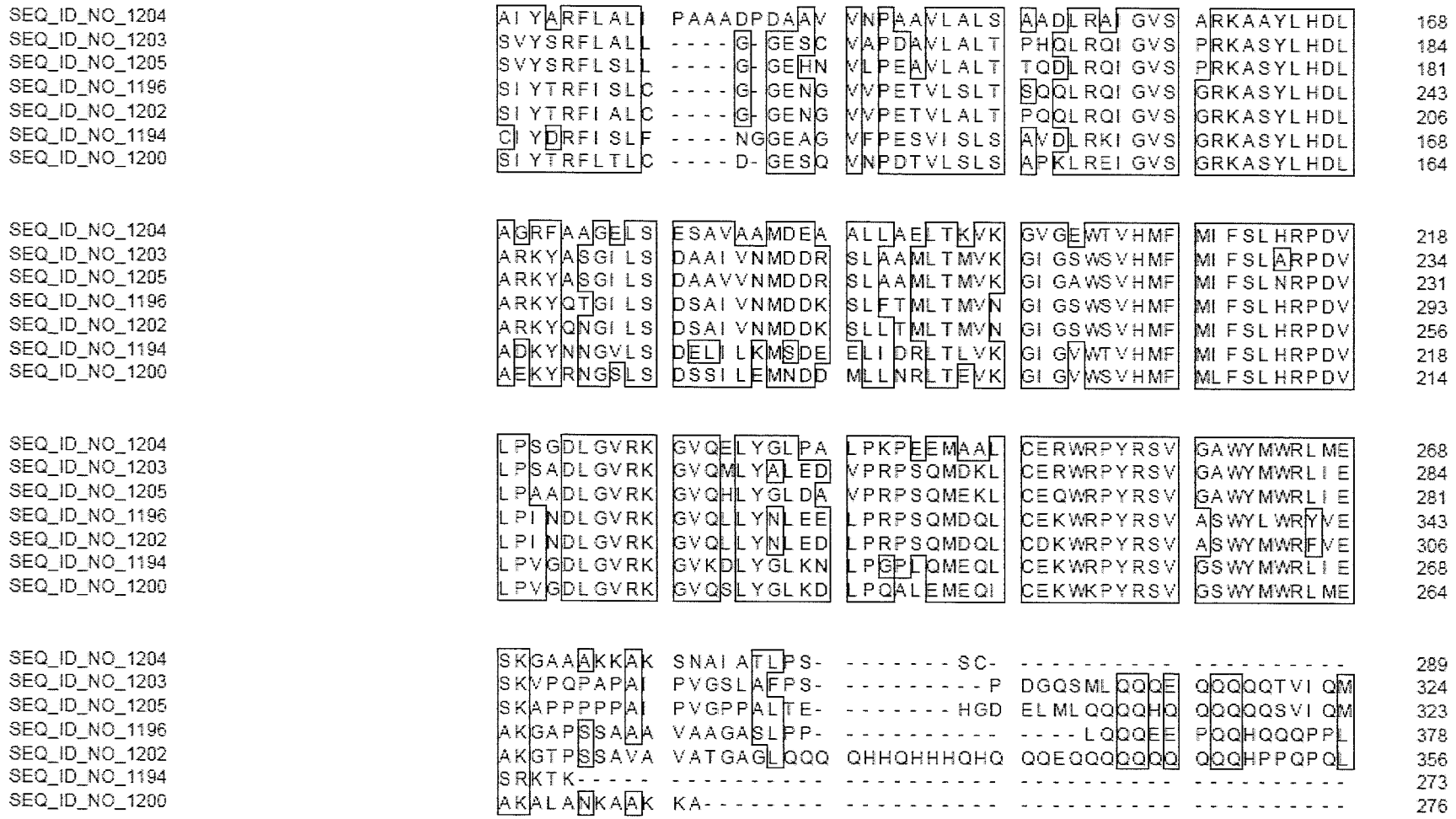

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SEQ_ID_NO_1205
SEQ_ID_NO_1196
SEQ_ID_NO_1202
SEQ_ID_NO_1194
SEQ_ID_NO_1200
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243
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168
164
218
234
231
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323
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276

Figure 41 (continued)

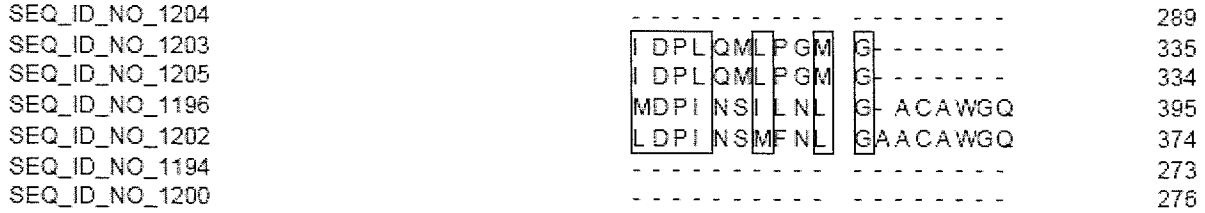


Figure 42

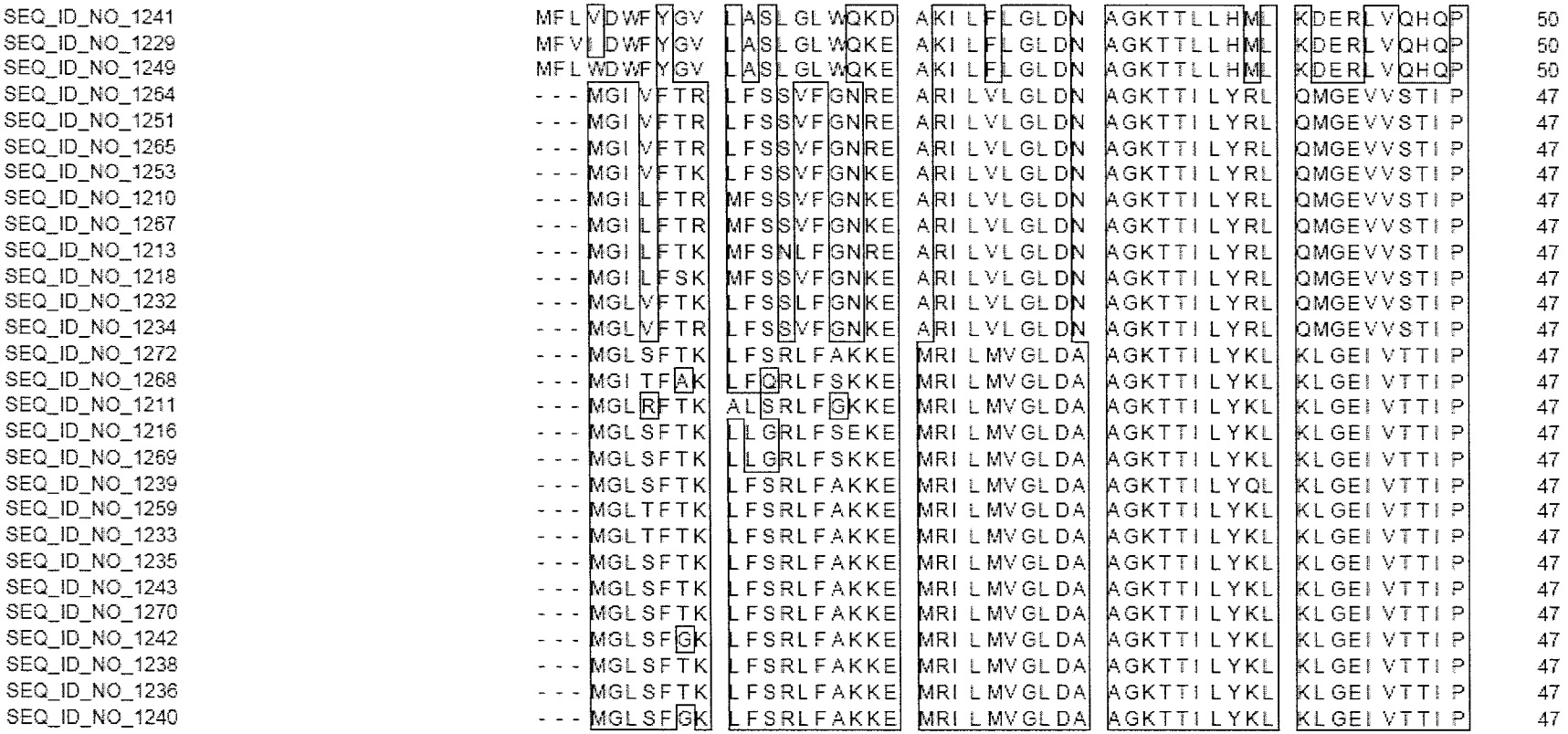

SEQ_ID_NO_1241 MFLVDWFYGV LASLGLWQKD AKILFLGLDN AGKTTLLHML KDERLVQHQP 50
SEQ_ID_NO_1229 MFVLDWFYGV LASLGLWQKE AKILFLGLDN AGKTTLLHML KDERLVQHQP 50
SEQ_ID_NO_1249 MFLWDWFYGV LASLGLWQKE AKILFLGLDN AGKTTLLHML KDERLVQHQP 50
SEQ_ID_NO_1264 ---MGIVFTR LFSSVFGNRE ARILVLGLDN AGKTTILYRL QMGEVVSTIP 47
SEQ_ID_NO_1251 ---MGIVFTR LFSSVFGNRE ARILVLGLDN AGKTTILYRL QMGEVVSTIP 47
SEQ_ID_NO_1265 ---MGIVFTR LFSSVFGNRE ARILVLGLDN AGKTTILYRL QMGEVVSTIP 47
SEQ_ID_NO_1253 ---MGIVFTK LFSSVFGNKE ARILVLGLDN AGKTTILYRL QMGEVVSTIP 47
SEQ_ID_NO_1210 ---MGILFTR MFSSVFGNKE ARILVLGLDN AGKTTILYRL QMGEVVSTIP 47
SEQ_ID_NO_1267 ---MGILFTR MFSSVFGNKE ARILVLGLDN AGKTTILYRL QMGEVVSTIP 47
SEQ_ID_NO_1213 ---MGILFTK MFSNLFGNRE ARILVLGLDN AGKTTILYRL QMGEVVSTIP 47
SEQ_ID_NO_1218 ---MGILFSK MFSSVFGNKE ARILVLGLDN AGKTTILYRL QMGEVVSTIP 47
SEQ_ID_NO_1232 ---MGLVFTK LFSSLFGNKE ARILVLGLDN AGKTTILYRL QMGEVVSTIP 47
SEQ_ID_NO_1234 ---MGLVFTR LFSSVFGNKE ARILVLGLDN AGKTTILYRL QMGEVVSTIP 47
SEQ_ID_NO_1272 ---MGLSFTK LFSRLFAKKE MRILMVGLDA AGKTTILYKL KLGEIVTTIP 47
SEQ_ID_NO_1268 ---MGITFAK LFQRLFSKKE MRILMVGLDA AGKTTILYKL KLGEIVTTIP 47
SEQ_ID_NO_1211 ---MGLRFTK ALSRLFGKKE MRILMVGLDA AGKTTILYKL KLGEIVTTIP 47
SEQ_ID_NO_1216 ---MGLSFTK LLGRLFSEKE MRILMVGLDA AGKTTILYKL KLGEIVTTIP 47
SEQ_ID_NO_1269 ---MGLSFTK LLGRLFSKKE MRILMVGLDA AGKTTILYKL KLGEIVTTIP 47
SEQ_ID_NO_1239 ---MGLSFTK LFSRLFAKKE MRILMVGLDA AGKTTILYQL KLGEIVTTIP 47
SEQ_ID_NO_1259 ---MGLTFTK LFSRLFAKKE MRILMVGLDA AGKTTILYKL KLGEIVTTIP 47
SEQ_ID_NO_1233 ---MGLTFTK LFSRLFAKKE MRILMVGLDA AGKTTILYKL KLGEIVTTIP 47
SEQ_ID_NO_1235 ---MGLSFTK LFSRLFAKKE MRILMVGLDA AGKTTILYKL KLGEIVTTIP 47
SEQ_ID_NO_1243 ---MGLSFTK LFSRLFAKKE MRILMVGLDA AGKTTILYKL KLGEIVTTIP 47
SEQ_ID_NO_1270 ---MGLSFTK LFSRLFAKKE MRILMVGLDA AGKTTILYKL KLGEIVTTIP 47
SEQ_ID_NO_1242 ---MGLSFGK LFSRLFAKKE MRILMVGLDA AGKTTILYKL KLGEIVTTIP 47
SEQ_ID_NO_1238 ---MGLSFTK LFSRLFAKKE MRILMVGLDA AGKTTILYKL KLGEIVTTIP 47
SEQ_ID_NO_1236 ---MGLSFTK LFSRLFAKKE MRILMVGLDA AGKTTILYKL KLGEIVTTIP 47
SEQ_ID_NO_1240 ---MGLSFGK LFSRLFAKKE MRILMVGLDA AGKTTILYKL KLGEIVTTIP 47

Figure 42 (continued)

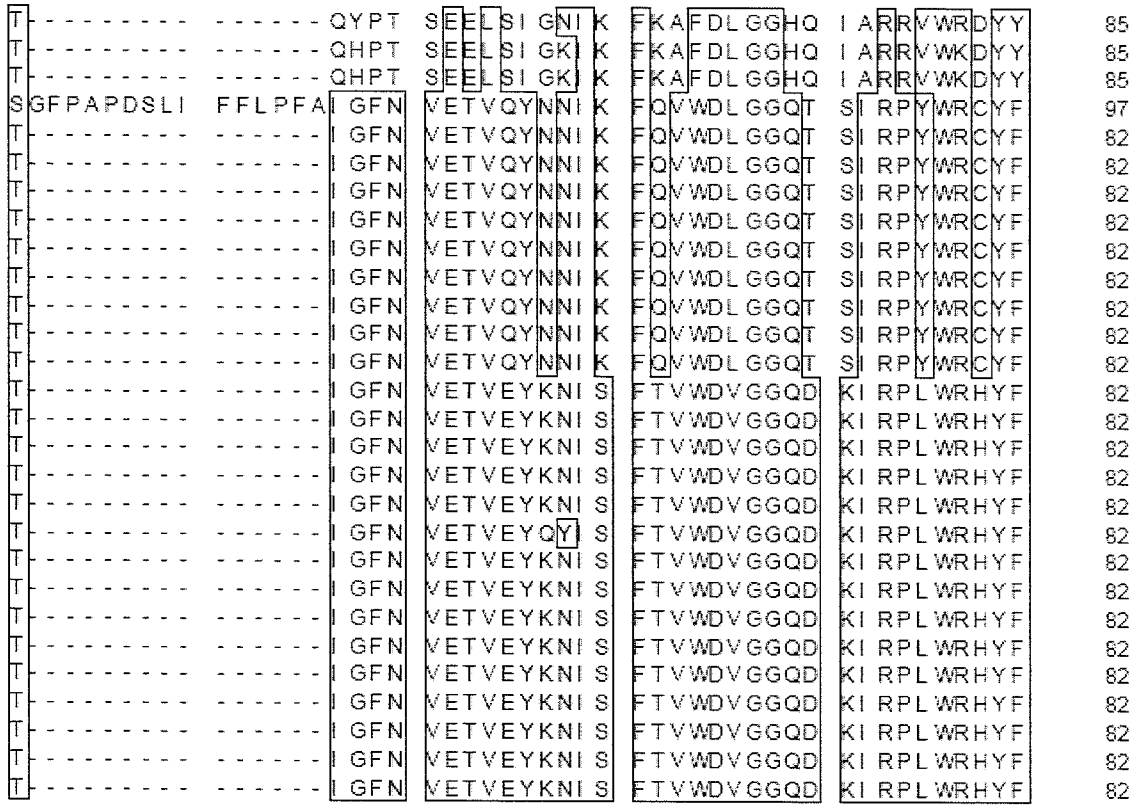


Figure 42 (continued)



Figure 42 (continued)

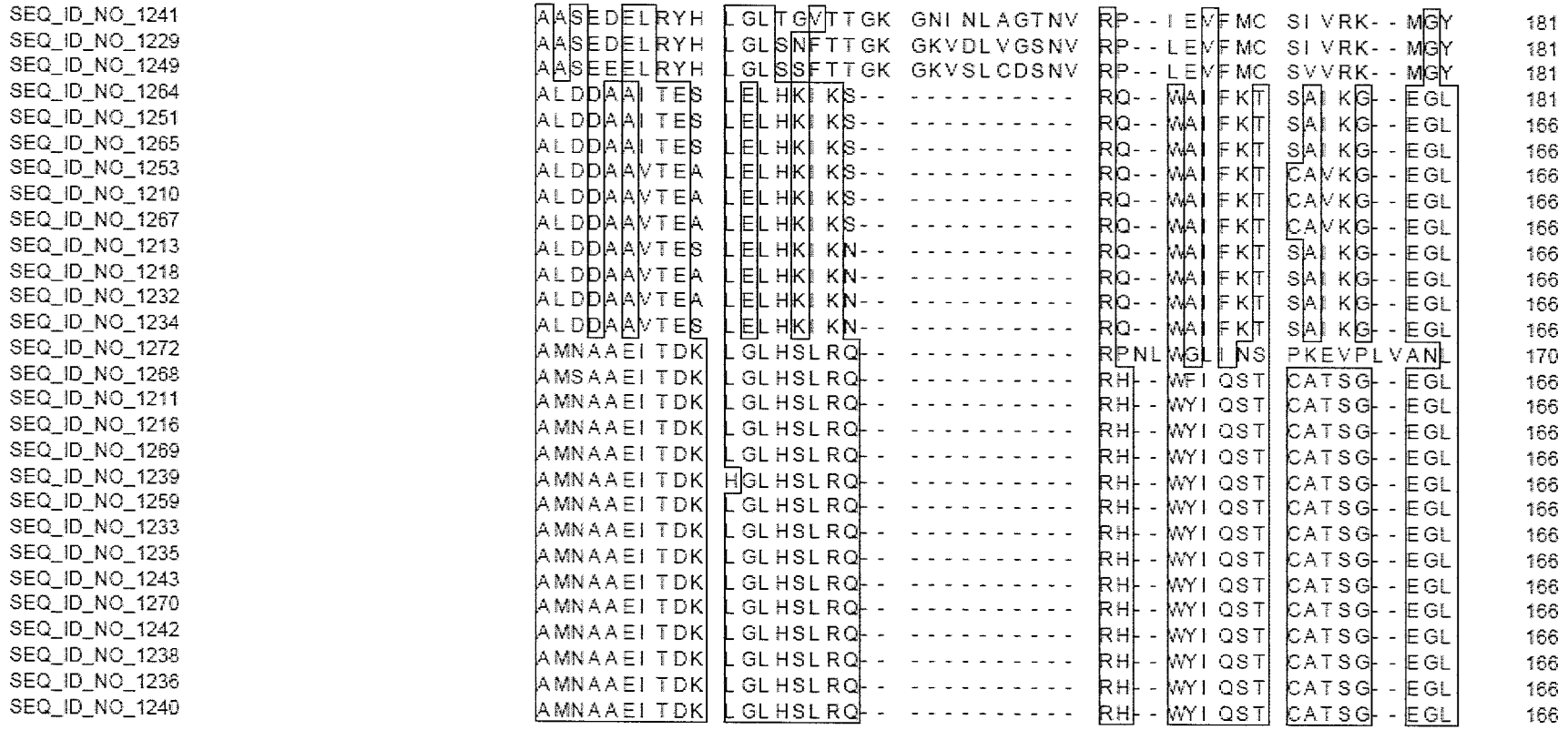


Figure 42 (continued)

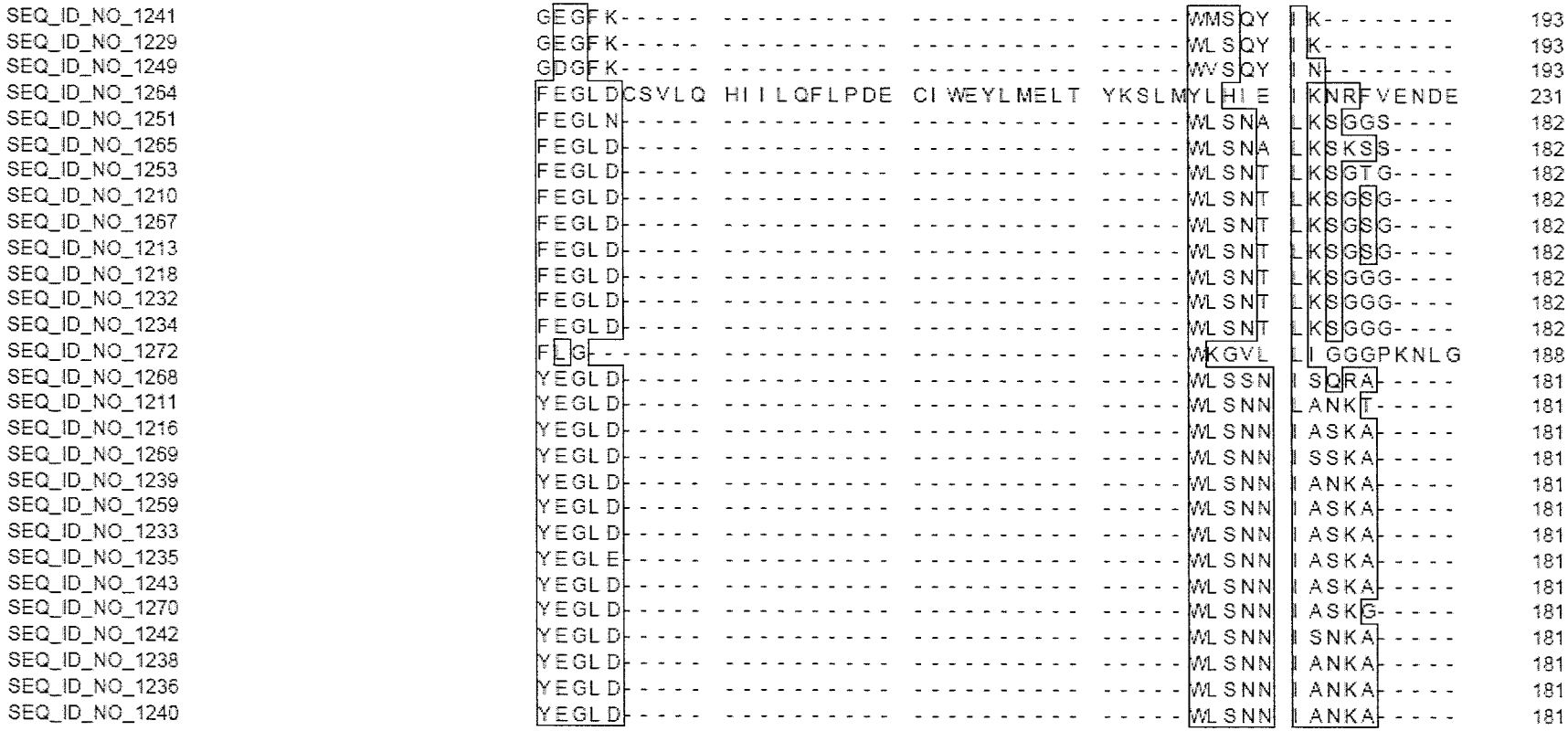
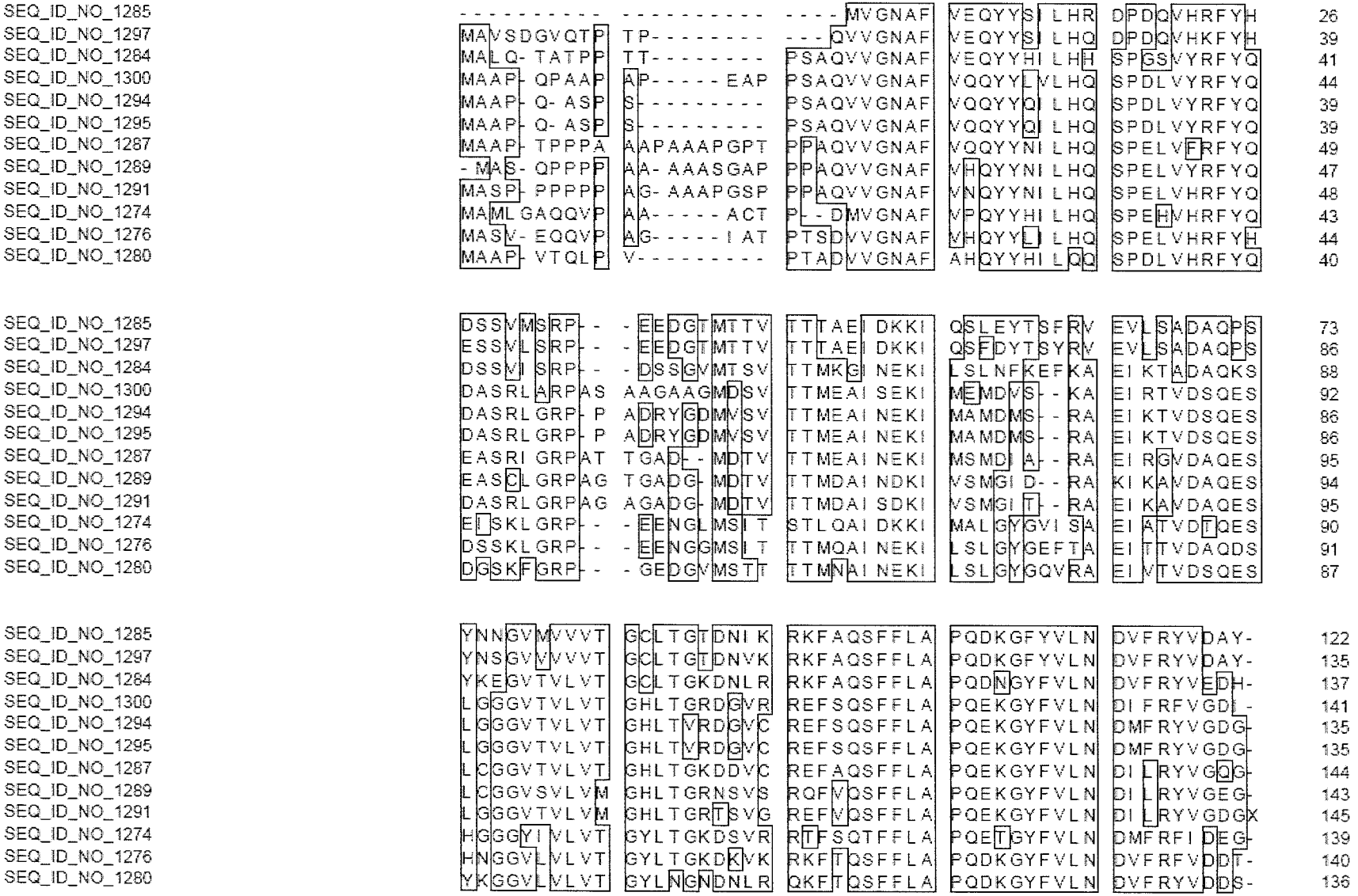


Figure 42 (continued)

SEQ_ID_NO_1241	- - - - - - - - - - - - -	193
SEQ_ID_NO_1229	- - - - - - - - - - - - -	193
SEQ_ID_NO_1249	- - - - - - - - - - - - -	193
SEQ_ID_NO_1264	QTVRTLGHWW LYP	244
SEQ_ID_NO_1251	- - - - - - - - - - - - -	182
SEQ_ID_NO_1265	- - - - - - - - - - - - -	182
SEQ_ID_NO_1253	- - - - - - - - - - - - -	182
SEQ_ID_NO_1210	- - - - - - - - - - - - -	182
SEQ_ID_NO_1267	- - - - - - - - - - - - -	182
SEQ_ID_NO_1213	- - - - - - - - - - - - -	182
SEQ_ID_NO_1218	- - - - - - - - - - - - -	182
SEQ_ID_NO_1232	- - - - - - - - - - - - -	182
SEQ_ID_NO_1234	- - - - - - - - - - - - -	182
SEQ_ID_NO_1272	LLSPKPK- - - - - -	195
SEQ_ID_NO_1268	- - - - - - - - - - - - -	181
SEQ_ID_NO_1211	- - - - - - - - - - - - -	181
SEQ_ID_NO_1216	- - - - - - - - - - - - -	181
SEQ_ID_NO_1269	- - - - - - - - - - - - -	181
SEQ_ID_NO_1239	- - - - - - - - - - - - -	181
SEQ_ID_NO_1259	- - - - - - - - - - - - -	181
SEQ_ID_NO_1233	- - - - - - - - - - - - -	181
SEQ_ID_NO_1235	- - - - - - - - - - - - -	181
SEQ_ID_NO_1243	- - - - - - - - - - - - -	181
SEQ_ID_NO_1270	- - - - - - - - - - - - -	181
SEQ_ID_NO_1242	- - - - - - - - - - - - -	181
SEQ_ID_NO_1238	- - - - - - - - - - - - -	181
SEQ_ID_NO_1236	- - - - - - - - - - - - -	181
SEQ_ID_NO_1240	- - - - - - - - - - - - -	181


SEQ_ID_NO_1285
SEQ_ID_NO_1297
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SEQ_ID_NO_1294
SEQ_ID_NO_1295
SEQ_ID_NO_1287
SEQ_ID_NO_1289
SEQ_ID_NO_1291
SEQ_ID_NO_1274
SEQ_ID_NO_1276
SEQ_ID_NO_1280
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136


SEQ_ID_NO_1285 --------KS IDIESVPANDADESAPSEAITPEPEPVHV PEVIPPTQTV 164
SEQ_ID_NO_1297 ---------K SVDIETVPANDADESAPSEAFTPDPEPIHV A-------ED 169
SEQ_ID_NO_1284 --------EP SELPPVTGDGDSAAVTVTPELEPSHVAD-- --------SC 169
SEQ_ID_NO_1300 --------PA PTAVEAQPEADAVVPPVAAPLANGTATPAV EPAIPDDHDA 183
SEQ_ID_NO_1294 -------PTP AAAAAAAAVEVQPEADAVAPPLANGTATAPL QPAAPDY-DG 177
SEQ_ID_NO_1295 ---------P TPAAAAAAAEVQPEADAVAPPLANGTATAPL QPAAPDY-DA 175
SEQ_ID_NO_1287 --EADPSLPP PQQQPPAPELDAVVAP-AAALANGTVAP-- VETVPREQEA 189
SEQ_ID_NO_1269 ----GGDEGA EKQPAPEVAADAEKTTSAPILANGTVGGDA TTVPQ---DA 186
SEQ_ID_NO_1291 GEEGAGHPPP PPQQPVQETVTGAEAVPAPILANGTVGG-D NETLPCEQDA 194
SEQ_ID_NO_1274 ---------- ----TVVHGNQIPVNNVQAPVNTYQDTAAA KEIPDDFVQE 175
SEQ_ID_NO_1276 ---------- ----KHQPGGQDPVNGFEASLTHEQGHS-- ---------- 164
SEQ_ID_NO_1280 ---------- ----THQNGNQEPASNFEAPVAPDQDTP-- ---------- 160
SEQ_ID_NO_1285 IPTAQTVIPPTQTVIADTETIISKEVSLPLENGKLSVT-- ---------- 202
SEQ_ID_NO_1297 IPTIQPVLADTDTNISK---EVSLPLENGKLSVT-- ---------- 200
SEQ_ID_NO_1284 APEPTNSHVNKGQTVAE---NAYELSNNHERQIPV- ---------- 201
SEQ_ID_NO_1300 VPQQENHVVDRSPPQPEEEDEA--EVYNPPPEEVV- ---------- 216
SEQ_ID_NO_1294 MPQEEPDVVEHAAVPPEEEE----EVYNPPLEEVEGGAV- ---------- 212
SEQ_ID_NO_1295 MPHEEPDVVENVAVPPEEEE----EVYNPPLEEVEGGAV- ---------- 210
SEQ_ID_NO_1287 SPQPELDLSESVPHTNEEEDPKE-EVYNPPNDVEVPV--- ---------- 225
SEQ_ID_NO_1269 SPQPECQVAEPALNPKEEVLNG--EVCNSLSDVEKPV--- ---------- 221
SEQ_ID_NO_1291 SPQPEQPAAESAPPTPEEEDLYGEEVYNPPNDMEKPV--- ---------- 231
SEQ_ID_NO_1274 KYVQENHAVKQTEVLSKSINEPE-KVFTPSEDEQVSA--- ---------- 211
SEQ_ID_NO_1276 -PVPENHTEQPAA-LPEECNGP--EVYNSSENGDGSIE-- ---------- 198
SEQ_ID_NO_1280 -HTQETHLSEPTAALSEEVIGG--EVYNPSESGDVSVEVE EEESGDVSFE 207
SEQ_ID_NO_1285 ENVIPVNHVKESSHHVKEPEQPTSIEKVASNTQEDTPKKS FASIVNALKD 252
SEQ_ID_NO_1297 ENVIPVNHVKESSHQEQMASIEKV----PSNTQEDTPKKS FASIVSAYKD 246
SEQ_ID_NO_1284 ENEGNVESHFQSNGNDDSQATELA-----SSAQDDAPKKS YASIVKVQKG 246
SEQ_ID_NO_1300 DEEQPVPEVINEVPNNVAPVAATT---VAPVLQEEAPKKS YASIVKVMKE 263
SEQ_ID_NO_1294 EEEQSVPEVINEVPNNVVPVVAPA---AAPVSHEEAPKKS YASIVKVMKE 259
SEQ_ID_NO_1295 EEEQSVPEVINEVPNNVVPVVAPA---DAPVSHEEAPKKS YASIVKVMKE 257
SEQ_ID_NO_1287 VEETLVPEVIDEVPNNVAASIPVS---APPVPHEEAPKKS YASIVKVMKA 272
SEQ_ID_NO_1269 AEETPVPDVINEVPNNVAVAPPIS---SPPVPLKEAPKKS YASIVKVMKE 268
SEQ_ID_NO_1291 VQETPVAEVINEVPNNVAVAAPSS---SPSIPIEEAPKKS YASIVKVMKE 278
SEQ_ID_NO_1274 AEEVLVTETVNEAPIEVQKVGESD------SRTGEIPKRS YASIVKVMKE 255
SEQ_ID_NO_1276 EEESPVAEVVDEIPDDSKMVSDSK------PEMEELPKKS YASILKVLKE 242
SEQ_ID_NO_1280 EEEEPMPEVVDEIPPDSQLVADSQVVVESSAKIEDTPKKS YASVVKVQKE 257


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SEQ_ID_NO_1276
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298
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Figure 43 (continued)



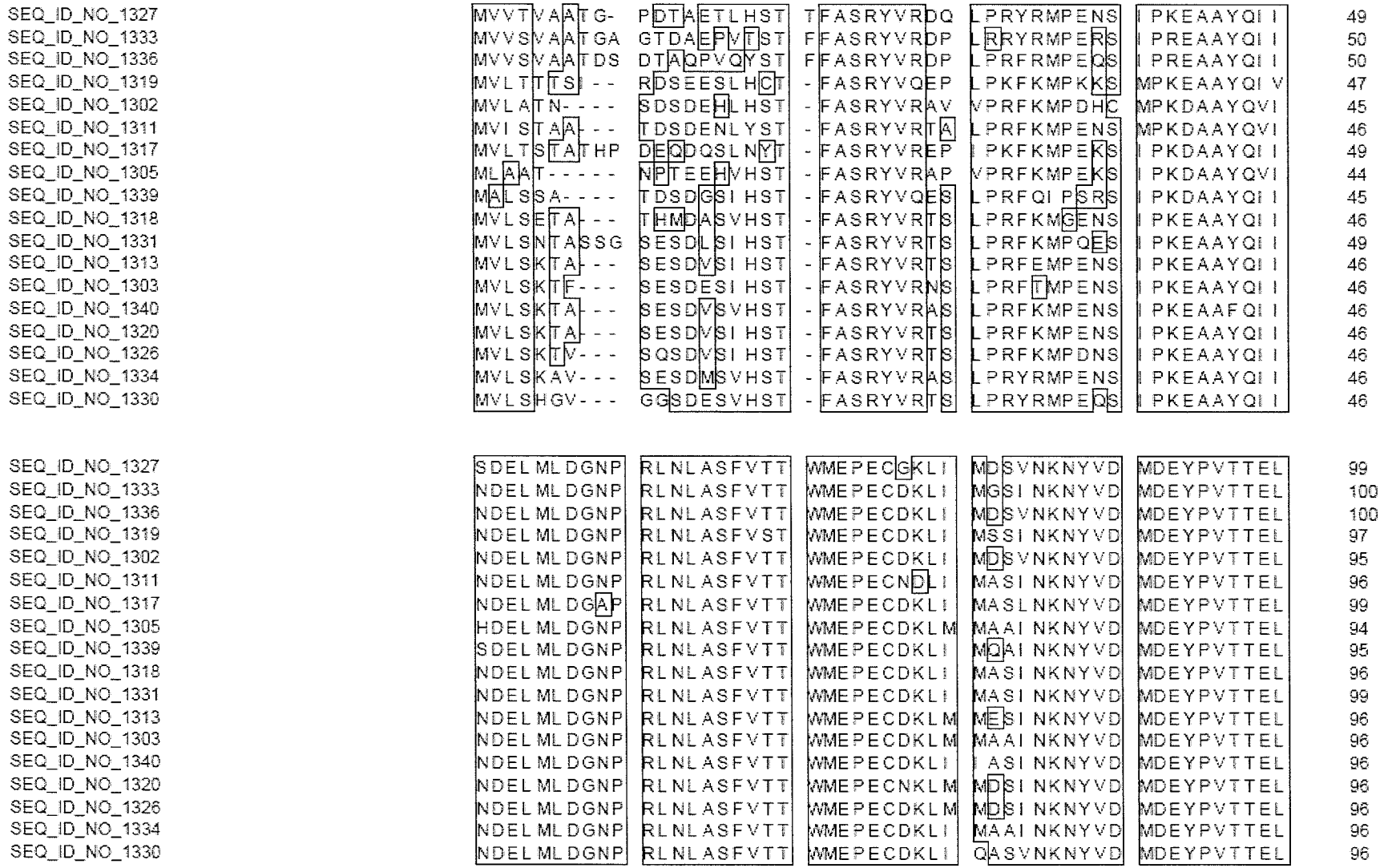

SEQ_ID_NO_1327 MVVTVAATG- PDTAETLHST TFASRYVRDQ LPRYRMPENS IPKEAAYQII 49
SEQ_ID_NO_1333 MVVSVAATGA GTDAEPVTST FFASRYVRDP LRRYRMPERS IPREAAYQII 50
SEQ_ID_NO_1336 MVVSVAATDS DTAQPVQYST FFASRYVRDP LPRFRMPEQS IPREAAYQII 50
SEQ_ID_NO_1319 MVLTTTSI-- RDSEESLHCT -FASRYVQEP LPKFKMPKKS MPKEAAYQIV 47
SEQ_ID_NO_1302 MVLATN---- SDSDEHLHST -FASRYVRAV VPRFKMPDHC MPKDAAYQVI 45
SEQ_ID_NO_1311 MVISTAA--- TDSDENLYST -FASRYVRTA LPRFKMPENS MPKDAAYQVI 46
SEQ_ID_NO_1317 MVLTSTATHP DEQDQSLNYT -FASRYVREP IPKFKMPEKS IPKDAAYQII 49
SEQ_ID_NO_1305 MLAAT----- NPTEEHVHST -FASRYVRAP VPRFKMPEKS IPKDAAYQVI 44
SEQ_ID_NO_1339 MALSSA---- TDSDGSIHST -FASRYVQES LPRFQIPSRS IPKDAAYQII 45
SEQ_ID_NO_1318 MVLSETA--- THMDASVHST -FASRYVRTS LPRFKMGENS IPKEAAYQII 46
SEQ_ID_NO_1331 MVLSNTASSG SESDLSIHST -FASRYVRTS LPRFKMPQES IPKEAAYQII 49
SEQ_ID_NO_1313 MVLSKTA--- SESDVSIHST -FASRYVRTS LPRFEMPENS IPKEAAYQII 46
SEQ_ID_NO_1303 MVLSKTF--- SESDESIHST -FASRYVRNS LPRFTMPENS IPKEAAYQII 46
SEQ_ID_NO_1340 MVLSKTA--- SESDVSVHST -FASRYVRAS LPRFKMPENS IPKEAAFQII 46
SEQ_ID_NO_1320 MVLSKTA--- SESDVSIHST -FASRYVRTS LPRFKMPENS IPKEAAYQII 46
SEQ_ID_NO_1326 MVLSKTV--- SQSDVSIHST -FASRYVRTS LPRFKMPDNS IPKEAAYQII 46
SEQ_ID_NO_1334 MVLSKAV--- SESDMSVHST -FASRYVRAS LPRYRMPENS IPKEAAYQII 46
SEQ_ID_NO_1330 MVLSHGV--- GGSDESVHST -FASRYVRTS LPRYRMPEQS IPKEAAYQII 46
SEQ_ID_NO_1327 SDELMLDGNP RLNLASFVTT WMEPECGKLI MDSVNKNYVD MDEYPVTTEL 99
SEQ_ID_NO_1333 NDELMLDGNP RLNLASFVTT WMEPECDKLI MGSINKNYVD MDEYPVTTEL 100
SEQ_ID_NO_1336 NDELMLDGNP RLNLASFVTT WMEPECDKLI MDSVNKNYVD MDEYPVTTEL 100
SEQ_ID_NO_1319 NDELMLDGNP RLNLASFVST WMEPECDKLI MSSINKNYVD MDEYPVTTEL 97
SEQ_ID_NO_1302 NDELMLDGNP RLNLASFVTT WMEPECDKLI MDSVNKNYVD MDEYPVTTEL 95
SEQ_ID_NO_1311 NDELMLDGNP RLNLASFVTT WMEPECNDLI MASINKNYVD MDEYPVTTEL 96
SEQ_ID_NO_1317 NDELMLDGAP RLNLASFVTT WMEPECDKLI MASLNKNYVD MDEYPVTTEL 99
SEQ_ID_NO_1305 HDELMLDGNP RLNLASFVTT WMEPECDKLM MAAINKNYVD MDEYPVTTEL 94
SEQ_ID_NO_1339 SDELMLDGNP RLNLASFVTT WMEPECDKLI MQAINKNYVD MDEYPVTTEL 95
SEQ_ID_NO_1318 NDELMLDGNP RLNLASFVTT WMEPECDKLI MASINKNYVD MDEYPVTTEL 96
SEQ_ID_NO_1331 NDELMLDGNP RLNLASFVTT WMEPECDKLI MASINKNYVD MDEYPVTTEL 99
SEQ_ID_NO_1313 NDELMLDGNP RLNLASFVTT WMEPECDKLM MESINKNYVD MDEYPVTTEL 96
SEQ_ID_NO_1303 NDELMLDGNP RLNLASFVTT WMEPECDKLM MAAINKNYVD MDEYPVTTEL 96
SEQ_ID_NO_1340 NDELMLDGNP RLNLASFVTT WMEPECDKLI IASINKNYVD MDEYPVTTEL 96
SEQ_ID_NO_1320 NDELMLDGNP RLNLASFVTT WMEPECNKLM MDSINKNYVD MDEYPVTTEL 96
SEQ_ID_NO_1326 NDELMLDGNP RLNLASFVTT WMEPECDKLM MDSINKNYVD MDEYPVTTEL 96
SEQ_ID_NO_1334 NDELMLDGNP RLNLASFVTT WMEPECDKLI MAAINKNYVD MDEYPVTTEL 96
SEQ_ID_NO_1330 NDELMLDGNP RLNLASFVTT WMEPECDKLI QASVNKNYVD MDEYPVTTEL 96

Figure 44 (continued)

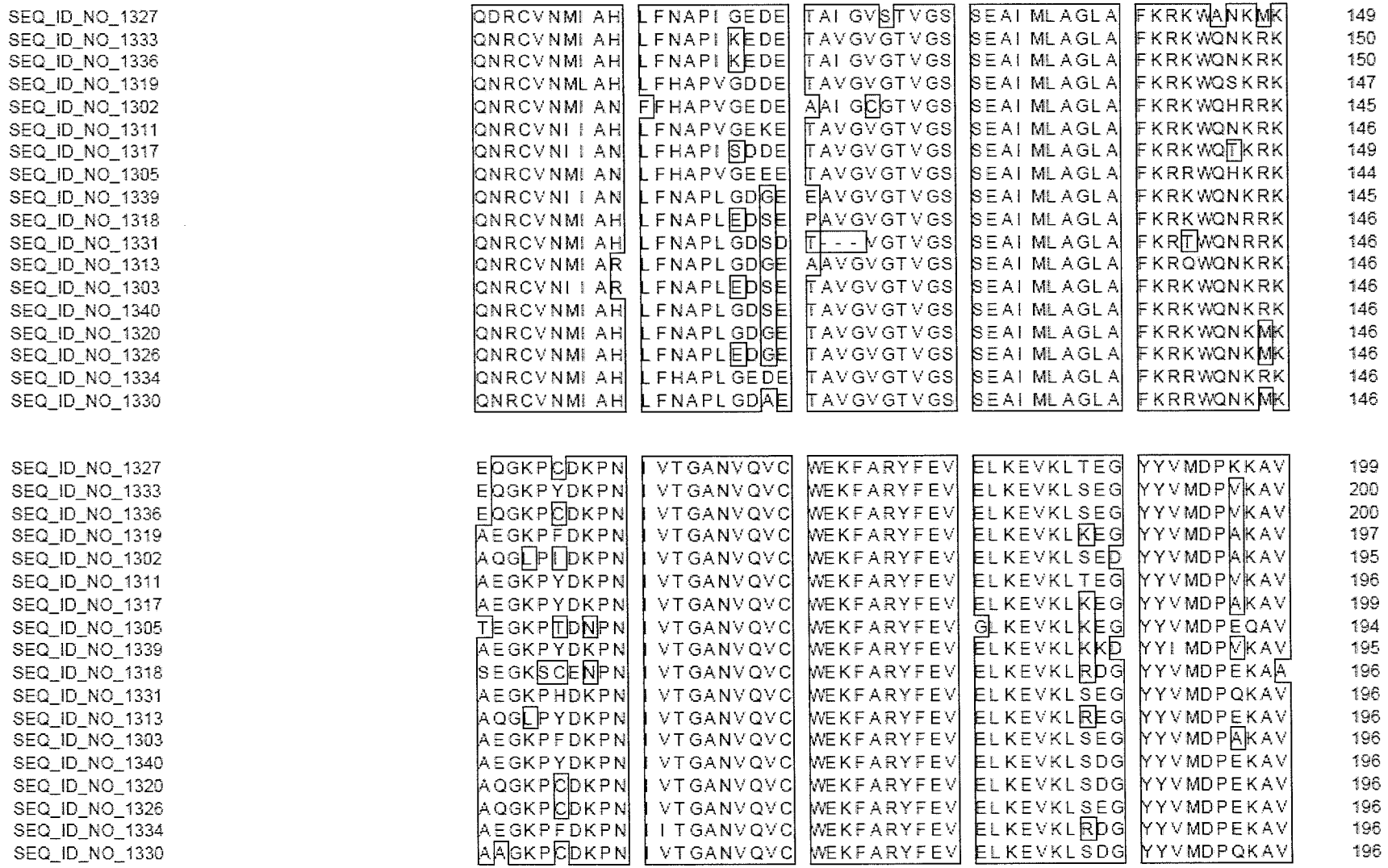


Figure 44 (continued)

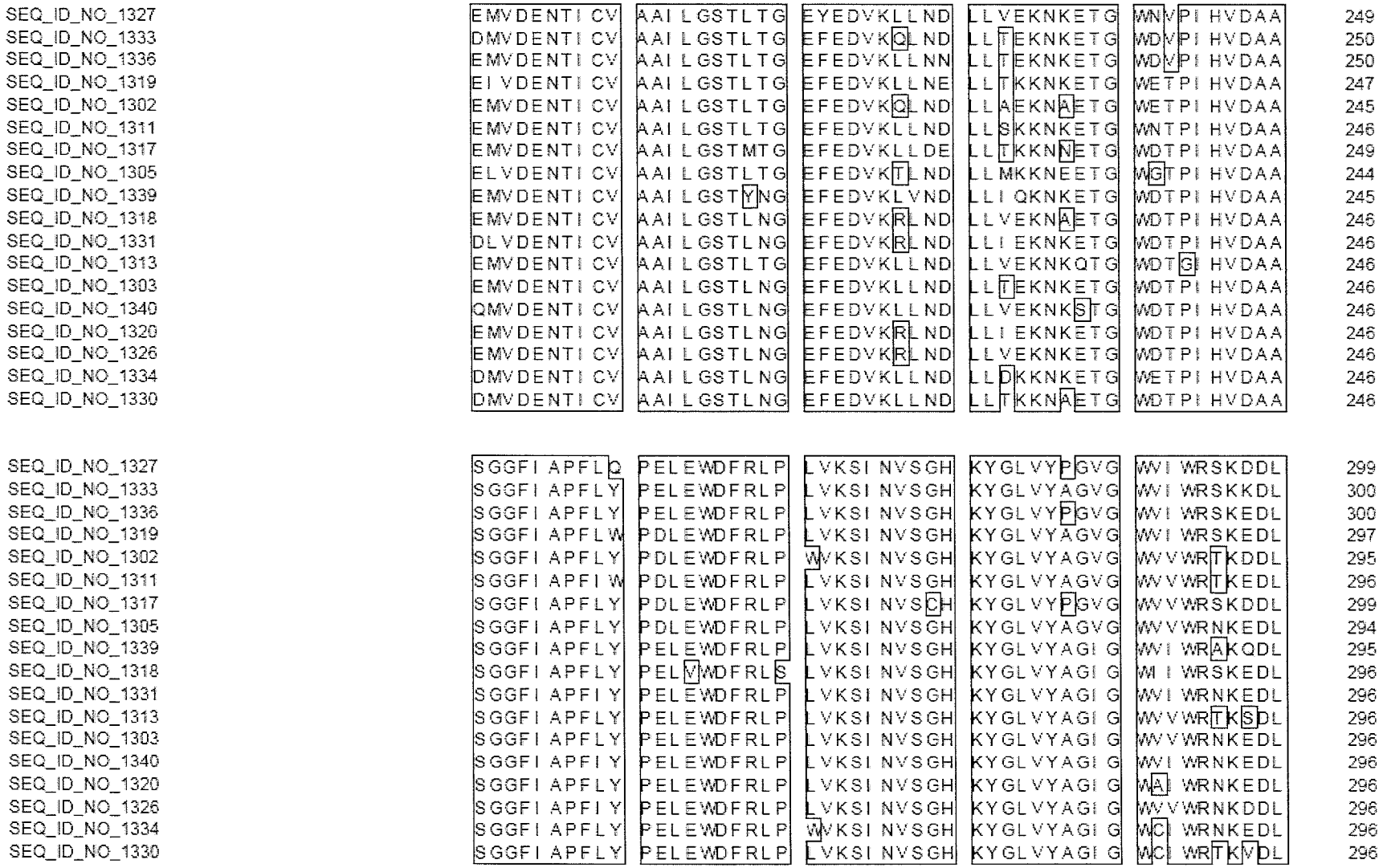


Figure 44 (continued)

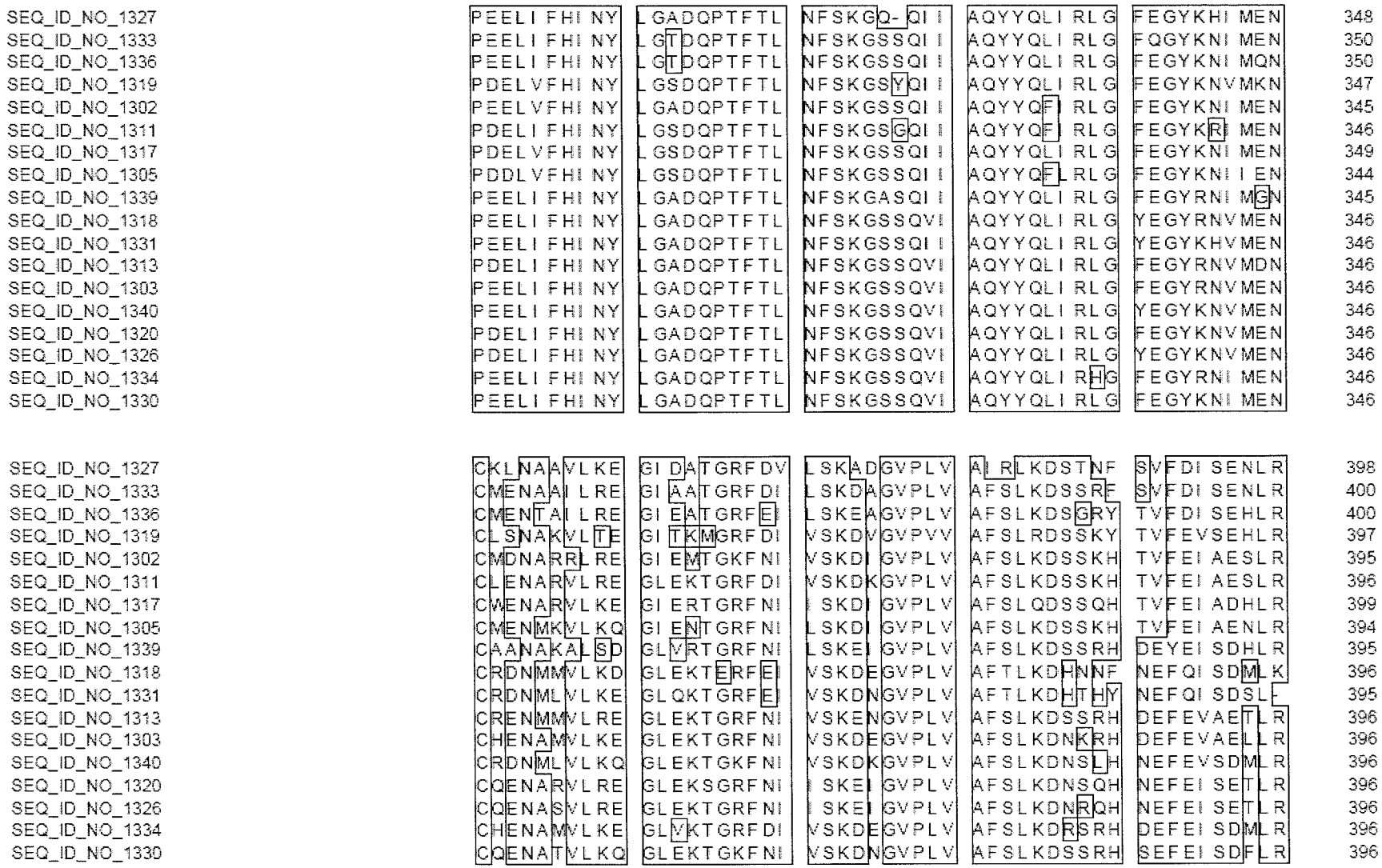


Figure 44 (continued)

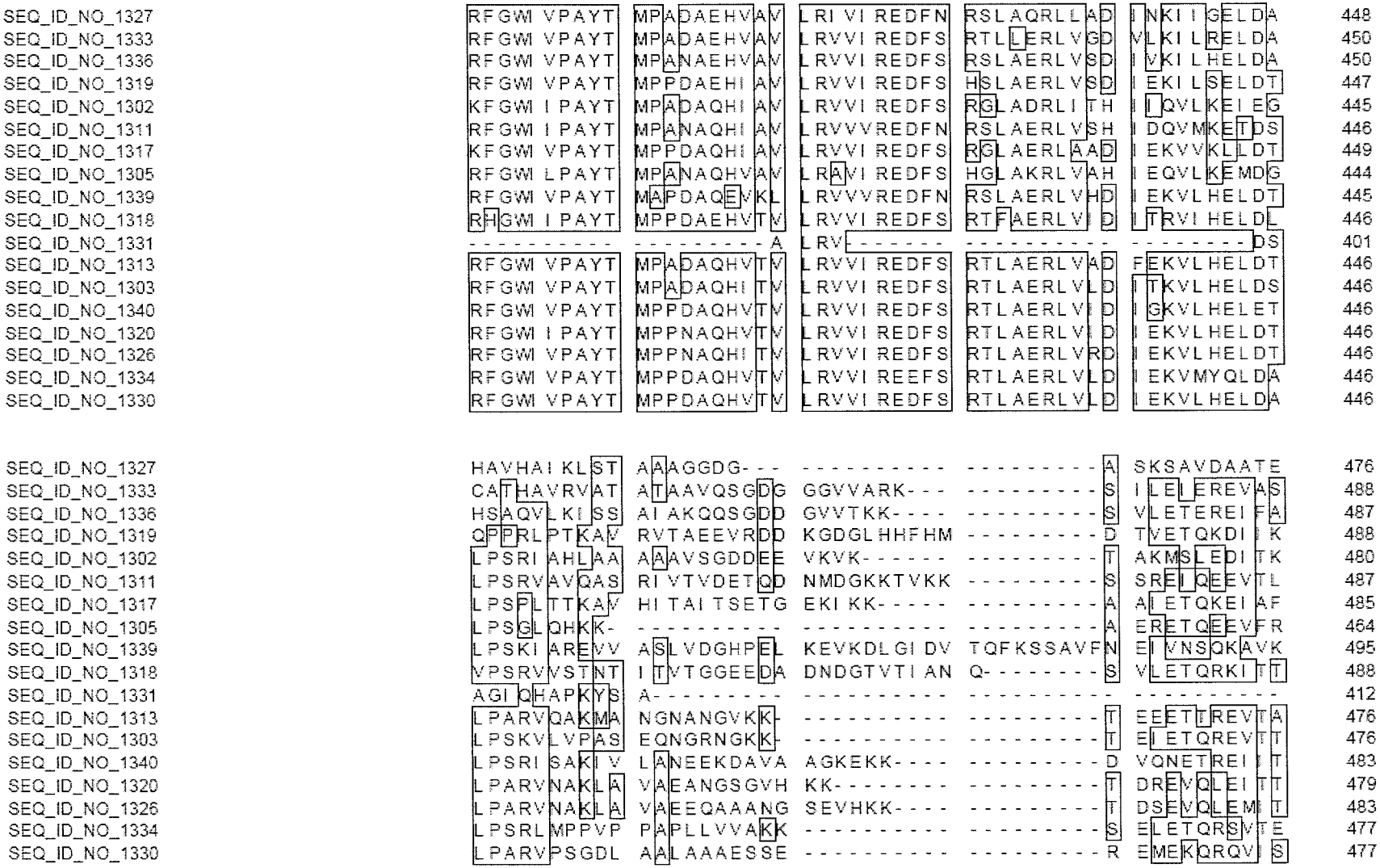


Figure 44 (continued)

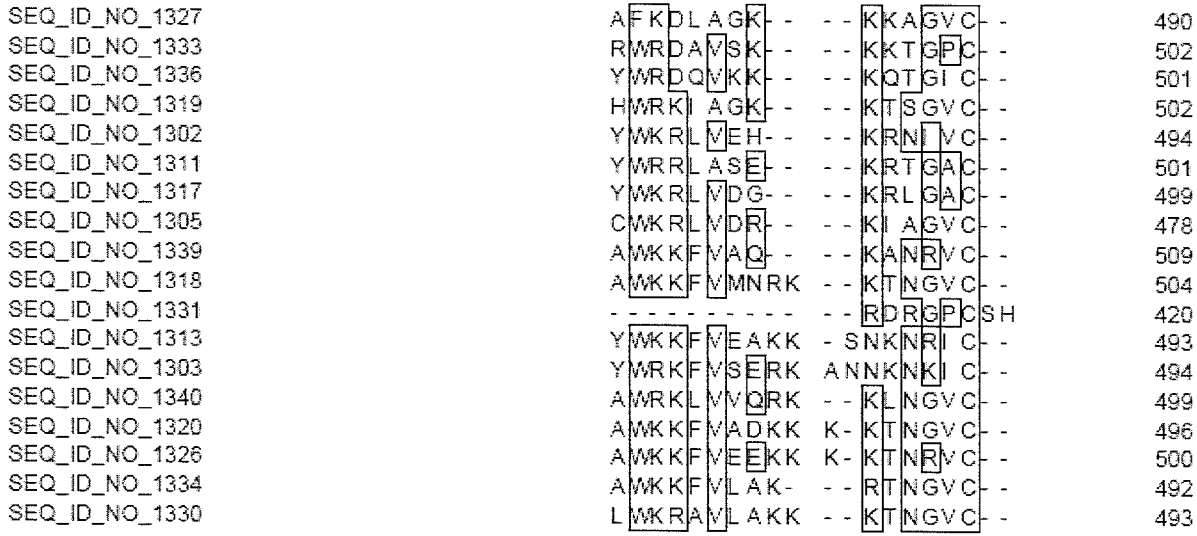


Figure 45


SEQ_ID_NO_1363 ---MSKTTNQ NRRPSFTSST 17
SEQ_ID_NO_1373 -------MVD 3
SEQ_ID_NO_1342 0
SEQ_ID_NO_1381 0
SEQ_ID_NO_1382 0
SEQ_ID_NO_1371 0
SEQ_ID_NO_1366 ---------M 1
SEQ_ID_NO_1370 0
SEQ_ID_NO_1346 0
SEQ_ID_NO_1372 0
SEQ_ID_NO_1374 --MKKQEKEA 8
SEQ_ID_NO_1355 0
SEQ_ID_NO_1364 0
SEQ_ID_NO_1378 MGSRHQVVQQ QNRGDVVPGA IKQKSMAVEK KNRRALGDIG NVV-TVRGVE 49
SEQ_ID_NO_1377 ---MNTNRAV LVPHRGEVGG KQKNGQADGR NNRRVLGDIG NLVTGAPVIE 47
SEQ_ID_NO_1379 MGSRAVVVPD QQPRGR--GG KQKNGQAEGR -NRRVLRDIG NLV-PVPTVE 46
SEQ_ID_NO_1380 ---MAGADEN HGAVKLANFR 17
SEQ_ID_NO_1383 0
SEQ_ID_NO_1363 ESSMRKRHGP SSSSSAVK-- PISNTAVMVA KKRAPLGNIT 55
SEQ_ID_NO_1373 EENKVPATAA ASRGSNKR-- AFDSIAITNE NDPLQISERP 41
SEQ_ID_NO_1342 0
SEQ_ID_NO_1381 -MADKENSTP ASAARLTRSS AAAGAQAKRS AAAGVADGGA 39
SEQ_ID_NO_1382 -MADKENSTP ASAARLTRSS AAAGAQAKRS AAAGVADGGA 39
SEQ_ID_NO_1371 -APSMTTPE- 8
SEQ_ID_NO_1366 ATSENNSSAR PQREAKKR-- AAAAISQIHG N- 30
SEQ_ID_NO_1370 MADQDNSTRR PQREAKKR-- AVAALCE--- 25
SEQ_ID_NO_1346 -MAEQENCTR VTRAAKKR-- AAALASTEDQ 27
SEQ_ID_NO_1372 -MADKENCIR VTRLAKKR-- AVEAMAASEQ Q- 28
SEQ_ID_NO_1374 IMADLENCGR VTRLAKKR-- AAEAMASHQQ Q- 37
SEQ_ID_NO_1355 MADEKENCVR MTRAATKRKA SMEAAIDKE- 29
SEQ_ID_NO_1364 -MAENQNSTR MTRAAAKR-- KASVTDEN-- 25
SEQ_ID_NO_1378 GKALPQVSRP ITRGFCAQLI ANAEAAAAEN NKNSLAVNAK GADGALPIKR 99
SEQ_ID_NO_1377 GKPKAQISRP ATRSFCAQLL ANAQAEKNKV KPLAEVVNKV 87
SEQ_ID_NO_1379 EKPQNQISRP VTRSLCVQ-- PAAAAEKKNK KPLAEVVNGG GEVKAAAAAH 94
SEQ_ID_NO_1380 ETTNRRALKD IKNFVGAP-- SFPCAANKRQ LKEVVCGNND 55
SEQ_ID_NO_1383 -MITGAQGVR QTRSKTTY-- EVPQQQQQQS FEW- 30

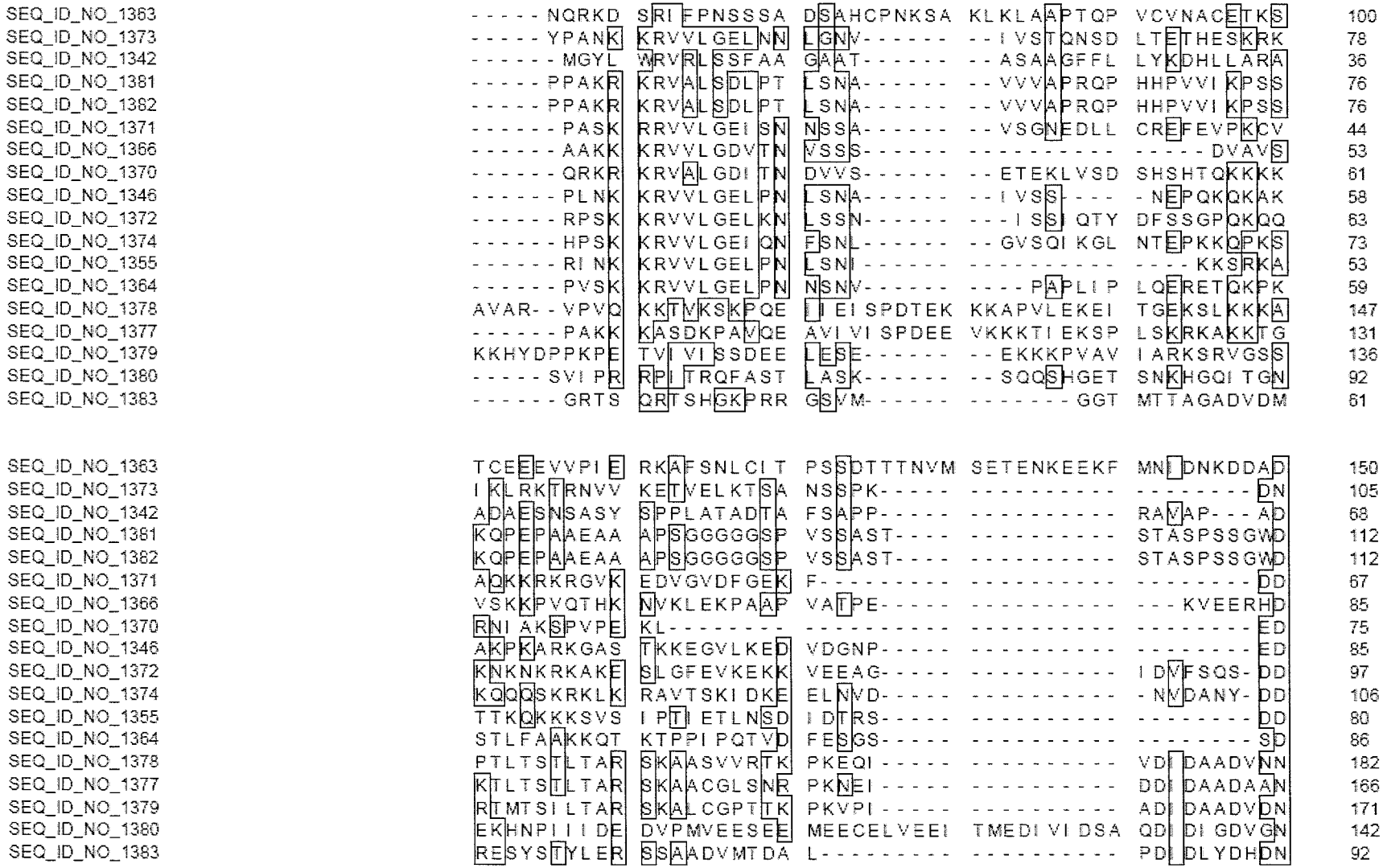

SEQ_ID_NO_1363 ------NQRKD SRIFPNSSSA DSAHCPNKSA KLKLAAPTQP VCVNACETKS 100
SEQ_ID_NO_1373 ------YPANK KRVVLGELNN LGNV------ --IVSTQNSD LTETHESKRK 78
SEQ_ID_NO_1342 -------MGYL WRVRLSSFAA GAAT------ --ASAAGFFL LYKDHLLARA 36
SEQ_ID_NO_1381 ------PPAKR KRVALSDLPT LSNA------ --VVVAPRQP HHPVVIKPSS 76
SEQ_ID_NO_1382 ------PPAKR KRVALSDLPT LSNA------ --VVVAPRQP HHPVVIKPSS 76
SEQ_ID_NO_1371 -------PASK RRVVLGEISN NSSA------ --VSGNEDLL CREFEVPKCV 44
SEQ_ID_NO_1366 -------AAKK KRVVLGDVTN VSSS------ ---------- -----DVAVS 53
SEQ_ID_NO_1370 -------QRKR KRVALGDITN DVVS------ --ETEKLVSD SHSHTQKKKK 61
SEQ_ID_NO_1346 -------PLNK KRVVLGELPN LSNA------ --IVSS---- -NEPQKQKAK 58
SEQ_ID_NO_1372 -------RPSK KRVVLGELKN LSSN------ ---ISSIQTY DFSSGPQKQQ 63
SEQ_ID_NO_1374 -------HPSK KRVVLGEIQN FSNL------ --GVSQIKGL NTEPKKQPKS 73
SEQ_ID_NO_1355 -------RINK KRVVLGELPN LSNI------ ---------- ----KKSRKA 53
SEQ_ID_NO_1364 -------PVSK KRVVLGELPN NSNV------ ----PAPLIP LQERETQKPK 59
SEQ_ID_NO_1378 AVAR--VPVQ KKTVKSKPQE IIEISPDTEK KKAPVLEKEI TGEKSLKKKA 147
SEQ_ID_NO_1377 ------PAKK KASDKPAVQE AVIVISPDEE VKKKTIEKSP LSKRKAKKTG 131
SEQ_ID_NO_1379 KKHYDPPKPE TVIVISSDEE LESE------ --EKKKPVAV IARKSRVGSS 136
SEQ_ID_NO_1380 -----SVIPR RPLTRQFAST LASK------ --SQQSHGET SNKHGQITGN 92
SEQ_ID_NO_1383 ------GRTS QRTSHGKPRR GSVM------ -------GGT MTTAGADVDM 61
SEQ_ID_NO_1363 TCEEEVVPIE RKAFSNLCIT PSSDTTTNVM SETENKEEKF MNIDNKDDAD 150
SEQ_ID_NO_1373 IKLRKTRNVV KETVELKTSA NSSPK----- ---------- ---------DN 105
SEQ_ID_NO_1342 ADAESNSASY SPPLATADTA FSAPP----- ---------- RAVAP---AD 68
SEQ_ID_NO_1381 KQPEPAAEAA APSGGGGGSP VSSAST---- ---------- STASPSSGWD 112
SEQ_ID_NO_1382 KQPEPAAEAA APSGGGGGSP VSSAST---- ---------- STASPSSGWD 112
SEQ_ID_NO_1371 AQKKRKRGVK EDVGVDFGEK F--------- ---------- ---------DD 67
SEQ_ID_NO_1366 VSKKPVQTHK NVKLEKPAAP VATPE----- ---------- ---KVEERHD 85
SEQ_ID_NO_1370 RNIAKSPVPE KL-------- ---------- ---------- ---------ED 75
SEQ_ID_NO_1346 AKPKARKGAS TKKEGVLKED VDGNP----- ---------- ---------ED 85
SEQ_ID_NO_1372 KNKNKRKAKE SLGFEVKEKK VEEAG----- ---------- IDVFSQS-DD 97
SEQ_ID_NO_1374 KQQQSKRKLK RAVTSKIDKE ELNVD----- ---------- -NVDANY-DD 106
SEQ_ID_NO_1355 TTKQKKKSVS IPTIETLNSD IDTRS----- ---------- ---------DD 80
SEQ_ID_NO_1364 STLFAAKKQT KTPPIPQTVD FESGS----- ---------- ---------SD 86
SEQ_ID_NO_1378 PTLTSTLTAR SKAASVVRTK PKEQI----- ---------- VDIDAADVNN 182
SEQ_ID_NO_1377 KTLTSTLTAR SKAACGLSNR PKNEI----- ---------- DDIDAADAAN 166
SEQ_ID_NO_1379 RTMTSILTAR SKALCGPTTK PKVPI----- ---------- ADIDAADVDN 171
SEQ_ID_NO_1380 EKHNPIIIDE DVPMVEESEE MEECELVEEI TMEDIVIDSA QDIDIGDVGN 142
SEQ_ID_NO_1383 RESYSTYLER SSAADVMTDA L--------- ---------- PDIDLYDHDN 92

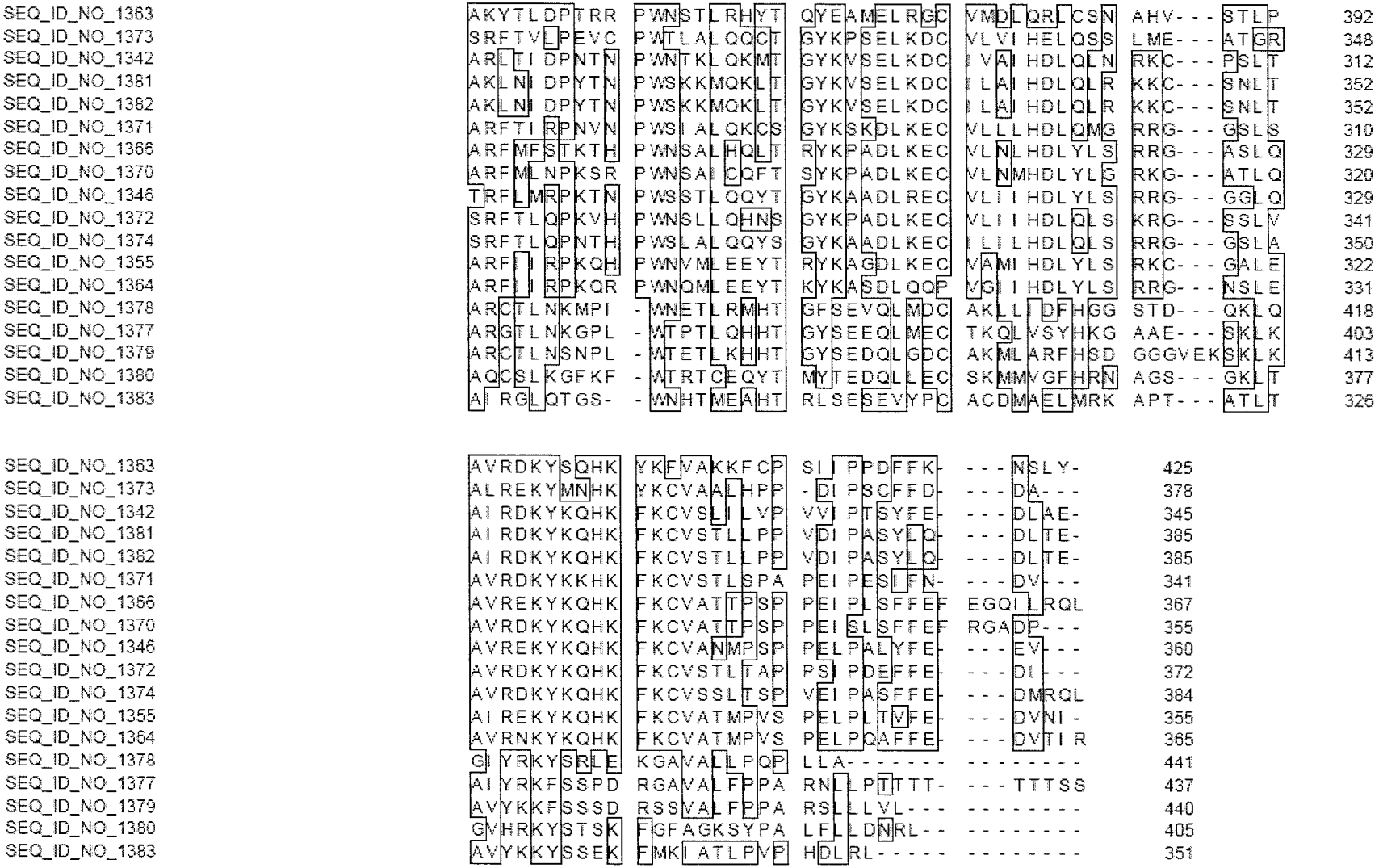
Figure 45 (continued)



Figure 45 (continued)



Figure 45 (continued)



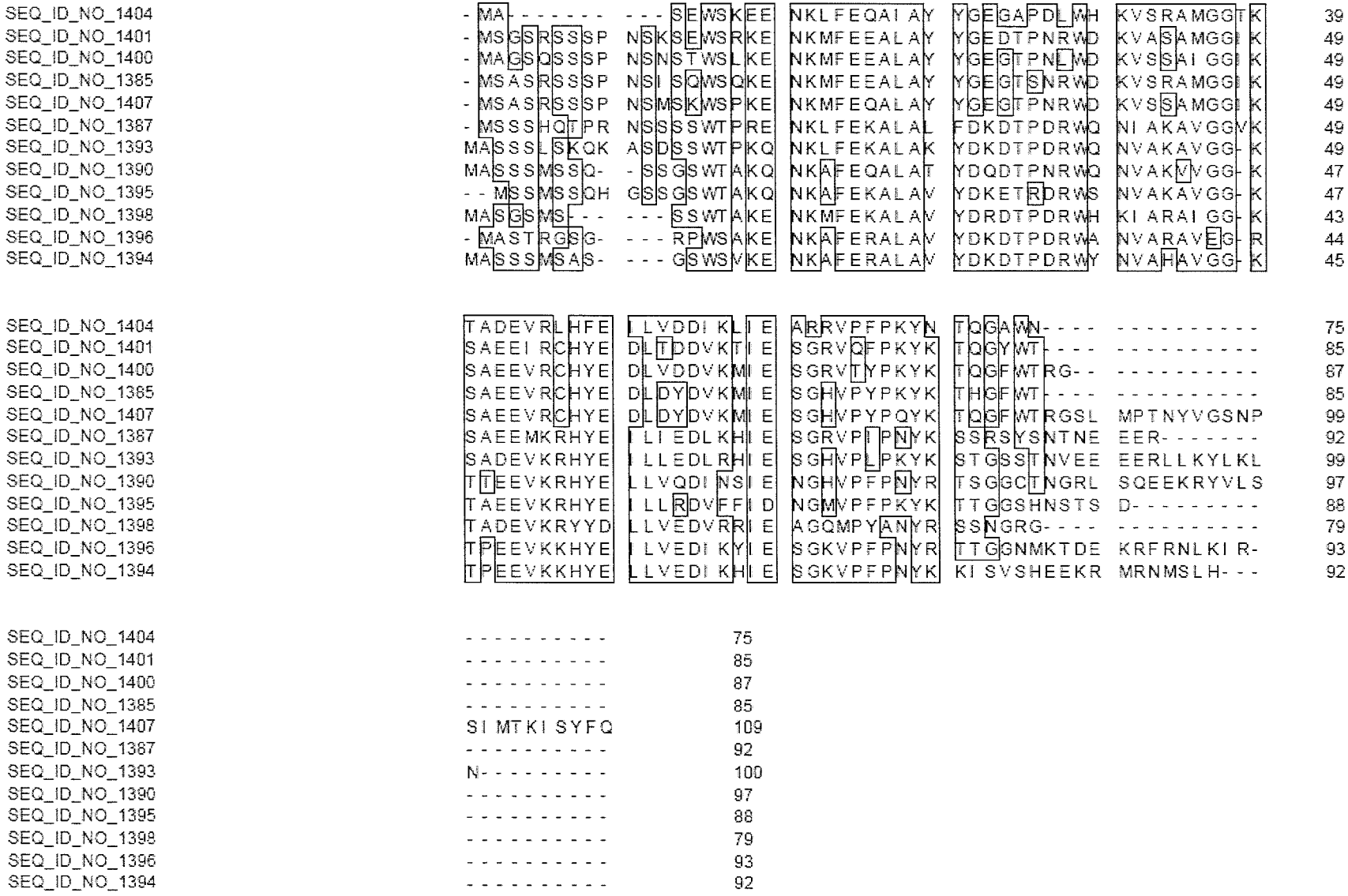

SEQ_ID_NO_1404
SEQ_ID_NO_1401
SEQ_ID_NO_1400
SEQ_ID_NO_1385
SEQ_ID_NO_1407
SEQ_ID_NO_1387
SEQ_ID_NO_1393
SEQ_ID_NO_1390
SEQ_ID_NO_1395
SEQ_ID_NO_1398
SEQ_ID_NO_1396
SEQ_ID_NO_1394
- MA- - - - - - - - - SEWSKEE NKLFEQAIAY YGEGAPDLWH KVSRAMGGTK 39
- MSGSRSSSP NSKSEWSRKE NKMFEEALAY YGEDTPNRWD KVASAMGGIK 49
- MAGSQSSSP NSNSTWSLKE NKMFEEALAY YGEGTPNLWD KVSSAIGGIK 49
- MSASRSSSP NSISQWSQKE NKMFEEALAY YGEGTSNRWD KVSRAMGGIK 49
- MSASRSSSP NSMSKWSPKE NKMFEQALAY YGEGTPNRWD KVSSAMGGIK 49
- MSSSHQTPR NSSSSWTPRE NKLFEKALAL FDKDTPDRWQ NIAKAVGGVK 49
MASSSLSKQK ASDSSWTPKQ NKLFEKALAK YDKDTPDRWQ NVAKAVGG-K 49
MASSSMSSQ- - SSGSWTAKQ NKAFEQALAT YDQDTPNRWQ NVAKVVGG-K 47
- - MSSMSSQH GSSGSWTAKQ NKAFEKALAV YDKETRDRWS NVAKAVGG-K 47
MASGSMS- - - - - - SSWTAKE NKMFEKALAV YDRDTPDRWH KIARAIGG-K 43
- MASTRGSG- - - - RPWSAKE NKAFERALAV YDKDTPDRWA NVARAVEG-R 44
MASSSMSAS- - - - GSWSVKE NKAFERALAV YDKDTPDRWY NVAHAVGG-K 45
TADEVRLHFE ILVDDIKLIE ARRVPFPKYN TQGAWN- - - - - - - - - - - - 75
SAEEIRCHYE DLTDDVKTIE SGRVQFPKYK TQGYWT- - - - - - - - - - - - 85
SAEEVRCHYE DLVDDVKMIE SGRVTYPKYK TQGFWTRG- - - - - - - - - - - 87
SAEEVRCHYE DLDYDVKMIE SGHVPYPKYK THGFWT- - - - - - - - - - - - 85
SAEEVRCHYE DLDYDVKMIE SGHVPYPQYK TQGFWTRGSL MPTNYVGSNP 99
SAEEMKRHYE ILIEDLKHIE SGRVPIPNYK SSRSYSNTNE EER- - - - - - - 92
SADEVKRHYE ILLEDLRHIE SGHVPLPKYK STGSSTNVEE EERLLKYLKL 99
TTEEVKRHYE LLVQDINSIE NGHVPFPNYR TSGGCTNGRL SQEEKRYVLS 97
TAEEVKRHYE ILLRDVFFID NGMVPFPKYK TTGGSHNSTS D- - - - - - - - - 88
TADEVKRYYD LLVEDVRRIE AGQMPYANYR SSNGRG- - - - - - - - - - - 79
TPEEVKKHYE ILVEDIKYIE SGKVPFPNYR TTGGNMKTDE KRFRNLKIR- 93
TPEEVKKHYE LLVEDIKHIE SGKVPFPNYK KISVSHEEKR MRNMSLH- - - 92
- - - - - - - - - - - 75
- - - - - - - - - - - 85
- - - - - - - - - - - 87
- - - - - - - - - - - 85
SIMTKISYFQ 109
- - - - - - - - - - - 92
N- - - - - - - - - - 100
- - - - - - - - - - - 97
- - - - - - - - - - - 88
- - - - - - - - - - - 79
- - - - - - - - - - - 93
- - - - - - - - - - - 92

Figure 47

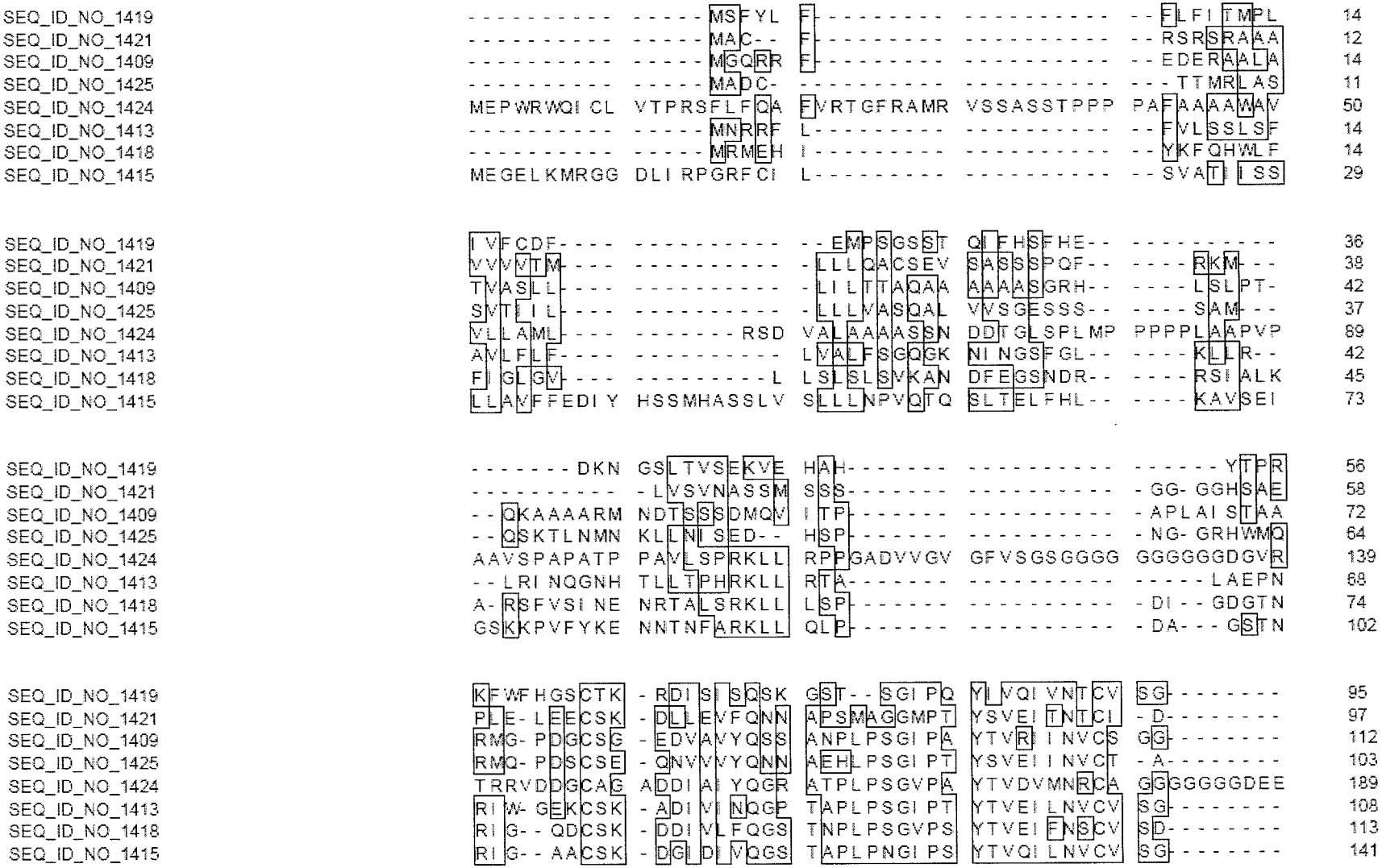
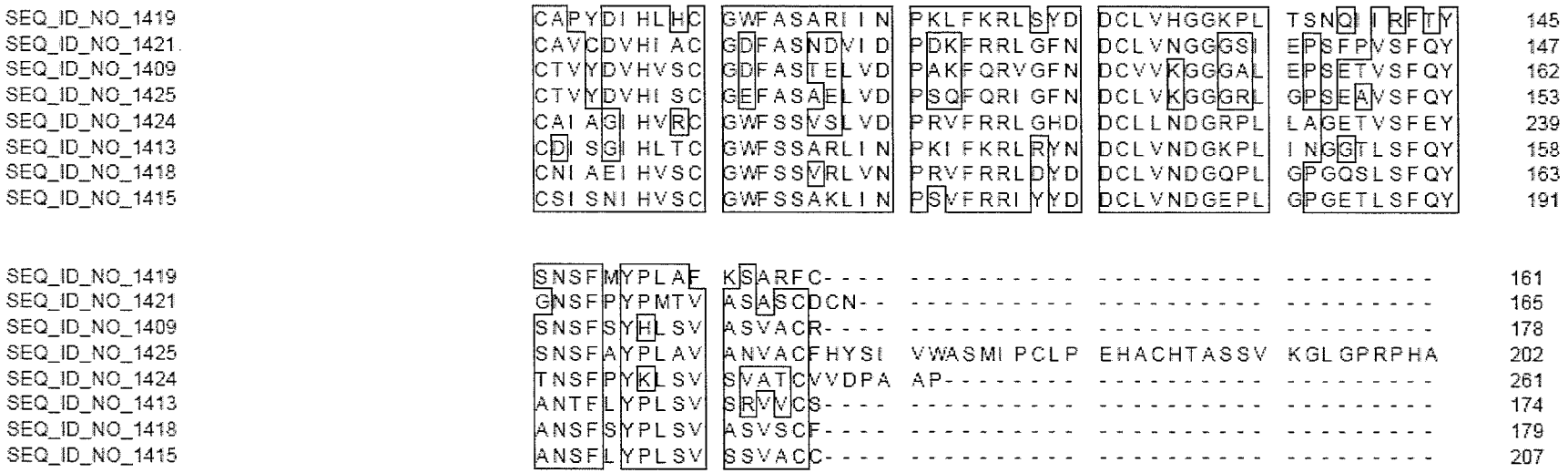

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SEQ_ID_NO_1424
SEQ_ID_NO_1413
SEQ_ID_NO_1418
SEQ_ID_NO_1415

Figure 47 (continued)



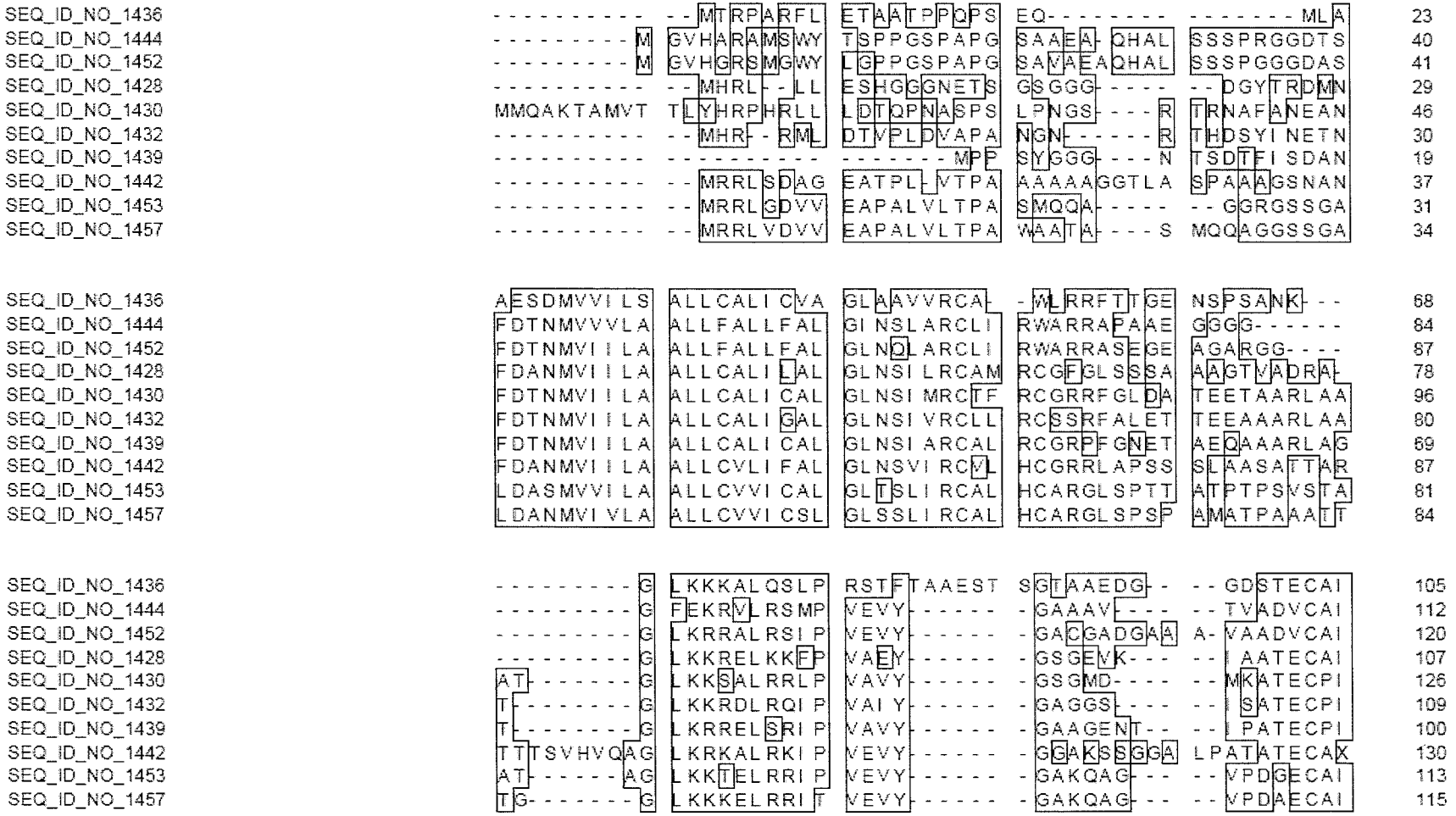
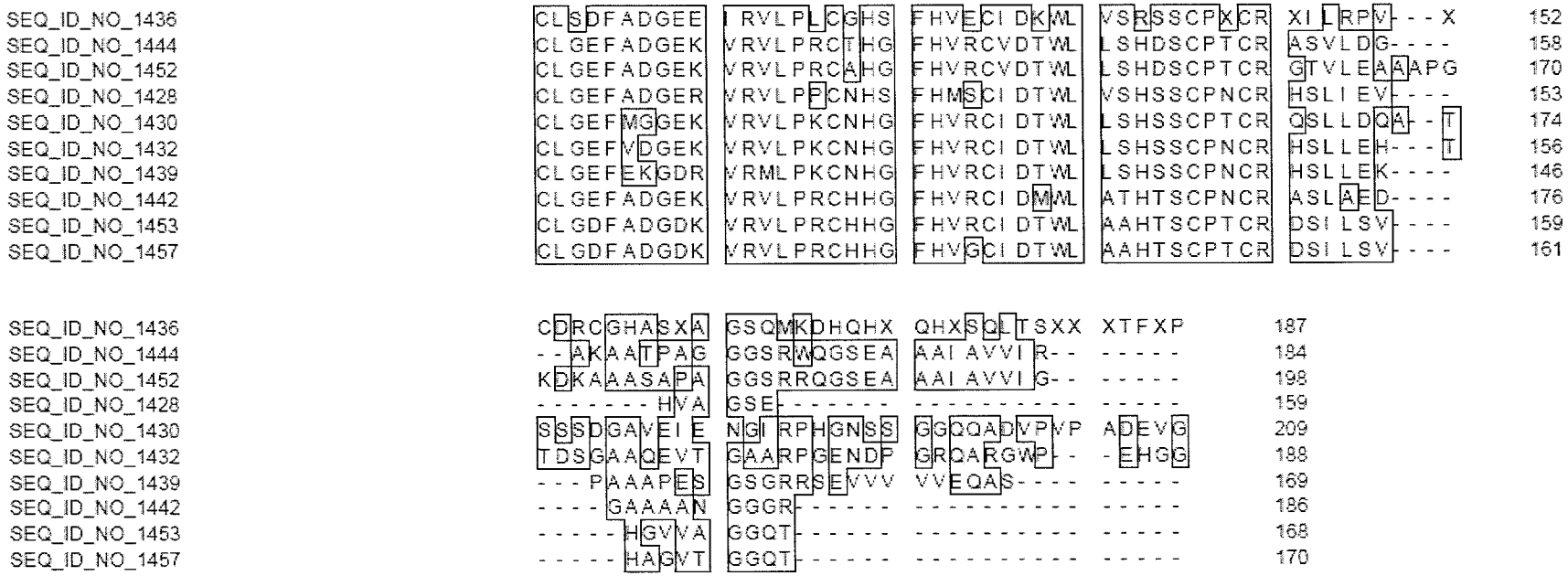

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SEQ_ID_NO_1428
SEQ_ID_NO_1430
SEQ_ID_NO_1432
SEQ_ID_NO_1439
SEQ_ID_NO_1442
SEQ_ID_NO_1453
SEQ_ID_NO_1457

Figure 48 (continued)



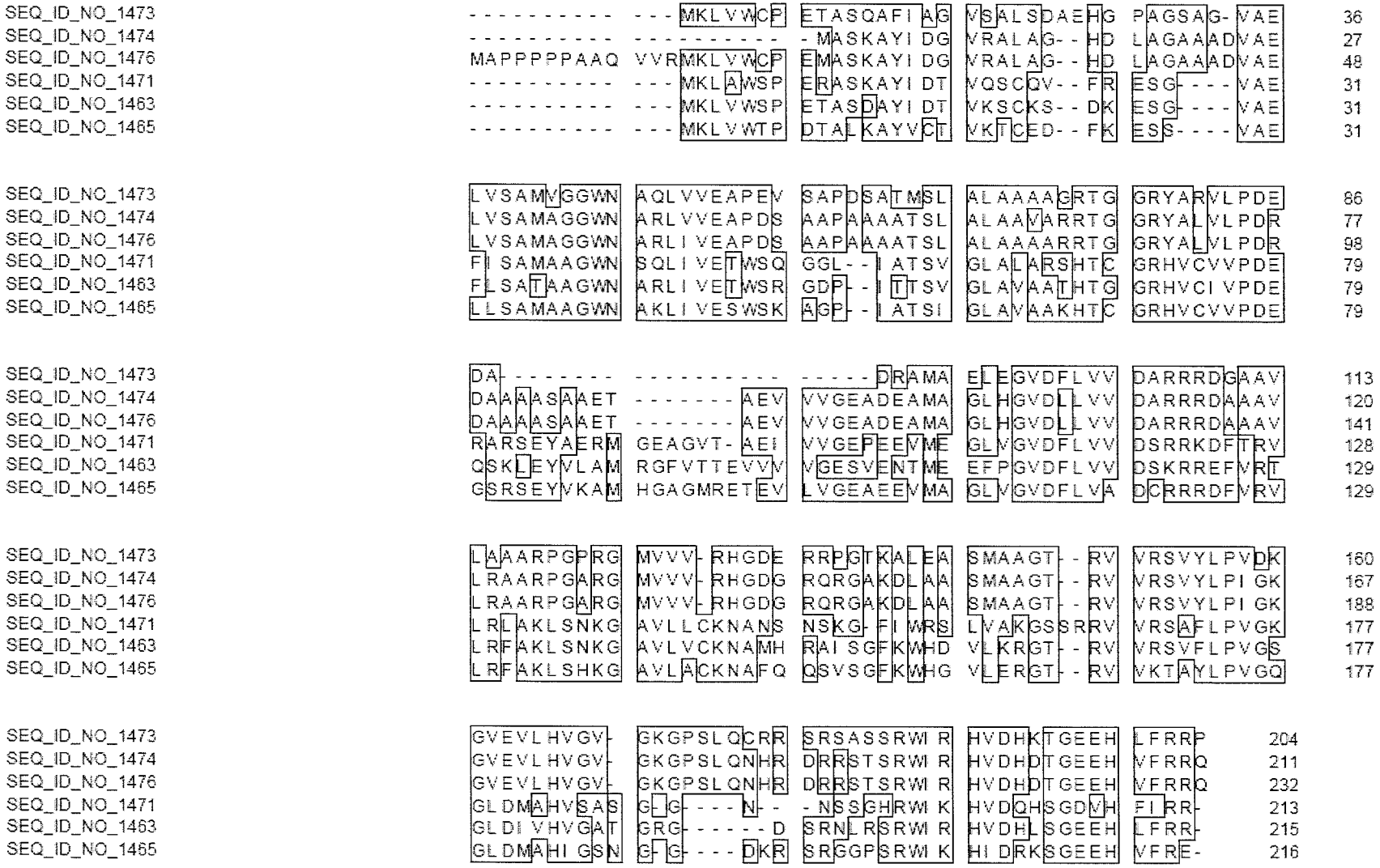

SEQ_ID_NO_1473
SEQ_ID_NO_1474
SEQ_ID_NO_1476
SEQ_ID_NO_1471
SEQ_ID_NO_1463
SEQ_ID_NO_1465
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216

Figure 50

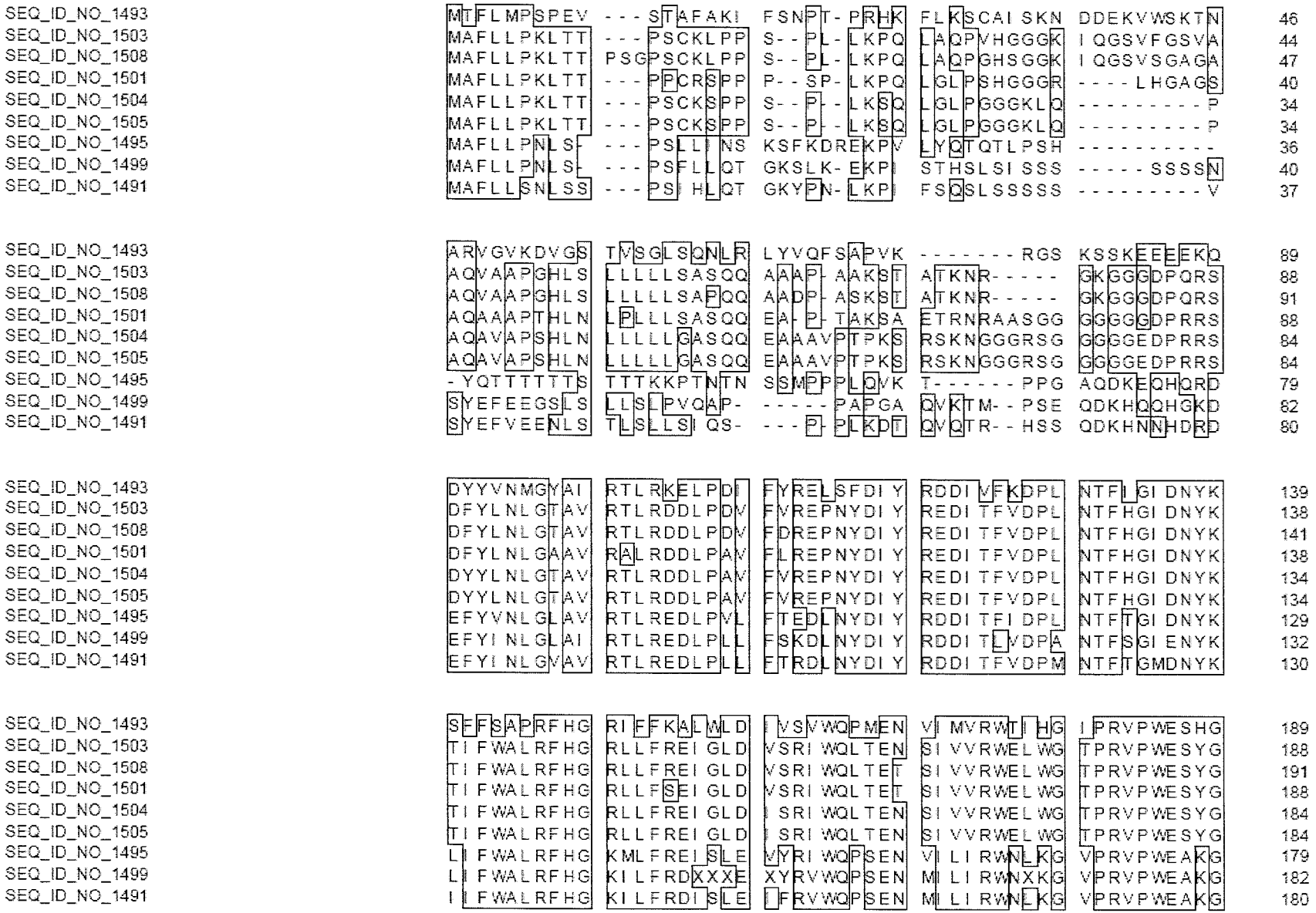
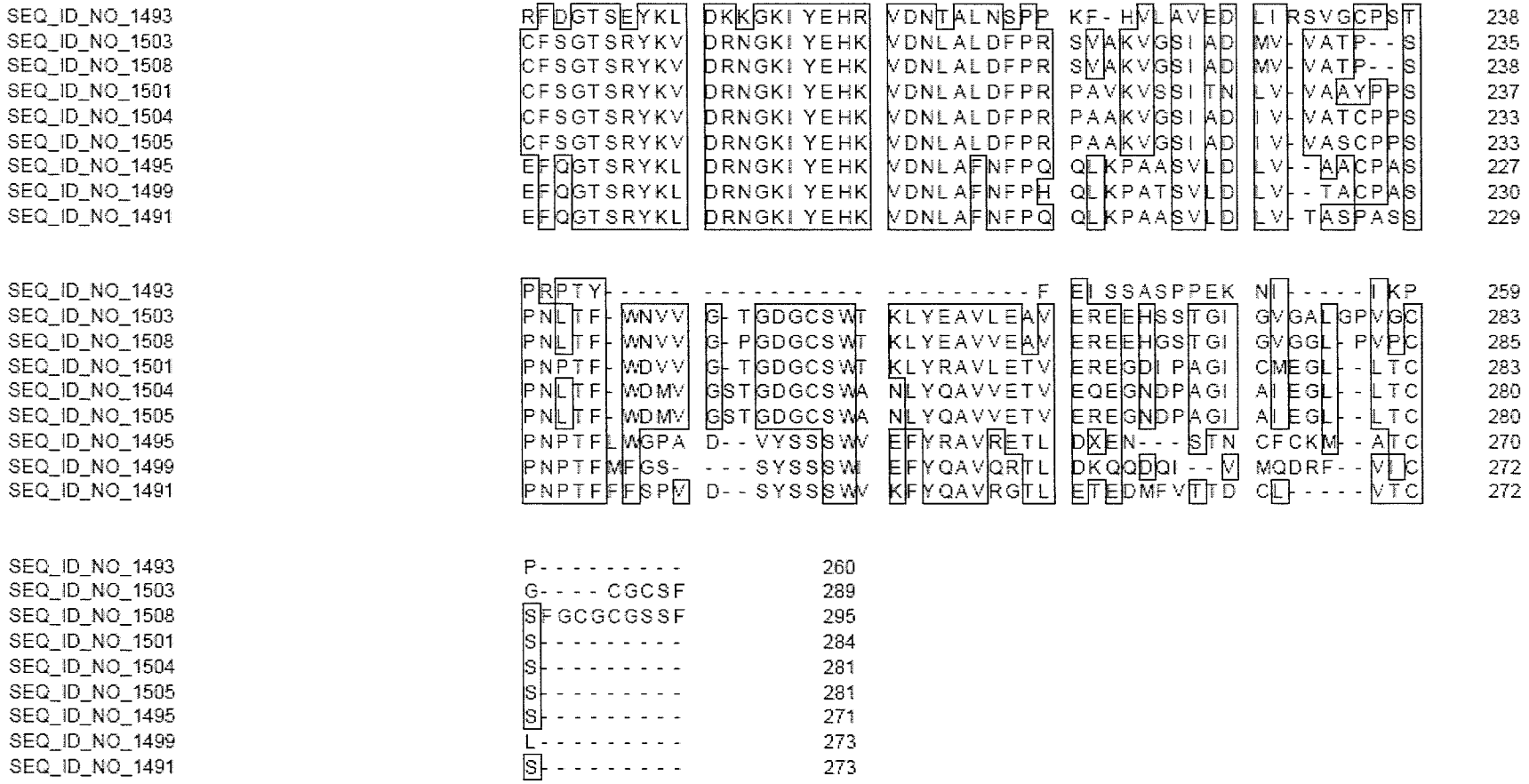

SEQ_ID_NO_1493
SEQ_ID_NO_1503
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SEQ_ID_NO_1501
SEQ_ID_NO_1504
SEQ_ID_NO_1505
SEQ_ID_NO_1495
SEQ_ID_NO_1499
SEQ_ID_NO_1491

Figure 50 (continued)




SEQ_ID_NO_1520 MDSLPKLR- - - - - - - - - - - HPSPFPTPL SSSLSFRSLP PPHFPSSSFR 37
SEQ_ID_NO_1510 MESLGKLQLH HQPFHLSFTH TSSSTFPKNL - - - - - FKSSI QPI SS- - - LK 42
SEQ_ID_NO_1512 MESLTKLHCR LQPLHLSFNH QRPS- FAKPI SSSVSFRTS- - - - SSSSPFK 45
SEQ_ID_NO_1516 MESVAKLHCR HQPFNLSLNP HRPS- FPKPI - ISLSFKTPP PSSSSPFKLS 48
SEQ_ID_NO_1520 LPSI RASSSP SQNDPAFRTP RNTPSLPPLL QTLTSFLSPL LETTCIVI- A 86
SEQ_ID_NO_1510 SASI KASSSK FQNS- - - ITP LPK- - - - - - SI- - - - PFRL FKSTCITLTT 78
SEQ_ID_NO_1512 LTSI RALSSS SSS- - - - SVP LHQTPKPSLL QT- - - - LAPL LKTTCITITA 87
SEQ_ID_NO_1516 STSI RASSSS SSR- - - - ITP LN- - - - - - - KN- - - - LGTI IKITSITLTA 82
SEQ_ID_NO_1520 AAAFFFMRFH HT- PAVLAAP LTSPAAETDT - - - - - AFTQE EAERLLEERL 130
SEQ_ID_NO_1510 AAALLLANLH LKSPAIAAPI APPPSVESKE - - - - - NVTLE EEERALDEHL 123
SEQ_ID_NO_1512 GAALLFMRFH QK- PALAATP TVTPTVEPAQ TDS- - NVSLE DQEKTIEEHL 134
SEQ_ID_NO_1516 AAALFFTRLN IK- PAIASPL TASSTVDPTE ESSKENVSYE EQERALQDYL 131
SEQ_ID_NO_1520 STNPRDTEAL HALMEVKIKA RKMDEAFEVL NRLIELEPEE QEWPLLKANM 180
SEQ_ID_NO_1510 ITHPSDVDAL RSLMEVKIKS RKLTEAVEVI DRLIKLEPEE KEWPVLKANI 173
SEQ_ID_NO_1512 TQYPNDVEAL QSLMEVRIKS RKLPQAIEVI DRLIQLEPED TEWPMLRAQI 184
SEQ_ID_NO_1516 SQNPNDIEAL RSLMEVRIKS KKLVEAIEVV DRLIELEPNE DEWPLLKSQI 181
SEQ_ID_NO_1520 HIYNDDHASA RKLFEEILKK DPLRVEAFHG LVMATAQSNE PLKSLLKRVE 230
SEQ_ID_NO_1510 FTYSGDLDLA KTGFEEILAK DPLRVEAYHG LLMAYSDAGL DLKEVESRIE 223
SEQ_ID_NO_1512 HSYSGDFALA KNEFEEILAK DPVRVEAFHG LVMASSESGQ KLKELEKRIE 234
SEQ_ID_NO_1516 YTYSGDFESA KDGFEAILKK DPLRVEAYHG LVMANSESGG SLEVVLKRIE 231
SEQ_ID_NO_1520 EAIEVCKKQK KDSDVRDFRL LIAQIKVMEG DYTEALKAYQ ELVKEEPRDF 280
SEQ_ID_NO_1510 EAMLKCKKEN NQNDFRDFKL LVAQIRVIEG KHSEALKLYQ ELVKEEPRDF 273
SEQ_ID_NO_1512 GAMEKCKKEK KNKDFRDFKL LIAQIRVIEG DHLEALKVYE GLVKEEPRDF 284
SEQ_ID_NO_1516 SAMDKCKKEK KTSDLRDFKL LVAQVRVMEE KYLDALKVYE ELVKEEPRDF 281
SEQ_ID_NO_1520 RPYLCQGIIY TLLRKKDEAD KQFNKFRRLV PKDHPYKDYF EDNMFATKFF 330
SEQ_ID_NO_1510 RPYLCQGIIY TLLKKKDKAE EQFDNFRKLV PKNHPYREYF MDNMIATKLF 323
SEQ_ID_NO_1512 RPYLCMGIIY SLMKKKDEAE KHFEKVRKLV PRNHPYREYF VDNMVATKLF 334
SEQ_ID_NO_1516 RPYLCQGIIY TLLRKKDEAE KKFEQFKKLV PKNHPYREYL VDNMFATKFF 331

Figure 51 (continued)

SEQ_ID_NO_1520	SQKLEREGA- - - - GARG	343
SEQ_ID_NO_1510	SEKAQREMAE EMAGSTS	340
SEQ_ID_NO_1512	SERAEREGA- - - - - - -	343
SEQ_ID_NO_1516	SDKVERERS- - - - - - -	340


SEQ_ID_NO_1525
SEQ_ID_NO_1535
SEQ_ID_NO_1527
SEQ_ID_NO_1534
39
39
48
50
77
85
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94
111
120
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138
160
156
180
181
193
190
228
230
239
239
270
275
276
274
314
319

Figure 52 (continued)

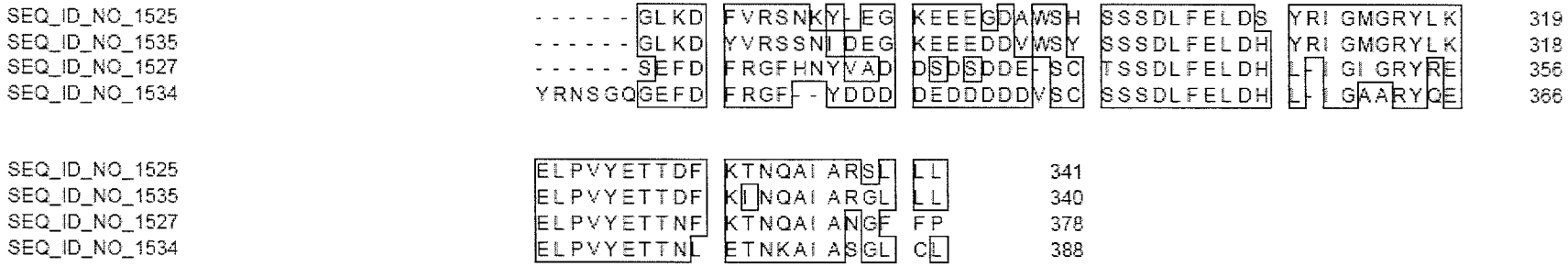


Figure 53

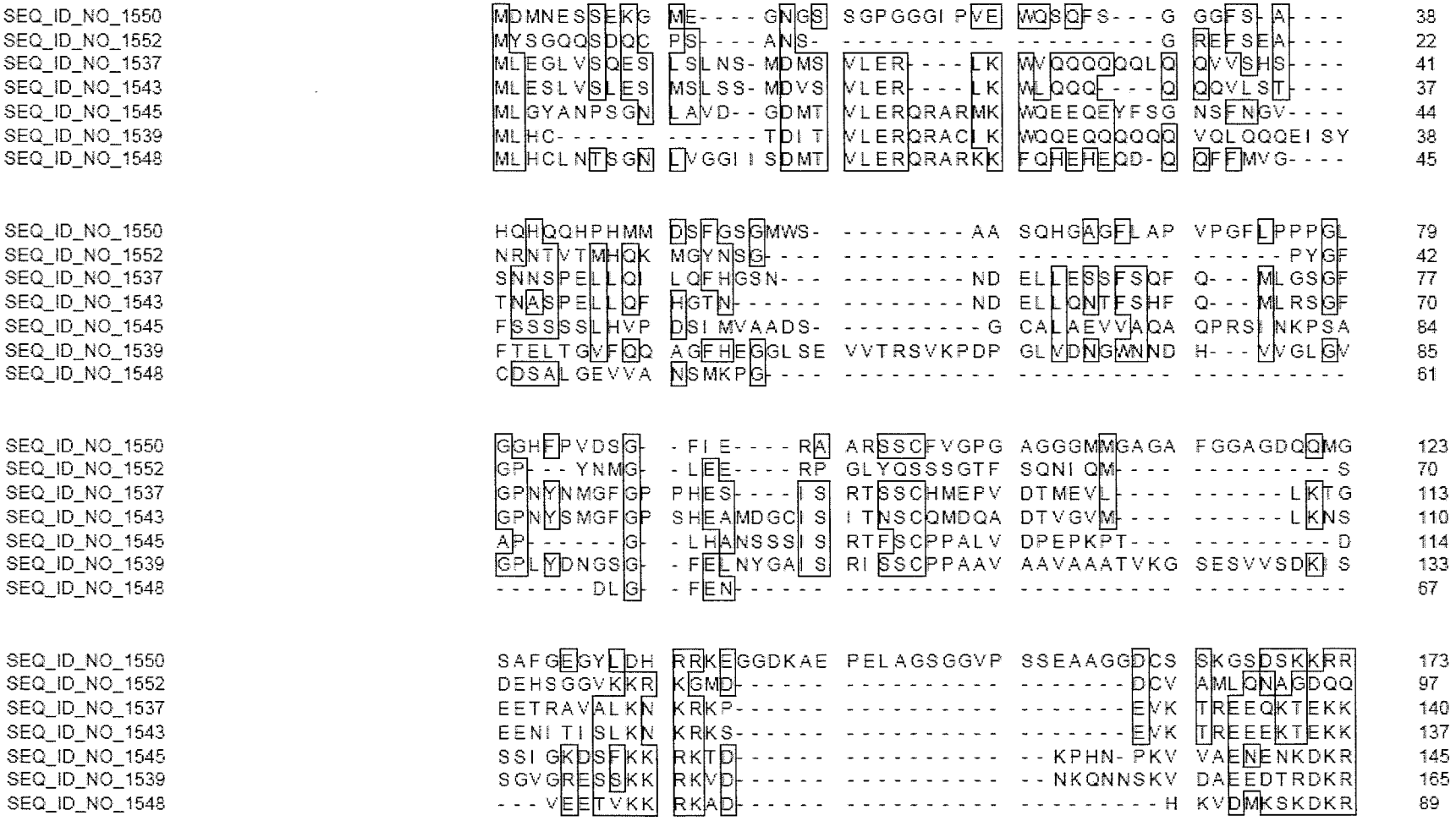

SEQ_ID_NO_1550
SEQ_ID_NO_1552
SEQ_ID_NO_1537
SEQ_ID_NO_1543
SEQ_ID_NO_1545
SEQ_ID_NO_1539
SEQ_ID_NO_1548

Figure 53 (continued)

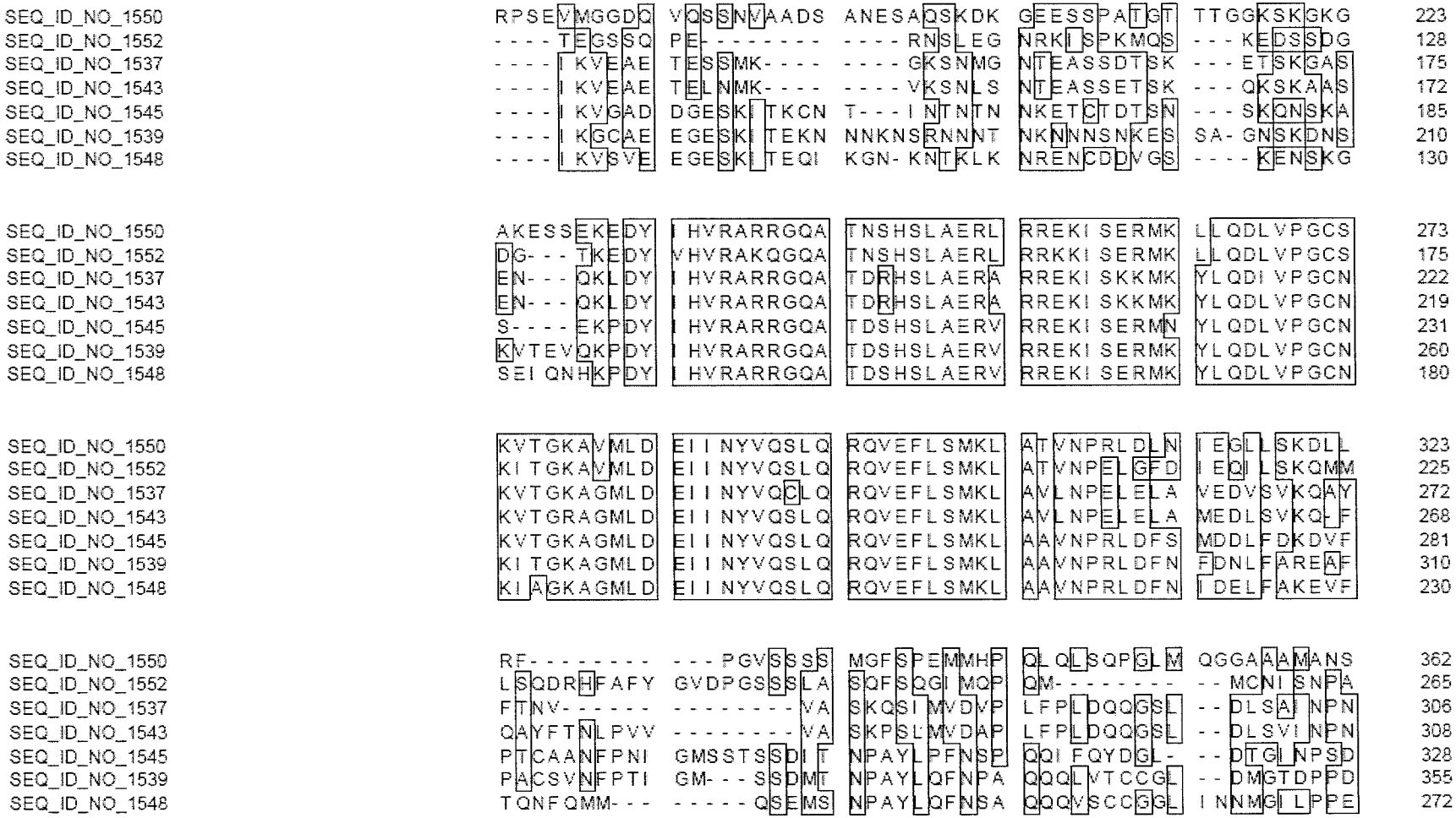


Figure 53 (continued)

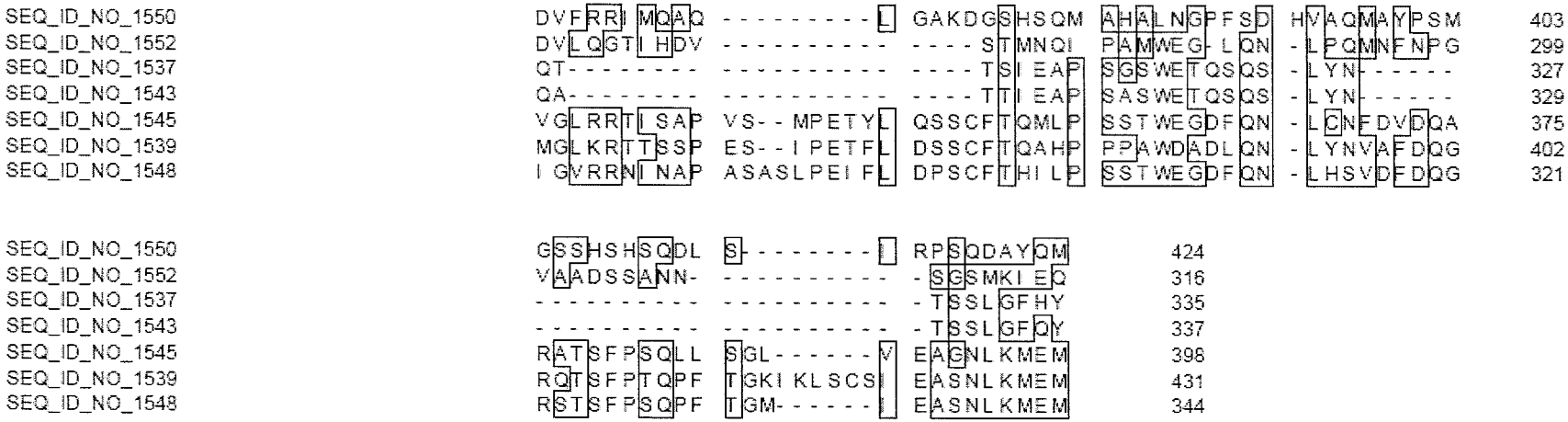


Figure 54

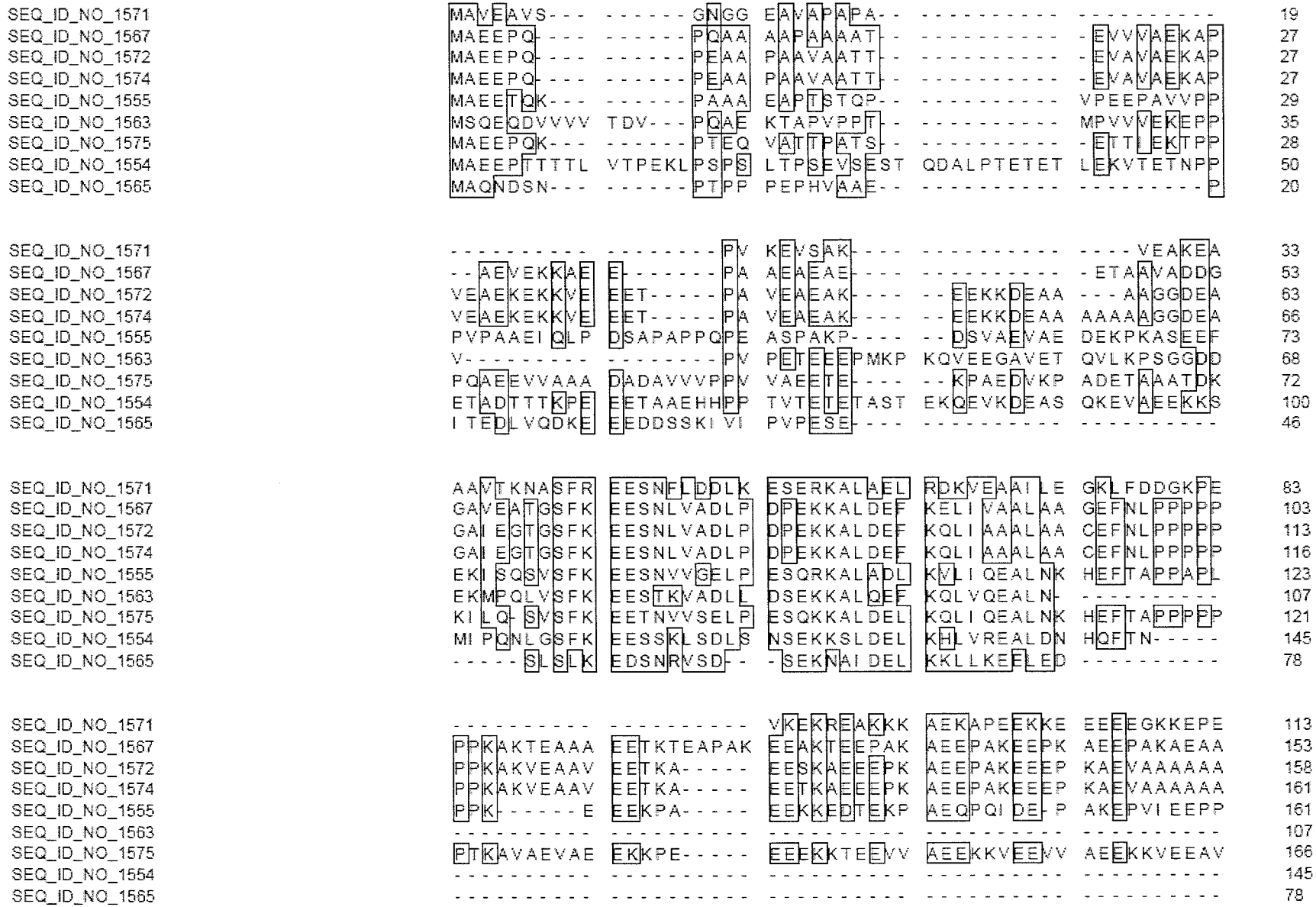

SEQ_ID_NO_1571
SEQ_ID_NO_1567
SEQ_ID_NO_1572
SEQ_ID_NO_1574
SEQ_ID_NO_1555
SEQ_ID_NO_1563
SEQ_ID_NO_1575
SEQ_ID_NO_1554
SEQ_ID_NO_1565

Figure 54 (continued)



Figure 54 (continued)



Figure 54 (continued)

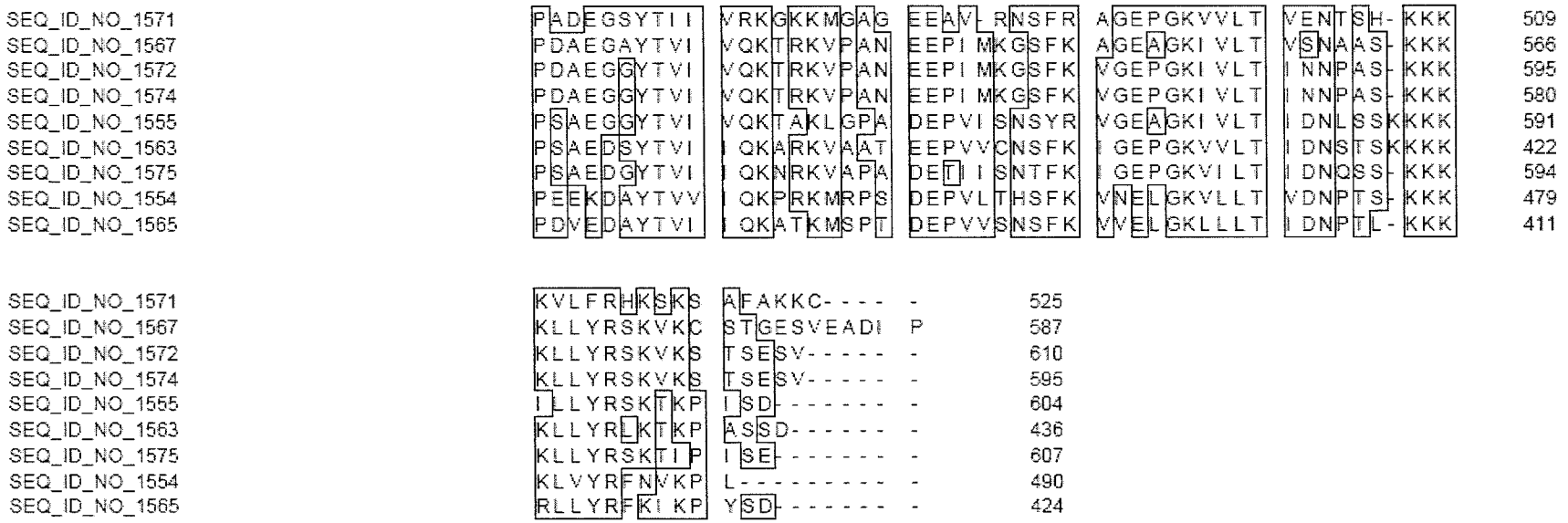


Figure 55


SEQ_ID_NO_1578
SEQ_ID_NO_1607
SEQ_ID_NO_1440
SEQ_ID_NO_1648
SEQ_ID_NO_1651
SEQ_ID_NO_1487
SEQ_ID_NO_1040
SEQ_ID_NO_1485
SEQ_ID_NO_1560
SEQ_ID_NO_1623
SEQ_ID_NO_1622
SEQ_ID_NO_1041
SEQ_ID_NO_1590
SEQ_ID_NO_1577
SEQ_ID_NO_1611
SEQ_ID_NO_1637
SEQ_ID_NO_1627
SEQ_ID_NO_1608
SEQ_ID_NO_1609
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82
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87

Figure 55 (continued)

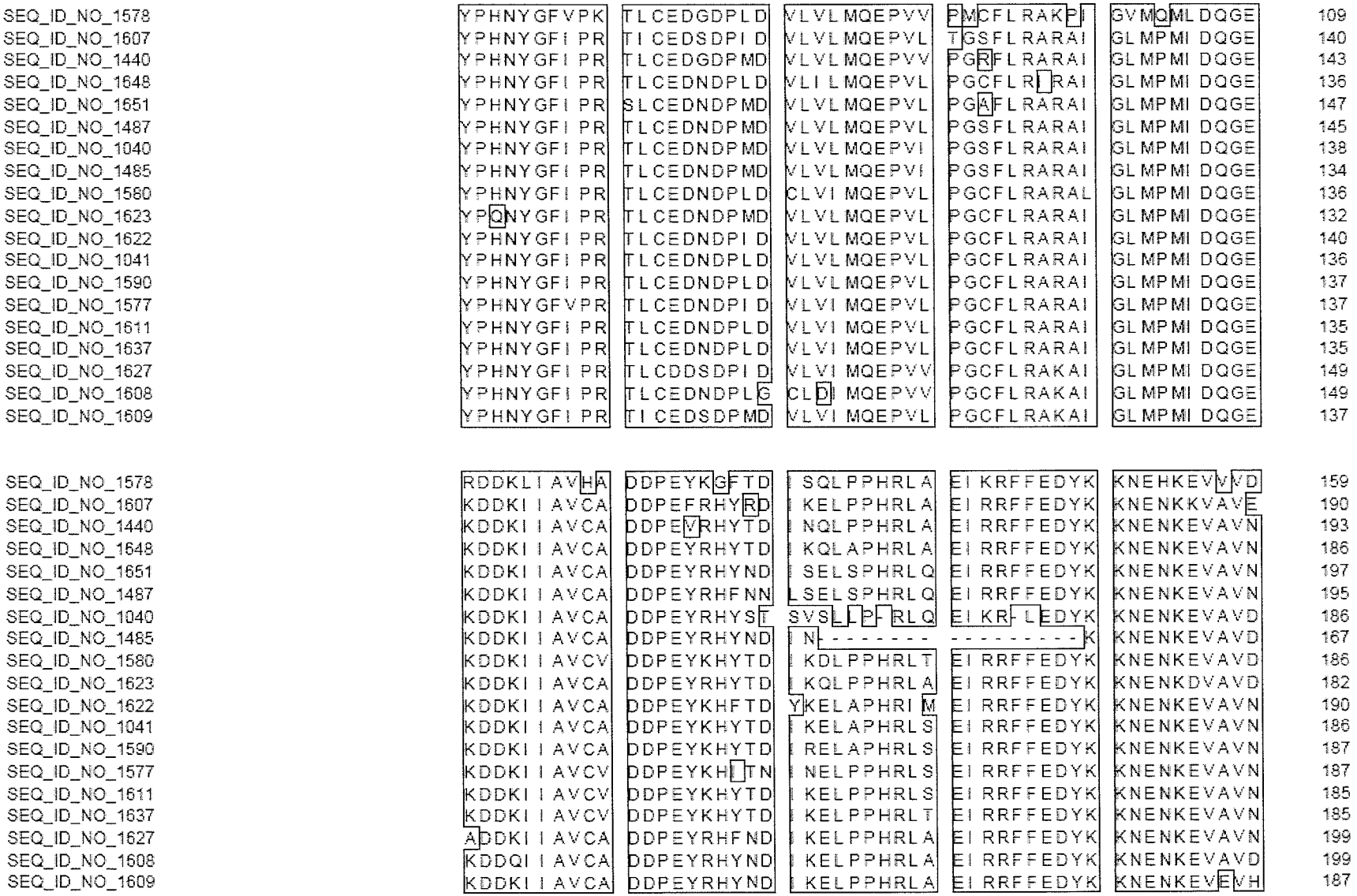


Figure 55 (continued)

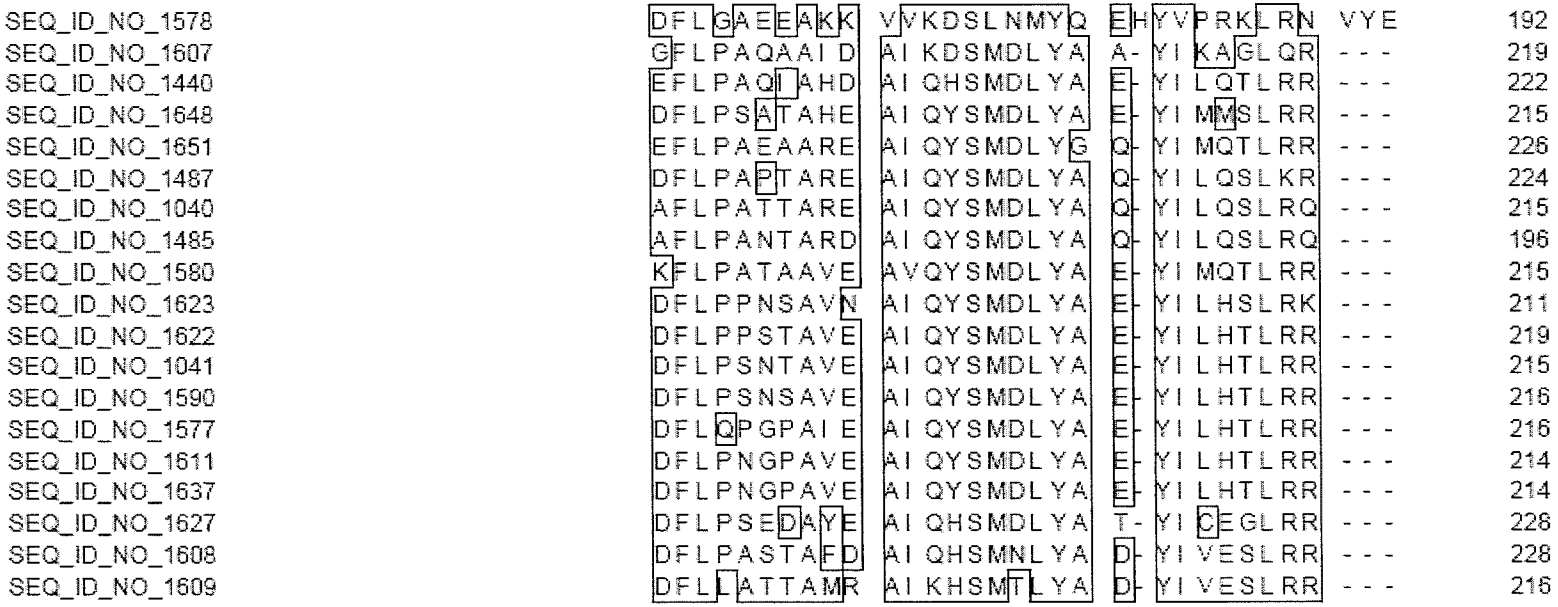


Figure 56

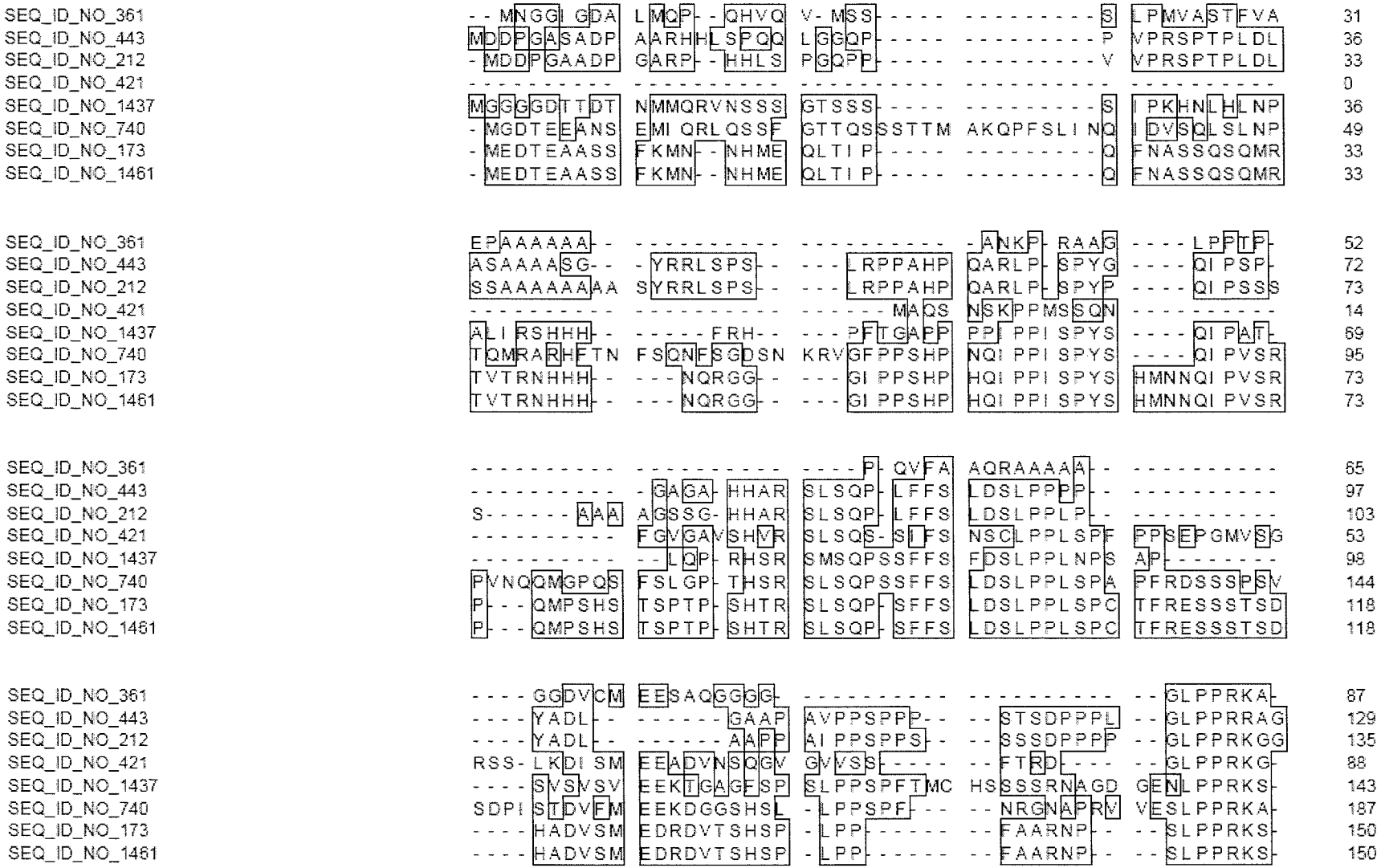

SEQ_ID_NO_361
SEQ_ID_NO_443
SEQ_ID_NO_212
SEQ_ID_NO_421
SEQ_ID_NO_1437
SEQ_ID_NO_740
SEQ_ID_NO_173
SEQ_ID_NO_1461

Figure 56 (continued)

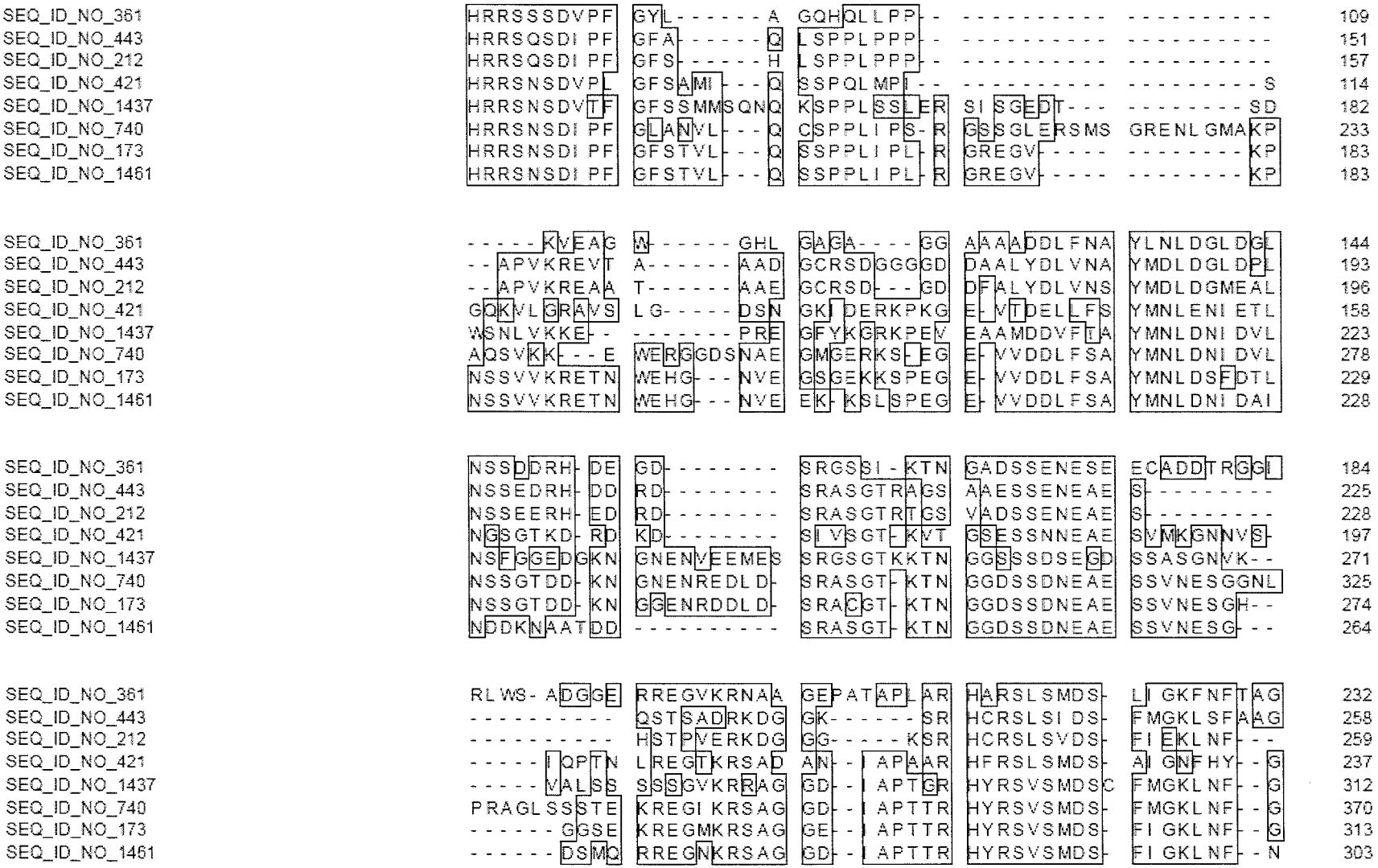


Figure 56 (continued)

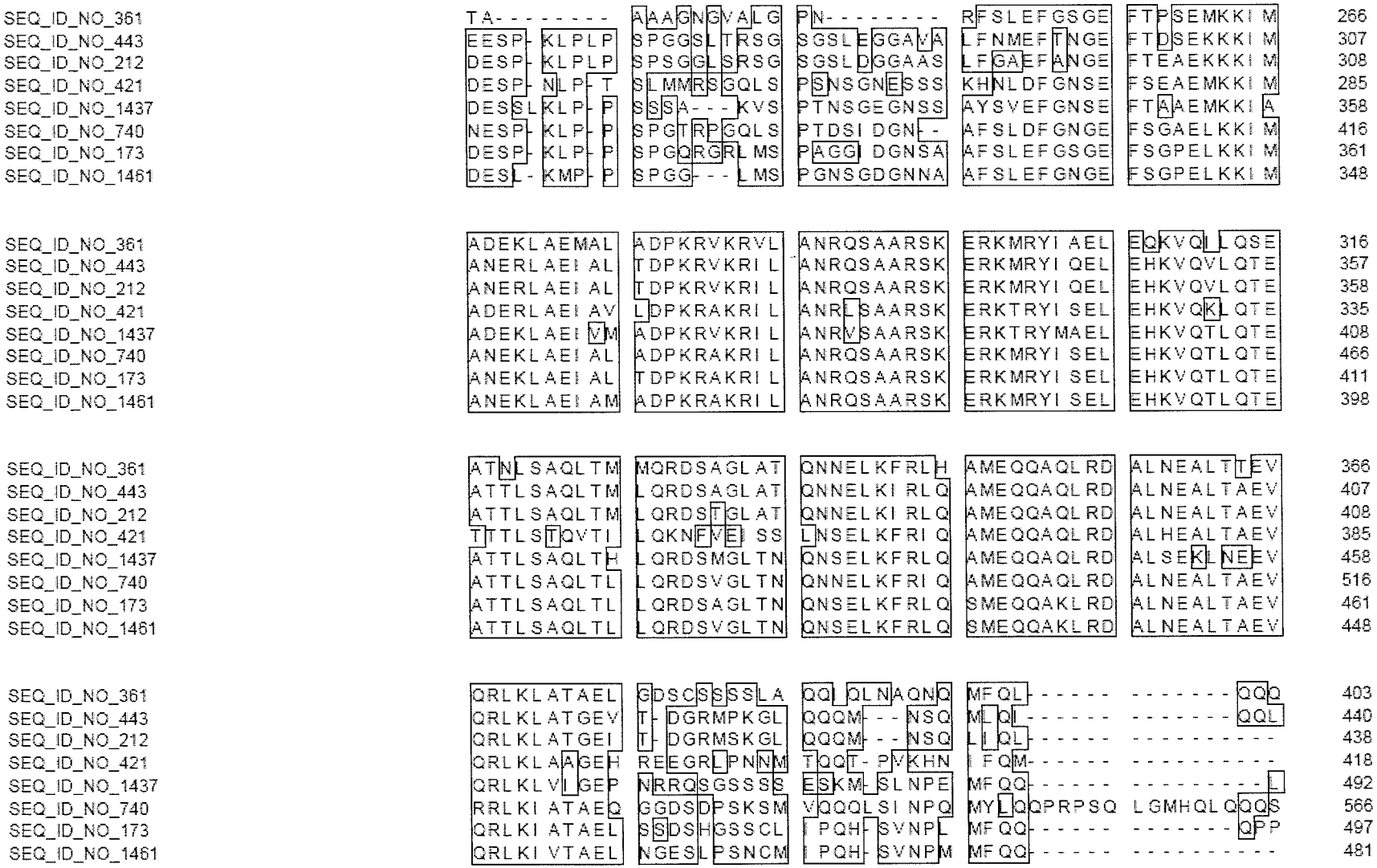


Figure 56 (continued)

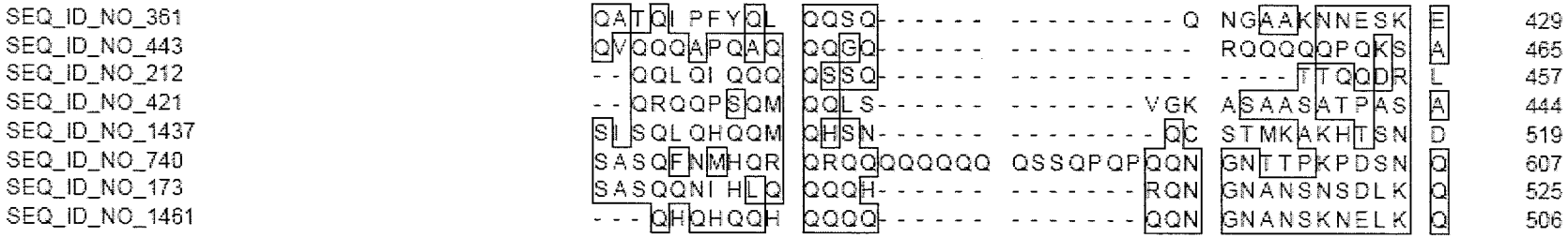
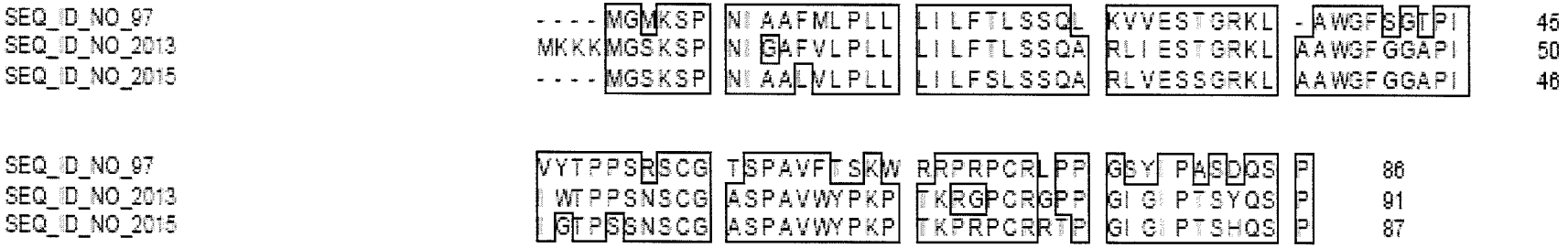


Figure 57


SEQ_ID_NO_97 ----MGMKSP NIAAFMLPLL LILFTLSSQL KVVESTGRKL -AWGFSSGTPI 45
SEQ_ID_NO_2013 MKKKMGSKSP NIGAFVLPLL LILFTLSSQA RLIESTGRKL AAWGFGGAPI 50
SEQ_ID_NO_2015 ----MGSKSP NIAALVLPLL LILFSLSSQA RLVESSGRKL AAWGFGGAPI 46
SEQ_ID_NO_97 VYTPPSRSCG TSPAVFTSKW RRPRPCRLPP GSYIPASDQS P 86
SEQ_ID_NO_2013 IWTPPSNSCG ASPAVWYPKP TKRGPCRGPP GIGIPTSYQS P 91
SEQ_ID_NO_2015 IGTPSSNSCG ASPAVWYPKP TKPRPCRRTP GIGIPTSHQS P 87