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(54) **CARBON FIXATION SYSTEMS IN PLANTS AND ALGAE**

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(57) **ABSTRACT**

Provided are heterologous nucleic acid constructs, vectors and methods for elevating cyclic electron transfer activity, improving carbon concentration, and enhancing carbon fixation in C3 and C4 plants, and algae, and producing biomass or other products from C3 or C4 plants, and algae, selected from among, for example, starches, oils, fatty acids, lipids, cellulose or other carbohydrates, alcohols, sugars, nutraceuticals, pharmaceuticals, fragrance and flavoring compounds, and organic acids, as well as transgenic plants produced thereby. These methods and transgenic plants and algae encompass the expression, or overexpression, of various combinations of genes that improve carbon concentrating systems in plants and algae, such as bicarbonate transport proteins, carbonic anhydrase, light driven proton pump, cyclic electron flow regulators, etc.

20 Claims, 13 Drawing Sheets

Specification includes a Sequence Listing.

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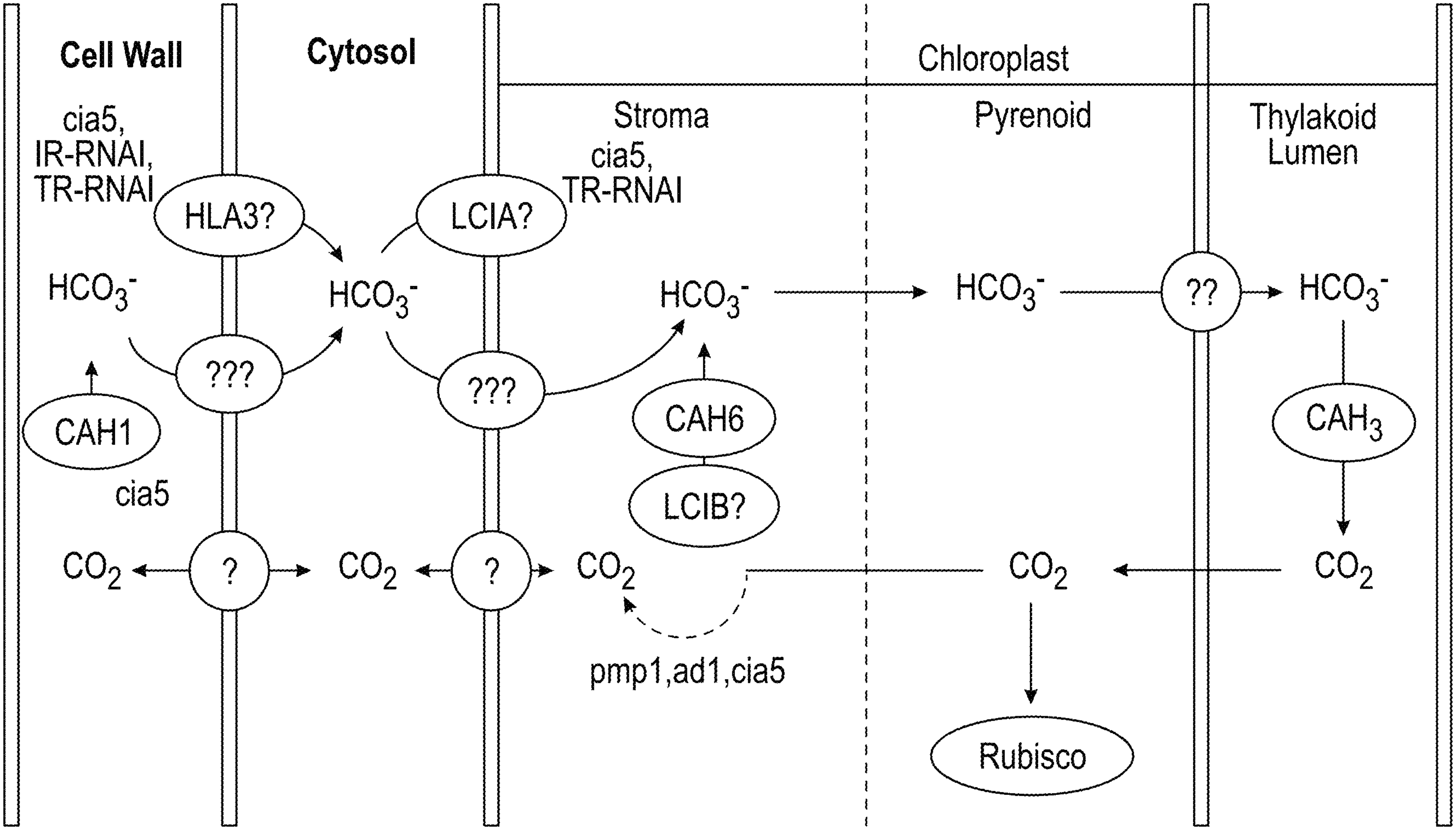

Cell Wall
Cytosol
Chloroplast
Stroma
Pyrenoid
Thylakoid Lumen
cia5, IR-RNAI, TR-RNAI
HLA3?
LCIA?
cia5, TR-RNAI
HCO_3^-
HCO_3^-
HCO_3^-
HCO_3^-
??
HCO_3^-
???
???
CAH1
CAH6
LCIB?
CAH_3
cia5
CO_2
?
CO_2
?
CO_2
CO_2
CO_2
pmp1,ad1,cia5
Rubisco

FIG. 1

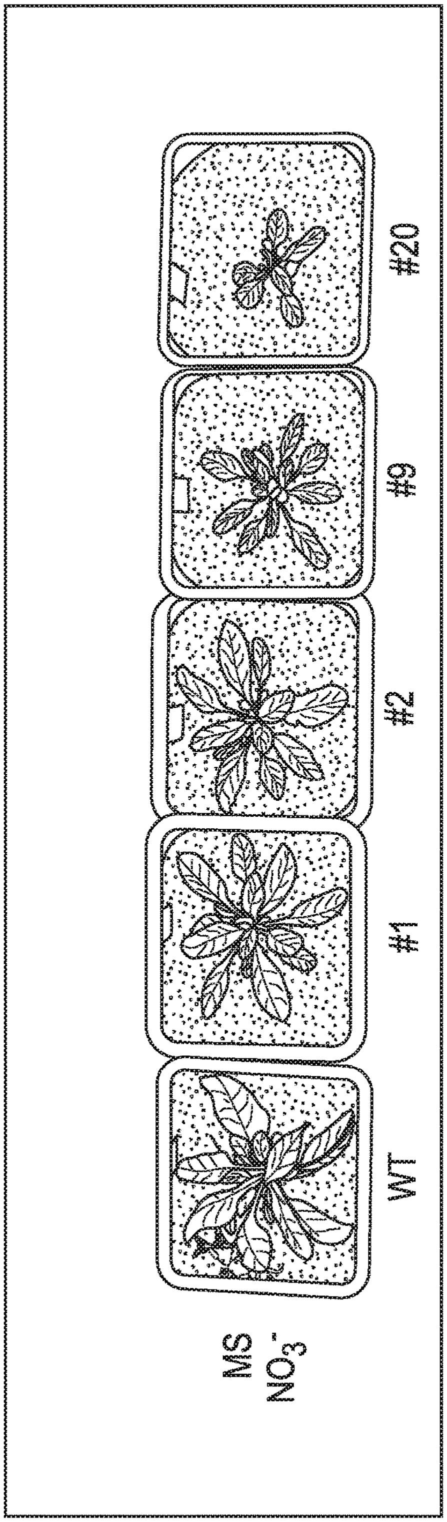


FIG. 2A

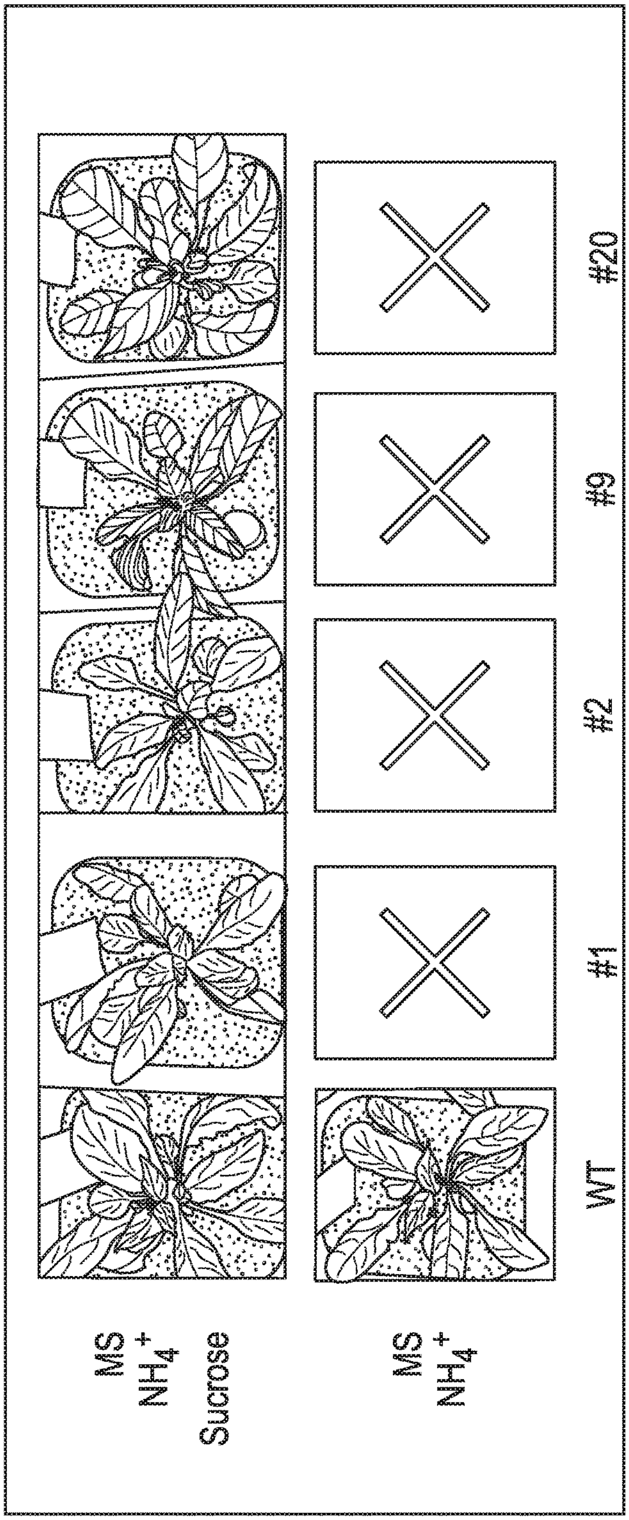


FIG. 2B

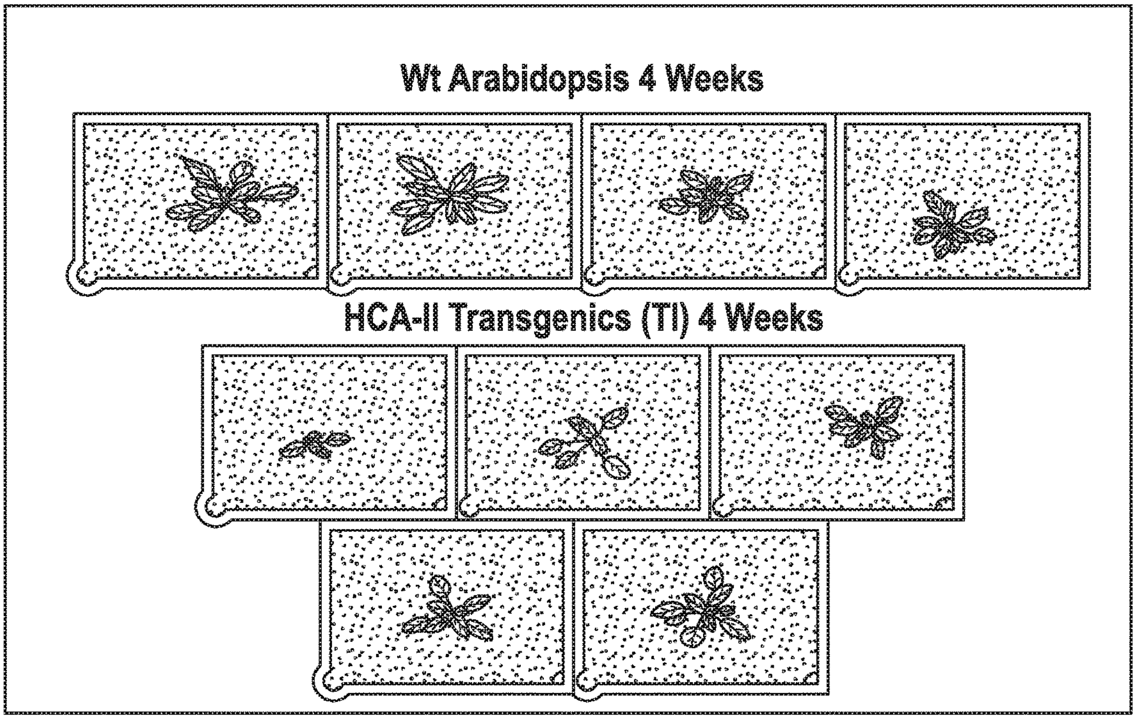


FIG. 3A

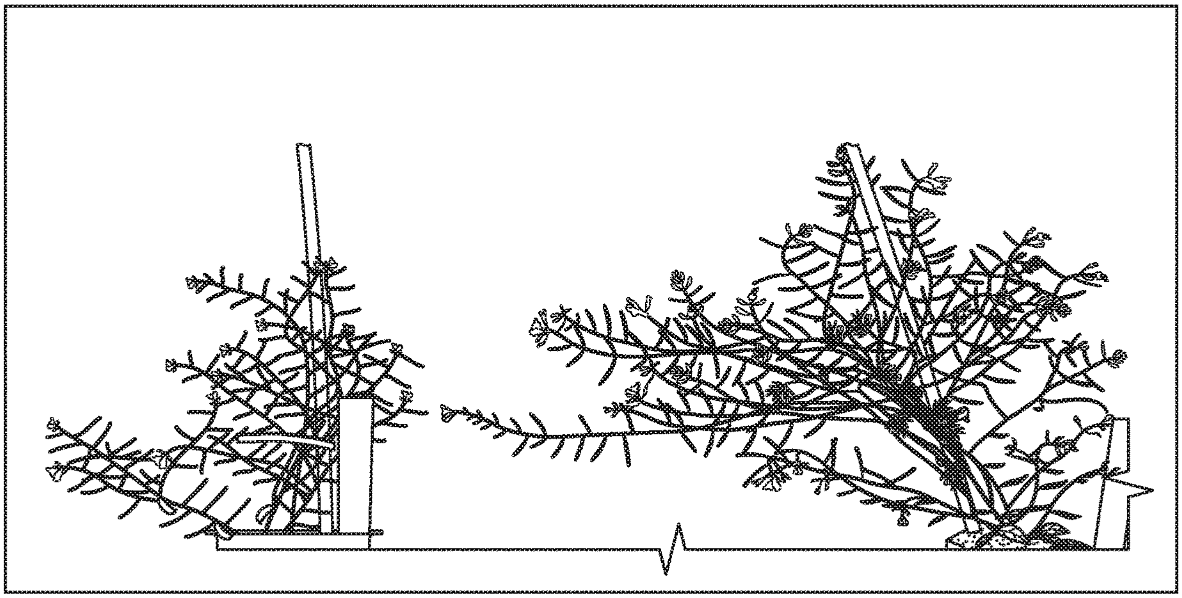


FIG. 3B

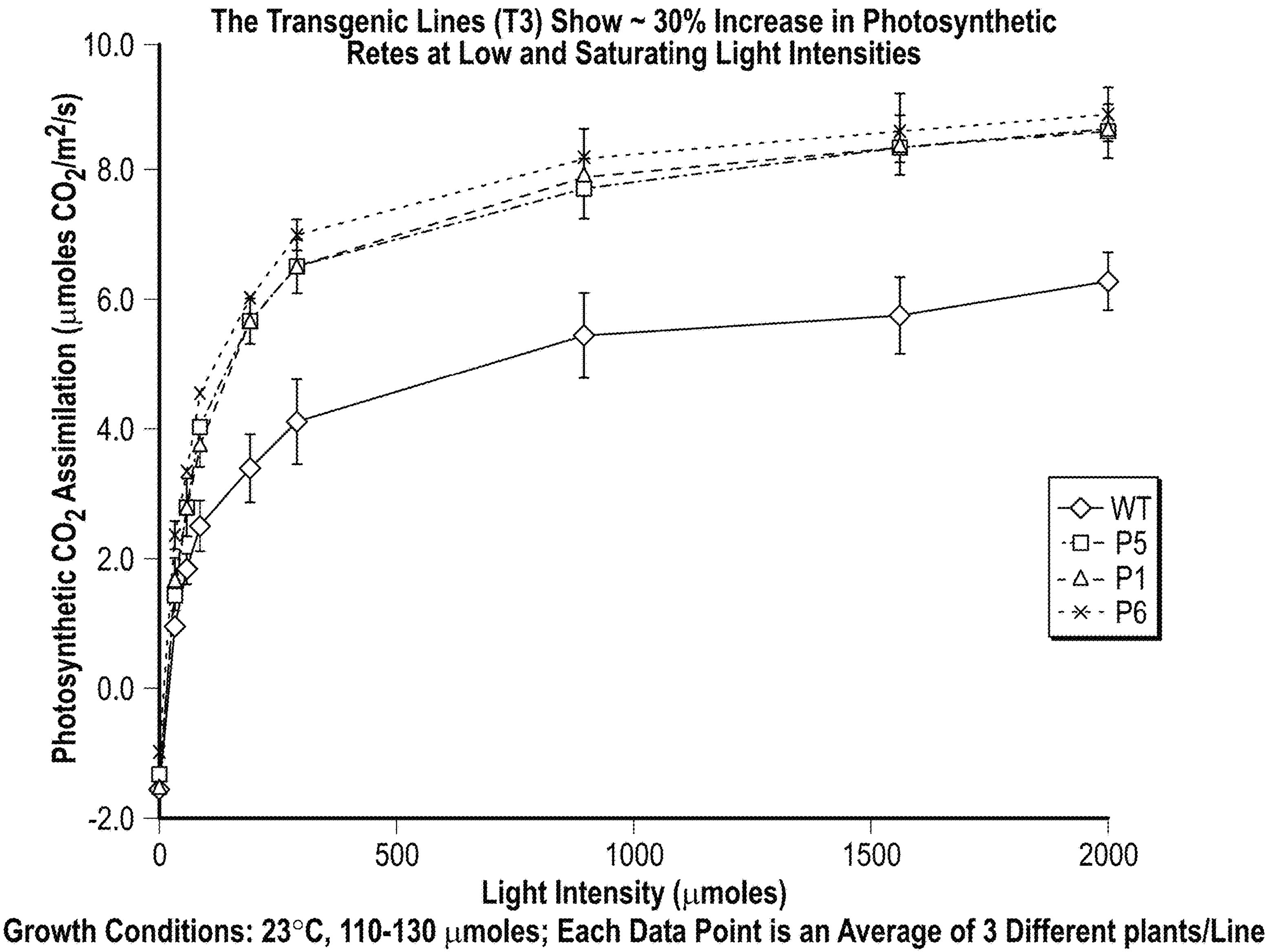

The Transgenic Lines (T3) Show ~ 30% Increase in Photosynthetic Retes at Low and Saturating Light Intensities
Photosynthetic CO$_2$ Assimilation (µmoles CO$_2$/m^2/s)
10.0
8.0
6.0
4.0
2.0
0.0
-2.0
0
500
1000
1500
2000
Light Intensity (µmoles)
WT
P5
P1
P6
Growth Conditions: 23°C, 110-130 µmoles; Each Data Point is an Average of 3 Different plants/Line

FIG. 4

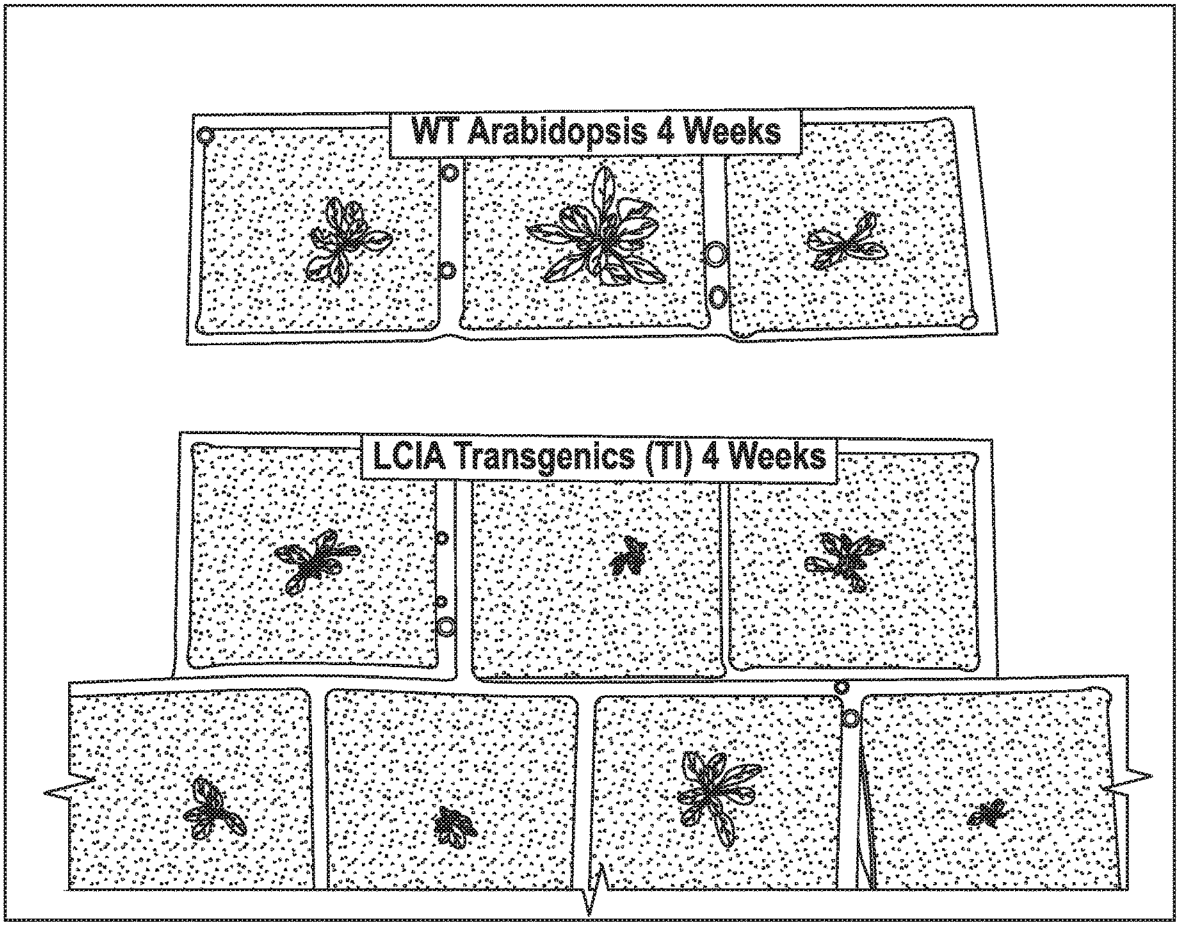

WT Arabidopsis 4 Weeks
LCIA Transgenics (TI) 4 Weeks

FIG. 5A

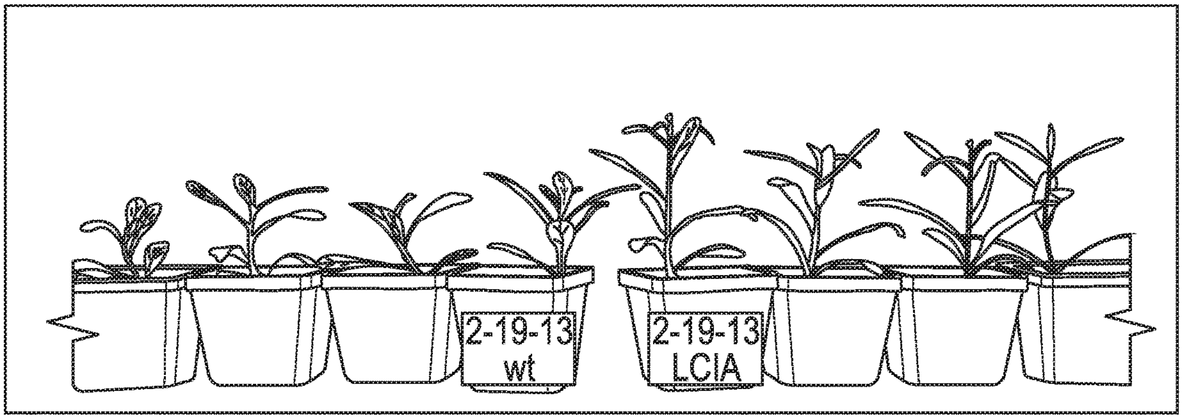

2-19-13
wt
2-19-13
LCIA

FIG. 5B

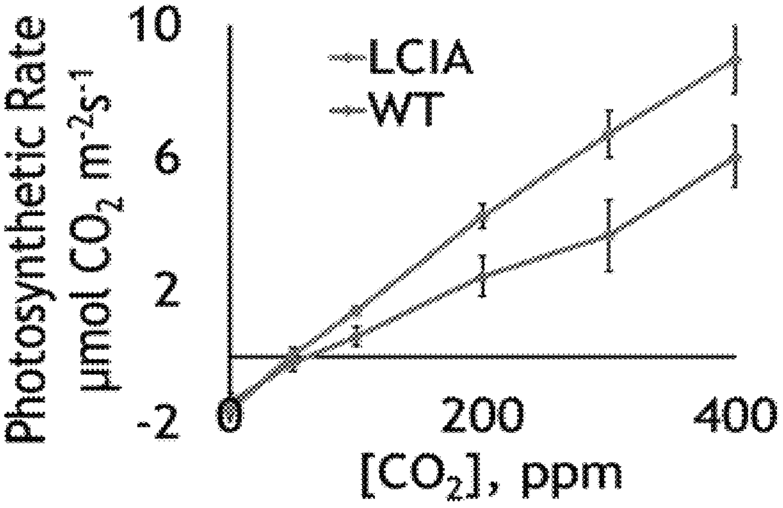
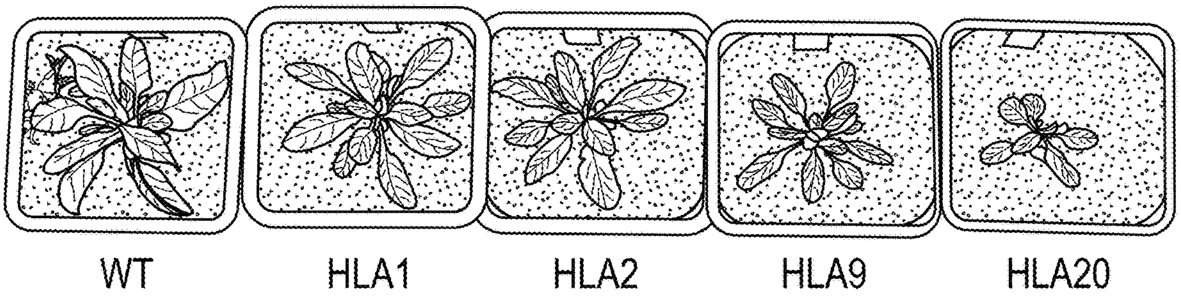

Photosynthetic Rate
μmol CO_2 $m^{-2}s^{-1}$
10
6
2
-2
0
200
400
$[CO_2]$, ppm
LCIA
WT

FIG. 5C



ATP	28.2±4.2	27.5±3.8	27.0±1.6	21.5±1.6	24.4±2.0
ADP	11.0±2.4	8.4±0.8	8.2±1.1	6.8±1.1	7.7±0.8
AMP	3.3±0.6	2.8±0.1	5.2±0.5	10.1±3.4	7.9±4.5
P_1	4.55±0.31	4.59±0.38	4.87±0.24	6.06±0.92	8.11±0.46
EC	0.80±0.00	0.82±0.02	0.77±0.01	0.66±0.06	0.71±0.09
NADPH	21.4±2.0	22.2±3.0	19.4±3.8	14.9±3.3	18.6±4.3
NADH	5.71±0.85	7.27±0.63	4.46±0.72	2.71±0.43	2.35±0.63
NADP	1.50±0.21	1.06±0.05	1.17±0.13	1.48±0.37	1.68±0.10
NAD	22.1±0.04	22.7±6.6	27.4±0.7	23.1±1.7	21.6±3.0
RP_1	0.53±0.03	0.57±0.05	0.45±0.05	0.41±0.05	0.46±0.07
RP_2	0.21±0.03	0.27±0.07	0.14±0.02	0.11±0.02	0.10±0.03

$$EC=\frac{ATP+0.5ADP}{ATP+ADP+AMP}\quad RP_1=\frac{NADPH+NADH}{NADP(H)+NAD(H)}\quad RP_2=\frac{NADH}{NADH+NAD}$$

FIG. 6

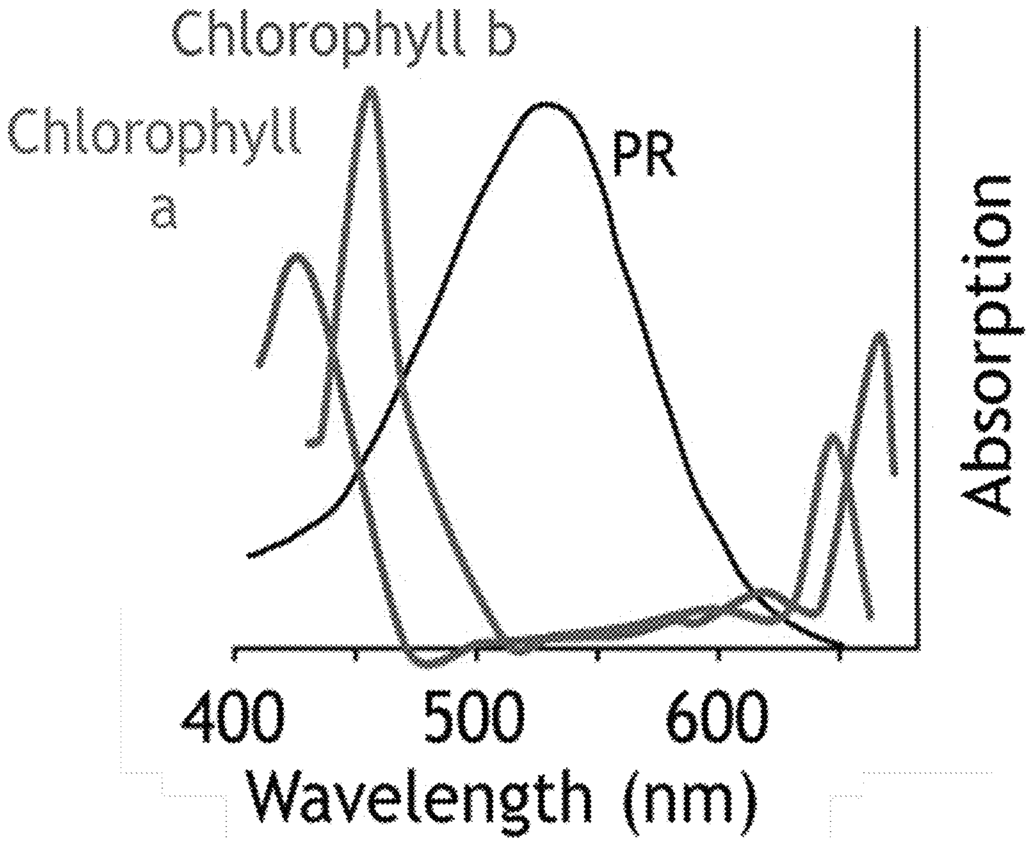

Chlorophyll b
Chlorophyll a
PR
Absorption
400
500
600
Wavelength (nm)

FIG. 7

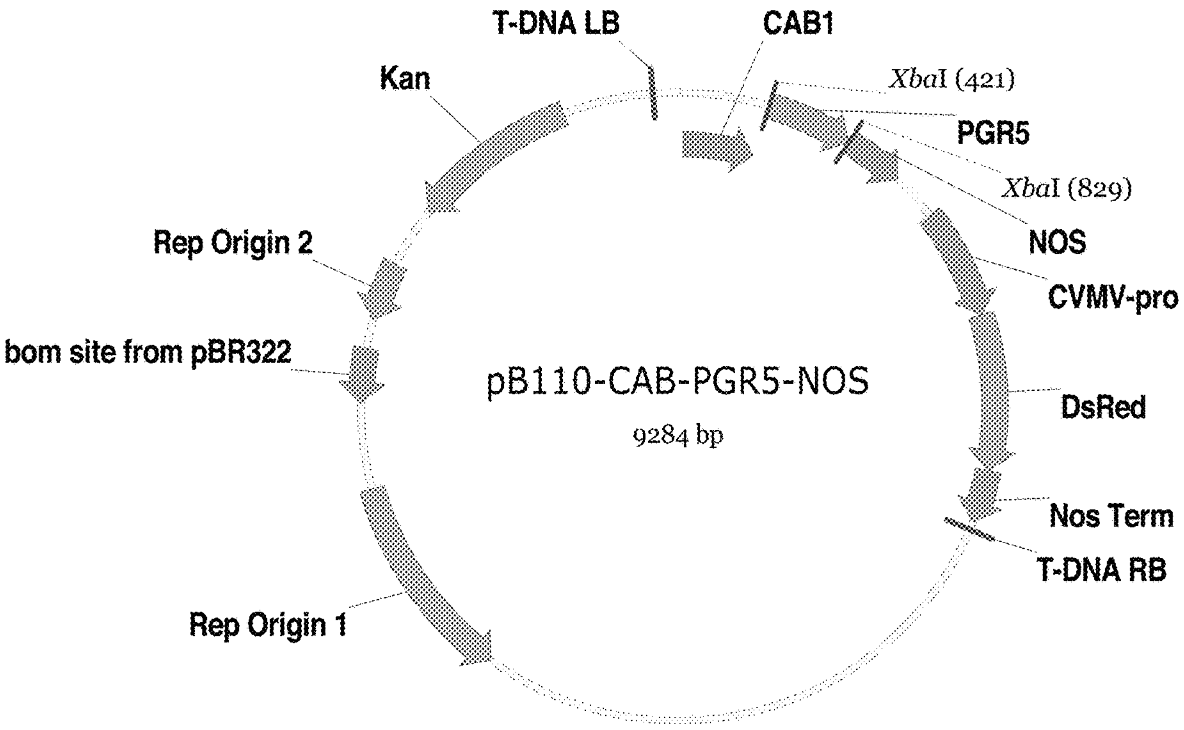

T-DNA LB
CAB1
XbaI (421)
Kan
PGR5
XbaI (829)
Rep Origin 2
NOS
CVMV-pro
bom site from pBR322
pB110-CAB-PGR5-NOS
9284 bp
DsRed
Nos Term
T-DNA RB
Rep Origin 1

FIG. 8

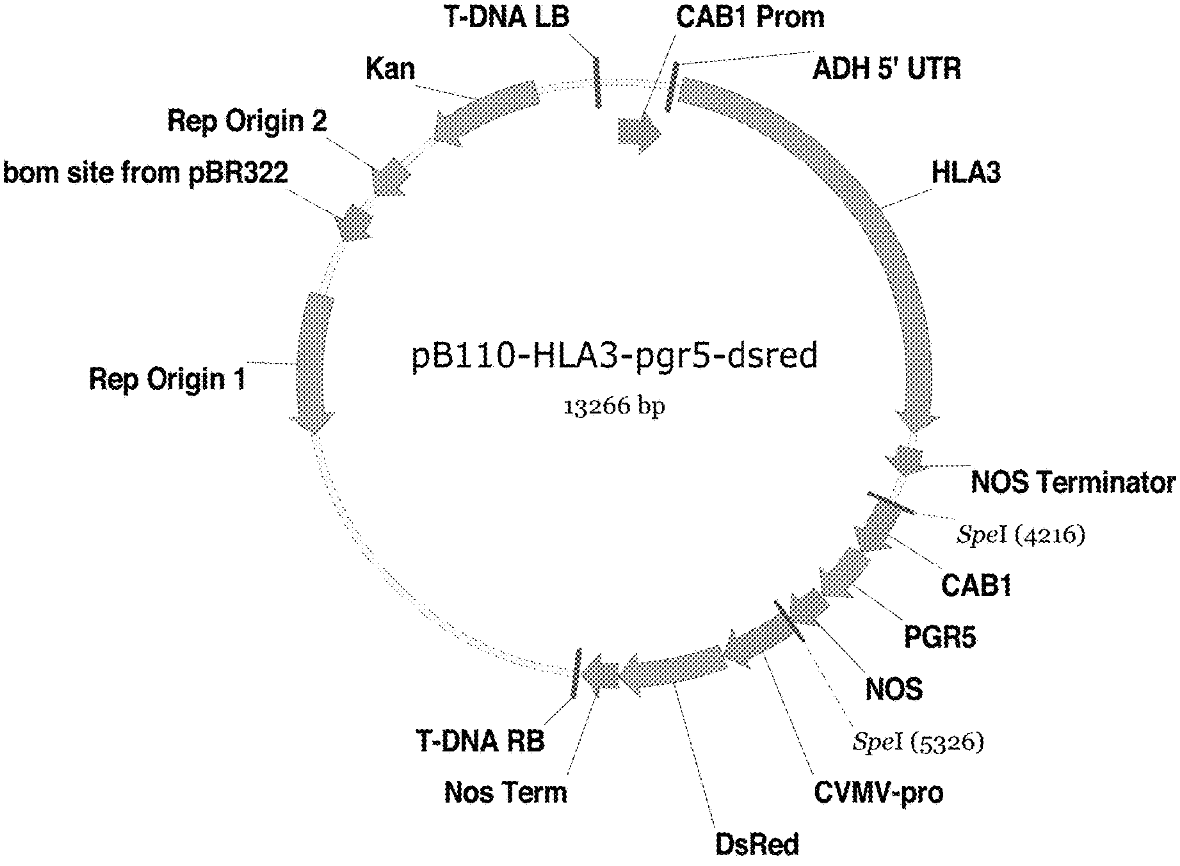

T-DNA LB
CAB1 Prom
ADH 5' UTR
Kan
Rep Origin 2
bom site from pBR322
HLA3
pB110-HLA3-pgr5-dsred
13266 bp
Rep Origin 1
NOS Terminator
*Spe*I (4216)
CAB1
PGR5
NOS
*Spe*I (5326)
T-DNA RB
Nos Term
CVMV-pro
DsRed

FIG. 9

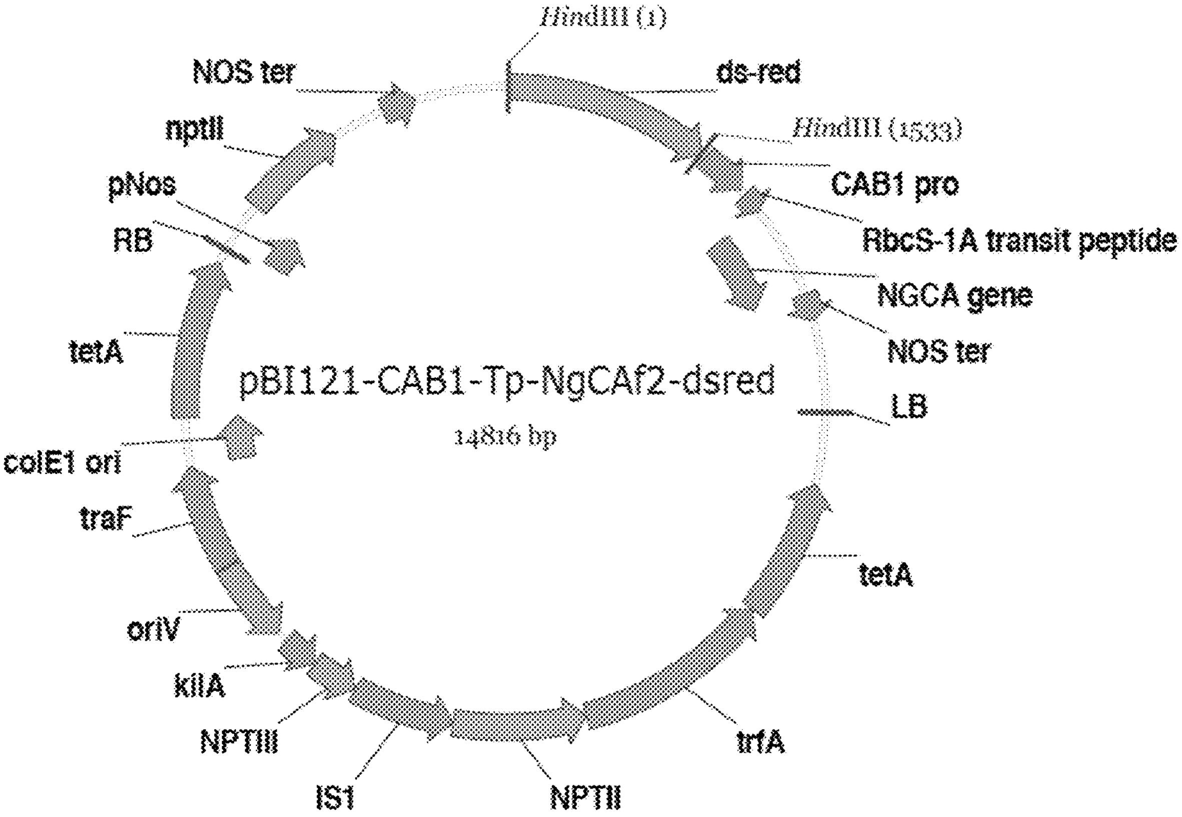

HindIII (1)
NOS ter
ds-red
HindIII (1533)
nptII
CAB1 pro
pNos
RB
RbcS-1A transit peptide
NGCA gene
NOS ter
tetA
pBI121-CAB1-Tp-NgCAf2-dsred
14816 bp
LB
colE1 ori
traF
tetA
oriV
kilA
NPTIII
IS1
NPTII
trfA

FIG. 10

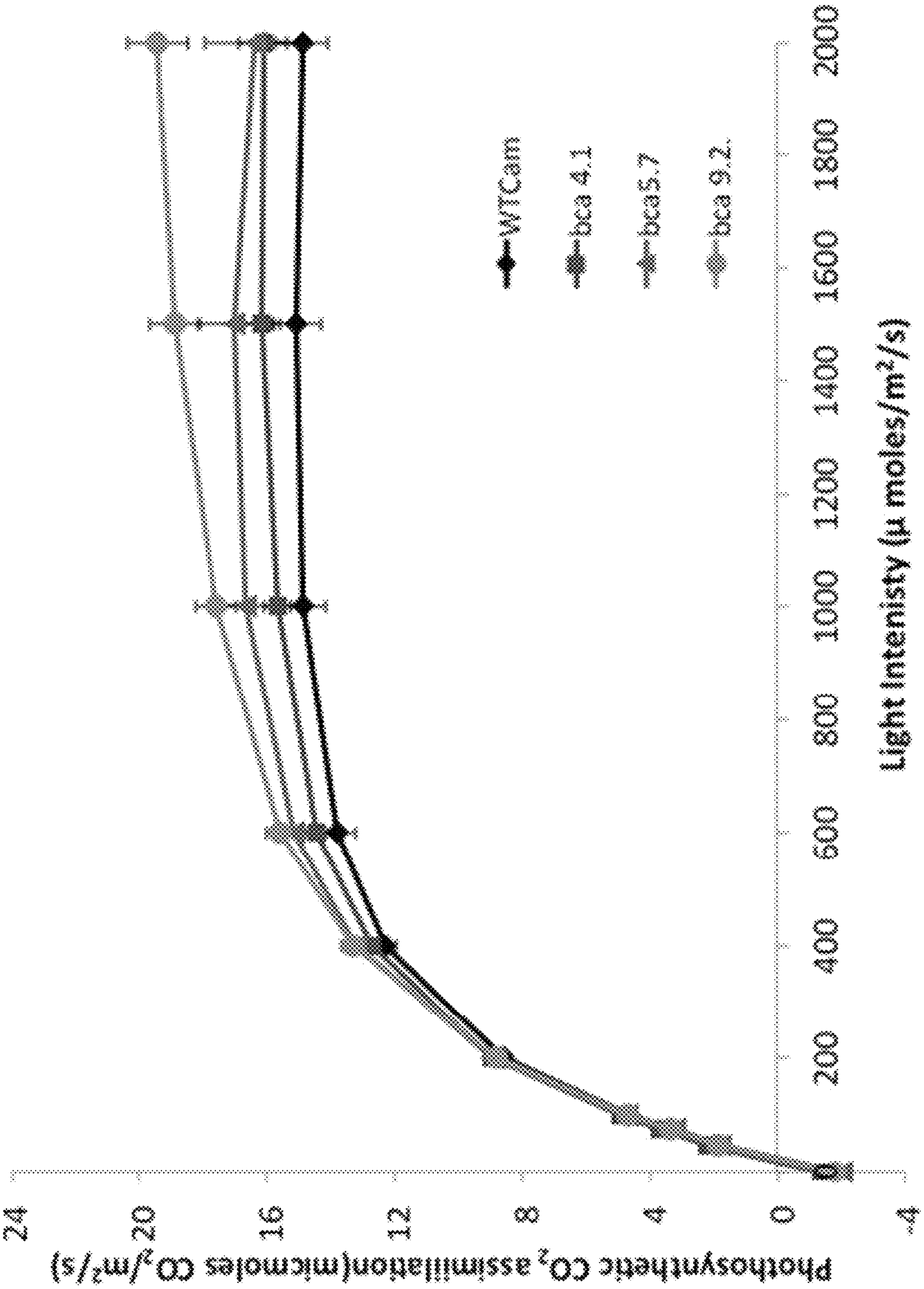

Photosynthetic CO_2 assimiliation(micmoles $CO_2/m^2/s$)
24
20
16
12
8
4
0
-4
Light Intenisty (µ moles/m^2/s)
200
400
600
800
1000
1200
1400
1600
1800
2000
WTCam
bca 4.1
bca5.7
bca 9.2.

FIG. 11

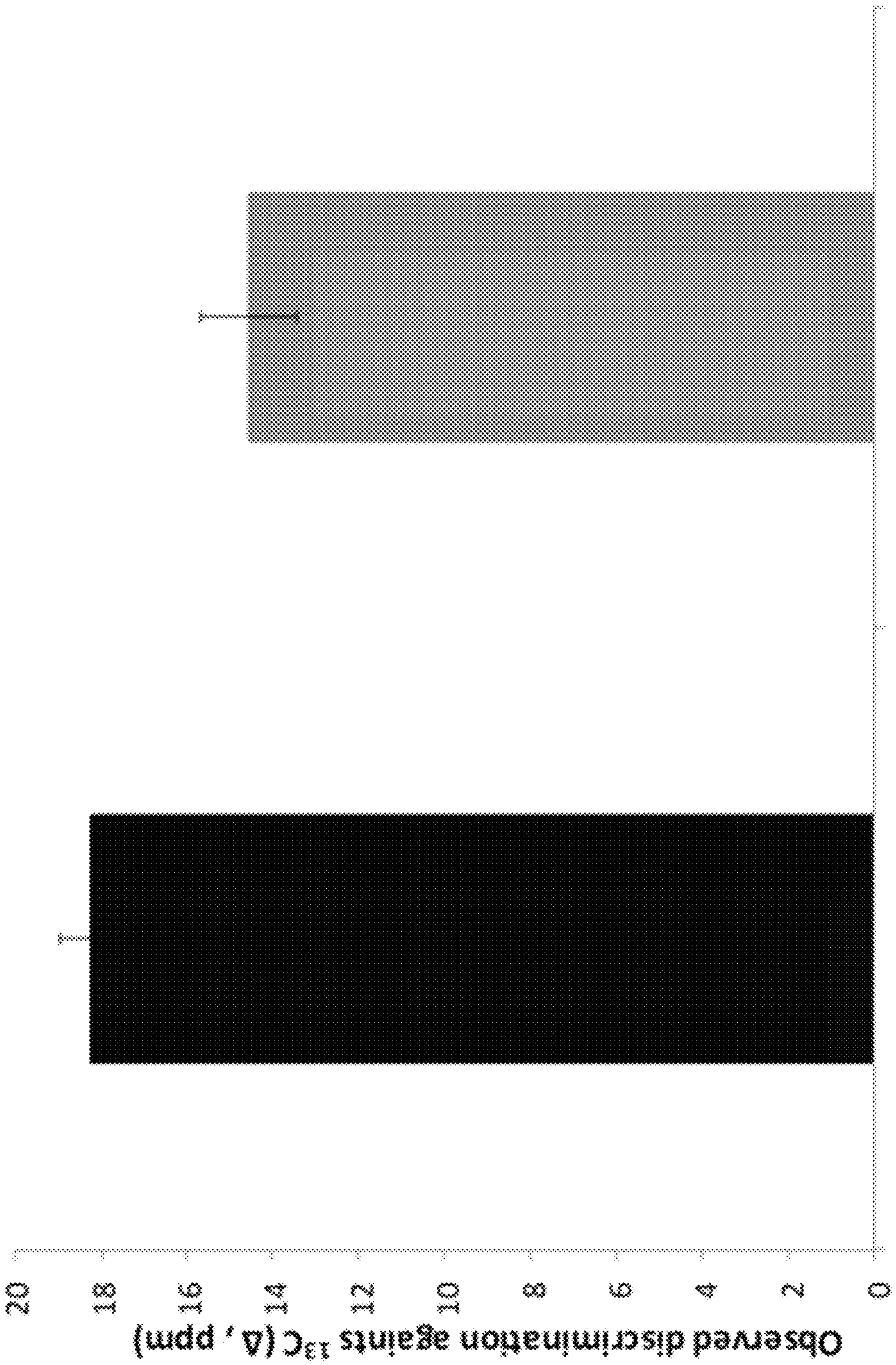

Observed discrimination againts ^{13}C (Δ , ppm)
20
18
16
14
12
10
8
6
4
2
0
Cam-WT
Cam-LCIA

FIG. 12

CARBON FIXATION SYSTEMS IN PLANTS AND ALGAE

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation of U.S. patent application Ser. No. 16/358,331, titled "Improved Carbon Fixation Systems in Plants and Algae", filed on Mar. 3, 2019, which claims priority to U.S. patent application Ser. No. 15/411,854, entitled "Improved Carbon Fixation Systems in Plants and Algae", filed on Jan. 20, 2017, and issued on Mar. 3, 2019 as U.S. Pat. No. 10,233,458, which is a continuation of International Patent Application No. PCT/US2015/041617, entitled "Improved Carbon Fixation Systems in Plants and Algae", filed on Jul. 22, 2015, which claims priority to and the benefit of the filing of U.S. Provisional Patent Application No. 62/027,354, entitled "Carbon Fixation Systems in Plants and Algae", filed on Jul. 22, 2014, and the specification and claims thereof are incorporated herein by reference.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

This invention was made with government support under grants Nos. DOE-CECO Prime No: DE-AR0000202, Sub No: 21018-N; DOE-CABS Prime No: DE-SC0001295, Sub No: 21017-NM NSF EF-1219603, NSF No:1219603. The U.S. government has certain rights in the invention.

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Apr. 5, 2017, is named 040517_NMC0001-101-US_Sequence_Listing_ST25.txt and is 286 KB in size.

INCORPORATION BY REFERENCE OF MATERIAL SUBMITTED ON A COMPACT DISC

Not Applicable.

COPYRIGHTED MATERIAL

Not Applicable.

BACKGROUND

A major factor limiting photosynthetic efficiency is the competitive inhibition of CO_2 fixation by oxygen, due to lack of specificity of the enzyme RuBisCO. Incorporation of oxygen by RuBisCO is the first-dedicated step in photorespiration, a pathway that respires CO_2, compounding photosynthetic inefficiency. Overall, photorespiration reduces photosynthetic productivity by as much as 50% [1]. To date, attempts to engineer reduced oxygenase activity in RuBisCO have been largely unsuccessful.

Significantly, the cyanobacteria, eukaryotic microalgae, and C4 plants have evolved mechanisms to reduce photorespiration by concentrating CO_2 near RuBisCO, competitively inhibiting oxygenase activity and leading to substantial increases in yield and water use efficiency per unit carbon fixed. However, carbon concentrating systems (CCMs) are not operational in the vast majority of plant species (i.e., C3 plants).

Attempts to reconstitute functional CCMs in C3 plants have been previously attempted by us and others, mainly focusing on engineering pathways that are directly involved in facilitating CO_2 transport into leaf chloroplasts. Note, for example, PCT International Publication WO 2012/125737; Sage and Sage (2009) Plant and Cell Physiol. 50(4):756-772; Zhu et al. (2010) J Interg. Plant Biol. 52(8):762-770; Furbank et al. (2009) Funct. Plant Biol. 36(11):845-856; Weber and von Caemmerer (2010) Curr. Opin. Plant Biol.; Price (2013) J. Exp. Bot. 64(3):753-68; and U.S. Patent Application Publication No. 2013/0007916 A1.

However, ATP and NADPH production through light harvesting and electron transfer steps must be coordinated with carbon assimilation and additional energy requiring steps including CCM systems to prevent photoinhibition and to improve growth. Additionally, assimilatory flux and storage rates can limit carbon fixation due to feedback inhibition when sink demand is not matched to source capacity [2].

Thus, there is a critical need to improve plant productivity through integrated systems engineering approaches that balance source/sink interactions with energy and reductant production to develop energy-requiring, artificial CCMs that can effectively mimic those found in nature.

BRIEF SUMMARY OF THE INVENTION

Accordingly, in response to this need, the present disclosure provides methods for elevating cyclic electron transfer activity, improving carbon concentration, and enhancing carbon fixation in C3 and C4 plants, and algae, and producing biomass or other products from C3 or C4 plants, and algae, selected from among, for example, starches, oils, fatty acids, lipids, cellulose or other carbohydrates, alcohols, sugars, nutraceuticals, pharmaceuticals, fragrance and flavoring compounds, and organic acids, as well as transgenic plants produced thereby. These methods and transgenic plants and algae encompass the expression, or overexpression, of various combinations of genes that improve carbon concentrating systems in plants and algae, such as bicarbonate transport proteins, carbonic anhydrase, light driven proton pump, cyclic electron flow regulators, etc. Thus, among its various embodiments, the present disclosure provides the following:

A first embodiment of the present invention provides for a transgenic plant or alga, comprising within its genome, and expressing or overexpressing, a combination of heterologous nucleotide sequences encoding an ATP dependent bicarbonate anion transporter localized to the plasma membrane and a cyclic electron transfer modulator protein. The cyclic electron transfer modulator protein may be selected from a PGRL1 protein (for example SEQ ID NO:3), a PGR5 protein (for example SEQ ID NO:1), a leaf FNR1 protein (for example SEQ ID NO:96), a leaf FNR2 protein (for example SEQ ID NO:97), a Fd1 protein (for example SEQ ID NO:95), or any combination thereof and for example the ATP dependent bicarbonate anion transporter localized to the plasma membrane may be a HLA3 protein (for example SEQ ID NO:77). The transgenic plant or alga described may further comprise within its genome, and expressing or overexpressing the heterologous nucleotide sequence encoding a bicarbonate anion transporter protein localized to the chloroplast envelope. The transgenic plant or alga described herein may further comprise within its genome, and expressing or overexpressing the heterologous nucleotide sequence a carbonic anhydrase protein. In a preferred embodiment, the cyclic electron transfer modulator protein is a PGR5 protein, in another preferred embodiment the cyclic electron transfer modulator protein is Fd1 protein, in yet another preferred embodiment, in still another preferred embodiment the cyclic electron transfer modulator protein is leaf FNR1, in a further preferred embodiment the cyclic electron transfer modulator protein is PGRL1. In a preferred embodiment the heterologous nucleotide sequences of the transgenic plant or alga encode i) a PGR5 protein, and a HLA3 protein; or ii) a PGR5 protein, a HLA3 protein and a PGRL1 protein ora PGR5 protein, a HLA3 protein, and a LCIA protein or a PGR5 protein, a HLA3 protein, a PGRL1 protein, a LCIA protein, and a BCA or HCA2 protein. In another preferred embodiment the heterologous nucleotide sequences the transgenic plant or alga of wherein encode a PGR5 protein, a HLA3 protein, a LCIA protein and a BCA or optionally a HCA2 protein. The transgenic plant or alga as described wherein the PGR5 protein has an amino acid sequence at least 80% identical to SEQ ID NO:1; the HLA3 protein has an amino acid sequence at least 80% identical to SEQ ID NO:77; the PGRL1 protein has an amino acid sequence at least 80% identical to SEQ ID NO:3; the LCIA protein has an amino acid sequence at least 80% identical to SEQ ID NO:18; and/or the BCA protein has an amino acid sequence at least 80% identical to SEQ ID NO:21. Alternatively, the sequence identity/sequence similarity is about 75%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 100% to those specifically disclosed which includes for example proteins without a transit peptide sequence and the functional protein.

A second embodiment provides for a transgenic plant or alga, comprising within its genome, and expressing or overexpressing, a combination of heterologous nucleotide sequences encoding:

LCIA protein and BCA protein or HCA protein is provided. In a preferred embodiment the heterologous nucleotide sequences encode transgenic plant or alga wherein the LCIA protein has an amino acid sequence at least 80% identical to SEQ ID NO:18; and/or the BCA protein has an amino acid sequence at least 80% identical to SEQ ID NO:21 and the HCA protein has an amino acid sequence at least 80% identical to SEQ ID NO:19. Alternatively, the sequence identity/sequence similarity is about 75%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 100% to those specifically disclosed which include for example proteins without a transit peptide sequence and the functional protein.

A third embodiment provides for a transgenic plant or alga, comprising within its genome, and expressing or overexpressing, a combination of heterologous nucleotide sequences encoding an ATP dependent bicarbonate anion transporter localized to the plasma membrane (for example SEQ ID NO:77), a bicarbonate anion transporter localized to the chloroplast envelope (for example SEQ ID NO:18), a carbonic anhydrase, a proteorhodopsin protein targeted to thylakoid membranes (for example SEQ ID NO:98), and a R carotene monooxygenase protein (for example SEQ ID NO:100). In another preferred embodiment the proteorhodopsin comprises a chloroplast transit peptide selected from among a psbX stop-transfer trans-membrane domain fused to its C-terminus, a DNAJ transit peptide, a CAB transit peptide, a PGR5 transit peptide, and a psaD transit peptide. In another preferred embodiment the β-carotene monooxygenase is expressed under the control of a promoter selected from among an ethanol inducible gene promoter and a green tissue/leaf-specific promoter selected from among CAB and rbcS. The proteorhodopsin may comprise an amino acid substitution selected from among L219E/T206S, M79T, and M79Y, and combinations thereof.

The carbonic anhydrase of the first, second, or third embodiment may be a BCA or optionally a HCA2 protein. The bicarbonate anion transporter localized to the chloroplast envelope of the first, second and third embodiment may be a LCIA protein. The ATP dependent bicarbonate anion transporter localized to the plasma membrane of the first and third embodiments may be HLA3.

A fourth embodiment provides for a method of making a transgenic plant or alga of a first embodiment wherein said method comprises expressing, or overexpressing, in a C3 plant, a C4 plant, or an alga, a combination of heterologous nucleotide sequences encoding an ATP dependent bicarbonate anion transporter localized to the plasma membrane and a cyclic electron transfer modulator protein. The cyclic electron transfer modulator protein may be selected from a PGRL1 protein, a PGR5 protein, a FNR1 protein, a FNR2 protein (leaf-form isotopes), a Fd1 protein, or any combination thereof and wherein the ATP dependent bicarbonate anion transporter localized to the plasma membrane is a HLA3 protein. The heterologous nucleotide sequences of the fourth embodiment further encoding a bicarbonate anion transporter protein localized to the chloroplast envelope for example the bicarbonate anion transporter protein is LCIA. Additionally, the heterologous nucleotide sequences encode a carbonic anhydrase protein for example a BCA protein or optionally a HCA2 protein. In a preferred embodiment the cyclic electron transfer modulator protein is a PGR5 protein and optionally a PGRL1 protein and or combination thereof.

A fifth embodiment provides a method of making a transgenic plant or alga as described in a second embodiment, wherein said method comprises expressing, or overexpressing, in a C3 plant, a C4 plant, or an alga, a combination of heterologous nucleotide sequences encoding a LCIA protein and a BCA protein or optionally a HCA protein.

A sixth embodiment provides a method of making a transgenic plant or alga of a third embodiment wherein said method comprises expressing, or overexpressing, in a C3 plant, a C4 plant, or an alga, a combination of heterologous nucleotide sequences encoding an ATP dependent bicarbonate anion transporter localized to the plasma membrane, a bicarbonate anion transporter, a carbonic anhydrase, a proteorhodopsin protein targeted to thylakoid membranes, and a R carotene monooxygenase protein. In a preferred embodiment the proteorhodopsin comprises a chloroplast transit peptide selected from among a psbX stop-transfer trans-membrane domain fused to its C-terminus, a DNAJ transit peptide, a CAB transit peptide, a PGR5 transit peptide, and a psaD transit peptide. In another preferred embodiment the β-carotene monooxygenase is expressed under the control of a promoter selected from among an ethanol inducible gene promoter and a green tissue/leaf-specific promoter selected from among CAB and rbcS. In a preferred embodiment the proteorhodopsin comprises an amino acid substitution selected from among L219E/T206S, M79T, and M79Y, and combinations thereof. In another preferred embodiment the ATP dependent bicarbonate anion transporter localized to the plasma membrane is HLA3.

The transgenic plant of an embodiment disclosed herein may be a C3 plant or a C4 plant such as a transgenic oilseed plant or a transgenic food crop plant which may include the genera *Brassica* (e.g., rapeseed/canola (*Brassica napus; Brassica carinata; Brassica nigra; Brassica oleracea*), Camelina, *Miscanthus*, and Jatropha; Jojoba (*Simmondsia* *chinensis*), coconut; cotton; peanut; rice; safflower; sesame; soybean; mustard other than *Arabidopsis*; wheat; flax (linseed); sunflower; olive; corn; palm; palm kernel; sugarcane; castor bean; switchgrass; *Borago officinalis; Echium plantagineum; Cuphea hookeriana; Cuphea pulcherrima; Cuphea lanceolata; Ricinus communis; Coriandrum sativum; Crepis alpina; Vernonia galamensis; Momordica charantia*; and *Crambe abyssinica*, wheat, rice, maize (corn), barley, oats, sorghum, rye, and millet; peanuts, chickpeas, lentils, kidney beans, soybeans, lima beans; potatoes, sweet potatoes, and cassavas; soybeans, corn, canola, peanuts, palm, coconuts, safflower, cottonseed, sunflower, flax, olive, and safflower; sugar cane and sugar beets; bananas, oranges, apples, pears, breadfruit, pineapples, and cherries; tomatoes, lettuce, carrots, melons, strawberry, asparagus, broccoli, peas, kale, cashews, peanuts, walnuts, pistachio nuts, almonds; forage and turf grasses; alfalfa, clover; coffee, cocoa, kola nut, poppy; vanilla, sage, thyme, anise, saffron, menthol, peppermint, spearmint and coriander and preferably wheat, rice and canola. The transgenic alga of an embodiment disclosed herein may be selected from among a *Chlorella* species, a *Nannochloropsis* species, and a *Chlamydomonas* species. The heterologous nucleotide sequences are described in an embodiment may be codon-optimized for expression in said transgenic plant or alga. One aspect of the present invention provides for a transgenic plant or alga as described in an embodiment which exhibits enhanced CO_2 fixation compared to an otherwise identical control plant grown under the same conditions for example wherein CO_2 fixation is enhanced in the range of from about 10% to about 50% compared to that of an otherwise identical control plant grown under the same conditions.

A fourth embodiment provides for a part of said transgenic plant or alga of any embodiment described herein. For example, the part of said transgenic plant may be selected from among a protoplast, a cell, a tissue, an organ, a cutting, an explant, a reproductive tissue, a vegetative tissue, biomass, an inflorescence, a flower, a sepal, a petal, a pistil, a stigma, a style, an ovary, an ovule, an embryo, a receptacle, a seed, a fruit, a stamen, a filament, an anther, a male or female gametophyte, a pollen grain, a meristem, a terminal bud, an axillary bud, a leaf, a stem, a root, a tuberous root, a rhizome, a tuber, a stolon, a corm, a bulb, an offset, a cell of said plant in culture, a tissue of said plant in culture, an organ of said plant in culture, a callus, propagation materials, germplasm, cuttings, divisions, and propagations.

A fifth embodiment provides for a progeny or derivative of said transgenic plant or alga of any embodiment described herein. For example, the progeny or derivatives may be selected from among clones, hybrids, samples, seeds, and harvested material thereof and may be produced sexually or asexually.

Another embodiment of the present invention provides a method of elevating CET activity in a C3 plant, C4 plant, or alga wherein said method comprises expressing, or overexpressing, in a C3 plant, a C4 plant, or an alga, a combination of heterologous nucleotide sequences encoding an ATP dependent bicarbonate anion transporter localized to the plasma membrane and cyclic electron transfer modulator protein.

Yet another embodiment provides a method of enhancing carbon fixation in a C3 plant, C4 plant, or alga wherein said method comprises expressing, or overexpressing, in a C3 plant, a C4 plant, or an alga, a combination of heterologous nucleotide sequences encoding an ATP dependent bicarbonate anion transporter localized to the plasma membrane and a cyclic electron transfer modulator protein.

Yet another method provides for a method of producing biomass or other products from a C3 plant, C4 plant, or an alga, wherein said products are selected from among starches, oils, fatty acids, triacylglycerols, lipids, cellulose or other carbohydrates, alcohols, sugars, nutraceuticals, pharmaceuticals, fragrance and flavoring compounds, and organic acids wherein said method comprises expressing, or overexpressing, in a C3 plant, a C4 plant, or an alga, a combination of heterologous nucleotide sequences encoding an ATP dependent bicarbonate anion transporter localized to the plasma membrane and a cyclic electron transfer modulator protein. This method further comprises growing said plant or alga and harvesting said biomass or recovering said product from said plant or alga. Another aspect of the present invention provides for biomass or other product produced from a plant or alga selected from among starches, oils, fatty acids, lipids, cellulose or other carbohydrates, alcohols, sugars, nutraceuticals, pharmaceuticals, fragrance and flavoring compounds, and organic acids, made by a method of any one of the method of making a transgenic plant or alga embodiments herein.

Another embodiment provides a method of elevating cyclic electron transfer (CET) activity in a C3 plant, C4 plant, or alga wherein said method comprises expressing, or overexpressing, in a C3 plant, a C4 plant, or an alga, a combination of heterologous nucleotide sequences encoding an ATP dependent bicarbonate anion transporter localized to the plasma membrane, a bicarbonate anion transporter, a carbonic anhydrase, a proteorhodopsin protein targeted to thylakoid membranes; and a R carotene monooxygenase protein.

Another embodiment provides a method of enhancing carbon fixation in a C3 plant, C4 plant, or alga wherein said method comprises expressing, or overexpressing, in a C3 plant, a C4 plant, or an alga, a combination of heterologous nucleotide sequences encoding an ATP dependent bicarbonate anion transporter localized to the plasma membrane, a bicarbonate anion transporter, a carbonic anhydrase, a proteorhodopsin protein targeted to thylakoid membranes; and a R carotene monooxygenase protein.

Another embodiment provides for a method of producing biomass or other products from a C3 plant, C4 plant, or an alga, wherein said products are selected from among starches, oils, fatty acids, triacylglycerols, lipids, cellulose or other carbohydrates, alcohols, sugars, nutraceuticals, pharmaceuticals, fragrance and flavoring compounds, and organic acids wherein said method comprises expressing, or overexpressing, in a C3 plant, a C4 plant, or an alga, a combination of heterologous nucleotide sequences encoding an ATP dependent bicarbonate anion transporter localized to the plasma membrane, a bicarbonate anion transporter, a carbonic anhydrase, a proteorhodopsin protein targeted to thylakoid membranes; and a ß carotene monooxygenase protein. The method further comprises growing said plant or alga and harvesting said biomass or recovering said product from said plant or alga.

Another embodiment provides for use of a construct comprising one or more nucleic acids encoding

a) a PGR5 protein, and a HLA3 protein;
b) a PGR5 protein, a HLA3 protein and a PGRL1 protein;
c) a PGR5 protein, a HLA3 protein, and a LCIA protein;
d) a PGR5 protein, a HLA3 protein, a LCIA protein and a BCA or HCA2 protein;
e) a PGR5 protein, a HLA3 protein, a PGRL1 protein and a LCIA protein;
f) a PGR5 protein, a HLA3 protein, a PGRL1 protein, a LCIA protein, and a BCA or HCA2 protein;

- g) a PGR5 protein, a HLA3 protein, and a BCA or HCA2 protein; or
- h) a PGR5 protein, a HLA3 protein, a PGRL1 protein, and a BCA or HCA2 protein

for

- i) making a transgenic plant or alga of a first embodiment;
- ii) elevating CET activity in a C3 plant, C4 plant, or alga;
- iii) enhancing carbon fixation in a C3 plant, C4 plant, or alga; or
- iv) producing biomass or other products from a C3 plant, C4 plant, or an alga, wherein said products are selected from among starches, oils, fatty acids, triacylglycerols, lipids, cellulose or other carbohydrates, alcohols, sugars, nutraceuticals, pharmaceuticals, fragrance and flavoring compounds, and organic acids.

Another embodiment provides for use of a construct comprising one or more nucleic acids encoding

- a) a LCIA protein and a BCA or HCA2 protein;

for

- i) making a transgenic plant or alga of a second embodiment;
- ii) elevating CET activity in a C3 plant, C4 plant, or alga;
- iii) enhancing carbon fixation in a C3 plant, C4 plant, or alga; or
- iv) producing biomass or other products from a C3 plant, C4 plant, or an alga, wherein said products are selected from among starches, oils, fatty acids, triacylglycerols, lipids, cellulose or other carbohydrates, alcohols, sugars, nutraceuticals, pharmaceuticals, fragrance and flavoring compounds, and organic acids.

One aspect of the present invention provides for a transgenic plant or alga, comprising within its genome, and expressing or overexpressing, a combination of heterologous nucleotide sequences encoding:

1. i) a PGRL1 protein, a PGR5 protein, and a HLA3 protein; or

- ii) a PGRL1 protein, a PGR5 protein, a HLA3 protein, a LCIA protein, and a BCA or HCA2 protein; or
- iii) a Fd1 protein, a HLA3 protein, a LCIA protein, and a BCA or HCA2 protein; or
- iv) a leaf FNR1 protein, a HLA3 protein, a LCIA protein, and a BCA or HCA2 protein; or
- v) a proteorhodopsin protein targeted to thylakoid membranes, a HLA3 protein, a LCIA protein, a BCA or HCA2 protein, and a β-carotene monooxygenase.

2. The transgenic plant or alga of 1, wherein said proteorhodopsin comprises a chloroplast transit peptide selected from among a psbX stop-transfer trans-membrane domain fused to its C-terminus, a DNAJ transit peptide, a CAB transit peptide, a PGR5 transit peptide, and a psaD transit peptide.

3. The transgenic plant or alga of 1 or 2, wherein said β-carotene monooxygenase is expressed under the control of a promoter selected from among an ethanol inducible gene promoter and a green tissue/leaf-specific promoter selected from among CAB and rbcS.

4. The transgenic plant or alga of any one of 1-3, wherein said proteorhodopsin comprises an amino acid substitution selected from among L219E/T206S, M79T, and M79Y, and combinations thereof.

5. The transgenic plant of any one of 1-4, which is a C3 plant or a C4 plant.

6. The transgenic plant of any one of 1-5, which is a transgenic oilseed plant or a transgenic food crop plant.

7. The transgenic oilseed plant of 6, which is selected from among plants of the genera *Brassica* (e.g., rapeseed/canola (*Brassica napus; Brassica carinata; Brassica nigra; Brassica oleracea*), Camelina, *Miscanthus*, and Jatropha; Jojoba (*Simmondsia chinensis*), coconut; cotton; peanut; rice; safflower; sesame; soybean; mustard other than *Arabidopsis*; wheat; flax (linseed); sunflower; olive; corn; palm; palm kernel; sugarcane; castor bean; switchgrass; *Borago officinalis; Echium plantagineum; Cuphea hookeriana; Cuphea* pulcherrima; *Cuphea lanceolata; Ricinus communis; Coriandrum sativum; Crepis alpina; Vernonia galamensis; Momordica charantia*; and *Crambe abyssinica.*

8. The transgenic alga of any one of 1-5, which is selected from among *Chlorella* sp., *Nannochloropsis* sp., and *Chlamydomonas* sp.

9. The transgenic plant or alga of any one of 1-8, wherein said heterologous nucleotide sequences are codon-optimized for expression in said transgenic plant or alga.

10. The transgenic plant or alga of any one of 1-9, which exhibits enhanced CO_2 fixation compared to an otherwise identical control plant grown under the same conditions.

11. The transgenic plant or alga of 10, wherein CO_2 fixation is enhanced in the range of from about 10% to about 50% compared to that of an otherwise identical control plant grown under the same conditions.

12. A part of said transgenic plant or alga of any one of 1-11.

13. The part of said transgenic plant of 12, which is selected from among a protoplast, a cell, a tissue, an organ, a cutting, an explant, a reproductive tissue, a vegetative tissue, biomass, an inflorescence, a flower, a sepal, a petal, a pistil, a stigma, a style, an ovary, an ovule, an embryo, a receptacle, a seed, a fruit, a stamen, a filament, an anther, a male or female gametophyte, a pollen grain, a meristem, a terminal bud, an axillary bud, a leaf, a stem, a root, a tuberous root, a rhizome, a tuber, a stolon, a corm, a bulb, an offset, a cell of said plant in culture, a tissue of said plant in culture, an organ of said plant in culture, a callus, propagation materials, germplasm, cuttings, divisions, and propagations.

14. Progeny or derivatives of said transgenic plant or alga of any one of 1-11.

15. The progeny or derivatives of 14, which is selected from among clones, hybrids, samples, seeds, and harvested material thereof.

16. The progeny of 14 or 15, which is produced sexually.

17. The progeny of 14 or 15, which is produced asexually.

Another aspect of the present invention provides for a method selected from among:

18. i) making a transgenic plant or alga of any one of 1-11;

ii) elevating CET activity in a C3 plant, C4 plant, or alga;

iii) enhancing carbon fixation in a C3 plant, C4 plant, or alga; and

iv) producing biomass or other products from a C3 plant, C4 plant, or alga, wherein said products are selected from among starches, oils, fatty acids, triacylglycerols, lipids, cellulose or other carbohydrates, alcohols, sugars, nutraceuticals, pharmaceuticals, fragrance and flavoring compounds, and organic acids,

wherein said method comprises expressing, or overexpressing, in a C3 plant, a C4 plant, or an alga, a combination of heterologous nucleotide sequences encoding:

- a) a PGRL1 protein, a PGR5 protein, and a HLA3 protein; or
- b) a PGRL1 protein, a PGR5 protein, a HLA3 protein, a LCIA protein, and a BCA or HCA2 protein; or
- c) a Fd1 protein, a HLA3 protein, a LCIA protein, and a BCA or HCA2 protein; or
- d) a leaf FNR1 protein, a HLA3 protein, a LCIA protein, and a BCA or HCA2 protein; or

e) a proteorhodopsin protein targeted to thylakoid membranes, a HLA3 protein, a LCIA protein, a BCA or HCA2 protein, and a β-carotene monooxygenase.

19. The method of 18, wherein step iv) further comprises growing said plant or alga and harvesting said biomass or recovering said product from said plant or alga.

20. The method of 18 or 19, wherein said proteorhodopsin comprises a chloroplast transit peptide selected from among a psbX stop-transfer trans-membrane domain fused to its C-terminus, a DNAJ transit peptide, a CAB transit peptide, a PGR5 transit peptide, and a psaD transit peptide.

21. The method of any one of 18-20, wherein said β-carotene monooxygenase is expressed under the control of a promoter selected from among an ethanol inducible gene promoter and a green tissue/leaf-specific promoter selected from among CAB and rbcS.

22. The method of any one of 18-21, wherein said proteorhodopsin comprises an amino acid substitution selected from among L219E/T206S, M79T, and M79Y, and combinations thereof.

23. The method of any one of 18-22, wherein said transgenic plant is a C3 plant, a C4 plant, or an alga.

24. The method of any one of 18-23, wherein said transgenic plant is a transgenic oilseed plant or a transgenic food crop plant.

25. The method of 24, wherein said transgenic oilseed plant is selected from among plants of the genera *Brassica* (e.g., rapeseed/canola (*Brassica napus; Brassica carinata; Brassica nigra; Brassica oleracea*), Camelina, *Miscanthus*, and Jatropha; Jojoba (*Simmondsia chinensis*), coconut; cotton; peanut; rice; safflower; sesame; soybean; mustard other than *Arabidopsis*; wheat; flax (linseed); sunflower; olive; corn; palm; palm kernel; sugarcane; castor bean; switchgrass; *Borago officinalis; Echium plantagineum; Cuphea hookeriana; Cuphea* pulcherrima; *Cuphea lanceolata; Ricinus communis; Coriandrum sativum; Crepis alpina; Vernonia galamensis; Momordica charantia*; and *Crambe abyssinica.*

26. The method of any one of 18-23, wherein said alga is selected from among *Chlorella* sp., *Nannochloropsis* sp., and *Chlamydomonas* sp.

27. The method of any one of 18-26, wherein said heterologous nucleotide sequences are codon-optimized for expression in said transgenic plant or alga.

28. The method of any one of 18-27, wherein said transgenic plant or alga exhibits enhanced CO_2 fixation compared to an otherwise identical control plant or alga grown under the same conditions.

29. The method of 28, wherein CO_2 fixation is enhanced in the range of from about 10% to about 50% compared to that of an otherwise identical control plant or alga grown under the same conditions.

Another aspect of the present invention provides for a transgenic plant or alga made by the method of any one of 18-29.

Yet another aspect of the present invention provides for a biomass or other product from a plant or alga, selected from among starches, oils, fatty acids, lipids, cellulose or other carbohydrates, alcohols, sugars, nutraceuticals, pharmaceuticals, fragrance and flavoring compounds, and organic acids, made by the method of any one of 18-29.

In addition to the various embodiments listed above, in the Examples below, and in the claims, this disclosure further variously encompasses the presently disclosed and claimed CCM protein combinations in further combinations with the genes and proteins focusing on engineering pathways that are directly involved in facilitating CO_2 transport into leaf chloroplasts, disclosed and claimed in the inventors' previous application PCT International Publication WO 2012/125737. The present disclosure encompasses any combination of genes disclosed herein with any combination of genes disclosed in WO 2012/125737 and in Tables D1-D9 to improve carbon concentrating systems (CCMs) in plants and algae.

Table D1 represents different classes of α-CAs found in mammals.

Table D2-D4 represents representative species, Gene bank accession numbers, and amino acid sequences for various species of suitable CA genes.

Table D5 represents the codon optimized DNA sequence for chloroplast expression in *Chlamydomonas reinhardtii*. In Table D5, the underlines sequences represent restriction sites, and bases changed to optimize chloroplast expression are listed in lower case. Table D6 provides a breakdown of the number and type of each codon optimized.

Representative species and Gene bank accession numbers for various species of bicarbonate transporter are listed below in Tables D8-D9.

Further scope of the applicability of the presently disclosed embodiments will become apparent from the detailed description and drawing(s) provided below. However, it should be understood that the detailed description and specific examples, while indicating preferred embodiments of this disclosure, are given by way of illustration only since various changes and modifications within the spirit and scope of these embodiments will become apparent to those skilled in the art from this detailed description.

BRIEF DESCRIPTION OF THE SEQUENCE LISTING

The disclosure can be more fully understood form the following detailed description and the accompanying Sequence Listing, which form a part of this application.

The sequence descriptions summarize the Sequence Listing attached hereto. The Sequence Listing contains standard symbols and format used for nucleotide and amino acid sequence data comply with the rules set forth in 37 C.F.R. § 1.822.

BRIEF DESCRIPTION OF THE DRAWINGS

The above and other aspects, features, and advantages of the present disclosure will be better understood from the following detailed descriptions taken in conjunction with the accompanying drawing(s), all of which are given by way of illustration only, and are not limitative of the presently disclosed embodiments, in which:

FIG. **1**. Model of the *Chlamydomonas* CCM showing the localization of inorganic carbon transporters (HLA3, LCIA) and carbonic anhydrase (CAH: CAH1, CAH3, and CAH6) [5]), and Rubisco. LCIB is an essential protein for CCM in *Chlamydomonas*. It's exact function is unknown.

FIG. **2**.(A-B) Growth phenotypes of VVT and HLA3 transgenic (T3) *Arabidopsis* initially grown on MS media (plus nitrate, NO_3^-). (B) MS media (plus ammonium (NH_4^+) and sucrose) or in soil (ammonium only). X indicates plants died. Numbers refer to plant lines.

FIG. **3**.(A-B) Growth phenotypes of VVT and HCA-II transgenic (T1) *Arabidopsis* 4 weeks after germination. (B) Growth phenotype of VVT *Arabidopsis* (Col-0, left) and the BCA transgenic (T3) (right).

FIG. **4**. Photosynthetic assimilation rate of CO_2 in three transgenic lines (P1, P5, P6) of *Arabidopsis* expressing BCA (bacterial carbonic anhydrase) measured using a LICOR 6400 gas analyzer. These lines showed ~30% increase in their photosynthetic efficiency when compared to WT *Arabidopsis* (Col.-0).

FIG. **5**.(A-C) Growth phenotypes of WT and LCIA transgenic (T1) *Arabidopsis* plants four weeks after germination. (B) Four-week-old WT (left 4 plants) and independent transgenic Camelina (right 4 plants) expressing LCIA. (C) CO_2-dependent photosynthetic rates of WT and LCIA transgenic Camelina.

FIG. **6**. Phenotype of HLA3 transgenics grown on nitrate. Energy charge and reductive potential of WT and HLA3 transgenic *Arabidopsis*. Adenylate, nucleotide cofactors, and inorganic phosphate levels measured as nmole/gFW for plants grown on nitrate. Values are averages±SE.

FIG. **7**. Photosynthetically active radiation in proteorhodopsin relative to plant-based chlorophyll [49].

FIG. **8**. Plasmid pB110-CAB-PGR5-NOS (Example 1).

FIG. **9**. Plasmid pB110-HLA3-pgr5-dsred (Example 1).

FIG. **10**. Plasmid pBI 121-CAB1-Tp-NgCAf2-dsred (Example 1).

FIG. **11** illustrates light response curves of Camelina BCA lines.

FIG. **12** illustrates expression of LCIA in Camelina vs WT.

DETAILED DESCRIPTION OF SEVERAL EMBODIMENTS

The following detailed description is provided to aid those skilled in the art in practicing the various embodiments of the present disclosure described herein, including all the methods, uses, compositions, etc., described herein. Even so, the following detailed description should not be construed to unduly limit the present disclosure, as modifications and variations in the embodiments herein discussed may be made by those of ordinary skill in the art without departing from the spirit or scope of the present discoveries.

The present disclosure is explained in greater detail below. This disclosure is not intended to be a detailed catalog of all the different ways in which embodiments of this disclosure can be implemented, or all the features that can be added to the instant embodiments. For example, features illustrated with respect to one embodiment may be incorporated into other embodiments, and features illustrated with respect to a particular embodiment may be deleted from that embodiment. In addition, numerous variations and additions to the various embodiments suggested herein will be apparent to those skilled in the art in light of the instant disclosure, which variations and additions do not depart from the scope of the instant disclosure. Hence, the following specification is intended to illustrate some particular embodiments of the disclosure, and not to exhaustively specify all permutations, combinations, and variations thereof.

Any feature, or combination of features, described herein is(are) included within the scope of the present disclosure, provided that the features included in any such combination are not mutually inconsistent as will be apparent from the context, this specification, and the knowledge of one of ordinary skill in the art. Additional advantages and aspects of the present disclosure are apparent in the following detailed description and claims.

The contents of all publications, patent applications, patents, and other references mentioned herein are incorporated by reference herein in their entirety. In case of conflict, the present specification, including explanations of terms, will control.

Definitions

The following definitions are provided to aid the reader in understanding the various aspects of the present disclosure. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by those of ordinary skill in the art to which the disclosure pertains.

As used herein and in the appended claims, the singular forms “a”, “an”, and “the” include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to “a plant” includes a plurality of such plants, reference to “a cell” includes one or more cells and equivalents thereof known to those skilled in the art, and so forth. Similarly, the word “or” is intended to include “and” unless the context clearly indicates otherwise. Hence “comprising A or B” means including A, or B, or A and B. Furthermore, the use of the term “including”, as well as other related forms, such as “includes” and “included”, is not limiting.

The term “about” as used herein is a flexible word with a meaning similar to “approximately” or “nearly”. The term “about” indicates that exactitude is not claimed, but rather a contemplated variation. Thus, as used herein, the term “about” means within 1 or 2 standard deviations from the specifically recited value, or ±a range of up to 20%, up to 15%, up to 10%, up to 5%, or up to 4%, 3%, 2%, or 1% compared to the specifically recited value.

The term “comprising” as used in a claim herein is open-ended, and means that the claim must have all the features specifically recited therein, but that there is no bar on additional features that are not recited being present as well. The term “comprising” leaves the claim open for the inclusion of unspecified ingredients even in major amounts. The term “consisting essentially of” in a claim means that the invention necessarily includes the listed ingredients, and is open to unlisted ingredients that do not materially affect the basic and novel properties of the invention. A “consisting essentially of” claim occupies a middle ground between closed claims that are written in a closed “consisting of” format and fully open claims that are drafted in a “comprising’ format”. These terms can be used interchangeably herein if, and when, this may become necessary. Furthermore, the use of the term “including”, as well as other related forms, such as “includes” and “included”, is not limiting.

“BCA” refers to bacterial carbonic anhydrase.

“CCMs” and the like refer to carbon concentrating systems.

“CET” refers to cyclic electron transfer.

“LET” refers to linear electron transfer.

“WT” refers to wild-type.

“Cyclic electron transfer modulator protein” refers to any protein natural or synthetic that improves the separation of charge across the thylakoid membrane resulting in improved photophosphorylation with the production of chemical energy. Examples of such modulators are the PGR5 and PRGL1 reductases, however improved proteins in the electron transport chain such as cytochromes, ATPases, ferredoxin-NADP reductase, NAD(P)H-plastoquinone reductase, and the like are also CET modulator proteins.

Unless otherwise stated, nucleic acid sequences in the text of this specification are given, when read from left to right, in the 5' to 3' direction. Nucleic acid sequences may be provided as DNA or as RNA, as specified; disclosure of one necessarily defines the other, as is known to one of ordinary skill in the art and is understood as included in embodiments where it would be appropriate. Nucleotides may be referred to by their commonly accepted single-letter codes. Unless otherwise indicated, amino acid sequences are written left to right in amino to carboxyl orientation, respectively. Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUM Biochemical Nomenclature Commission. It is further to be understood that all base sizes or amino acid sizes, and all molecular weight or molecular mass values, given for nucleic acids or polypeptides are approximate, and are provided for description purposes and are not to be unduly limiting.

Regarding disclosed ranges, the endpoints of all ranges directed to the same component or property are inclusive and independently combinable (e.g., ranges of "up to about 25 wt. %, or, more specifically, about 5 wt. % to about 20 wt. %," is inclusive of the endpoints and all intermediate values of the ranges of "about 5 wt. % to about 25 wt. %," etc.). Numeric ranges recited with the specification are inclusive of the numbers defining the range and include each integer within the defined range.

As used herein, "altering level of production" or "altering level of expression" means changing, either by increasing or decreasing, the level of production or expression of a nucleic acid sequence or an amino acid sequence (for example a polypeptide, an siRNA, a miRNA, an mRNA, a gene), as compared to a control level of production or expression.

"Conservative amino acid substitutions": It is well known that certain amino acids can be substituted for other amino acids in a protein structure without appreciable loss of biochemical or biological activity. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence substitutions can be made in a protein sequence, and, of course, its underlying DNA coding sequence, and nevertheless obtain a protein with like properties. Thus, various changes can be made in the amino acid sequences disclosed herein, or in the corresponding DNA sequences that encode these amino acid sequences, without appreciable loss of their biological utility or activity.

Proteins and peptides biologically functionally equivalent to the proteins and peptides disclosed herein include amino acid sequences containing conservative amino acid changes in the fundamental amino acid sequence. In such amino acid sequences, one or more amino acids in the fundamental sequence can be substituted, for example, with another amino acid(s), the charge and polarity of which is similar to that of the native amino acid, i.e., a conservative amino acid substitution, resulting in a silent change.

It should be noted that there are a number of different classification systems in the art that have been developed to describe the interchangeability of amino acids for one another within peptides, polypeptides, and proteins. The following discussion is merely illustrative of some of these systems, and the present disclosure encompasses any of the "conservative" amino acid changes that would be apparent to one of ordinary skill in the art of peptide, polypeptide, and protein chemistry from any of these different systems.

As disclosed in U.S. Pat. No. 5,599,686, certain amino acids in a biologically active peptide, polypeptide, or protein can be replaced by other homologous, isosteric, and/or isoelectronic amino acids, wherein the biological activity of the original molecule is conserved in the modified peptide, polypeptide, or protein. The following list of amino acid replacements is meant to be illustrative and is not limiting:

Original Amino Acid	Replacement Amino Acid(s)
Ala	Gly
Arg	Lys, ornithine
Asn	Gln
Asp	Glu
Glu	Asp
Gln	Asn
Gly	Ala
Ile	Val, Leu, Met, Nle (norleucine)
Leu	Ile, Val, Met, Nle
Lys	Arg
Met	Leu, Ile, Nle, Val
Phe	Tyr, Trp
Ser	Thr
Thr	Ser
Trp	Phe, Tyr
Tyr	Phe, Trp
Val	Leu, Ile, Met, Nle

In another system, substitutes for an amino acid within a fundamental sequence can be selected from other members of the class to which the naturally occurring amino acid belongs. Amino acids can be divided into the following four groups: (1) acidic amino acids; (2) basic amino acids; (3) neutral polar amino acids; and (4) neutral non-polar amino acids. Representative amino acids within these various groups include, but are not limited to: (1) acidic (negatively charged) amino acids such as aspartic acid and glutamic acid; (2) basic (positively charged) amino acids such as arginine, histidine, and lysine; (3) neutral polar amino acids such as glycine, serine, threonine, cysteine, cystine, tyrosine, asparagine. and glutamine; (4) neutral nonpolar (hydrophobic) amino acids such as alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine.

Conservative amino acid changes within a fundamental peptide, polypeptide, or protein sequence can be made by substituting one amino acid within one of these groups with another amino acid within the same group.

Some of the other systems for classifying conservative amino acid interchangeability in peptides, polypeptides, and proteins applicable to the sequences of the present disclosure include, for example, the following:

Functionally defining common properties between individual amino acids by analyzing the normalized frequencies of amino acid changes between corresponding proteins of homologous organisms (Schulz, G. E. and R. H. Schirmer (1979) Principles of Protein Structure (Springer Advanced Texts in Chemistry), Springer-Verlag). According to such analyses, groups of amino acids can be defined where amino acids within a group exchange preferentially with each other, and therefore resemble each other most in their impact on overall protein structure;

Making amino acid changes based on the hydropathic index of amino acids as described by Kyte and Doolittle (1982) J. Mol. Biol. 157(1):105-32. Certain amino acids can be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, i.e., still obtain a biological functionally equivalent protein. In making such changes, the substitution of amino acids whose hydropathic indices are within +2 is preferred, those that are within +1 are particularly preferred, and those within +0.5 are even more particularly preferred;

Substitution of like amino acids on the basis of hydrophilicity. U.S. Pat. No. 4,554,101 states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein. As detailed in this patent, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0.+0.1); glutamate (+3.0.+0.1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (−0.4); proline (−0.5.+0.1); alanine (−0.5); histidine (−0.5); cysteine (−1.0); methionine (−1.3); valine (−1.5); leucine (−1.8); isoleucine (−1.8); tyrosine (−2.3); phenylalanine (−2.5); tryptophan (−3.4). Betts and Russell ((2003), "Amino Acid Properties and Consequences of Substitutions", Bioinformatics for Geneticists, Michael R. Barnes and Ian C. Gray, Eds., John Wiley & Sons, Ltd, Chapter 14, pp. 289-316) review the nature of mutations and the properties of amino acids in a variety of different protein contexts with the purpose of aiding in anticipating and interpreting the effect that a particular amino acid change will have on protein structure and function. The authors point out that features of proteins relevant to considering amino acid mutations include cellular environments, three-dimensional structure, and evolution, as well as the classifications of amino acids based on evolutionary, chemical, and structural principles, and the role for amino acids of different classes in protein structure and function in different contexts. The authors note that classification of amino acids into categories such as those shown in FIG. **14.3** of their review, which involves common physico-chemical properties, size, affinity for water (polar and non-polar; negative or positive charge), aromaticity and aliphaticity, hydrogen-bonding ability, propensity for sharply turning regions, etc., makes it clear that reliance on simple classifications can be dangerous, and suggests that alternative amino acids could be engineered into a protein at each position. Criteria for interpreting how a particular mutation might affect protein structure and function are summarized in section 14.7 of this review, and include first inquiring about the protein, and then about the particular amino acid substitution contemplated.

Biologically/enzymatically functional equivalents of the proteins and peptides disclosed herein can have 10 or fewer conservative amino acid changes, more preferably seven or fewer conservative amino acid changes, and most preferably five or fewer conservative amino acid changes, i.e., 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 conservative amino acid changes. The encoding nucleotide sequence (e.g., gene, plasmid DNA, cDNA, codon-optimized DNA, or other synthetic DNA) will thus have corresponding base substitutions, permitting it to code for the biologically functionally equivalent form of protein or peptide. Due to the degeneracy of the genetic code, i.e., the existence of more than one codon for most of the amino acids naturally occurring in proteins, other DNA (and RNA) sequences that contain essentially the same genetic information as these nucleic acids, and which encode the same amino acid sequence as that encoded by these nucleic acids, can be used in the methods disclosed herein. This principle applies as well to any of the other nucleotide sequences disclosed herein.

"Control" or "control level" means the level of a molecule, such as a polypeptide or nucleic acid, normally found in nature under a certain condition and/or in a specific genetic background. In certain embodiments, a control level of a molecule can be measured in a cell or specimen that has not been subjected, either directly or indirectly, to a treatment. A control level is also referred to as a wildtype or a basal level. These terms are understood by those of ordinary skill in the art. A control plant, i.e. a plant that does not contain a recombinant DNA that confers (for instance) an enhanced trait in a transgenic plant, is used as a baseline for comparison to identify an enhanced trait in the transgenic plant. A suitable control plant may be a non-transgenic plant of the parental line used to generate a transgenic plant. A control plant may in some cases be a transgenic plant line that comprises an empty vector or marker gene, but does not contain the recombinant DNA, or does not contain all of the recombinant DNAs, in the test plant.

The terms "enhance", "enhanced", "increase", or "increased" refer to a statistically significant increase. For the avoidance of doubt, these terms generally refer to about a 5% increase in a given parameter or value, about a 10% increase, about a 15% increase, about a 20% increase, about a 25% increase, about a 30% increase, about a 35% increase, about a 40% increase, about a 45% increase, about a 50% increase, about a 55% increase, about a 60% increase, about a 65% increase, about 70% increase, about a 75% increase, about an 80% increase, about an 85% increase, about a 90% increase, about a 95% increase, about a 100% increase, or more over the control value. These terms also encompass ranges consisting of any lower indicated value to any higher indicated value, for example "from about 5% to about 50%", etc.

"Expression" or "expressing" refers to production of a functional product, such as, the generation of an RNA transcript from an introduced construct, an endogenous DNA sequence, or a stably incorporated heterologous DNA sequence. A nucleotide encoding sequence may comprise intervening sequence (e.g., introns) or may lack such intervening non-translated sequences (e.g., as in cDNA). Expressed genes include those that are transcribed into mRNA and then translated into protein and those that are transcribed into RNA but not translated (for example, siRNA, transfer RNA, and ribosomal RNA). The term may also refer to a polypeptide produced from an mRNA generated from any of the above DNA precursors. Thus, expression of a nucleic acid fragment, such as a gene or a promoter region of a gene, may refer to transcription of the nucleic acid fragment (e.g., transcription resulting in mRNA or other functional RNA) and/or translation of RNA into a precursor or mature protein (polypeptide), or both.

An "expression cassette" refers to a nucleic acid construct, which when introduced into a host cell, results in transcription and/or translation of a RNA or polypeptide, respectively.

The term "genome" as it applies to a plant cells encompasses not only chromosomal DNA found within the nucleus, but organelle DNA found within subcellular components (e.g., mitochondrial, plastid) of the cell. As used herein, the term "genome" refers to the nuclear genome unless indicated otherwise. However, expression in a plastid genome, e.g., a chloroplast genome, or targeting to a plastid genome such as a chloroplast via the use of a plastid targeting sequence, is also encompassed by the present disclosure.

The term "heterologous" refers to a nucleic acid fragment or protein that is foreign to its surroundings. In the context of a nucleic acid fragment, this is typically accomplished by introducing such fragment, derived from one source, into a different host. Heterologous nucleic acid fragments, such as coding sequences that have been inserted into a host organism, are not normally found in the genetic complement of the host organism. As used herein, the term "heterologous" also refers to a nucleic acid fragment derived from the same organism, but which is located in a different, e.g., non-native, location within the genome of this organism. Thus, the organism can have more than the usual number of copy(ies) of such fragment located in its(their) normal position within the genome and in addition, in the case of plant cells, within different genomes within a cell, for example in the nuclear genome and within a plastid or mitochondrial genome as well. A nucleic acid fragment that is heterologous with respect to an organism into which it has been inserted or transferred is sometimes referred to as a "transgene."

A "heterologous" PGRL1 protein or CAB transit peptide protein-encoding nucleotide sequence, etc., can be one or more additional copies of an endogenous PGRL1 protein or CAB transit peptide protein-encoding nucleotide sequence, or a nucleotide sequence from another plant or other source. PGRL1 is a putative ferredoxin-plastoquinone reductase involved in photosynthetic cyclic electron flow. Furthermore, these can be genomic or non-genomic nucleotide sequences. Non-genomic nucleotide sequences encoding such proteins and peptides include, by way of non-limiting examples, mRNA; synthetically produced DNA including, for example, cDNA and codon-optimized sequences for efficient expression in different transgenic plants algae reflecting the pattern of codon usage in such plants; nucleotide sequences encoding the same proteins or peptides, but which are degenerate in accordance with the degeneracy of the genetic code; which contain conservative amino acid substitutions that do not adversely affect their activity, etc., as known by those of ordinary skill in the art.

The term "homology" describes a mathematically based comparison of sequence similarities which is used to identify genes or proteins with similar functions or motifs. The nucleic acid and protein sequences of the present invention can be used as a "query sequence" to perform a search against public databases to, for example, identify other family members, related sequences, or homologs. The term "homologous" refers to the relationship between two nucleic acid sequence and/or proteins that possess a "common evolutionary origin", including nucleic acids and/or proteins from superfamilies (e.g., the immunoglobulin superfamily) in the same species of animal, as well as homologous nucleic acids and/or proteins from different species of animal (for example, myosin light chain polypeptide, etc.; see Reeck et al., (1987) Cell, 50:667). Such proteins (and their encoding nucleic acids) may have sequence homology, as reflected by sequence similarity, whether in terms of percent identity or by the presence of specific residues or motifs and conserved positions. The methods disclosed herein contemplate the use of the presently disclosed nucleic and protein sequences, as well as sequences having sequence identity and/or similarity, and similar function.

"Host cell" means a cell which contains a vector and supports the replication and/or expression of the vector. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells. Alternatively, the host cells are monocotyledonous or dicotyledonous plant cells.

The term "introduced" means providing a nucleic acid (e.g., an expression construct) or protein into a cell. "Introduced" includes reference to the incorporation of a nucleic acid into a eukaryotic or prokaryotic cell where the nucleic acid may be incorporated into the genome of the cell, and includes reference to the transient provision of a nucleic acid or protein to the cell. "Introduced" includes reference to stable or transient transformation methods, as well as sexually crossing. Thus, "introduced" in the context of inserting a nucleic acid fragment (e.g., a recombinant DNA construct/expression construct) into a cell, can mean "transfection" or "transformation" or "transduction", and includes reference to the incorporation of a nucleic acid fragment into a eukaryotic or prokaryotic cell where the nucleic acid fragment may be incorporated into the genome of the cell (e.g., chromosome, plasmid, plastid, or mitochondrial DNA), converted into an autonomous replicon, or transiently expressed (e.g., transfected mRNA).

The term "isolated" refers to a material such as a nucleic acid molecule, polypeptide, or small molecule, that has been separated from the environment from which it was obtained. It can also mean altered from the natural state. For example, a polynucleotide or a polypeptide naturally present in a living animal is not "isolated" but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is "isolated", as the term is employed herein. Thus, a polypeptide or polynucleotide produced and/or contained within a recombinant host cell is considered isolated. Also intended as "isolated polypeptides" or "isolated nucleic acid molecules", etc., are polypeptides or nucleic acid molecules that have been purified, partially or substantially, from a recombinant host cell or from a native source.

As used herein, "nucleic acid" or "nucleotide sequence" means a polynucleotide (or oligonucleotide), including single or double-stranded polymers of deoxyribonucleotide or ribonucleotide bases, and unless otherwise indicated, encompasses naturally occurring and synthetic nucleotide analogues having the essential nature of natural nucleotides in that they hybridize to complementary single-stranded nucleic acids in a manner similar to naturally occurring nucleotides. Nucleic acids may also include fragments and modified nucleotide sequences. Nucleic acids disclosed herein can either be naturally occurring, for example genomic nucleic acids, or isolated, purified, non-genomic nucleic acids, including synthetically produced nucleic acid sequences such as those made by solid phase chemical oligonucleotide synthesis, enzymatic synthesis, or by recombinant methods, including for example, cDNA, codon-optimized sequences for efficient expression in different transgenic plants reflecting the pattern of codon usage in such plants, nucleotide sequences that differ from the nucleotide sequences disclosed herein due to the degeneracy of the genetic code but that still encode the protein(s) of interest disclosed herein, nucleotide sequences encoding the presently disclosed protein(s) comprising conservative (or non-conservative) amino acid substitutions that do not adversely affect their normal activity, PCR-amplified nucleotide sequences, and other non-genomic forms of nucleotide sequences familiar to those of ordinary skill in the art.

The protein-encoding nucleotide sequences, and promoter nucleotide sequences used to drive their expression, disclosed herein can be genomic or non-genomic nucleotide sequences. Non-genomic nucleotide protein-encoding sequences and promoters include, for example, naturally-occurring mRNA, synthetically produced mRNA, naturally-occurring DNA, or synthetically produced DNA. Synthetic nucleotide sequences can be produced by means well known in the art, including by chemical or enzymatic synthesis of oligonucleotides, and include, for example, cDNA, codon-optimized sequences for efficient expression in different transgenic plants and algae reflecting the pattern of codon usage in such organisms, variants containing conservative (or non-conservative) amino acid substitutions that do not adversely affect their normal activity, PCR-amplified nucleotide sequences, etc.

"A PGRL1 protein", "a PGR5 protein", "a HLA3 protein", "a CAB transit peptide", "a PGR5 transit peptide", or any other protein or peptide presently broadly disclosed and utilized in any of the CCM methods and plants and algae disclosed herein refers to a protein or peptide exhibiting enzymatic/functional activity similar or identical to the enzymatic/functional activity of the specifically named protein or peptide. Enzymatic/functional activities of the proteins and peptides disclosed herein are described below. "Similar" enzymatic/functional activity of a protein or peptide can be in the range of from about 75% to about 125% or more of the enzymatic/functional activity of the specifically named protein or peptide when equal amounts of both proteins or peptides are assayed, tested, or expressed as described below under identical conditions, and can therefore be satisfactorily substituted for the specifically named proteins or peptides in the present enhanced CCM methods and transgenic plants and algae.

"Nucleic acid construct" or "construct" refers to an isolated polynucleotide which can be introduced into a host cell. This construct may comprise any combination of deoxyribonucleotides, ribonucleotides, and/or modified nucleotides. This construct may comprise an expression cassette that can be introduced into and expressed in a host cell.

"Operably linked" refers to a functional arrangement of elements. A first nucleic acid sequence is operably linked with a second nucleic acid sequence when the first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter effects the transcription or expression of the coding sequence. The control elements need not be contiguous with the coding sequence, so long as they function to direct the expression thereof. Thus, for example, intervening untranslated yet transcribed sequences can be present between a promoter and the coding sequence and the promoter can still be considered "operably linked" to the coding sequence.

The terms "plant" or "plants" that can be used in the present methods broadly include the classes of higher and lower plants amenable to transformation techniques, including angiosperms (monocotyledonous and dicotyledonous plants), gymnosperms, ferns, and unicellular and multicellular algae. The term "plant" also includes plants which have been modified by breeding, mutagenesis, or genetic engineering (transgenic and non-transgenic plants). It includes plants of a variety of ploidy levels, including aneuploid, polyploid, diploid, haploid, and hemizygous. The plant may be in any form including suspension cultures, embryos, meristematic regions, callus tissue, gametophytes, sporophytes, pollen, microspores, whole plants, shoot vegetative organs/structures (e.g. leaves, stems and tubers), roots, flowers and floral organs/structures, seed (including embryo, endosperm, and seed coat) and fruit, plant tissue (e.g. vascular tissue, ground tissue, and the like) and cells, and progeny of same.

Embodiments of the present disclosure also include parts of plants or algae, which can be selected from among a protoplast, a cell, a tissue, an organ, a cutting, an explant, a reproductive tissue, a vegetative tissue, biomass, an inflorescence, a flower, a sepal, a petal, a pistil, a stigma, a style, an ovary, an ovule, an embryo, a receptacle, a seed, a fruit, a stamen, a filament, an anther, a male or female gametophyte, a pollen grain, a meristem, a terminal bud, an axillary bud, a leaf, a stem, a root, a tuberous root, a rhizome, a tuber, a stolon, a corm, a bulb, an offset, a cell of said plant in culture, a tissue of said plant in culture, an organ of said plant in culture, a callus, propagation materials, germplasm, cuttings, divisions, and propagations.

Other embodiments include progeny or derivatives of transgenic plants and algae disclosed herein selected, for example, from among clones, hybrids, samples, seeds, and harvested material. Progeny can be asexually or sexually produced by methods well known in the art.

Useful C3 and C4 Plants

Plants to which the methods disclosed herein can be advantageously applied include both C3 and C4 plants, including "food crop" and "oilseed" plants, as well as algae.

Food Crop Plants

The term "food crop plant" refers to plants that are either directly edible, or which produce edible products, and that are customarily used to feed humans either directly, or indirectly through animals. Non-limiting examples of such plants include:

1. Cereal crops: wheat, rice, maize (corn), barley, oats, sorghum, rye, and millet;
2. Protein crops: peanuts, chickpeas, lentils, kidney beans, soybeans, lima beans;
3. Roots and tubers: potatoes, sweet potatoes, and cassavas;
4. Oil crops: soybeans, corn, canola, peanuts, palm, coconuts, safflower, cottonseed, sunflower, flax, olive, and safflower;
5. Sugar crops: sugar cane and sugar beets;
6. Fruit crops: bananas, oranges, apples, pears, breadfruit, pineapples, and cherries;
7. Vegetable crops and tubers: tomatoes, lettuce, carrots, melons, asparagus, etc.
8. Nuts: cashews, peanuts, walnuts, pistachio nuts, almonds;
9. Forage and turf grasses;
10. Forage legumes: alfalfa, clover;
11. Drug crops: coffee, cocoa, kola nut, poppy;
12. Spice and flavoring crops: vanilla, sage, thyme, anise, saffron, menthol, peppermint, spearmint, coriander.

In certain embodiments of this disclosure, the food crop plants are soybean, canola, tomato, potato, cassava, wheat, rice, oats, lettuce, broccoli, beets, sugar beets, beans, peas, kale, strawberry, and peanut.

"Oilseed Plants", "Oil Crop Plants", "Biofuels Crops", "Energy Crops"

The terms "oilseed plant" or "oil crop plant", and the like, to which the present methods and compositions can also be applied, refer to plants that produce seeds or fruit with oil content in the range of from about 1 to 2%, e.g., wheat, to about 20%, e.g., soybeans, to over 40%, e.g., sunflowers and rapeseed (canola). These include major and minor oil crops, as well as wild plant species which are used, or are being investigated and/or developed, as sources of biofuels due to their significant oil production and accumulation.

Exemplary oil seed or oil crop plants useful in practicing the methods disclosed herein include, but are not limited to, plants of the genera *Brassica* (e.g., rapeseed/canola (*Brassica napus; Brassica carinata; Brassica nigra; Brassica oleracea*), Camelina, *Miscanthus*, and Jatropha; Jojoba (*Simmondsia chinensis*), coconut; cotton; peanut; rice; safflower; sesame; soybean; mustard; wheat; flax (linseed); sunflower; olive; corn; palm; palm kernel; sugarcane; castor bean; switchgrass; *Borago officinalis; Echium plantagineum; Cuphea hookeriana; Cuphea pulcherrima; Cuphea lanceolata; Ricinus communis; Coriandrum sativum; Crepis alpina; Vernonia galamensis; Momordica charantia*; and *Crambe abyssinica.*

A non-limiting example of a tuber that accumulates significant amounts of reserve lipids is the tuber of *Cyperus esculentus* (chufa or tigernuts), which has been proposed as an oil crop for biofuel production. In the case of chufa, use of a constitutive or tuber-specific promoter would be useful in the methods disclosed herein.

Useful Algae

Algae useful in practicing various methods of the present disclosure include members of the following divisions: Chlorophyta and Heterokontophyta.

In certain embodiments, useful algae include members of the following classes: Chlorophyceae, Bacillariophyceae, Eustigmatophyceae, and Chrysophyceae. In certain embodiments, useful algae include members of the following genera: *Nannochloropsis, Chlorella, Dunaliella, Scenedesmus, Selenastrum, Oscillatoria, Phormidium, Spirulina, Amphora*, and *Ochromonas*. In one embodiment, members of the genus *Chlorella* are preferred.

Some algal species of particular interest include, without limitation: Bacillariophyceae strains, Chlorophyceae, Cyanophyceae, Xanthophyceae, Chrysophyceae, *Chlorella, Crypthecodinium, Schizocytrium, Nannochloropsis, Ulkenia, Dunaliella, Cyclotella, Navicula, Nitzschia, Cyclotella, Phaeodactylum*, and *Thaustochytrid.*

Non-limiting examples of algae species that can be used with the methods of the present disclosure include, for example, *Achnanthes orientalis, Agmenellum* spp., *Amphiprora hyaline, Amphora coffeiformis, Amphora coffeiformis* var. *linea, Amphora coffeiformis* var. *punctata, Amphora coffeiformis* var. *taylori, Amphora coffeiformis* var. *tenuis, Amphora delicatissima, Amphora delicatissima* var. *capitata, Amphora* sp., *Anabaena, Ankistrodesmus, Ankistrodesmus falcatus, Boekelovia hooglandii, Borodinella* sp., *Botryococcus braunii, Botryococcus sudeticus, Bracteococcus minor, Bracteococcus medionucleatus, Carteria, Chaetoceros gracilis, Chaetoceros muelleri, Chaetoceros muelleri* var. *subsalsum, Chaetoceros* sp., *Chlamydomas perigranulata, Chlorella* anitrata, *Chlorella* antarctica, *Chlorella aureoviridis, Chlorella Candida, Chlorella capsulate, Chlorella desiccate, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca* var. *vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum* var. *actophila, Chlorella infusionum* var. *auxenophila, Chlorella kessleri, Chlorella lobophora, Chlorella luteoviridis, Chlorella luteoviridis* var. *aureoviridis, Chlorella luteoviridis* var. *lutescens, Chlorella miniata, Chlorella minutissima, Chlorella mutabilis, Chlorella nocturna, Chlorella ovalis, Chlorella parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides, Chlorella protothecoides* var. *acidicola, Chlorella regularis, Chlorella regularis* var. *minima, Chlorella regularis* var. *umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella saccharophila* var. *ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella* sp., *Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella vulgaris, Chlorella vulgaris* fo. *tertia, Chlorella vulgaris* var. *autotrophica, Chlorella vulgaris* var. *viridis, Chlorella vulgaris* var. *vulgaris, Chlorella vulgaris* var. *vulgaris* fo. *tertia, Chlorella vulgaris* var. *vulgaris* fo. *viridis, Chlorella* xanthella, *Chlorella zofingiensis, Chlorella trebouxioides, Chlorella vulgaris, Chlorococcum infusionum, Chlorococcum* sp., *Chlorogonium, Chroomonas* sp., *Chrysosphaera* sp., *Cricosphaera* sp., *Crypthecodinium cohnii, Cryptomonas* sp., *Cyclotella cryptica, Cyclotella meneghiniana, Cyclotella* sp., *Chlamydomonas moewusii Chlamydomonas reinhardtii Chlamydomonas* sp. *Dunaliella* sp., *Dunaliella bardawil, Dunaliella bioculata, Dunaliella granulate, Dunaliella maritime, Dunaliella minuta, Dunaliella parva, Dunaliella peircei, Dunaliella primolecta, Dunaliella salina, Dunaliella terricola, Dunaliella tertiolecta, Dunaliella viridis, Dunaliella tertiolecta, Eremosphaera viridis, Eremosphaera* sp., *Ellipsoidon* sp., *Euglena* spp., *Franceia* sp., *Fragilaria crotonensis, Fragilaria* sp., *Gleocapsa* sp., *Gloeothamnion* sp., *Haematococcus pluvialis, Hymenomonas* sp., *Isochrysis* aff. *galbana, Isochrysis galbana, Lepocinclis, Micractinium, Micractinium, Monoraphidium minutum, Monoraphidium* sp., *Nannochloris* sp., *Nannochloropsis* salina, *Nannochloropsis* sp., *Navicula acceptata, Navicula biskanterae, Navicula pseudotenelloides, Navicula pelliculosa, Navicula saprophila, Navicula* sp., *Nephrochloris* sp., *Nephroselmis* sp., *Nitschia communis, Nitzschia alexandrina, Nitzschia closterium, Nitzschia communis, Nitzschia dissipata, Nitzschia frustulum, Nitzschia hantzschiana, Nitzschia inconspicua, Nitzschia intermedia, Nitzschia microcephala, Nitzschia pusilla, Nitzschia pusilla elliptica, Nitzschia pusilla monoensis, Nitzschia quadrangular, Nitzschia* sp., *Ochromonas* sp., *Oocystis parva, Oocystis pusilla, Oocystis* sp., *Oscillatoria limnetica, Oscillatoria* sp., *Oscillatoria subbrevis, Parachlorella kessleri, Pascheria acidophila, Pavlova* sp., *Phaeodactylum tricomutum, Phagus, Phormidium, Platymonas* sp., *Pleurochrysis carterae, Pleurochrysis dentate, Pleurochrysis* sp., *Prototheca wickerhamii, Prototheca stagnora, Prototheca portoricensis, Prototheca moriformis, Prototheca zopfii, Pseudochlorella aquatica, Pyramimonas* sp., *Pyrobotrys, Rhodococcus opacus, Sarcinoid chrysophyte, Scenedesmus armatus, Schizochytrium, Spirogyra, Spirulina platensis, Stichococcus* sp., *Synechococcus* sp., *Synechocystisf, Tagetes erecta, Tagetes patula, Tetraedron, Tetraselmis* sp., *Tetraselmis suecica, Thalassiosira weissflogii*, and *Viridiella fridericiana.*

In certain embodiments of this disclosure, the algae are species of *Chlorella, Nannochloropsis*, and *Chlamydomonas* listed above.

Exemplary food crop plant include wheat, rice, maize (corn), barley, oats, sorghum, rye, and millet; peanuts, chickpeas, lentils, kidney beans, soybeans, lima beans; potatoes, sweet potatoes, and cassavas; soybeans, corn, canola, peanuts, palm, coconuts, safflower, cottonseed, sunflower, flax, olive, and safflower; sugar cane and sugar beets; bananas, oranges, apples, pears, breadfruit, pineapples, and cherries; tomatoes, lettuce, carrots, melons, strawberry, asparagus, broccoli, peas, kale, cashews, peanuts, walnuts, pistachio nuts, almonds; forage and turf grasses; alfalfa, clover; coffee, cocoa, kola nut, poppy; vanilla, sage, thyme, anise, saffron, menthol, peppermint, spearmint and coriander and preferably wheat, rice and canola.

The terms “peptide”, “polypeptide”, and “protein” are used to refer to polymers of amino acid residues. These terms are specifically intended to cover naturally occurring biomolecules, as well as those that are recombinantly or synthetically produced, for example by solid phase synthesis.

The term “promoter” or “regulatory element” refers to a region or nucleic acid sequence located upstream or downstream from the start of transcription and which is involved in recognition and binding of RNA polymerase and/or other proteins to initiate transcription of RNA. Promoters need not be of plant or algal origin. For example, promoters derived from plant viruses, such as the CaMV35S promoter, or from other organisms, can be used in variations of the embodiments discussed herein. Promoters useful in the present methods include, for example, constitutive, strong, weak, tissue-specific, cell-type specific, seed-specific, inducible, repressible, and developmentally regulated promoters.

A skilled person appreciates that a promoter sequence can be modified to provide for a range of expression levels of an operably linked heterologous nucleic acid molecule. Less than the entire promoter region can be utilized and the ability to drive expression retained. However, it is recognized that expression levels of mRNA can be decreased with deletions of portions of the promoter sequence. Thus, the promoter can be modified to be a weak or strong promoter. A promoter is classified as strong or weak according to its affinity for RNA polymerase (and/or sigma factor); this is related to how closely the promoter sequence resembles the ideal consensus sequence for the polymerase. Generally, by "weak promoter" is intended a promoter that drives expression of a coding sequence at a low level. By "low level" is intended levels of about 1/10,000 transcripts to about 1/100,000 transcripts to about 1/500,000 transcripts. Conversely, a strong promoter drives expression of a coding sequence at a high level, or at about 1/10 transcripts to about 1/100 transcripts to about 1/1,000 transcripts. The promoter of choice is preferably excised from its source by restriction enzymes, but can alternatively be PCR-amplified using primers that carry appropriate terminal restriction sites. It should be understood that the foregoing groups of promoters are non-limiting, and that one skilled in the art could employ other promoters that are not explicitly cited herein.

The term "purified" refers to material such as a nucleic acid, a protein, or a small molecule, which is substantially or essentially free from components which normally accompany or interact with the material as found in its naturally occurring environment, and/or which may optionally comprise material not found within the purified material's natural environment. The latter may occur when the material of interest is expressed or synthesized in a non-native environment. Nucleic acids and proteins that have been isolated include nucleic acids and proteins purified by standard purification methods. The term also encompasses nucleic acids and proteins prepared by recombinant expression in a host cell as well as chemically synthesized nucleic acids.

"Recombinant" refers to a nucleotide sequence, peptide, polypeptide, or protein, expression of which is engineered or manipulated using standard recombinant methodology. This term applies to both the methods and the resulting products. As used herein, a "recombinant construct", "expression construct", "chimeric construct", "construct" and "recombinant expression cassette" are used interchangeably herein.

As used herein, the phrase "sequence identity" or "sequence similarity" is the similarity between two (or more) nucleic acid sequences, or two (or more) amino acid sequences. Sequence identity is frequently measured as the percent of identical nucleotide or amino acid residues at corresponding positions in two or more sequences when the sequences are aligned to maximize sequence matching, i.e., taking into account gaps and insertions.

One of ordinary skill in the art will appreciate that sequence identity ranges are provided for guidance only. It is entirely possible that nucleic acid sequences that do not show a high degree of sequence identity can nevertheless encode amino acid sequences having similar functional activity. It is understood that changes in nucleic acid sequence can be made using the degeneracy of the genetic code to produce multiple nucleic acid molecules that all encode substantially the same protein. Means for making this adjustment are well-known to those of skill in the art. When percentage of sequence identity is used in reference to amino acid sequences it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g., charge or hydrophobicity) and therefore do not change the functional properties of the molecule. Where sequences differ in conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences which differ by such conservative substitutions are said to have "sequence similarity" or "similarity". Means for making this adjustment are well-known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity.

"Percentage of sequence identity" is determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity.

Sequence identity (or similarity) can be readily calculated by known methods, including but not limited to those described in: Computational Molecular Biology, Lesk, A. M., ed., Oxford University Press, New York, 1988; Biocomputing: Informatics and Genome Projects, Smith, D. W., ed., Academic Press, New York, 1993; Computer Analysis of Sequence Data, Part I, Griffin, A. M., and Griffin, H. G., eds., Humana Press, New Jersey, 1994; Sequence Analysis in Molecular Biology, von Heinje, G., Academic Press, 1987; and Sequence Analysis Primer, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; and Carillo, H., and Lipman, D., SIAM J. Applied Math., 48: 1073 (1988). Methods to determine identity are designed to give the largest match between the sequences tested. Moreover, methods to determine identity are codified in publicly available computer programs. Optimal alignment of sequences for comparison can be conducted, for example, by the local homology algorithm of Smith & Waterman, by the homology alignment algorithms, by the search for similarity method or, by computerized implementations of these algorithms (GAP, BESTFIT, PASTA, and TFASTA in the GCG Wisconsin Package, available from Accelrys, Inc., San Diego, Calif., United States of America), or by visual inspection. See generally, (Altschul, S. F. et al., J. Mol. Biol. 215: 403-410 (1990) and Altschul et al. Nucl. Acids Res. 25: 3389-3402 (1997)).

One example of an algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in (Altschul, S., et al., NCBI NLM NIH Bethesda, Md. 20894; & Altschul, S., et al., J. Mol. Biol. 215: 403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length Win the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold. These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value, the cumulative score goes to zero or below due to the accumulation of one or more negative-scoring residue alignments, or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=−4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915).

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul, Proc. Nat'l. Acad. Sci. USA 90: 5873-5877 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P (N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. BLAST searches assume that proteins can be modeled as random sequences. However, many real proteins comprise regions of nonrandom sequences which may be homopolymeric tracts, short-period repeats, or regions enriched in one or more amino acids. Such low-complexity regions may be aligned between unrelated proteins even though other regions of the protein are entirely dissimilar. A number of low-complexity filter programs can be employed to reduce such low-complexity alignments. For example, the SEG (Wooten and Federhen, Comput. Chem., 17: 149-163 (1993)) and XNU (Claverie and States, Comput. Chem., 17: 191-201 (1993)) low-complexity filters can be employed alone or in combination.

The constructs and methods disclosed herein encompass nucleic acid and protein sequences having sequence identity/sequence similarity at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 100% to those specifically and/or sequences having the same or similar function for example if a protein or nucleic acid is identified with a transit peptide and the transit peptide is cleaved leaving the protein sequence without the transit peptide then the sequence identity/sequence similarity is compared to the protein with and/or without the transit peptide.

A "transgenic" organism, such as a transgenic plant, is a host organism that has been stably or transiently genetically engineered to contain one or more heterologous nucleic acid fragments, including nucleotide coding sequences, expression cassettes, vectors, etc. Introduction of heterologous nucleic acids into a host cell to create a transgenic cell is not limited to any particular mode of delivery, and includes, for example, microinjection, floral dip, adsorption, electroporation, vacuum infiltration, particle gun bombardment, whiskers-mediated transformation, liposome-mediated delivery, *Agrobacterium*-mediated transfer, the use of viral and retroviral vectors, etc., as is well known to those skilled in the art.

Conventional techniques of molecular biology, recombinant DNA technology, microbiology, and chemistry useful in practicing the methods of the present disclosure are described, for example, in Green and Sambrook (2012) Molecular Cloning: A Laboratory Manual, Fourth Edition, Cold Spring Harbor Laboratory Press; Ausubel et al. (2003 and periodic supplements) Current Protocols in Molecular Biology, John Wiley & Sons, New York, N.Y.; Amberg et al. (2005) Methods in Yeast Genetics: A Cold Spring Harbor Laboratory Course Manual, 2005 Edition, Cold Spring Harbor Laboratory Press; Roe et al. (1996) DNA Isolation and Sequencing: Essential Techniques, John Wiley & Sons; J. M. Polak and James O'D. McGee (1990) In Situ Hybridization: Principles and Practice; Oxford University Press; M. J. Gait (Editor) (1984) Oligonucleotide Synthesis: A Practical Approach, IRL Press; D. M. J. Lilley and J. E. Dahlberg (1992) Methods in Enzymology: DNA Structure Part A: Synthesis and Physical Analysis of DNA, Academic Press; and Lab Ref: A Handbook of Recipes, Reagents, and Other Reference Tools for Use at the Bench, Edited by Jane Roskams and Linda Rodgers (2002) Cold Spring Harbor Laboratory Press; Burgess and Deutscher (2009) Guide to Protein Purification, Second Edition (Methods in Enzymology, Vol. 463), Academic Press. Note also U.S. Pat. Nos. 8,178,339; 8,119,365; 8,043,842; 8,039,243; 7,303,906; 6,989,265; US20120219994A1; and EP1483367B1. The entire contents of each of these texts and patent documents are herein incorporated by reference.

Preliminary Results: Transgenic Plants Expressing Algal CCM Genes

Previously, reconstitution of a functional inorganic CCM in C3 plants to suppress photo-respiration and enhance photosynthesis was proposed. In WO 2012/125737, it was hypothesized that expression of a minimum of three algal CCM proteins would be sufficient to elevate internal plastid CO_2 concentrations high enough to suppress photorespiration. These three algal CCM genes included the *Chlamydomonas* plasma membrane-localized and ATP-dependent bicarbonate transporter, HLA3; the chloroplast envelope localized bicarbonate anion transporter, LCIA; and a chloroplast stromal-localized carbonic anhydrase (HCA-II) to accelerate conversion of bicarbonate into CO_2. These genes have individually been shown to be important to the CCM in prior studies ([3-5]). To test this hypothesis, we generated multiple independent transgenic *Arabidopsis* and Camelina plants expressing each CCM gene as a single gene construct, as well as a stacked 3-gene construct. The expression of each gene was controlled by the light-regulated Cab1 gene promoter [6].

The results of phenotypic analyses of *Arabidopsis* and Camelina plants transformed with the single CCM gene constructs were as follows:

HLA3 *Arabidopsis* transgenics varied in their phenotypes, but generally had reduced growth phenotypes relative to wild-type (WT) plants (FIG. **6**). When the same plasmid was used to transform Camelina, no viable seeds were recovered from any transformation event after multiple attempts, indicating that HLA3 expression was likely toxic to Camelina.

With respect to carbonic anhydrase (CA) transgenics, we expressed a human carbonic anhydrase-2 (HCA2 (SEQ ID NO:17)) or a bacterial *Neisseria gonorrhoeae* carbonic anhydrase (BCA SEQ ID NO: 4)) in the chloroplast stroma [7]. We choose these CAs because each has a turnover number (Kcat=106 sec-1) that is approximately 10× faster than plant/algal Cas. In both *Arabidopsis* and Camelina, we observed phenotypes that were either similar to WT (HCA2) or substantially larger (BCA) than WT plants (FIG. **3**B).

Transgenic *Arabidopsis* plants expressing the LCIA gene were substantially impaired in growth (FIG. **5**A). In contrast, Camelina LCIA transgenics grew better than WT, had up to 25% higher photosynthetic rates at ambient CO_2 concentrations, and had reduced CO_2 compensation points (FIG. **5**B).

The fact that expression of individual CCM genes impaired growth in C3 plants suggested that additional traits may need to be expressed or silenced to achieve optimal photosynthetic performance.

To determine if we could reconstitute a fully functional CCM complex in C3 plants, we transformed *Arabidopsis* and Camelina with a triple-gene CCM construct in which the expression of the HLA3, CA, and LCIA genes was driven by the green-tissue specific Cab1 promoter. In both *Arabidopsis* and Camelina there was either a substantial impairment in growth, or the plants did not survive (results not shown).

Thus, co-expression of the HLA3 gene with any other CCM gene(s) impaired growth even in plants in which expression of the other CCM genes, e.g., LCIA in Camelina, or BCA in *Arabidopsis*, enhanced growth. These results indicated that HLA3 expression was problematic.

Since the HLA3 protein catalyzes active bicarbonate transport and is the first-dedicated step in the engineered CCM, we re-focused our efforts on trying to determine why HLA3 expression was toxic to plants and how to mitigate its effects. We considered two possible hypotheses for HLA3 toxicity: 1) expression of the HLA3 ABC-transporter increases ATP demand (1 ATP/COO for photosynthesis by 25% and depletes cytoplasmic ATP levels [3-5,8] and 2) elevated bicarbonate levels in HLA3 transgenic plants negatively impact cytoplasmic pH levels. With respect to the latter hypothesis, it is noteworthy that unlike cyanobacteria, plants have robust cytoplasmic CA activity, potentially mitigating the effects of elevated bicarbonate levels on cytoplasmic pH.

The Role of ATP Demand and Cyclic Electron Transfer Activity in CCMs

In contrast to air-grown algae (4 ATP/2 NADPH/CO_2) and C4 plants (5 ATP/2 NADPH/CO_2) which have increased ATP demands for photosynthesis, C3 plants (3 ATP/2 NADPH/CO_2) have limited capacity to generate additional ATP for each electron transferred [8-10]. Increasing ATP demand by 25% per carbon fixed in HLA3 transgenic plants, therefore, could deplete cytoplasmic ATP levels as well as alter the redox state of the cell [8,10]. One mechanism to increase ATP synthesis for each light-driven electron transferred is by cyclic electron transfer (CET) activity. Light-driven CET is catalyzed by photosystem I (PSI) mediated charge separation leading to the reduction of ferredoxin (fd) and the PGR5 protein. The PGR5 protein reduces and protonates plastoquinone (PQ). PQH2 is then oxidized by the cytochrome b6f complex (Cyt b6f). Protons released from the oxidation of PQH2 drive ATP synthesis. The electron transfer cycle is completed by the reduction of plastocyanin (PC) by Cyt b6f, which in turn is oxidized by the PSI primary donor P700+. Significantly, molecular studies have demonstrated that genes encoding proteins functional in CET are substantially overexpressed (4-10×) in C4 plants and air-grown algae relative to related C3 species or high CO_2 grown algae [9,11-17]. These CET genes include: the Proton Gradient Regulation Genes PGR5 and PGRL1, and certain members of the Fd and ferredoxin NADP reductase (FNR) gene families [8-15]: Accession Nos.: PGR5:NM_126585; PGRL1: NM_179091; Fd: AtFd1: At1g10960; AtFd2:At1g60950; FNR: LFNR1:At5g66190; LFRN2: At1g20020) [15]. The sequence for the PRG5 protein with the transit peptide amino acid sequence underlined is provided as

(SEQ ID NO: 1)

MAAASISAIG CNQTLIGTSF YGGWGSSISG EDYQTMLSKT

VAPPQQARVS RKAIRAVPMMKNVNEGKGLF APLVVVTRNL

VGKKRFNQLR GKAIALHSQV ITEFCKSIGA

DAKQRQGLIRAKKNGERLG FL.

The transit peptide is cleaved to produce the functional PGR5 protein.

To test the hypothesis that ATP depletion in HLA3 transgenics resulted in growth impairment, we compared the phenotypes of VVT and HLA3 transgenics grown on nitrate which would require more linear electron transport (LET) to facilitate the reduction of nitrate. Significantly, the additional ATP produced by LET is not required for conversion of nitrate to ammonium and thus total ATP levels are expected to increase. In contrast, plants grown on ammonium do not require additional LET. Finally, we also grew transgenics on ammonium with sucrose which would presumably provide additional ATP via respiration [15,17]. We hypothesized that growth on nitrate or ammonium with sucrose would provide additional ATP that could potentially drive HLA3 activity.

As shown in FIG. **2**B, none of the *Arabidopsis* HLA3 transgenics (4 independent lines) grew in the presence of ammonium, but all HLA3 lines were rescued when grown on ammonium with sucrose. Furthermore, plants grown on ammonium plus sucrose were phenotypically similar to VVT (FIG. **2**B). In contrast, all HLA3 plants grown on nitrate survived, but some lines (#9, #20) had substantially impaired growth phenotypes. Identical results were observed for the germination and growth of VVT and HLA3 transgenic seeds on MS media agar plates using either nitrate (HLA3 transgenics survived) or ammonium (HLA3 transgenics died) as the sole nitrogen source (results not shown). Based on these observations, we propose that increased ATP synthesis associated with nitrate-driven LET and/or sucrose metabolism reduces the depletion of cytoplasmic ATP levels in HLA3 transgenics and rescues them.

This interpretation was corroborated by comparative metabolite analyses of leaf energy charge (EC) status (ATP), inorganic phosphate levels, and leaf reductive potential (RP) of VVT and HLA3 transgenic *Arabidopsis* grown on nitrate. As shown in FIG. **6**, HLA3 transgenics grown on nitrate had reduced EC and RP ratios relative to WT. Energy charge is defined as ([ATP]+½[ADP])/([ATP]+[ADP]+[AMP]). The reduction potential is a measurement of the capacity of the system to gain or lose electrons.

Significantly, inorganic phosphate levels were two-fold higher in HLA3 line #20, while the NADH level was two-fold lower than WT.

These results are consistent with the hypothesis that HLA3 expression places increased ATP demand on plants. This increased ATP demand in HLA3 transgenics may be met in part via NAD(P)H oxidation via the malate/oxaloacetate redox shunt between the mitochondria and chloroplasts [16].

LCIA Phenotype Depends on Plant Species

As previously indicated, LCIA expression in transgenic *Arabidopsis* resulted in plants with severely depressed growth phenotypes (FIG. **5**A). In contrast, transgenic Camelina expressing LCIA had increased growth rates as well as higher CO_2-dependent photosynthetic rates relative to WT (FIG. **5**B). We propose that the substantially greater carbon sink-strength of Camelina relative to *Arabidopsis* accounts for the enhanced growth phenotype observed in Camelina LCIA plants. In support of this hypothesis, we observed that Camelina LCIA transgenics had higher CO_2-dependent rates of photosynthesis and lower CO_2 compensation points (40 vs. 53 ppm CO_2) than WT plants indicative of facilitated inorganic carbon uptake by LCIA (FIG. **5**C).

Overview: Enhancing photosynthetic carbon fixation by increasing ATP production and limiting CO_2 diffusion out of artificial CCM lines; Strategies for facilitating CET and ATP synthesis in C3 plants

Prior attempts to subvert the limitations of photosynthesis have focused on engineering RuBisCO throughput and specificity [35] by introduction of engineered and non-native forms of the enzyme [36], through alterations in the regenerative capacity of the Calvin cycle [37,38] or by engineering photorespiratory bypasses [39]. These studies produced mixed results, thus advocating for a more comprehensive systems-level approach to enhance and/or redirect photosynthetic carbon flux.

As evidenced by our prior work described above, we postulate that both the carbon assimilatory steps and the light-based generation of ATP and NAPDH must be considered to develop a competent CCM with significantly improved photosynthetic capacity. To demonstrate proof of concept, an *Arabidopsis* line that contains a functional CCM that includes mechanisms to adjust ATP levels to meet transporter demand will be generated.

Enhancing CET and ATP Synthesis to Support HLA3-Dependent Bicarbonate Uptake

To exploit the expression of an algal CCM in C3 plants requires that we meet the additional energy demands required to actively transport inorganic carbon. As previously discussed in the section entitled "The role of ATP demand and cyclic electron transfer activity in CCMs", C4 plants and algae have robust CET activity, and overexpress a variety of genes involved in CET [13,16,40-45] compared to C3 plants.

Several strategies are identified in the following examples, to increase ATP synthesis to support HLA3-dependent bicarbonate transport. Several of these strategies focus on elevating CET activity in C3 plants. Another approach involves the expression of a green photon-driven bacterial proton pump in thylakoids to supplement proton-driven ATP synthesis. Each approach is designed to complement existing CCM lines in *Arabidopsis*, Camelina, and potato we have created, and are evaluated based upon measured adenylate levels, plant biomass production, and photosynthetic measurements of carbon assimilation. The materials and methods employed in the examples below are for illustrative purposes only, and are not intended to limit the practice of the present embodiments thereto. Any materials and methods similar or equivalent to those described herein as would be apparent to one of ordinary skill in the art can be used in the testing or practice of the present embodiments, i.e., the materials, methods, and examples are illustrative only and not intended to be limiting.

Example 1: Enhancing CET Based on Overexpressing the Proton Gradient Regulatory Proteins PGR5 and PGRL1 in C3 Plants

Enhancing CET is based on overexpressing the proton gradient regulatory proteins PGR5 and/or PGRL1 which have previously been shown to be important to CET [37]. It has recently been demonstrated that the PGRL1 protein has antimycin A-sensitive (AA), ferredoxin-plastoquinone reductase (FQR) activity [46]. In *Chlamydomonas*, PGRL1 is part of the Cytb6f/PSI supercomplex which mediates CET. Significantly, PGRL1 forms homodimers as well as heterodimers with PGR5 via redox active cysteine residues. Under high-light conditions, thioredoxinred reduces PGRL1 dimers present in grana stacks, increasing the abundance of PGRL1 monomers and enhancing CET [47]. Mutational studies have shown that the PGR5 protein is required for Fd oxidation and PGRL1 reduction, but not for PQ reduction. In addition, it has been shown that PGRL1/PGR5 heterodimers are more active in CET than PGRL1 monomers. In C4 plants PGR5 and PGRL1 expression levels are elevated (4×) relative to C3 plants [9]. Similarly, PGR5 expression is up-regulated in air-grown *Chlamydomonas* (active CCM and HLA3 activity) relative to high CO_2 (low CCM) grown cells [16,43]. Significantly, overexpression of PGRL1 and PGR5 has also been shown to increase AA-sensitive CET in transgenic *Arabidopsis* [48]. One embodiment of the present invention provides for an overexpression of PGRL1 gene (SEQ ID NO:106) and PGR5 gene with chloroplast targeting sequence (SEQ ID NO:2) with HLA3 gene (SEQ ID NO:12) or with HLA3 gene (SEQ ID NO:12) and LCIA gene (SEQ ID NO:16) and BCA gene codon optimized for expression in *Arabidopsis* (SEQ ID NO:4) to yield substantially increased photosynthetic rates, particularly in plants with enhanced sink strength (Camelina and potato for example). Co-expression of the PGR5 gene (SEQ ID NO:2) along with the HLA3 gene (SEQ ID NO:12) in Camelina rescued the HLA3 gene and it was no longer lethal. These results indicate that the PGR5 gene is enabling the production of sufficient ATP to meet the demands of the HLA3 gene product.

HLA3 (SEQ ID NO:12) and PGR5 (SEQ ID NO:2) are introduced as a double construct into *Arabidopsis* or Camelina, by *Agrobacterium*-mediated Ti plasmid transformation using, for example, plasmid pB110-HLA3-pgr5-dsred (FIG. **9**). Since PGR5 protein (SEQ ID NO:1) is naturally targeted to the thylakoid membranes, no additional targeting sequences are introduced. Similarly, since HLA3 protein (SEQ ID NO:77) is naturally targeted to the chloroplast envelope, no additional targeting sequences are added. HLA3 is codon optimized for plant expression.

In one embodiment, the expression of each protein is driven by the light sensitive leaf-specific CAB1 promoter (SEQ ID NO:7) and Nos terminator (SEQ ID NO:9) (FIG. **9**).

The BCA gene (AAW89307; SEQ ID NO:4), under the control of CAB1 promoter, is introduced in to *Arabidopsis* by *Agrobacterium*-mediated Ti plasmid transformation by floral dip method using the construct shown in FIG. **10**.

As a visual marker, the plasmid also includes a gene for expression of fluorescent DsRed protein under the control of CVMV promoter and Nos terminator (FIG. **10**).

Plants are transformed by vacuum infiltration method (Lu and Kang (February, 2008) Plant Cell Rep. 27(2):273-8), and will be screened for biomass yield parameters (including plant weight, height, branching and seed yield) and photosynthetic efficiency measured as CO_2 absorption with the aid of a LiCor 6400 gas exchange analyzer.

The PGRL1 gene from *Arabidopsis* (NM_179091 SEQ ID NO:3) will be subcloned into pCambia1301-based binary plasmid under control of the CAB1 promoter (SEQ ID NO:7) and Nos terminator (SEQ ID NO:9). The plasmid will also carry a gene for hygromycin selection marker. *Agrobacterium*-mediated transformation takes place by the standard floral dip method followed by germination of seeds on hygromycin to select for transformants. The expression of PRGL1 will be confirmed by RT-PCR, and the resulting transgenic plant lines will be crossed with HLA3/PGR5 plants and screened for biomass yield and photosynthesis rate (CO_2 fixation).

Example 2: Determining if Fd1 Gene Overexpression can Support Algal CCM and Increased Photosynthetic Rates

It has recently been demonstrated that specific members of the ferredoxin (Fd) gene family facilitate CET. Overexpression of pea ferredoxin1 (Fd1) enhanced CET at the expense of LET in tobacco [16,40].

Therefore, another embodiment of the present invention provides enhancing ATP production and titrating the expression of the pea Fd1 gene in the three model C3 plants with and without co-expression of the CCM genes to determine if Fd1 overexpression can support the algal CCM and increased photosynthetic rates. Earlier results demonstrated that Fd1 overexpression slightly impaired Linear Electron Transfer (LET), resulting in a stunted phenotype [40]. We expect that the additional ATP demand in HLA3 transgenics, however, will mitigate these effects.

Fd1 gene (At1g10960) will be introduced by *Agrobacterium*-mediated Ti plasmid transformation. Fd1 gene will be subcloned into pCambia1301-based binary plasmid under control of CAB1 promoter (SEQ ID NO:7) and Nos terminator (SEQ ID NO:9). The plasmid will also carry a gene for hygromycin selection as a marker. *Agrobacterium*-mediated transformation takes place by the standard floral dip method, followed by germination of seeds on hygromycin to select for transformants. The expression of FD1 (SEQ ID NO:93) will be confirmed by real time QPCR, and the resulting plant lines exhibiting different levels of FD1 expression will be crossed with CCM-expressing plants and screened for biomass yield and photosynthesis rate with the aid of a LiCor 6400 CO_2-gas exchange analyzer.

Example 3: Overexpression of Unique Ferredoxin NADP Reductase (FNR) Gene Family Members Associated with CET

Yet another embodiment is based on overexpression of unique ferredoxin NADP reductase (FNR) gene family members associated with CET. Leaf FNR (LFNR) catalyzes the reduction of Fd and is involved in both LET and CET [15]. It was recently demonstrated that there are three LFNR gene family members expressed in maize leaves: Accession Nos. BAA88236 (LFNR1), BAA88237 (LFNR2), and ACF85815 (LFNR3).

LFNR-1 was shown to be localized to thylakoid membranes and associated with Cytb6f complexes. LFNR2 was present in thylakoids and stroma associated with Cytb6f complexes. LFNR3 was soluble and not associated with Cytb6f complexes.

Significantly, when plants were grown with nitrate instead of ammonium, expression of LFNR1 and LFNR2 was elevated but not that of LFNR3. In contrast, studies using *Arabidopsis* LFNR1 knock out mutants demonstrated that PGA-dependent oxygen evolution (which requires additional ATP) is more negatively affected than is nitrate-dependent oxygen evolution (no additional ATP demand), suggesting that LFNR1 may play a role in regulating CET [15]. However, this interpretation remains equivocal.

To determine if CET activity and HLA3 mediated inorganic carbon uptake can be altered by differential expression of LFNR1, we will both over-express (CAB1 promoter (SEQ ID NO:7)) and under-express (LFNR1 RNAi) LFNR1 in transgenic *Arabidopsis* to determine the impact of altered LFNR1 expression on functional CCM activity.

For overexpression of the LFNR1, the gene (At5g66190) will be introduced by *Agrobacterium*-mediated Ti plasmid transformation by floral dipping. The LFNR1gene will be subcloned into pCambia1301-based binary plasmid under control of the CAB1 promoter (SEQ ID NO:7) and Nos terminator (SEQ ID NO:9). The plasmid will also carry a gene for hygromycin selection as a marker. The expression of LFNR1 will be confirmed by real time QPCR, the resulting plant lines will be crossed with CCM-expressing plants, and screened for biomass yield and photosynthesis rate with the aid of a LiCor 6400 CO_2-gas exchange analyzer.

For downregulaton of the LFNR1 levels, an RNAi construct containing a partial sequence of the LFNR1 (At5g66190 or BAA88236) and reverse complementary sequence of LFNR1 will be subcloned into pCambia1301-based binary plasmid under control of the CAB1 promoter (SEQ ID NO:7) and Nos terminator (SEQ ID NO:9). The plasmid will also carry a gene for hygromycin selection as a marker. The reduced level of LFNR1 expression will be confirmed by real time QPCR.

The resulting lines will be crossed with CCM-expressing lines to generate double mutants. Those mutants will be screened for biomass yield parameters (including plant weight, height, branching and seed yield) and photosynthetic efficiency measured as CO_2 absorption with the aid of a LiCor 6400 gas exchange analyzer.

Example 4: Facilitated Vectoral Proton Transport Using Proteorhodopsin (PR)

In yet another embodiment green photons, not absorbed by chlorophyll, to drive proton transport across thylakoids by expressing modified PR [49]) will be employed to enhance ATP synthesis (FIG. **7**).

PR is a seven-helix transmembrane-spanning protein similar to bacteriorhodopsin that contains retinal in its active site. Green light-driven cis-trans isomerization of retinal drives vectoral proton transfer across the membrane [50-55]. Significantly, it has been demonstrated that a functional PR could be expressed in a respiration-impaired mutant of *E. coli* when supplemented with exogenous all-trans retinal [56]. More recently, hydrogen production was shown to increase nearly two-fold in PR-expressing *E. coli* when cells were exposed to increasing light intensities (70 to 130 μE), indicating that PR can efficiently absorb light even at low intensities [57]. To the best of our knowledge, retinal complementation of other rhodopsins has not been reported. Significantly, PR-expressing *E. coli* respiratory mutants generated sufficient proton-motive force to support ATP synthesis levels, leading to enhanced cell viability and motility when transgenics were exposed to sunlight as the only energy source.

These results suggest that targeting PR to the thylakoid membrane using appropriate targeting sequences (e.g., nuclear-encoded, N-terminal, light harvesting complex signal sequences) and supplementation with exogenous retinal or retinal derived from β-carotene cleavage) could drive additional ATP synthesis. One concern is that the optical cross section of retinal is small and light harvesting by PR is not supplemented by antenna complexes. This constraint may be overcome in part by overexpressing PR in thylakoids. Regardless, the additional proton gradient necessary to support HLA3 activity is substantially less than that required to support overall CO_2 fixation. The best achievable PR expression levels will be determined empirically using different gene promoters, e.g., psaD (SEQ ID NO:10), rbcs (SEQ ID NO:11), and cab1 (SEQ ID NO:7), to drive its expression.

Generation of Improved PR and its Functional Reconstitution in Chloroplasts

PR (AF279106), for example (SEQ ID NO:98), will be introduced into *Arabidopsis*, Camelina, and potato by Ti plasmid transformation and targeted to the thylakoid membrane using the DNAJ transit peptide (At5g21430, SEQ ID NO: 22) or psbX stop-transfer trans-membrane domain (At2g06520 SEQ ID NO:23) fused to the C-terminus of PR [58], or transit peptides from nuclear encoded chloroplast proteins such as CAB (SEQ ID NO:13), PGR5 (SEQ ID NO:14), and psaD (SEQ ID NO:15). Reconstitution with exogenous retinal will be carried out in a manner similar to strategies described for *E. coli*, except that retinal will be painted on the surface of the leaf [56] to demonstrate proof of concept. Retinal reconstitution will be followed by monitoring the absorption of the thylakoid membranes at 540 nm [59].

If exogenously applied retinal is not incorporated into PR, we will express low levels of a plant codon-optimized β-carotene monooxygenase for example (SEQ ID NO:100) in plastids to cleave a small fraction of β-carotene to generate retinal. Non-limiting examples of β-carotene monooxygenases that can be used include, for example, mouse, human, zebra fish, and rat enzymes (Accession Nos. AW044715, AK001592, AJ290390, and NM_053648, respectively). Alternatively, if β-carotene levels are severely depleted, we will transiently express β-carotene monooxygenase under the control of a transient inducible promoter such as an ethanol inducible gene promoter. This is available as an EcoRl/Pstl fragment from Syngenta-Construct: pJL67-5S::AlcR/AlcA::GUS in pMLBART (Weigel World, Max Planck Institute for Developmental Biology, Tubingen, Germany) for periods of time sufficient to fully saturate PR [60,61]. Operation of a functional retinal photocycle in PR will be confirmed by transient absorption spectroscopy [62].

Alternatively, promoters such as the green tissue/leaf-specific promoters such as the CAB (At3g54890 SEQ ID NO:7) and rbcS (At5g38420 SEQ ID NO:11) promoters can be used, for example see SEQ ID NO:5 for the BCA protein with a rbc-1a transit peptide. As the skilled person will be well aware, various promoters may be used to promote the transcription of the nucleic acid of the invention, i.e. the nucleic acid which when transcribed yields an RNA molecule that modulates the expression and/or activity of a protein according to the invention. Such promoters include for example constitutive promoters, inducible promoters (e.g. light inducible promoters, stress-inducible promoters, drought-inducible promoters, hormone-inducible promoters, chemical-inducible promoters, etc.), tissue-specific promoters, developmentally regulated promoters and the like.

Thus, a plant expressible promoter can be a constitutive promoter, i.e. a promoter capable of directing high levels of expression in most cell types (in a spatio-temporal independent manner). Examples of plant expressible constitutive promoters include promoters of bacterial origin, such as the octopine synthase (OCS) and nopaline synthase (NOS) promoters from *Agrobacterium*, but also promoters of viral origin, such as that of the cauliflower mosaic virus (CaMV) 35S transcript (Hapster et al., 1988, Mol. Gen. Genet. 212: 182-190) or 19S RNAs genes (Odell et al., 1985, Nature. 6; 313(6005):810-2; U.S. Pat. No. 5,352,605; WO 84/02913; Benfey et al., 1989, EMBO J. 8:2195-2202), the enhanced 2×35S promoter (Kay at al., 1987, Science 236:1299-1302; Datla et al. (1993), Plant Sci 94:139-149) promoters of the cassava vein mosaic virus (CsVMV; WO 97/48819, U.S. Pat. No. 7,053,205), 2×CsVMV (WO2004/053135) the circovirus (AU 689 311) promoter, the sugarcane bacilliform badnavirus (ScBV) promoter (Samac et al., 2004, Transgenic Res. 13(4):349-61), the figwort mosaic virus (FMV) promoter (Sanger et al., 1990, Plant Mol Biol. 14(3):433-43), the subterranean clover virus promoter No 4 or No 7 (WO 96/06932) and the enhanced 35S promoter as described in U.S. Pat. Nos. 5,164,316, 5,196,525, 5,322,938, 5,359,142 and 5,424,200. Among the promoters of plant origin, mention will be made of the promoters of the promoter of the *Arabidopsis thaliana* histone H4 gene (Chabouté et al., 1987), the ubiquitin promoters (Holtorf et al., 1995, Plant Mol. Biol. 29:637-649, U.S. Pat. No. 5,510,474) of Maize, Rice and sugarcane, the Rice actin 1 promoter (Act-1, U.S. Pat. No. 5,641,876), the histone promoters as described in EP 0 507 698 A1, the Maize alcohol dehydrogenase 1 promoter (Adh-1) (from the world wide web at patentlens.net/daisy/promoters/242.html)).

A variety of plant gene promoters that regulate gene expression in response to environmental, hormonal, chemical, developmental signals, and in a tissue-active manner can be used for expression of a sequence in plants. Choice of a promoter is based largely on the phenotype of interest and is determined by such factors as tissue (e.g., seed, fruit, root, pollen, vascular tissue, flower, carpel, etc.), inducibility (e.g., in response to heat, cold, drought, light etc.), timing, developmental stage, and the like.

Promoters that can be used to practice this invention include those that are green tissue specific such as the promoter of light harvesting complex protein 2 (Sakamoto et al. Plant Cell Physiology, 1991, 32(3): 385-393) or the promoter of the cytosolic fructose-1, 6-bisphosphatase from rice (Si et al. Acta Botanica Sinica 45: 3(2003): 359-364). Alternative embodiments include light inducible promoters such as promoters of the plant ribulose-biscarboxylase/oxygenase (Rubisco) small subunit promoter (U.S. Pat. No. 4,962,028; WO99/25842) from *Zea mays* and sunflower. Also the small subunit promoter from *Chrysanthemum* may be used, combined or not combined with the use of the respective terminator (Outchkourov et al., Planta, 216: 1003-1012, 2003).

Additional promoters that can be used to practice this invention are those that elicit expression in response to stresses, such as the RD29 promoters that are activated in response to drought, low temperature, salt stress, or exposure to ABA (Yamaguchi-Shinozaki et al., 2004, Plant Cell, Vol. 6, 251-264; WO12/101118), but also promoters that are induced in response to heat (e.g., see Ainley et al. (1993) Plant Mol. Biol. 22: 13-23), light (e.g., the pea rbcS-3A promoter, Kuhlemeier et al. (1989) Plant Cell 1: 471-478, and the maize rbcS promoter, Schaffher and Sheen (1991) Plant Cell 3: 997-1012); wounding (e.g., wunl, Siebertz et al. (1989) Plant Cell 1: 961-968); pathogens (such as the PR-I promoter described in Buchel et al. (1999) Plant Mol. Biol. 40: 387-396, and the PDF 1.2 promoter described in Manners et al. (1998) Plant Mol. Biol. 38: 1071-1080), and chemicals such as methyl jasmonate or salicylic acid (e.g., see Gatz (1997) Annu. Rev. Plant Physiol. Plant Mol. Biol. 48: 89-108). In addition, the timing of the expression can be controlled by using promoters such as those acting at senescence (e.g., see Gan and Amasino (1995) Science 270: 1986-1988); or late seed development (e.g., see Odell et al. (1994) Plant Physiol. 106: 447-458).

Use may also be made of salt-inducible promoters such as the salt-inducible NHX1 promoter of rice landrace Pokkali (PKN) (Jahan et al., 6th International Rice Genetics symposium, 2009, poster abstract P4-37), the salt inducible promoter of the vacuolar H+-pyrophosphatase from *Thellungiella halophila* (TsVP1) (Sun et al., BMC Plant Biology 2010, 10:90), the salt-inducible promoter of the *Citrus sinensis* gene encoding phospholipid hydroperoxide isoform gpx1 (Avsian-Kretchmer et al., Plant Physiology July 2004 vol. 135, p 1685-1696).

In alternative embodiments, tissue-specific and/or developmental stage-specific promoters are used, e.g., promoter that can promote transcription only within a certain time frame of developmental stage within that tissue. See, e.g., Blazquez (1998) Plant Cell 10:791-800, characterizing the *Arabidopsis* LEAFY gene promoter. See also Cardon (1997) Plant J 12:367-77, describing the transcription factor SPL3, which recognizes a conserved sequence motif in the promoter region of the *A. thaliana* floral meristem identity gene API; and Mandel (1995) Plant Molecular Biology, Vol. 29, pp 995-1004, describing the meristem promoter eIF4. Tissue specific promoters which are active throughout the life cycle of a particular tissue can be used. Other promoters that can be used to express the nucleic acids of the invention include, a leaf-specific promoter (see, e.g., Busk (1997) Plant J. 11:1285 1295, describing a leaf-specific promoter in maize); a tomato promoter active during fruit ripening, senescence and abscission of leaves, a guard-cell preferential promoter e.g. as described in PCT/EP12/065608, and, to a lesser extent, of flowers can be used (see, e.g., Blume (1997) Plant J. 12:731 746); the Blec4 gene from pea, which is active in epidermal tissue of vegetative and floral shoot apices of transgenic alfalfa making it a useful tool to target the expression of foreign genes to the epidermal layer of actively growing shoots or fibers; the ovule-specific BELI gene (see, e.g., Reiser (1995) Cell 83:735-742, GenBank No. U39944); and/or, the promoter in Klee, U.S. Pat. No. 5,589,583, describing a plant promoter region is capable of conferring high levels of transcription in meristematic tissue and/or rapidly dividing cells. Further tissue specific promoters that may be used according to the invention include, promoters active in vascular tissue (e.g., see Ringli and Keller (1998) Plant Mol. Biol. 37: 977-988), carpels (e.g., see Ohl et al. (1990) Plant Cell 2. In alternative embodiments, plant promoters which are inducible upon exposure to plant hormones, such as auxins, are used to express the nucleic acids used to practice the invention. For example, the invention can use the auxin-response elements EI promoter fragment (AuxREs) in the soybean {*Glycine max* L.) (Liu (1997) Plant Physiol. 115:397-407); the auxin-responsive *Arabidopsis* GST6 promoter (also responsive to salicylic acid and hydrogen peroxide) (Chen (1996) Plant J. 10: 955-966); the auxin-inducible parC promoter from tobacco (Sakai (1996) 37:906-913); a plant biotin response element (Streit (1997) Mol. Plant Microbe Interact. 10:933-937); and, the promoter responsive to the stress hormone abscisic acid (ABA) (Sheen (1996) Science 274:1900-1902). Further hormone inducible promoters that may be used include auxin-inducible promoters (such as that described in van der Kop et al. (1999) Plant Mol. Biol. 39: 979-990 or Baumann et al., (1999) Plant Cell 11: 323-334), cytokinin-inducible promoter (e.g., see Guevara-Garcia (1998) Plant Mol. Biol. 38: 743-753), promoters responsive to gibberellin (e.g., see Shi et al. (1998) Plant Mol. Biol. 38: 1053-1060, Willmott et al. (1998) Plant Molec. Biol. 38: 817-825) and the like.

In alternative embodiments, nucleic acids used to practice the invention can also be operably linked to plant promoters which are inducible upon exposure to chemicals reagents which can be applied to the plant, such as herbicides or antibiotics. For example, the maize In2-2 promoter, activated by benzenesulfonamide herbicide safeners, can be used (De Veylder (1997) Plant Cell Physiol. 38:568-577); application of different herbicide safeners induces distinct gene expression patterns, including expression in the root, hydathodes, and the shoot apical meristem. Coding sequence can be under the control of, e.g., a tetracycline-inducible promoter, e.g., as described with transgenic tobacco plants containing the *Avena sativa* L. (oat) arginine decarboxylase gene (Masgrau (1997) Plant J. 11:465-473); or, a salicylic acid-responsive element (Stange (1997) Plant J. 11:1315-1324). Using chemically- {e.g., hormone- or pesticide) induced promoters, i.e., promoter responsive to a chemical which can be applied to the transgenic plant in the field, expression of a polypeptide of the invention can be induced at a particular stage of development of the plant. Use may also be made of the estrogen-inducible expression system as described in U.S. Pat. No. 6,784,340 and Zuo et al. (2000, Plant J. 24: 265-273) to drive the expression of the nucleic acids used to practice the invention.

In alternative embodiments, a promoter may be used whose host range is limited to target plant species, such as corn, rice, barley, wheat, potato or other crops, inducible at any stage of development of the crop.

In alternative embodiments, a tissue-specific plant promoter may drive expression of operably linked sequences in tissues other than the target tissue. In alternative embodiments, a tissue-specific promoter that drives expression preferentially in the target tissue or cell type, but may also lead to some expression in other tissues as well, is used.

According to the invention, use may also be made, in combination with the promoter, of other regulatory sequences, which are located between the promoter and the coding sequence, such as transcription activators ("enhancers"), for instance the translation activator of the tobacco mosaic virus (TMV) described in Application WO 87/07644, or of the tobacco etch virus (TEV) described by Carrington & Freed 1990, J. Virol. 64: 1590-1597, for example.

Other regulatory sequences that enhance the expression of the nucleic acid of the invention may also be located within the chimeric gene. One example of such regulatory sequences is introns. Introns are intervening sequences present in the pre-mRNA but absent in the mature RNA following excision by a precise splicing mechanism. The ability of natural introns to enhance gene expression, a process referred to as intron-mediated enhancement (IME), has been known in various organisms, including mammals, insects, nematodes and plants (WO 07/098042, p 11-12). IME is generally described as a posttranscriptional mechanism leading to increased gene expression by stabilization of the transcript. The intron is required to be positioned between the promoter and the coding sequence in the normal orientation. However, some introns have also been described to affect translation, to function as promoters or as position and orientation independent transcriptional enhancers (Chaubet-Gigot et al., 2001, Plant Mol Biol. 45(1):17-30, p 27-28).

Examples of genes containing such introns include the 5' introns from the rice actin 1 gene (see U.S. Pat. No. 5,641,876), the rice actin 2 gene, the maize sucrose synthase gene (Clancy and Hannah, 2002, Plant Physiol. 130(2):918-

29), the maize alcohol dehydrogenase-1 (Adh-1) and Bronze-1 genes (Callis et al. 1987 Genes Dev. 1(10):1183-200; Mascarenhas et al. 1990, Plant Mol Biol. 15(6):913-20), the maize heat shock protein 70 gene (see U.S. Pat. No. 5,593,874), the maize shrunken 1 gene, the light sensitive 1 gene of *Solanum tuberosum*, and the heat shock protein 70 gene of *Petunia hybrida* (see U.S. Pat. No. 5,659,122), the replacement histone H3 gene from alfalfa (Keleman et al. 2002 Transgenic Res. 11(1):69-72) and either replacement histone H3 (histone H3.3-like) gene of *Arabidopsis thaliana* (Chaubet-Gigot et al., 2001, Plant Mol Biol. 45(1):17-30).

Other suitable regulatory sequences include 5' UTRs. As used herein, a 5' UTR, also referred to as a leader sequence, is a particular region of a messenger RNA (mRNA) located between the transcription start site and the start codon of the coding region. It is involved in mRNA stability and translation efficiency. For example, the 5' untranslated leader of a petunia chlorophyll a/b binding protein gene downstream of the 35S transcription start site can be utilized to augment steady-state levels of reporter gene expression (Harpster et al., 1988, Mol Gen Genet. 212(1):182-90). WO95/006742 describes the use of 5' non-translated leader sequences derived from genes coding for heat shock proteins to increase transgene expression.

The chimeric gene may also comprise a 3' end region, i.e. a transcription termination or polyadenylation sequence, operable in plant cells. As a transcription termination or polyadenylation sequence, use may be made of any corresponding sequence of bacterial origin, such as for example the nos terminator of *Agrobacterium tumefaciens*, of viral origin, such as for example the CaMV 35S terminator, or of plant origin, such as for example a histone terminator as described in published Patent Application EP 0 633 317 A1. The polyadenylation region can be derived from the natural gene, from a variety of other plant genes, or from T-DNA. The 3' end sequence to be added may be derived from, for example, the nopaline synthase or octopine synthase genes, or alternatively from another plant gene, or less preferably from any other eukaryotic gene.

The expression and targeting of proteorhodopsin to the thylakoid membranes will take advantage of the green energy spectrum that is inaccessible to chlorophyll. An increase in the amount of ATP is expected under photosynthesis conditions, from proton gradient generated both by the photosystems and the proteorhodopsin pump. Under conditions of inhibition of electron transfer through the photosystems, we should be able to observe a steady rate of ATP synthesis well above the basal rate through the activity of the proteorhodopsin proton pump.

Under normal pH conditions, protons are pumped into the bacterial periplasmic space by PR [50]. The photo-driven retinal cycle begins with photoisomerization of all trans-retinal to 13-cis retinal. The resulting conformational change poises the system for transfer of a proton from the Schiff base (SB; pKa~11) to the counter ion, Asp 97 (pKa~7.5). The proton is transferred to the lumen via a proton-conducting channel, and the SB is reprotonated from the cytoplasm. The mechanism of proton release in PR is not as well understood as in bacteriorhodopsin (BR); however, the main events of the photocycle are expected to be similar to those of BR. One potential challenge for pumping protons by PR in thylakoid membranes is the pH gradient-dependent reversibility of proton transfer by PR. At periplasmic pHs, <5.5, proton flow in PR is reversed, potentially depleting the proton gradient and impairing ATP synthesis. Thus, at the lumenal pH of thylakoids (4.5), reversed proton transduction via PR is possible. One of the critical residues involved in reversible proton flow is Asp97, which acts as the proton acceptor from retinal. The pKa of Asp97 in PR is ~7.5, while the pKa of its counterpart in BR is ~2.5. Due to the extremely low pKa of the counter ion, BR is able to retain its forward pumping activity at pHs as low as 3.5. The ability of PR to act as a proton pump in the thylakoid membrane thus entails maintaining the pumping efficiency at low pH conditions prevailing in the lumen. We propose that vectoral pumping of protons into the thylakoid lumen can be achieved by lowering the pKa of Asp97 and/or by protecting the SB from the lumenal pH through rational, site-specific mutagenesis. The electrostatic environment around the SB in PR is presumably maintained by the counter ions, Asp97, Asp227 (analogous to BR Asp212), Arg94 (analogous to BR Arg82) and His75. In BR, the low pKa of Asp85 is attributed to its strong hydrogen bonding interactions with Thr89 and Arg82 [53,54]. Since, interactions that reduce the pKa of Asp97 will promote proton-pumping activity at low external pH, mutation of Met79 to a residue that can hydrogen bond to His75 and Asp212, like Tyr or Thr, will be explored. These mutations are proposed by overlaying the structures of BR and PR, and identifying residues which are in a position to effect the desired behavior. Finally, the ability of a modified PR to work as an efficient H+ pump at acidic pHs will also entail shielding the SB from the extracellular environment. To this end, a L219E/T206S mutant will be generated, wherein E219 and S206 will form a Glu-Ser gate regulating vectoral proton transfer as occurs in BR.

To determine if any transgenes alter CET or ATP synthesis activity, we will compare the dark reduction kinetics of the photosystem I primary donor, P700+ in VVT and transgenic plants, with and without dibromothymoquinone (DBMIB), an inhibitor of Cytb6f-mediated CET. Dark P700+ reduction kinetics are expected to be faster in plants with more active CET. In addition, we will assess the amplitude of the After Glow (AG) thermoluminescence band (−40° C.) associated with CET activity [11,14,16,43,63]. Pool sizes of ATP will also be assessed in VVT and transgenic plants by mass spectroscopy.

Referring now to FIG. **11**, additional transgenic Camelina lines were produced that expressed the BCA gene (SEQ ID NO:4) in the chloroplast stroma. These lines were produced using the *Agrobacterium*-mediated transformation procedures as described previously. Three lines were evaluated for their ability to accumulate biomass and provide improved photosynthetic rates. Wildtype Camelina and the BCA mutant lines were not significantly different at lower light levels (0-400 umol/m^2/s) in their ability to assimilate carbon dioxide. However, as light intensity increased the BCA transformants showed between 10 and 30% higher accumulation of CO_2 at 2000 μmoles/m^2/s than wildtype. The BCA line 9.2 was the highest while lines BCA 4.1 and BCA 5.7 were both about 10% higher than wildtype. This improved ability to assimilate CO_2 was reflected in two of the lines (BCA-5.7 and BCA-9.2) into increased biomass accumulation, with these lines having about 15% greater biomass accumulation than wildtype. The BCA-4.1 line did not show improved biomass accumulation compared to control.

Referring now to FIG. **12**, the ability of the chloroplast enveloped localized bicarbonate transporter bicarbonate transporter (LCIA) protein to transport bicarbonate and improve the capture of inorganic carbon by transgenic Camelina was determined following the method of Farquhar and colleagues (1989). LCIA transgenic Camelina were produced using the *Agrobacterium*-mediated transformation processed described previously. A LCIA expressing mutant line (CAM-LCIA) was compared to wildtype Camelina

(Cam-WT) for the observed discrimination of the stable isotope ^{13}C. This carbon isotope discrimination is expressed as the difference between the ^{13}C in the air and in a plant which has been previously exposed to $^{13}CO_2$, the carbon isotope discrimination is symbolized by A and expressed in parts per million (ppm) and is described by Farquhar and colleagues (1989). In the LCIA transgenic lines, the observed discrimination by the plant was 20% less than that observed in the wildtype. This indicates that the insertion of LCIA provides the plant the ability to better accumulate and retain inorganic carbon than the wildtype plant and shows decreased "leakiness" vs wildtype. Reference for ^{13}C discrimination: Carbon isotope discrimination and photosynthesis, G. D. Farquhar, J. R. Ehlieringer and K. T. Hubick. *Annu. Rev. Plant Physiol. Plant Mol. Biol.* 1989, 40, 503-537.

TABLE D1

Isoenzyme	Kcat (s−1)	Km (mM)	Kcat/ Km ($M^{-1}s^{-1}$)	Ki (nM)	Subcellular localization	Tissue I organ localization
hCAI	2×10^5	4.0	5.0×10^7	250	cytosol	E, GI
hCAII	1.4×10^{6o}	9.3	1.5×10^8	12	cytosol	E, eye, GI, BO, K, L, T, B
hCAIII	1.0×10^4	33.3	3.0×10^5	2×10^5	cytosol	SM, A
hCAIV	1.0×10^6	21.5	5.1×10^7	74	membrane	K, L, P, B, C, H
hCAVA	2.9×10^5	10.0	2.9×10^7	63	mitochondria	Li
hCAVB	9.5×10^5	9.7	9.8×10^7	54	mitochondria	H, SM, P, K, SC, GI
hCAVI	3.4×10^5	6.9	4.9×10^7	11	secreted	G
hCAVII	9.5×10^5	11.4	8.3×10^1	2.5	cytosol	CNS
hCAVIII					cytosol	CNS
hCAIX	3.8×10^5	6.9	5.5×10^7	25	transmembrane	TU, GI
hCAX					cytosol	CNS
hCAXI					cytosol	CNS
hCAXII	4.2×10^5	12.0	3.5×10^7	5.7	transmembrane	R, I, RE, eye, TU
hCAXIII	1.5×10^5	13.8	1.1×10^7	16	cytosol	K, B, L, GI, RE
hCAXIV	3.1×10^5	7.9	3.9×10^7	41	transmembrane	K, B, L
hCAXV	4.7×10^5	14.2	3.3×10^7	72	membrane	K

H = Human;
M = Mouse;
hCAVIII, X, and XI are devoid of catalytic activity.
E = Erthrocyes;
GI = GI tract;
BO = Bone osteoclasts;
K = kidney,
L = Lung;
T = testis;
B = brain;
SM = skeletal muscle;
A = Adipocytes;
P = pancreas;
C = colon;
H = heart;
Li = liver;
SC = spinal cord;
G = salivary and mammary gland;
R = renal;
I = intestinal;
TU = tumors,
RE = Reproductive

TABLE D2

Exemplary Type II Carbonic Anhydrases

Organism	Sequence	Accession Number	SEQ. ID. NO
Human	MSHHWGYGKH NGPEHWHKDF PIAKGERQSP VDIDTHTAKY DPSLKPLSVS YDQATSLRIL NNGHAFNVEF DDSQDKAVLK GGPLDGTYRL IQFHFHWGSL DGQGSEHTVD KKKYAAELHL VHWNTKYGDF GKAVQQPDGL AVLGIFLKVG SAKPGLQKVV DVLDSIKTKG KSADFTNFDP RGLLPESLDY WTYPGSLTTP PLLECVTWIV LKEPISVSSE QVLKFRKLNF NGEGEPEELM VDNWRPAQPL KNRQIKASFK	NP-000058.1	SEQ. ID. NO. 19
Macaca fascicularis (crab-eating macaque)	MSHHWGYGKH NGPEHWHKDF PIAKGQRQSP VDIDTHTAKY DPSLKPLSVS YDQATSLRIL NNGHSFNVEF DDSQDKAVIK GGPLDGTYRL IQFHFHWGSL DGQGSEHTVD KKKYAAELHL VHWNTKYGDF GKAVQQPDGL AVLGIFLKVG SAKPGLQKVV DVLDSIKTKG KSADFTNFDP RGLLPESLDY WTYPGSLTTP PLLECVTWIV LKEPISVSSE QMSKFRKLNF NGEGEPEELM VDNWRPAQPL KNRQIKASFK	BAE91302.1	SEQ. ID. NO. 24

TABLE D2-continued

Exemplary Type II Carbonic Anhydrases

Organism	Sequence	Accession Number	SEQ. ID. NO
Pan troglodytes	MSHHWGYGKH NGPEHWHKDF PIAKGERQSP VDIDTHTAKY DPSLKPLSVS YGQATSLRIL NNGHAFNVEF DDSQDKAVLK GGPLDGTYRL IQFHFHWGSL DGQGSEHTVD KKKYAAELHL VHWNTKYGDF GKAVQQPDGL AVLGIFLKVG SAKPGLQKVV DVLDSIKTKG KSADFTNFDP HGLLPESLDY WTYPGSLTTP PLLECVTWIV LKEPISVSSE QMLKFRKLNF NGEGEPEELM VDNWRPAQPL KNRQIKASFK	NP_001181853	SEQ. ID. NO. 25
Macaca mulatta	MSHHWGYGKH NGPEHWHKDF PIAKGQRQSP VDINTHTAKY DPSLKPLSVS YDQATSLRIL NNGHSFNVEF DDSQDKAVIK GGPLDGTYRL IQFHFHWGSL DGQGSEHTVD KKKYAAELHL VHWNTKYGDF GKAVQQPDGL AVLGIFLKVG SAKPGLQKVV DVLDSIKTKG KSADFTNFDP RGLLPESLDY WTYPGSLTTP PLLECVTWIV LKEPISVSSE QMSKFRKLNF NGEGEPEELM VDNWRPAQPL KNRQIKASFK	NP_001182346	SEQ. ID. NO. 26
Pongo abelii	MSHHWGYGKH NGPEHWHKDF PIAKGERQSP VDIDTHTAKY DPSLKPLSVC YDQATSLRIL NNGHSFNVEF DDSQDKAVLK GGPLDGTYRL IQFHFHWGSL DGQGSEHTVD KKKYAAELHL VHWNTKYGDF GKAVQQPDGL AVLGIFLKVG SAKPGLQKVV DVLDSIKTKG KCADFTNFDP RGLLPASLDY WTYPGSLTTP PLLECVTWIV LKEPISVSSE QMLKFRKLNF NGEGEPEELM VDNWRPAQPL KKRQIKASFK	XP_002819286	SEQ. ID. NO. 27
Callithrix jacchus	MSHHWGYGKH NGPEHWHKDF PIAKGERQSP VDIDTHTAKY DPSLKPLSVS YDQATSWRIL NNGHSFNVEF DDSQDKAVLK GGPLDGTYRL IQFHFHWGST DGQGSEHTVD KKKYAAELHL VHWNTKYGDF GKAAQQPDGL AVLGIFLKVG SAKPGLQKVV DVLDSIKTKG KSADFTNFDP RGLLPESLDY WTYPGSLTTP PLLESVTWIV LKEPISVSSE QILKFRKLNF SGEGEPEELM VDNWRPAQPL KNRQIKASFK	XP_002759086	SEQ. ID. NO. 28
Lemur catta	MSHHWGYGKH NGPEHWHKDF PIAKGERQSP VDINTGAAKH DPSLKPLSVY YEQATSRRIL NNGHSFNVEF DDSQDKAVLK GGPLDGTYRL IQFHFHWGSL DGQGSEHTVD KKKYAAELHL VHWNTKYGDF GKAVQQPDGL AVLGIFLKVG SAKPGLQKVV DVLDSIKTKG KSADFTNFDP RGLLPESLDY WTYLGSLTTP PLLECVTWIV LKEPISVSSE QMMKFRKLSF SGEGEPEELM VDNWRPAQPL KNRQIKASFK	ADD83028	SEQ. ID. NO. 29
Ailuropoda melanoleuca	MAHHWGYGKH NGPEHWYKDF PIAKGQRQSP VDIDTKAAIH DPALKALCPT YEQAVSQRVI NNGHSFNVEF DDSQDNAVLK GGPLTGTYRL IQFHFHWGSS DGQGSEHTVD KKKYAAELHL VHWNTKYGDF GKAVQQPDGL AVLGIFLKIG DARPGLQKVL DALDSIKTKG KSADFTNFDP RGLLPESLDY WTYPGSLTTP PLLECVTWIV LKEPISVSSE QMLKFRRLNF NKEGEPEELM VDNWRPAQPL HNRQINASFK	XP_002916939	SEQ. ID. NO. 30
Eguus caballus	MSHHWGYGQH NGPKHWHKDF PIAKGQRQSP VDIDTKAAVH DAALKPLAVH YEQATSRRIV NNGHSFNVEF DDSQDKAVLQ GGPLTGTYRL IQFHFHWGSS DGQGSEHTVD KKKYAAELHL VHWNTKYGDF GKAVQQPDGL AVVGVFLKVG GAKPGLQKVL DVLDSIKTKG KSADFTNFDP RGLLPESLDY WTYPGSLTTP PLLECVTWIV LREPISVSSE QLLKFRSLNF NAEGKPEDPM VDNWRPAQPL NSRQIRASFK	XP_001488540	SEQ. ID. NO. 31
Canis lupus familiaris	MAHHWGYAKH NGPEHWHKDF PIAKGERQSP VDIDTKAAVH DPALKSLCPC YDQAVSQRII NNGHSFNVEF DDSQDKTVLK GGPLTGTYRL IQFHFHWGSS DGQGSEHTVD KKKYAAELHL VHWNTKYGEF GKAVQQPDGL AVLGIFLKIG GANPGLQKIL DALDSIKTKG KSADFTNFDP RGLLPESLDY WTYPGSLTTP PLLECVTWIV LKEPISVSSE QMLKFRKLNF NKEGEPEELM MDNWRPAQPL HSRQINASFK	NP_001138642	SEQ. ID. NO. 32
Oryctolagus cuniculus	MSHHWGYGKH NGPEHWHKDF PIANGERQSP IDIDTNAAKH DPSLKPLRVC YEHPISRRII NNGHSFNVEF DDSHDKTVLK EGPLEGTYRL IQFHFHWGSS DGQGSEHTVN KKKYAAELHL VHWNTKYGDF GKAVKHPDGL AVLGIFLKIG SATPGLQKVV DTLSSIKTKG KSVDFTDFDP RGLLPESLDY WTYPGSLTTP PLLECVTWIV LKEPITVSSE QMLKFRNLNF NKEAEPEEPM VDNWRPTQPL KGRQVKASFV	NP_001182637	SEQ. ID. NO. 33
Ailuropoda melanoleuca	GPEHWYKDFP IAKGQRQSPV DIDTKAAIHD PALKALCPTY EQAVSQRVIN NGHSFNVEFD DSQDNAVLKG GPLTGTYRLI QFHFHWGSSD GQGSEHTVDK KKYAAELHLV HWNTKYGDFG	EFB24165	SEQ. ID. NO. 34

TABLE D2-continued

Exemplary Type II Carbonic Anhydrases

Organism	Sequence	Accession Number	SEQ. ID. NO
	KAVQQPDGLA VLGIFLKIGD ARPGLQKVLD ALDSIKTKGK SADFTNFDPR GLLPESLDYW TYPGSLTTPP LLECVTWIVL KEPISVSSEQ MLKFRRLNFN KEGEPEELMV DNWRPAQPLH NRQINASFK		
Sus scrofa	MSHHWGYDKH NGPEHWHKDF PIAKGDRQSP VDINTSTAVH DPALKPLSLC YEQATSQRIV NNGHSFNVEF DSSQDKGVLE GGPLAGTYRL IQFHFHWGSS DGQGSEHTVD KKKYAAELHL VHWNTKYKDF GEAAQQPDGL AVLGVFLKIG NAQPGLQKIV DVLDSIKTKG KSVEFTGFDP RDLLPGSLDY WTYPGSLTTP PLLESVTWIV LREPISVSSG QMMKFRTLNF NKEGEPEHPM VDNWRPTQPL KNRQIRASFQ	XP_001927840.1	SEQ. ID. NO. 35
Callithrix jacchus	MSHHWGYGKH NGPEHWHKDF PIAKGERQSP VDIDTHTAKY DPSLKPLSVS YDQATSWRIL NNGHSFNVEF DDSQDKAVLK GGPLDGTYRL IQLHLVHWNT KYGDFGKAAQ QPDGLAVLGI FLKVGSAKPG LQKVVDVLDS IKTKGKSADF TNFDPRGLLP ESLDYWTYPG SLTTPPLLES VTWIVLKEPI SVSSEQILKF RKLNFSGEGE PEELMVDNWR PAQPLKNRQI KASFK	XP_002759087	SEQ. ID. NO. 36
Mus musculus	MSHHWGYSKH NGPENWHKDF PIANGDRQSP VDIDTATAQH DPALQPLLIS YDKAASKSIV NNGHSFNVEF DDSQDNAVLK GGPLSDSYRL IQFHFHWGSS DGQGSEHTVN KKKYAAELHL VHWNTKYGDF GKAVQQPDGL AVLGIFLKIG PASQGLQKVL EALHSIKTKG KRAAFANFDP CSLLPGNLDY WTYPGSLTTP PLLECVTWIV LREPITVSSE QMSHFRTLNF NEEGDAEEAM VDNWRPAQPL KNRKIKASFK	NP_033931	SEQ. ID. NO. 37
Bos taurus	MSHHWGYGKH NGPEHWHKDF PIANGERQSP VDIDTKAVVQ DPALKPLALV YGEATSRRMV NNGHSFNVEY DDSQDKAVLK DGPLTGTYRL VQFHFHWGSS DDQGSEHTVD RKKYAAELHL VHWNTKYGDF GTAAQQPDGL AVVGVFLKVG DANPALQKVL DALDSIKTKG KSTDFPNFDP GSLLPNVLDY WTYPGSLTTP PLLESVTWIV LKEPISVSSQ QMLKFRTLNF NAEGEPELLM LANWRPAQPL KNRQVRGFPK	NP_848667	SEQ. ID. NO. 38
Oryctolagus cuniculus	GKHNGPEHWH KDFPIANGER QSPIDIDTNA AKHDPSLKPL RVCYEHPISR RIINNGHSFN VEFDDSHDKT VLKEGPLEGT YRLIQFHFHW GSSDGQGSEH TVNKKKYAAE LHLVHWNTKY GDFGKAVKHP DGLAVLGIFL KIGSATPGLQ KVVDTLSSIK TKGKSVDFTD FDPRGLLPES LDYWTYPGSL TTPPLLECVT WIVLKEPITV SSEQMLKFRN LNFNKEAEPE EP	AAA80531	SEQ. ID. NO. 39
Rattus norvegicus	MSHHWGYSKS NGPENWHKEF PIANGDRQSP VDIDTGTAQH DPSLQPLLIC YDKVASKSIV NNGHSFNVEF DDSQDFAVLK EGPLSGSYRL IQFHFHWGSS DGQGSEHTVN KKKYAAELHL VHWNTKYGDF GKAVQHPDGL AVLGIFLKIG PASQGLQKIT EALHSIKTKG KRAAFANFDP CSLLPGNLDY WTYPGSLTTP PLLECVTWIV LKEPITVSSE QMSHFRKLNF NSEGRAEELM VDNWRPAQPL KNRKIKASFK	NP062164	SEQ. ID. NO. 40

TABLE D3

Exemplary Type VII Carbonic Anhydrases

Organism	Sequence	Accession Number	SEQ. ID. NO
Human	MSLSITNNGH SVQVDFNDSD DRTVVTGGPL EGPYRLKQFH FHWGKKHDVG SEHTVDGKSF PSELHLVHWN AKKYSTFGEA ASAPDGLAVV GVFLETGDEH PSMNRLTDAL YMVRFKGTKA QFSCFNPKCL LPASRHYWTY PGSLTTPPLS ESVTWIVLRE PICISERQMG KFRSLLFTSE DDERIHMVNN FRPPQPLKGR VVKASFRA		SEQ. ID. NO. 41
Pongo abelii	MTGHHGWGYG QDDGPSHWHK LYPIAQGDRQ SPINIISSQA VYSPSLQPLE LSYEACMSLS ITNNGHSVQV DFNDSDDRTV VTGGPLEGPY RLKQFHFHWG KKHDVGSEHT VDGKSFPSEL HLVHWNAKKY STFGEAASAP DGLAVVGVFL ETGDEHPSMN RLTDALYMVR FKGTKAQFSCFNPKSLLPAS RHYWTYPGSL TTPPLSESVT WIVLREPICI SERQMGKFRS LLFTSEDDER IHMVNNFRPP QPLKGRVVKA SFRA	XP_002826555	SEQ. ID. NO. 42

TABLE D3-continued

Exemplary Type VII Carbonic Anhydrases

Organism	Sequence	Accession Number	SEQ. ID. NO
Pan troglodytes	MEFGLSPELS PSRCFKRLLR GSERGRSRSP NERTEPTGQV HGCGDGSGMT GHHGWGYGQD DGPSHWHKLY PIAQGDRQSP INIISSQAVY SPSLQPLELS YEACMSLSIT NNGHSVQVDF NDSDDRTVVT GGPLEGPYRL KQFHFHWGKK HDVGSEHTVD GKSFPSELHL VHWNAKKYST FGEAASAPDG LAVVGVFLET GDEHPSMNRL TDALYMVRFK GTKAQFSCFN PKCLLPASRH YWTYPGSLTT PPLSESVTWI VLREPICISE RQMRKFRSLL FTSEDDERIH MVNNFRPPQP LKGRVVKASF RA	XP_001143159.1	SEQ. ID. NO. 43
Callithrix jacchus	MTGHHGWGYG QDDGPSHWHK LYPIAQGDRQ SPINIISSQA VYSPSLQPLE LSYEACMSLS ITNNGHSVQV DFNDSDDRTV VTGGPLEGPY RLKQFHFHWG KKHDVGSEHT VDGKSFPSEL HLVHWNAKKY STFGEAASAP DGLAVVGVFL ETGDEHPSMN RLTDALYMVR FKGTKAQFSC FNPKCLLPAS WHYWTYPGSL TTPPLSESVT WIVLREPICI SERQMGKFRS LLFTSEDDER VHMVNNFRPP QPLKGRVVKA SFRA	XP_002761099	SEQ. ID. NO. 44
Ailuropoda melanoleuca	GPSQWHKLYP IAQGDRQSPI NIVSSQAVYS PSLKPLELSY EACISLSIAN NGHSVQVDFN DSDDRTVVTG GPLDGPYRLK QFHFHWGKKH SVGSEHTVDG KSFPSELHLV HWNAKKYSTF GEAASAPDGL AVVGVFLETG DEHPSMNRLT DALYMVRFKG TKAQFSCFNP KCLLPASRHY WTYPGSLTTP PLSESVTWIV LREPISISER QMEKFRSLLF TSEDDERIHM VNNFRPPQPL KGRVVKASFR A	EFB15849	SEQ. ID.NO. 45
Canis familiaris	MTGHHCWGYG QNDEIQASLS PSLSTPAGPS QWHKLYPIAQ GDRQSPINIV SSQAVYSPSL KPLELSYEAC ISLSITNNGH SVQVDFNDSD DRTAVTGGPL DGPYRLKQLH FHWGKKHSVG SEHTVDGKSF PSELHLVHWN AKKYSTFGEA ASAPDGLAVV GIFLETGDEH PSMNRLTDAL YMVRFKGTKA QFSCFNPKCL LPASRHYWTY PGSLTTPPLS ESVTWIVLRE PISISERQME KFRSLLFTSE EDERIHMVNN FRPPQPLKGR VVKASFRA	XP_546892	SEQ. ID. NO. 46
Bos taurus	MTGHHGWGYG QNDGPSHWHK LYPIAQGDRQ SPINIVSSQA VYSPSLKPLE ISYESCTSLS IANNGHSVQV DFNDSDDRTV VSGGPLDGPY RLKQFHFHWG KKHGVGSEHT VDGKSFPSEL HLVHWNAKKY STFGEAASAP DGLAVVGVFL ETGDEHPSMN RLTDALYMVR FKGTKAQFSC FNPKCLLPAS RHYWTYPGSL TTPPLSESVT WIVLREPIRI SERQMEKFRS LLFTSEEDER IHMVNNFRPP QPLKGRVVKA SFRA	XP_002694851	SEQ. ID. NO. 47
Rattus norvegicus	MTVLWWPMLR EELMSKLRTG GPSNWHKLYP IAQGDRQSPI NIISSQAVYS PSLQPLELFY EACMSLSITN NGHSVQVDFN DSDDRTVVAG GPLEGPYRLK QLHFHWGKKR DVGSEHTVDG KSFPSELHLV HWNAKKYSTF GEAAAAPDGL AVVGIFLETG DEHPSMNRLT DALYMVRFKD TKAQFSCFNP KCLLPTSRHY WTYPGSLTTP PLSESVTWIV LREPIRISER QMEKFRSLLF TSEDDERIHM VNNFRPPQPL KGRVVKASFQ S	EDL87229	SEQ. ID. NO. 48
Oryctolagus cuniculus	MTGHHGWGYG QDDGGRPSHW HKLYPIAQGD RQSPINIVSS QAVYSPGLQP LELSYEACTS LSIANNGHSV QVDFNDSDDR TVVTGGPLEG PYRLKQFHFH WGKRRDAGSE HTVDGKSFPS ELHLVHWNAR KYSTFGEAAS APDGLAVVGV FLETGNEHPS MNRLTDALYM VRFKGTKAQF SCFNPKCLLP SSRHYWTYPG SLTTPPLSES VTWIVLREPI SISERQMEKF RSLLFTSEDD ERVHMVNNFR PPQPLRGRVV KASFRA	XP_002711604	SEQ. ID. NO. 49
Mus musculus	GQDDGPSNWH KLYPIAQGDR QSPINIISSQ AVYSPSLQPL ELFYEACMSL SITNNGHSVQ VDFNDSDDRT VVSGGPLEGP YRLKQLHFHW GKKRDMGSEH TVDGKSFPSE LHLVHWNAKK YSTFGEAAAA PDGLAVVGVF LETGDEHPSM NRLTDALYMV RFKDTKAQFS CFNPKCLLPT SRHYWTYPGS LTTPPLSESV TWIVLREPIR ISERQMEKFR SLLFTSEDDE RIHMVDNFRP PQPLKGRVVK ASFQA	AAG16230.1	SEQ. ID. NO. 50
Monodelphis domestic	MTGHHGWGYG QEDGPSEWHK LYPIAQGDRQ SPIDIVSSQA VYDPTLKPLV LAYESCMSLS IANNGHSVMV EFDDVDDRTV VNGGPLDGPY RLKQFHFHWG KKHSLGSEHT VDGKSFSSEL HLVHWNGKKY KTFAEAAAAP DGLAVVGIFL ETGDEHASMN RLTDALYMVR FKGTKAQFNS FNPKCLLPMN LSYWTYPGSL TTPPLSESVT WIVLKEPITI SEKQMEKFRS LLFTAEEDEK VRMVNNFRPP QPLKGRVVQA SFRS	XP_001364411.1	SEQ. ID. NO. 51
Gallus gallus	MTGHHSWGYG QDDGPAEWHK SYPIAQGNRQ SPIDIISAKA VYDPKLMPLV ISYESCTSLN ISNNGHSVMV EFEDIDDKTV	XP_414152.1	SEQ. ID. NO. 52

TABLE D3-continued

Exemplary Type VII Carbonic Anhydrases

Organism	Sequence	Accession Number	SEQ. ID. NO
	ISGGPFESPF RLKQFHFHWG AKHSEGSEHT IDGKPFPCEL HLVHWNAKKY ATFGEAAAAP DGLAVVGVFL EIGKEHANMN RLTDALYMVK FKGTKAQFRS FNPKCLLPLS LDYWTYLGSL TTPPLNESVI WVVLKEPISI SEKQLEKFRM LLFTSEEDQK VQMVNNFRPP QPLKGRTVRA SFKA		
Taeniopygia guttata	MTGQHSWGYG QADGPSEWHK AYPIAQGNRQ SPIDIDSARA VYDPSLQPLL ISYESCSSLS ISNTGHSVMV EFEDTDDRTA ISGGPFQNPF RLKQFHFHWG TTHSQGSEHT IDGKPFPCEL HLVHWNARKY TTFGEAAAAP DGLAVVGVFL EIGKEHASMN RLTDALYMVK FKGTKAQFRG FNPKCLLPLS LDYWTYLGSL TTPPLNESVT WIVLKEPIRI SVKQLEKFRM LLFTGEEDQR IQMANNFRPP QPLKGRIVRA SFKA	XP_002190292.1	SEQ. ID. NO. 53

TABLE D4

Exemplary Type XIII Carbonic Anhydrases

Organism	Sequence	Accession Number	SEQ. ID. NO
Human	MSRLSWGYRE HNGPIHWKEF FPIADGDQQS PIEIKTKEVK YDSSLRPLSI KYDPSSAKII SNSGHSFNVD FDDTENKSVL RGGPLTGSYR LRQVHLHWGS ADDHGSEHIV DGVSYAAELH VVHWNSDKYP SFVEAAHEPD GLAVLGVFLQ IGEPNSQLQK ITDTLDSIKE KGKQTRFTNF DLLSLLPPSW DYWTYPGSLT VPPLLESVTW IVLKQPINIS SQQLAKFRSL LCTAEGEAAA FLVSNHRPPQ PLKGRKVRAS FH	NP_940986.1	SEQ. ID. NO. 54
Pan troglodytes	MSRLSWGYRE HNGPIHWKEF FPIADGDQQS PIEIKTKEVK YDSSLRPLSI KYDPSSAKII SNSGHSFNVD FDDTENKSVL RGGPLTGSYR LRQFHLHWGS ADDHGSEHIV DGVSYAAELH VVHWNSDKYP SFVEAAHEPD GLAVLGVFLQ IGEPNSQLQK ITDTLDSIKE KGKQTRFTNF DPLSLLPPSW DYWTYPGSLT VPPLLESVTW IVLKQPINIS SQQLAKFRSL LCTAEGEAAA FLVSNHRPPQ PLKGRKVRAS FH	XP_001169377.1	SEQ. ID. NO. 55
Macaca mulatta	MSRLSWGYRE HNGPIHWKEF FPIADGDQQS PIEIKTQEVK YDSSLRPLSI KYDPSSAKII SNSGHSFNVD FDDTEDKSVL RGGPLAGSYR LRQFHLHWGS ADDHGSEHIV DGVSYAAELH VVHWNSDKYP SFVEAAHEPD GLAVLGVFLQ IGEPNSQLQK ITDILDSIKE KGKQTRFTNF DPLSLLPPSW DYWTYPGSLT VPPLLESVIW IVLKQPINVS SQQLAKFRSL LCTAEGEAAA FLLSNHRPPQ PLKGRKVRAS FR	XP_001095487.1	SEQ. ID. NO. 56
Oryctolagus cuniculus	MSRISWGYGE HNGPIHWNQF FPIADGDQQS PIEIKTKEVK YDSSLRPLSI KYDPSSAKII SNSGHSFNVD FDDTEDKSVL RGGPLTGNYR LRQFHLHWGS ADDHGSEHVV DGVRYAAELH VVHWNSDKYP SFVEAAHEPD GLAVLGVFLQ IGEYNSQLQK ITDILDSIKE KGKQTRFTNF DPLSLLPSSW DYWTYPGSLT VPPLLESVTW IVLKQPINIS SQQLAKFRSL LCSAEGESAA FLLSNHRPPQ PLKGRKVRAS FH	XP_002710714.1	SEQ. ID. NO. 57
Ailuropoda melanoleuca	MSRLSWGYGE HNGPIHWNKF FPIADGDQQS PIEIKTKEVK YDSSLRPLSI KYDANSAKII SNSGHSFSVD FDDTEDKSVL RGGPLTGSYR LRQFHLHWGS ADDHGSEHVV DGVRYAAELH VVHWNSDKYP SFVEAAHEPD GLAVLGVFLQ IGEHNSQLQK ITDILDSIKE KGKQTRFTNF DPLSLLPPSW DYWTYPGSLT VPPLLESVTW IVLKQPINIS SEQLATFRTL LCTAEGEAAA FLLSNHRPPQ PLKGRKVRAS FH	XP_002916937.1	SEQ. ID. NO. 58
Sus scrofa	MSRFSWGYGE HNGPVHWNEF FPIADGDQQS PIEIKTKEVK YDSSLRPLSI KYDPSSAKII SNSGHSFSVD FDDTEDKSVL RGGPLTGSYR LRQFHLHWGS ADDHGSEHVV DGVKYAAELH VVHWNSDKYP SFVEAAHEPD GLAVLGVFLQ IGEHNSQLQK ITDILDSIKE KGKQTRFTNF DPLSLLPPSW DYWTYPGSLT VPPLLESVTW IILKQPINIS SQQLATFRTL LCTKEGEEAA FLLSNHRPLQ PLKGRKVRAS FH	XP_001924497.1	SEQ. ID. NO. 59
Callithrix jacchus	MSRLSWGYGE HNGPIHWNEF FPIADGDRQS PIEIKAKEVK YDSSLRPLSI KYDPSSAKII SNSGHSFNVD FDDTEDKSVL HGGPLTGSYR LRQFHLHWGS ADDHGSEHVV DGVRYAAELH	XP_002759085.1	SEQ. ID. NO. 60

TABLE D4-continued

Exemplary Type XIII Carbonic Anhydrases

Organism	Sequence	Accession Number	SEQ. ID. NO
	VVHWNSEKYP SFVEAAHEPD GLAVLGVFLQ IGEPNSQLQK IIDILDSIKE KGKOIRFTNF DPLSLFPPSW DYWTYSGSLT VPPLLESVTW ILLKQPINIS SQQLAKFRSL LCTAEGEAAA FLLSNYRPPQ PLKGRKVRAS FR		
Rattus norvegicus	MARLSWGYDE HNGPIHWNEL FPIADGDQQS PIEIKTKEVK YDSSLRPLSI KYDPASAKII SNSGHSFNVD FDDTEDKSVL RGGPLTGSYR LRQFHLHWGS ADDHGSEHVV DGVRYAAELH VVHWNSDKYP SFVEAAHESD GLAVLGVFLQ IGEHNPQLQK ITDILDSIKE KGKQTRFTNF DPLCLLPSSW DYWTYPGSLT VPPLLESVTW IVLKQPISIS SQQLARFRSL LCTAEGESAA FLLSNHRPPQ PLKGRRVRAS FY	NP_001128465.1	SEQ. ID. NO. 61
Mus musculus	MARLSWGYGE HNGPIHWNEL FPIADGDQQS PIEIKTKEVK YDSSLRPLSI KYDPASAKIISNSGHSFNVD FDDTEDKSVL RGGPLTGNYR LRQFHLHWGS ADDHGSEHVV DGVRYAAELH VVHWNSDKYP SFVEAAHESD GLAVLGVFLQ IGEHNPQLQK ITDILDSIKE KGKQTRFTNFDPLCLLPSSW DYWTYPGSLT VPPLLESVTW IVLKQPISIS SQQLARFRSL LCTAEGESAA FLLSNHRPPQ PLKGRRVRAS FY	NP_078771.1	SEQ. ID. NO. 62
Canis familiaris	MPPRRHGPNT FLSAGTKGQQ NFWTKNQKSG PIHWNKFFPI ADGDQQSPIE IKTKEVKYDS SLRPLSIKYD ANSAKIISNS GHSFSVDFDD TEDKSVLRGG PLTGSYRLRQ FHLHWGSADD HGSEHVVDGV RYAAELHVVH WNSDKYPSFV EAAHEPDGLA VLGVFLQIGE HNSQLQKITD ILDSIKEKGK QTRFTNFDPL SLLPPSWDYW TYPGSLTVPP LLESVTWIVL KQPINISSQQ LATFRTLLCT AEGEAAAFLL SNHRPPQPLK GRKVRASFH	XP_544159	SEQ. ID. NO. 63
Eguus caballus	MSGPVHWNEF FPIADGDQQS PIEIKTKEVK YDSSLRPLTI KYDPSSAKII SNSGHSFSVG FDDTENKSVL RGGPLTGSYR LRQFHLHWGS ADDHGSEHVV DGVRYAAELH IVHWNSDKYP SFVEAAHEPD GLAVLGVFLQ VGEHNSQLQK ITDTLDSIKE KGKQTLFTNF DPLSLLPPSW DYWTYPGSLT VPPLLESVTW IILKQPINIS SQQLVKFRTL LCTAEGETAA FLLSNHRPPQ PLKGRKVRAS FR	XP_001489984.2	SEQ. ID. NO. 64
Bos taurus	MSGFSWGYGE RDGPVHWNEF FPIADGDQQS PIEIKTKEVR YDSSLRPLGI KYDASSAKII SNSGHSFNVD FDDTDDKSVL RGGPLTGSYR LRQFHLHWGS TDDHGSEHVV DGVRYAAELH VVHWNSDKYP SFVEAAHEPD GLAVLGIFLQ IGEHNPQLQK ITDILDSIKE KGKQTRFTNF DPVCLLPPCR DYWTYPGSLT VPPLLESVTW IILKQPINIS SQQLAAFRTL LCSREGETAA FLLSNHRPPQ PLKGRKVRAS FR	XP_002692875.1	SEQ. ID. NO. 65
Monodelphis domestica	MSRLSWGYCE HNGPVHWSEL FPIADGDYQS PIEINTKEVK YDSSLRPLSI KYDPASAKII SNSGHSFSVD FDDSEDKSVL RGGPLIGTYR LRQFHLHWGS TDDQGSEHTV DGMKYAAELH VVHWNSDKYP SFVEAAHEPD GLAVLGIFLQ TGEHNLQMQK ITDILDSIKE KGKQIRFTNF DPATLLPQSW DYWTYPGSLT VPPLLESVTW IVLKQPITIS SQQLAKFRSL LYTGEGEAAA FLLSNYRPPQ PLKGRKVRAS FR	XP_001366749.1	SEQ. ID. NO. 66

TABLE D4-continued

Exemplary Type XIII Carbonic Anhydrases			
Organism	Sequence	Accession Number	SEQ. ID. NO
Ornithorhynchus anatinus	MKKGVGSFYE LAVNRWSVVN RVQIMIVESI TEPLLCGSRA LALTLSPTQA LAVAPALALA VVQALALTVV QALALAVSPA LALSVAPALA LAVVQALALA VVQALALAVA QALALAVAQA LALAVAQALA LALPQALALT LPQALALTLS PTLALSVAPA LALAVAPALA LADSPALALA LARPHPSSGS SPALDCELVL FGDCHTVLLK WMRMGNYSSV SPLEERNSSC PLGPIHWNEL FPIADGDRQS PIEIKTKEVK YDSSLRPLSI KYDPTSAKII SNSGHSFSVD FDDTEDKSVL RGGPLSGTYR LRQFHFHWGS ADDHGSEHTV DGMEYSAELH VVHWNSDKYS SFVEAAHEPD GLAVLGIFLK RGEHNLQLQK ITDILDAIKE KGKQMRFTNF DPLSLLPLTR DYWTYPGSLT VPPLLESVIW IIFKQPISIS SQQLAKFRNL LYTAEGEAAD FMLSNHRPPQ PLKGRKVRAS FRS	XP_001507177.1	SEQ. ID. NO. 67

TABLE D5

Exemplary CA II DNA expression constructs for chloroplast expression	
ATGTCCCATC ACTGGGGGTA CGGCAAACAC AACGGACCTG AGCACTGGCA TAAGGACTTC CCCATTGCCA AGGGAGAGCG CCAGTCCCCT GTTGACATCG ACACTCATAC AGCCAAGTAT GACCCTTCCC TGAAGCCCCT GTCTGTTTCC TATGATCAAG CAACTTCCCT GAGGATCCTC AACAATGGTC ATGCTTTCAA CGTGGAGTTT GATGACTCTC AGGACAAAGC AGTGCTCAAG GGAGGACCCC TGGATGGCAC TTACAGATTG ATTCAGTTTC ACTTTCACTG GGGTTCACTT GATGGACAAG GTTCAGAGCA TACTGTGGAT AAAAAGAAAT ATGCTGCAGA ACTTCACTTG GTTCACTGGA ACACCAAATA TGGGGATTTT GGGAAAGCTG TGCAGCAACC TGATGGACTG GCCGTTCTAG GTATTTTTTT GAAGGTTGGC AGCGCTAAAC CGGGCCTTCA GAAAGTTGTT GATGTGCTGG ATTCCATTAA AACAAAGGGC AAGAGTGCTG ACTTCACTAA CTTCGATCCT CGTGGCCTCC TTCCTGAATC CTTGGATTAC TGGACCTACC CAGGCTCACT GACCACCCCT CCTCTTCTGG AATGTGTGAC CTGGATTGTG CTCAAGGAAC CCATCAGCGT CAGCAGCGAG CAGGTGTTGA AATTCCGTAA ACTTAACTTC AATGGGGAGG GTGAACCCGA AGAACTGATG GTGGACAACT GGCGCCCAGC TCAGCCACTG AAGAACAGGC AAATCAAAGC TTCCTTCAAA TAA	SEQ. ID. NO. 94 (human cDNA sequence)
gaattcATGTCtCATCAtTGGGGtTAtGGtAAACACAAtGGtCCTGAaCACTGGCATAAaGACTT tCCaATTGCaAAaGGtGAaCGtCAaTCaCCTGTTGAtATtGACACTCATACAGCtAAaTATGACC CTTCttTaAAaCCatTaTCTGTTTCaTATGATCAAGCAACTTCttTacGtATttTaAACAATGGT CATGCTTTtAAtGTaGAaTTTGATGACTCTCAaGAtAAAGCAGTatTaAAaGGtGGtCCatTaGA TGGtACTTACcGtTTaATTCAaTTTCACTTTCACTGGGGTTCAtTaGATGGtCAAGGTTCAGAaC ATACTGTaGATAAAAAaAAATATGCTGCAGAAtTaCACTTaGTTCACTGGAACACaAAATATGGt GATTTTGGtAAAGCTGTaCAaCAACCTGATGGttTaGCtGTTtTAGGTATTTTTTTaAAaGTTGG tAGtGCTAAACCaGGtCTTCAaAAAGTTGTTGATGTatTaGATTCaATTAAAACAAAaGGtAAaA GTGCTGACTTtACTAAtTTCGATCCTCGTGGttTaCTTCCTGAATCtTTaGATTACTGGACaTAt CCAGGtTCAtTaACaACaCCTCCTCTTtTaGAATGTGTaACaTGGATTGTatTaAAaGAACCaAT tAGtGTaAGtAGtGAaCAaGTaTTaAAATTCCGTAAACTTAAtTTCAATGGtGAaGGTGAACCaG AAGAAtTaATGGTtGAtAACTGGCGtCCAGCTCAaCCAtTaAAaAAtcGtCAAATtAAAGCTTCa TTCAAATAAgcatgc	SEQ. ID. NO. 108 (Optimized for chloroplast Expression)

TABLE D6

Codons in Human CA II optimized for expression in chloroplast of *Chlamydomonas reinhardtii*				
Amino acid	Total number	Number of codons that were optimized	No. of amino acids of each codon	Expected ratio of codons
Ser(S)	18	12	TCT TCA AGT (7:7:5)	1:1:1
Phe(F)	12	3	TIT TTC (8:4)	2:1
Leu(L)	26	19	TIA CTT (21:5)	5:1
Val(V)	17	10	GTT GTA (8:9)	1:1
Pro(P)	17	6	CCT CCA (8:9)	3:4
Thr(T)	12	5	ACT ACA (5:7)	2:3
Ala(A)	13	3	GCT GCA (9:4)	2:1
Tyr(Y)	8	2	TAT TAC (6:2)	2:1
His(H)	12	1	CAT CAC (6:6)	1:1
Asn(N)	10	4	AAT AAC (7:3)	2.5 1
A(D)	19	3	GAT GAC (14:5)	2.5 1
Ile(I)	9	4	ATT (9)	1
Met(M)	2	0	ATG (2)	1
Gln(Q)	11	7	CAA (11)	1
Glu(E)	13	6	GAA (13)	1
Lys(K)	24	11	AAA (24)	1
Cys(C)	1	0	TGT (1)	1
Tf£__(W)	7	0	TGG (7)	1
Gly(G)	22	17	GGT (22)	1
Arg(R)	7	5	CGT (7)	1

TABLE D7

Exemplary algal bicarbonate transporter types				
Transport Type	Mechanism	Substrate affinity	Flux rate	Photosynthetic affinity ko.6
BicA	Na+ dependent	Low-medium	High	90-170 µM HC0$_{3-}$
SbtA	Na+ dependent HC0$_{3-}$ uptake	High	Low	<5 µM HC0$_3$

TABLE D7-continued

Exemplary algal bicarbonate transporter types				
Transport Type	Mechanism	Substrate affinity	Flux rate	Photosynthetic affinity ko.6
BicA	Na+ dependent	Low-medium	High	90-170 µM HC0$_{3-}$
SbtA	Na+ dependent HC0$_{3-}$ uptake	High	Low	<5 µM HC0$_3$

TABLE D8

Exemplary plasma membrane localized Bicarbonate transporters			
Organism	Sequence	Accession Number	SEQ. ID. NO
Chlamydomonas reinhardtii	MLPGLGVILL VLPMQYYFGY KIVQIKLQNA KHVALRSAIM QEVLPAIKLV KYYAWEQFFE NQISKVRREE IRLNFWNCVM KVINVACVFC VPPMTAFVIF TTYEFQRARL VSSVAFTTLS LFNILRFPLV VLPKALRAVS EANASLQRLE AYLLEEVPSG TAAVKTPKNA PPGAVIENGV FHHPSNPNWH LHVPKFEVKP GQVVAVVGRI AAGKSSLVQA ILGNMVKEHG SFNVGGRISY VPQNPWLQNL SLRDNVLFGE QFDENKYTDV IESCALTLDL QILSNGDQSK AGIRGVNFSG GQRQRVNLAR CAYADADLVL LDNALSAVDH HTAHHIFDKC IKGLFSDKAV VLVTHQIEFM PRCDNVAIMD EGRCLYFGKW NEEAQHLLGK LLPITHLLHA AGSQEAPPAP KKKAEDKAGP QKSQSLQLTL APTSIGKPTE KPKDVQKLTA YQAALIYTWY GNLFLVGVCF FFFLAAQCSR QISDFWVRWW VNDEYKKFPV KGEQDSAATT FYCLIYLLLV GLFYIFMIFR GATFLWWVLK SSETIRRKAL HNVLNAPMGF FLVTPVGDLL LNFTKDQDIM DENLPDAVHF MGIYGLILLA TTITVSVTIN FFAAFTGALI IMTLIMLSIY LPAATALKKA RAVSGGMLVG LVAEVLEGLG VVQAFNKQEY FIEEAARRTN ITNSAVFNAE ALNLWLAFWC DFIGACLVGV VSAFAVGMAK DLGGATVGLA FSNIIQMLVF YTWVVRFISE SISLFNSVEG MAYLADYVPH DGVFYDQRQK DGVAKQIVLP DGNIVPAASK VQVVVDDAAL ARWPATGNIR FEDVWMQYRL DAPWALKGVT FKINDGEKVG AVGRTGSGKS TTLLALYRMF ELGKGRILVD GVDIATLSLK RLRTGLSIIP QEPVMFTGTV RSNLDPFGEF KDDAILWEVL KKVGLEDQAQ HAGGLDGQVD GTGGKAWSLG QMQLVCLARA ALRAVPILCL DEATAAMDPH TEAIVQQTIK KVFDDRTTIT IAHRLDTIIE SLMEYESPSK LLANRDSMFS KLVDKTGPAA AAALRKMAED FWSTRSAQGR NQ	EDP07736.1	SEQ. ID. NO. 77
Volvox carteri f. nagariensis	MGTISHPARG NDPTAGFFNK EAFGWMFKHV SEARKNGDID LDKMGMPPEN HAHEAYDMFA SNWAAEMKLK DSGAKPSLVR ALRKSFGLVY LLGGVFKCFW STFVITGAFY FVRSLLAHVN GIKDGRLYSK TVSGWCLMAG FTLDAWLLGL SLQRMGYICM SVGIRARAAL VQAVTHKAFR LSSVRADQSA AIVNFVSSDI QKIYDGALEF HYLWTAPFEA AAILALLGYL TNDSMLPGLG VILLVLPLQY FFGYKIIQIK LQNAKHVALR SSILQEVLPA IKLVKYYAWE QFFEDEISKI RREEMRLSFW NAMMKVINVA CVFCVPPMTA FVIFTTYEFQ KARLVSGVAF TTLSLFNILR FPLVVLPKAL RAVSEAHASL QRLESYLLED VPQGTASGGK SSKSSAPGVH IDNAVYHHPS NPNWHLHVPR FDVRPGQVVA VVGRIGAGKS SLVQAILGNM VKEHGSQQVG GRISYVPQNP WLQNLSIRDN VTFGEGWDEN KYEAVIDACA LTMDLQILPQ GDQSKAGIRG VNFSGGQRQR VNLARCAYAD ADLVLLDNAL SAVDHHTAHH IFDKCIKGLF SDKAVVLITH QIEFMPRCDA VAIMDEGRCL YFGKWNEESQ HLLGKLLPIT HLLHAAGSQE APPAAPKKKD DKATPQKSQS LQLTLAPTSI GKPTQKDTKA APKLTAFKAA LIYTYYGNIL LVFVCFITFL AAQTCRQMSD FWVRWWVNDE YKHFPKRTGV REESATKFYA LIYLLLVGLF YFTMVARGST FLWWVLRSSE NIRKKALNNV LNAPMGFFLV TPVGDLLLNF TKDQDIMDEN LPDAIHFMGI YGLILLATTI TVSVTINFFG AFTGFLIIMT LIMLAIYLPA ATALKKARAV SGGQLVGLVA EVLEGLNVVQ AFSKQEYFIE EAARRTDVTN AAVFNAESLN LWLAFWCDLI GASLVGVVSA FAVGLKDQLG AATVGLAFSN IIQMLVFYTW VVRFIAESIS LFNSVEAMAW	XP_002950646.1	SEQ. ID. NO. 69

TABLE D8-continued

Exemplary plasma membrane localized Bicarbonate transporters

Organism	Sequence	Accession Number	SEQ. ID. NO
	LADYVPKDGI FYDQKQLDGV AKSITLPDGQ IVPATSKVQV VVDDAALARW PATGNIRFED VWMQYRLDAA WALKGVTFKI NDGEKVGAVG RTGSGKSTTL LALYRMFELG KGRILIDGVD IATLSLKRLR TGLSIIPQEP VMFTGTVRSN LDPFGEFKDD SVLWEVLQKV GLEAQAQHAG GLDGRVDGTG GKAWSLGQMQ LVCLARAALR AVPILCLDEA TAAMDPHTEQ VVQETIKKVF DDRTTITIAH RLDTIIESDK VLVMEAGELK EFAPPAQLLA NRETMFSKLV DKTGPAAAAA LRKMADEHFS KSQARAAAQR H		
Chlorella variabilis	MVPLLAQRGR IRSQAPRTWH PDPQPLHAER SRQCPGRGVR AAAKRGGGSG GATHKSKKSK ELDEVAAFEQ LMCDWDDAFA ADCYDNERAA RMARLAEEGY QHHGRGFVFV RSRLDKRSRK ARNDSGASKG FGAAAKALSV EQGTPLENNP QLHLLSWTAC YIASSQLDSL GGLFSTQEGV LLPDSGSLLT DGGSGASGSN AADAVGELQR VLRGQDLSQL RGYVGAPPQA RPASGSDDDG SSTTGSNNGA AGEGSEVEEG TAMGGIRRYE PESGELVVLL SCKIGGKPAV GAELLAVAQA EDGKHAPGAS PDTRLCKEPS QSAFDLWSFG WMNKIVPAAR RGEVEVADLP LPEAQQAEPC YEELNTNWEA AVQEAKKAGK EPKLMKVLWK TYGKDIVLAG IFKLMWSVFV ILGAYYFTRS ILMCIRTLEG KDDSIYDTEW KGWVLTGFFF LDAWLLGMML QRMAFNCLKV GIKARAALTT MIARKCYNMA HLTKDTAAEA VGFVASDINK VFEGIQEVHY LWGAPVEAGA ILALLGTLVG VYCIGGVIIV CMVVPLQYYF GYKIIKNKIK NAPNVTERWS IIQEILPAMK LVKYYAWERF FEKHVADMRT RERHYMFWNA VVKTVNVTMV FGVPPMVTFA VLVPYELWHV DSSTSEPYIK PQTAFTMLSL FNVLRFPLVV LPKAMRCVSE ALRSVGNLEK FLAEPVAPRQ DLEGKPGAQL SKAVLRHEMD TSGFTLRVPE FSVKAGELVA VVGRVGAGKS SILQAMLGNM QTASGLAKCQ HSASSCLPFL VEGTAHSGGR IAYVPQTAWC QNLSLRDNIT FGQPWDEAKY KQVIHACALE LDLAILAAGD QSKAGLRGIN LSGGQRQRLN LARCAYFDGD LVLLDNALSA VDHHTAHHIF EHCVRGMFRD KATVLVTHQV EFLPQCDKVA IMDDGTCVYF GPWNAAAQQL LSKYLPASHL LAAGGNAEQP RDTKKKVVKK EETKKTEDAG KAKRVHSASL TLKSALWEYC WDARWIIFCL SLFFFLTAQA SRQLADYFIR WWTRDHYNKY GVLCIDEGDN PCGPLFYVQY YGILGLLCFI VLMAFRGAFL YTWSLGASYR QHEKSIHRVL YAPLGFFLTT PVGDLLVSFT KDQDVMDDAL PDALYYAGIY GLILLATAIT VSVTIPLFSA LAGGLFVVSG IMLAIYLPAA THLKKLRMGT SGDVVTLIAE ALDGLGVIQA YGKQAYFTTI TSQYVNDAHR ALFGAESLNL WLAFICDFFG ACMVLSVACF GIGQWSTLGS SSVGLAFSQS IQMLVFYTWS IRLVAECIGL FGSAEKIAWL ANHTPQEAGS LDPPSLPGSG ETKAAPKKRG TAGKFLPPLK DEDLAIVPTG GPKLPSGWPR TGVLEFNQVV MKYAPHLPPA LRGVSFKVKS GDKVGVVGRT GSGKSTLLLA LYRMFNLESG AITLDGIDIS TLTLEQLRRG LSVIPQEPTV FSGTVRTNLD PFGEFGADAI LWEALRDCGL EEQVKACGGL DAKLDGTGGN AWSIGQQQLM CLARAALKKV PVLCLDEATA AMDPHTEAHV LEIIERIFSD RTMLTIAHRL DNVIRSDLVV VMDAGQVCEM GTPDELLANP_QSAFSQLVDK TGAASAAALR KMAADFLDER ARGQKLGFKP RPSLEESHIC VAPSPSLILS TLLFPPAFMA NVTALLLPKP VLSHAPVSSQ TVNTYIRLNI IQLQCNVLHP ATKEATWSSR RITFTAHLSS SGSKPPPPLP PLTELPEGRG LDWSSAGYRD GREAIPSPSA KYSAADYGAA GDGVTDDTQA LQVAVAAAHE DDEGGVVYLG AGTFVLTQPL SIAGSNVVIR GAGEDATTIF VPLPLSDVFP GTWSMDASGK VTSPWITRGG FLAFSGRRTK SSDSSTLLAT VAGSVEQGAS VIPVDSTAEF RLGQWVRIII NDASTDASAG GGTLERGSSE VQESETMIAE GATGGGAGVR AQWTGVLHAF EPTVQCSGVE QLTIRFNHSM MAAHLAERGY NAIELEDVVD CWIRQVTILN ADNAIRLRGT DHSTLSGQAC SGGGVVAVVP VWCRRGLPSP ADVTVGVTEL RWEPDTREVN GHHAITVSKG HANLVTRFRI TAPFYHDISL EGGALLNVIS SGGGANLNLD LHRSGPWGNL FSQLGMGLAA RPFDAGGRDG RGAHAGRQNT FWNLQPGDVA AAAPALQPSA AAGDARRLLV DGDSLLHAGT GQARLLRQLE ADDSAEPLLL PSCEFGPLLN FVGGFAGELC KSSGWLVAGL PDDRPDLHAS QVTARLQHGA ADNKTHA	EFN52914.1	SEQ. ID. NO. 70
Synechococcus elongatus PCC 7942.J	MDFLSNFLMD FVKQLQSPTL SFLIGGMVIA ACGSQLQIPE SICKIIVFML LTKIGLTGGM AIRNSNLTEM VLPALFSVAI GILIVFIARY TLARMPKVKT VDAIATGGLF GAVSGSTMAA ALTLLEEQKI PYEAWAGALY PFMDIPALVT AIVVANIYLN KKKRKEAAFA SAQGAYSKQP VAAGDYSSSS DYPSSRREYA QQESGDHRVK IWPIVEESLQ GPALSAMLLG VALGLFARPE	ABB57505.1	SEQ. ID. No. 71

TABLE D8-continued

Exemplary plasma membrane localized Bicarbonate transporters

Organism	Sequence	Accession Number	SEQ. ID. NO
	SVYEGFYDPL FRGLLSILML VMGMEAWSRI SELRKVAQWY VVYSIVAPLA HGFIAFGLGM IAHYATGFSM GGVVVLAVIA ASSSDISGPP TLRAGIPSAN PSAYIGASTA IGTPVAIGIA IPLFLGLAQT IGG		
Synechocystis sp. PCC 6803	MDFLSNFLTD FVGQLQSPTL AFLIGGMVIA ALGTQLVIPE AISTIIVFML LTKIGLTGGM AIRNSNLTEM LLPVAFSVIL GILIVFIARF TLAKLPNVRT VDALATGGLF GAVSGSTMAA ALTTLEESKI SYEAWAGALY PFMDIPALVT AIVVANIYLN KRKRKSAAAS IEESFSKQPV AAGDYGDQTD YPRTRQEYLS QQEPEDNRVK IWPIIEESLQ GPALSAMLLG LALGIFTKPE SVYEGFYDPL FRGLLSILML IMGMEAWSRI GELRKVAQWY VVYSLIAPIV HGFIAFGLGM IAHYATGFSL GGVVVLAVIA ASSSDISGPP TLRAGIPSAN PSAYIGSSTA IGTPIAIGVC IPLFIGLAQT LGAG	NP_441340	SEQ. ID. No.72
Nostoc sp. PCC 712	MDFFSLFLMD FVKQLQSPTL GFLIGGMVIA ALGSELIIPE AICQIIVFML LTKIGLTGGI AIRNSNLTEM VLPAASAVAV GVLVVFIARY TLAKLPKVNT VDAIATGGLF GAVSGSTMAA ALTLLEEQKI QYEAWAAALY PFMDIPALVT AIVVANIYLN KKKRSAAGEY LSKQSVAAGE YPDQQDYPSS RQEYLRKQQS ADNRVKIWPI VKESLQGPAL SAMLLGIALG LFTQPESVYK SFYDPLFRGL LSILMLVMGM EAWSRIGELR KVAQWYVVYS VVAPLVHGFI AFGLGMIAHY ATGFSLGGVV ILAVIAASSS DISGPPTLRA GIPSANPSAY IGASTAIGTP IAIGLAIPLF LGLAQAIGGR	NP_486174	SEQ. ID. No. 73
Cyanothece sp. PCC 7425	MDFWSYFLMD FVKQLQSPTL GFLIGGMVIA ALGSQLVIPE AICQIIVFML LTKIGLTGGM AIRNSNLTEM VLPAAFSVIS GILIVFIARY TLAKLPKVRT VDAIATGGLF GAVSGSTMAA ALTLLEEEKI PYEAWAGALY PFMDIPALVT AIVIANIYLN KKKRRAESEA LSKQEYLGKQ SIVAGDYPAQ QDYPSTRQEY LSKQQGPENN RVKIWPIVQE SLQGPALSAM LLGVALGILT KPESVYESFY DPLFRGLLSI LMLVMGMEAW SRIGELRKVA QWYVVYSVVA PFVHGLIAFG LGMFAHYTMG FSMGGVVVLA VIASSSSDIS GPPTLRAGIP SANPSAYIGA STAIGTPIAI GLCIPFFIGL AQTLGGG	YP_002485721	SEQ. ID. No. 74
Microcysti *aeruginosa* NIES-843	MDFFSLFVMD FIQQLQSPTL AFLIGGMIIA ALGSELVIPE SICTIIVFML LTKIGLTGGI AIRNSNLTEM VLPMIFAVIV GIIVVFVARY TLANLPKVKV VDAIATGGLF GAVSGSTMAA GLTVLEEQKI PYEAWAGALY PFMDIPALVT AIVVANIYLN KKKQKEAAYD QESFSKQPVA AGNYSDQQDY PSSRQEYLSQ QQPADNRVKI WPIIEESLRG PALSAMLLGL ALGIFTQPES VYKSFYDPLF RGLLSVLMLV MGMEAWSRVG ELRKVAQWYV VYSVIAPFVH GLIAFGLGMI AHYATGFSWG GVVMLAVIAS SSSDISGPPT LRAGIPSANP SAYIGASTAI GTPVAIGLCI PFFVGLAQAL SGG	YP_001661223	SEQ. ID. No. 75
Anabaena *variabills* ATCC 29413	MDFVSLFVKD FIAQLQSPTL AFLIGGMIIA ALGSELVIPE SICTIIVFML LTKIGLTGGI AIRNSNLTEM VLPMIFAVIT GITIVFISRY TLAKLPKVKV VDAIATGGLF GAVSGSTMAA GLTVLEEQKM AYEAWAGALY PFMDIPALVT AIVIANIYLN KKKRKEAVYS TEQPVAAGDY PDQKDYPSSR QEYLSQQKGD EDNRVKIWPI IEESLRGPAL SAMLLGLALG LFTQPESVYK SFYDPAFRGL LSILMLVMGM EAWSRIGELR KVAQWYVVYS VVAPFVHGLI AFGLGMIAHY TMNFSMGGVV ILAVIASSSS DISGPPTLRA GIPSANPSAY IGASTAVGTP VAIGLCIPFF LGLAQAIGG	YP_323532	SEQ. ID. No. 86
Cyanothece sp. PCC 880	MDFLSLFVKD FIIQLQSPTL AFLIGGMVIA ALGSELVIPE SICTIIVFML LTKIGLTGGI AIRNSNLTEM VLPMICAVIV GIVVVFIARY TLAKLPKVNV VDAIATGGLF GAVSGSTMAA GLTVLEEQKI PYEAWAGALY PFMDIPALVT AIVVANIYLN KKKRKATVMQ ESLSKQPVAA GDYPSSRQEY VSQQQPEDNR VKIWPIIEES LRGPALSAML LGLALGILTQ PESVYKGFYD PPFRGLLSIL MLVMGMEAWS RIGELRKVAQ WYVVYSVAAP FIHGLLAFGL GMIAHYTMGF SMGGVVILAV IASSSSDISG PPTLRAGIPS ANPSAYIGAS TAIGTPVAIG LCIPFFVGLA QAIGGF	YP_002371470.1	SEQ. ID. No. 87
Arthrospia *platensis* str. *Paraca*	MDFLSGFLTR FLAQLQSPTL GFLIGGMVIA AVNSQLQIPD AIYKFVVFML LMKVGLSGGI AIRGSNLTEM LLPAVFALVT GIVIVFIGRY TLAKLPNVKT VDAIATAGLF GAVSGSTMAA ALTLLEEQGM EYEAWAAALY PFMDIPALVS AIVLASIYVS	ZP.06383808.1	SEQ. ID. No. 88

TABLE D8-continued

Exemplary plasma membrane localized Bicarbonate transporters

Organism	Sequence	Accession Number	SEQ. ID. NO
	KQKHSDMADE SLSKHESLSK QPVAAGDYPS KPEYPTTRQE YLSQQRGSAN QGVEIWPIIK ESLQGSALSA LLLGLALGLL TRPESVFQSF YEPLFRGLLS ILMLVMGMEA TARLGELRKV AQWYAVYAFI APLLHGLIAF GLGMIAHVVT GFSLGGVVIL AVIASSSSDI SGPPTLRAGI PSANPSAYIG SSTAVGTPVA IALGIPLYIG LAQALMGG		

TABLE D9

Exemplary chloroplast envelope localized Bicarbonate transporters

Organism	Sequence	Accession Number	SEQ. ID. NO
Chlamydomonas reinhardtii	MQTTMTRPCL AQPVLRSRVL RSPMRVVAAS APTAVTTVVT SNGNGNGHFQ AATTPVPPTP APVAVSAPVR AVSVLTPPQV YENAINVGAY KAGLTPLATF VQGIQAGAYI AFGAFLAISV GGNIPGVAAA NPGLAKLLFA LVFPVGLSMV TNCGAELFTG NTMMLTCALI EKKATWGQLL KNWSVSYFGN FVGSIAMVAA VVATGCLTTN TLPVQMATLK ANLGFTEVLS RSILCNWLVC CAVWSASAAT SLPGRILALW PCITAFVAIG LEHSVANMFV IPLGMMLGAE VTWSQFFFNN LIPVTLGNTI AGVLMMAIAY SISFGSLGKS AKPATA	BAD16681.1	SEQ. ID. NO.89
Volvox carteri f. nagariensis	MQTTMSVTRP CVGLRPLPVR NVRSLIRAQA APQQVSTAVS TNGNGNGVAA ASLSVPAPVA APAQAVSTPV RAVSVLTPPQ VYENAANVGA YKASLGVLAT FVQGIQAGAY IAFGAFLACS VGGNIPGITA SNPGLAKLLF ALVFPVGLSM VTNCGAELYT GNTMMLTCAI FEKKATWAQL VKNWVVSYAG NFVGSIAMVA AVVATGLMAS NQLPVNMATA KSSLGFTEVL SRSILCNWLV CCAVWSASAA TSLPGRILGL WPPITAFVAI GLEHSVANMF VIPLGMMLGA DVTWSQFFFN NLVPVTLGNT IAGVVMMAVA YSVSYGSLGK TPKPATA	XP_002951507.1	SEQ. ID. NO. 79

TABLE D10

Transit Peptides

Organism	SEQ ID NO	Name
Arabidopsis thaliana	8	Rbcs-1a transit peptide
Arabidopsis thaliana	14	PGR5 transit peptide
Arabidopsis thaliana	15	psaD transit peptide
Arabidopsis thaliana	22	DNAJ transit peptide
Cyanophora paradoxa	102	psaD trasit peptide
Arabidopsis thaliana	104	CAB transit peptide
Arabidopsis thaliana	105	PGR5 transit peptide

TABLE D11

Cyclic Electron Transfer modulator proteins

Organism	SEQ ID NO	Name	Accession No.	Function
Arabidopsis thaliana	93	Ferredoxin1 (FD1)	AEE28669.1	cyclic electron transfer modulator protein
Arabidopsis thaliana	95	Ferredoxin2 (FD2)	AAG40057.1	cyclic electron transfer modulator protein
Arabidopsis thaliana	96	ferredoxin-NADP(+) oxidoreductase (FNR1)	AT5G66190 partial	cyclic electron transfer modulator protein
Arabidopsis thaliana	97	ferredoxin-NADP(+) oxidoreductase (FNR2)	BAH19611.1	cyclic electron transfer modulator protein

An exemplary optimized DNA sequence for the plasma membrane localized bicarbonate transporter is shown in SEQ ID NO. 91

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                                                              (SEQ ID NO: 91)
atgctgcccg gcctgggcgt catcctgctg gtgctgccca tgcagtacta cttcggctac      60

aagatcgtgc agatcaagct gcagaacgcc aagcacgtcg ccctgcgctc cgccatcatg     120

caggaggtgc tgcccgccat caagctggtc aagtactacg cctgggagca gttctttgag     180

aaccagatca gcaaggtccg ccgcgaggag atccgcctca acttctggaa ctgcgtgatg     240

aaggtcatca acgtggcctg cgtgttctgc gtgccgccca tgaccgcctt cgtcatcttc     300

accacctacg agttccagcg cgcccgcctg gtgtccagcg tcgccttcac caccctgtcg     360

ctgttcaaca ttctgcgctt cccccctggtc gtgctgccca aggccctgcg tgccgtgtcc     420

gaggccaacg cgtctctcca gcgcctggag gcctacctgc tggaggaggt gccctcgggc     480

actgccgccg tcaagacccc caagaacgct ccccccggcg ccgtcatcga gaacggtgtg     540

ttccaccacc cctccaaccc caactggcac ctgcacgtgc ccaagttcga ggtcaagccc     600

ggccaggtcg ttgctgtggt gggccgcatc gccgccggca agtcgtccct ggtgcaggcc     660

atcctcggca acatggtcaa ggagcacggc agcttcaacg tgggcggccg catctcctac     720

gtgccgcaga acccctggct gcagaacctg tccctgcgtg acaacgtgct gtttggcgag     780

cagttcgatg agaacaagta caccgacgtc atcgagtcct gcgccctgac cctggacctg     840

cagatcctgt ccaacggtga ccagtccaag gccggcatcc gcggtgtcaa cttctccggt     900

ggccagcgcc agcgcgtgaa cctggcccgc tgcgcctacg ccgacgccga cctggtgctg     960

ctcgacaacg ccctgtccgc cgtggaccac cacaccgccc accacatctt cgacaagtgc    1020

atcaagggcc tgttctccga caaggccgtg gtgctggtca cccaccagat cgagttcatg    1080

ccccgctgcg acaacgtggc catcatggac gagggccgct gcctgtactt cggcaagtgg    1140

aacgaggagg cccagcacct gctcggcaag ctgctgccca tcacccacct gctgcacgcc    1200

gccggctccc aggaggctcc ccccgccccc aagaagaagg ccgaggacaa ggccggcccc    1260

cagaagtcgc agtcgctgca gctgaccctg gcccccacct ccatcggcaa gcccaccgag    1320

aagcccaagg acgtccagaa gctgactgcc taccaggccg ccctcatcta cacctggtac    1380

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An exemplary optimized DNA sequence for Chloroplast envelope localized Bicarbonate transporter is shown in SEQ ID NO: 92

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Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the disclosure specifically described herein. For example a transgenic plant or alga of an embodiment disclosed herein further comprising within its genome, and expressing or overexpressing, a combination of heterologous nucleotide sequences encoding additionally a Rubisco (for example SEQ ID NO:107). Further still a transit peptide amino acid sequence at the amine terminal portion of a protein sequence identified herein may be cleaved leaving the protein sequence alone. The percent homology applies to the protein sequence without the transit peptide sequence also. Such equivalents are intended to be encompassed within the scope of the following claims.

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SEQUENCE LISTING

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```

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Thr Val Val Ala Leu Gly Leu Phe Phe Phe Leu Asp Asp Ile Thr Gly
    210                 215                 220

Phe Glu Ile Thr Tyr Ile Met Glu Leu Pro Glu Pro Tyr Ser Phe Ile
225                 230                 235                 240

Phe Thr Trp Phe Ala Ala Val Pro Val Ile Val Tyr Leu Ala Leu Ser
                245                 250                 255

Ile Thr Lys Leu Ile Ile Lys Asp Phe Leu Ile Leu Lys Gly Pro Cys
            260                 265                 270

Pro Asn Cys Gly Thr Glu Asn Thr Ser Phe Phe Gly Thr Ile Leu Ser
        275                 280                 285

Ile Ser Ser Gly Gly Lys Thr Asn Thr Val Lys Cys Thr Asn Cys Gly
    290                 295                 300

Thr Ala Met Val Tyr Asp Ser Gly Ser Arg Leu Ile Thr Leu Pro Glu
305                 310                 315                 320

Gly Ser Gln Ala
```

<210> SEQ ID NO 4
<211> LENGTH: 975
<212> TYPE: DNA
<213> ORGANISM: Neisseria gonorrhoeae
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: codon optimized for Arabidopsis thaliana

<400> SEQUENCE: 4

```
atgggtagca agatgttgtt tagtttgaca agtcctcgac ttttctccgc cgtttctcgc      60

aaaccttcct cttctttctc tccttctcct ccgtcgccgt cttcgaggac tcaatggact     120

cagctcagcc ctggaaaatc gatttctttg agaagaagag tcttcttgtt gcctgctaaa     180

gccacaacag agcaatcagg tccagtagga ggagacaacg tcgatagcaa tgttttgccc     240

tattgtagca tcaacaaggc tgagaagaaa acaattggtg aaatggaaca agagtttctc     300

caagcgttgc aatctttcta ttatgatggc aaagcgatca tgtctaatga agagtttgat     360

aaccttaaag aagagttaat gtgggaagga agcagtgttg tgatgctaag ttccgatgaa     420

caaagattct tggaagcttc catggcttat gtttctggaa atccaatctt gaatgatgaa     480

gaatatgata agctcaaact caaactaaag attgatggta gcgacattgt gagcgagggt     540

ccaagatgca gtctccgtag taaaaaggtg tatagtgatc tcgctgtaga ttatttcaaa     600

atgttattgt tgaatgttcc agcaaccgtt gttgctctcg gactcttttt cttcctggac     660

gacattacag gttttgagat cacatacatc atggagcttc cagaaccata cagtttcata     720

ttcacttggt tcgctgctgt gcctgtgatt gtatatctgg ctttatcaat caccaaattg     780

atcatcaagg acttcttgat cttgaagggt ccttgtccga attgtggaac ggaaaacacc     840

tccttctttg gaacaattct gtcaatctcc agcggcggca aaaccaacac tgtcaaatgc     900

accaactgcg gaaccgcgat ggtgtatgac tcgggttcta ggttgatcac attgccagaa     960

ggaagccaag cttaa                                                      975
```

<210> SEQ ID NO 5
<211> LENGTH: 280
<212> TYPE: PRT
<213> ORGANISM: Neisseria gonorrhoeae
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(54)
<223> OTHER INFORMATION: Bacterial carbonic anhydrase (BCA) amino acid
sequence with rbcs-1a transit peptide

```
<400> SEQUENCE: 5

Met Ala Ser Ser Met Leu Ser Ser Ala Thr Met Val Ala Ser Pro Ala
1               5                   10                  15

Gln Ala Thr Met Val Ala Pro Phe Asn Gly Leu Lys Ser Ser Ala Ala
            20                  25                  30

Phe Pro Ala Thr Arg Lys Ala Asn Asn Asp Ile Thr Ser Ile Thr Ser
        35                  40                  45

Asn Gly Gly Arg Val Asn His Gly Asn His Thr His Trp Gly Tyr Thr
    50                  55                  60

Gly His Asp Ser Pro Glu Ser Trp Gly Asn Leu Ser Glu Glu Phe Arg
65                  70                  75                  80

Leu Cys Ser Thr Gly Lys Asn Gln Ser Pro Val Asn Ile Thr Glu Thr
                85                  90                  95

Val Ser Gly Lys Leu Pro Ala Ile Lys Val Asn Tyr Lys Pro Ser Met
            100                 105                 110

Val Asp Val Glu Asn Asn Gly His Thr Ile Gln Val Asn Tyr Pro Glu
        115                 120                 125

Gly Gly Asn Thr Leu Thr Val Asn Gly Arg Thr Tyr Thr Leu Lys Gln
    130                 135                 140

Phe His Phe His Val Pro Ser Glu Asn Gln Ile Lys Gly Arg Thr Phe
145                 150                 155                 160

Pro Met Glu Ala His Phe Val His Leu Asp Glu Asn Lys Gln Pro Leu
                165                 170                 175

Val Leu Ala Val Leu Tyr Glu Ala Gly Lys Thr Asn Gly Arg Leu Ser
            180                 185                 190

Ser Ile Trp Asn Val Met Pro Met Thr Ala Gly Lys Val Lys Leu Asn
        195                 200                 205

Gln Pro Phe Asp Ala Ser Thr Leu Leu Pro Lys Arg Leu Lys Tyr Tyr
    210                 215                 220

Arg Phe Ala Gly Ser Leu Thr Thr Pro Pro Cys Thr Glu Gly Val Ser
225                 230                 235                 240

Trp Leu Val Leu Lys Thr Tyr Asp His Ile Asp Gln Ala Gln Ala Glu
                245                 250                 255

Lys Phe Thr Arg Ala Val Gly Ser Glu Asn Asn Arg Pro Val Gln Pro
            260                 265                 270

Leu Asn Ala Arg Val Val Ile Glu
        275                 280


<210> SEQ ID NO 6
<211> LENGTH: 684
<212> TYPE: DNA
<213> ORGANISM: Neisseria gonorrhoeae

<400> SEQUENCE: 6

aaccacggca atcacaccca ttggggctat accggacacg actctcccga aagctggggc      60

aatctgtcag aagaattccg tttgtgctcc accggcaaaa accaatctcc ggtaaacatt     120

accgaaaccg tttccggcaa actgcccgcc atcaaagtca attacaaacc gagtatggtt     180

gacgtggaaa acaacggcca caccattcag gtcaattatc ccgaaggcgg caataccctg     240

accgtgaacg gcagaaccta taccctgaaa cagttccact tccacgtgcc gagcgaaaac     300

caaatcaaag gcagaacttt cccgatggaa gctcacttcg tccacttaga cgaaaacaaa     360

cagcctttag tattagccgt gctgtatgaa gccggcaaaa ccaacgggag actgtcttcc     420
```

atctggaacg tcatgccgat gaccgcagga aaagtgaaac tcaaccaacc gttcgacgca 480

tccaccctac tgccgaaaag attgaaatac tacagatttg ccggttcgct gaccacgccg 540

ccgtgcacag agggcgtatc atggttggtg ttgaaaactt atgaccacat cgaccaagcg 600

caagcggaaa aattcaccag agccgtcggt tcggaaaaca acagacccgt acagcctctg 660

aatgcacgtg tagttattga ataa 684

<210> SEQ ID NO 7
<211> LENGTH: 356
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 7

ggtttacatt gatgctctca ggatttcata aggatagaga gatctattcg tatacgtgtc 60

acgtcatgag tgggtgtttc gccaatccat gaaacgcacc tagatatcta aaacacatat 120

caattgcgaa tctgcgaagt gcgagccatt aaccacgtaa gcaaacaaac aatctaaacc 180

ccaaaaaaaa tctatgacta gccaatagca acctcagaga ttgatatttc aagataagac 240

agtatttaga tttctgtatt atatatagcg aaaatcgcat caataccaaa ccacccattt 300

cttggcttac aacaacaaat cttaaacgtt ttactttgtg ctgcactact caacct 356

<210> SEQ ID NO 8
<211> LENGTH: 162
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Rbcs-1a transit peptide

<400> SEQUENCE: 8

atggcttcct ctatgctctc ttccgctact atggttgcct ctccggctca ggccactatg 60

gtcgctcctt tcaacggact taagtcctcc gctgccttcc cagccaccag aaaggctaac 120

aacgacatta cttccatcac aagcaacggc ggaagagtta ac 162

<210> SEQ ID NO 9
<211> LENGTH: 207
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: NOS terminator from cloning vector.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Nos terminator

<400> SEQUENCE: 9

atcgttcaaa catttggcaa taaagtttct taagattgaa tcctgttgcc ggtcttgcga 60

tgattatcat ataatttctg ttgaattacg ttaagcatgt aataattaac atgtaatgca 120

tgacgttatt tatgagatgg gtttttatga ttagagtccc gcaattatac atttaatacg 180

cgatagaaaa caaaatatag cgcgcaa 207

<210> SEQ ID NO 10
<211> LENGTH: 251
<212> TYPE: DNA
<213> ORGANISM: Nicotiana sylvestris

<400> SEQUENCE: 10

tgtggtcaca cctcaaacta aatcaaccag tttgcatttt tttccttctc aatgttaatt 60

tgctgacttg gctagggtgc gaatcaaatc acacgttcta attgggcaaa atccgtatat 120 caccttatcc tatatccttt ttctccacca cccatcatct cttctatgca acaaaaatag 180

cttcttcctt ttcatttttc acttctctca atccaacttt tctatggcca tggcatccca 240

agcttccctt t 251

<210> SEQ ID NO 11
<211> LENGTH: 255
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 11

tatacaaagc aaccgatcaa gtggagacta gtaaaccata cacaatcact catttcctca 60

caaaagaaag ataagataag ggtgtcaaca cctttcctta atcatgtggt agtgaacgag 120

ttatcatgaa tcccggaccc tttgatcatt agggcttttt gcctcttacg gttctcacta 180

tataaagatg acaaaaccaa tagaaaaaca attaagcaaa agaagaagaa gaagaagtaa 240

tggcttcctc tatgc 255

<210> SEQ ID NO 12
<211> LENGTH: 3249
<212> TYPE: DNA
<213> ORGANISM: Chlamydomonas reinhardtii

<400> SEQUENCE: 12

atgcttcctg gtcttggtgt catccttctt gtgcttccta tgcagtacta cttcggttac 60

aagatcgtgc agatcaagct tcagaacgct aagcacgtcg ctcttcgttc tgctatcatg 120

caggaggtgc ttcctgctat caagcttgtc aagtactacg cttgggagca gttctttgag 180

aaccagatct ctaaggtccg tcgtgaggag atccgtctca acttctggaa ctgcgtgatg 240

aaggtcatca acgtggcttg cgtgttctgc gtgccgccta tgaccgcttt cgtcatcttc 300

accacctacg agttccagcg tgctcgtctt gtgtcttctg tcgctttcac cacccttttct 360

cttttcaaca ttcttcgttt ccctcttgtc gtgcttccta aggctcttcg tgctgtgtct 420

gaggctaacg cttctctcca gcgtcttgag gcttaccttc ttgaggaggt gccttctggt 480

actgctgctg tcaagacccc taagaacgct cctcctggtg ctgtcatcga gaacggtgtg 540

ttccaccacc cttctaaccc taactggcac cttcacgtgc ctaagttcga ggtcaagcct 600

ggtcaggtcg ttgctgtggt gggtcgtatc gctgctggta agtcttctct tgtgcaggct 660

atcctcggta acatggtcaa ggagcacggt tctttcaacg tgggtggtcg tatctcttac 720

gtgccgcaga acccttggct tcagaacctt tctcttcgtg acaacgtgct tttggtgag 780

cagttcgatg agaacaagta caccgacgtc atcgagtctt gcgctcttac ccttgacctt 840

cagatccttt ctaacggtga ccagtctaag gctggtatcc gtggtgtcaa cttctctggt 900

ggtcagcgtc agcgtgtgaa ccttgctcgt tgcgcttacg ctgacgctga ccttgtgctt 960

ctcgacaacg ctctttctgc tgtggaccac cacaccgctc accacatctt cgacaagtgc 1020

atcaagggtc ttttctctga caaggctgtg gtgcttgtca cccaccagat cgagttcatg 1080

cctcgttgcg acaacgtggc tatcatggac gagggtcgtt gcctttactt cggtaagtgg 1140

aacgaggagg ctcagcacct tctcggtaag cttcttccta tcacccacct tcttcacgct 1200

gctggttctc aggaggctcc tcctgctcct aagaagaagg ctgaggacaa ggctggtcct 1260

cagaagtctc agtctcttca gcttaccctt gctcctacct ctatcggtaa gcctaccgag 1320

aagcctaagg acgtccagaa gcttactgct taccaggctg ctctcatcta cacctggtac 1380

-continued

ggtaaccttt tccttgttgg tgtgtgcttc ttcttcttcc ttgctgctca gtgctctcgt 1440

cagatctctg atttctgggt gcgttggtgg gtgaacgacg agtacaagaa gttccctgtg 1500

aagggtgagc aggactctgc tgctaccacc ttctactgcc tcatctacct tcttcttgtg 1560

ggtcttttct acatcttcat gatcttccgt ggtgctactt tcctttggtg ggtgctcaag 1620

tcttctgaga ccatccgtag gaaggctctt cacaacgtcc tcaacgctcc tatgggtttc 1680

ttccttgtca cgccggtcgg tgaccttctt ctcaacttca ccaaggacca ggacattatg 1740

gatgagaacc ttcctgatgc tgttcacttc atgggtatct acggtcttat tcttcttgct 1800

accaccatca ccgtgtctgt caccatcaac ttcttcgctg ctttcaccgg tgctcttatc 1860

atcatgaccc tcatcatgct ctctatctac cttcctgctg ctactgctct taagaaggct 1920

cgtgctgtgt ctggtggtat gcttgtcggt cttgttgctg aggttcttga gggtcttggt 1980

gtggttcagg ctttcaacaa gcaggagtac ttcattgagg aggctgctcg tcgtaccaac 2040

atcaccaact ctgctgtctt caacgctgag gctcttaacc tttggcttgc tttctggtgc 2100

gacttcatcg gtgcttgcct tgtgggtgtg gtgtctgctt tcgctgtggg tatggctaag 2160

gaccttggtg gtgctaccgt cggtcttgct ttctctaaca tcattcagat gcttgtgttc 2220

tacacctggg tggtccgttt catctctgag tctatctctc tcttcaactc tgtcgagggt 2280

atggcttacc tcgctgacta cgtgcctcac gatggtgtct tctatgacca gcgtcagaag 2340

gacggtgtcg ctaagcaaat cgtccttcct gacggtaaca tcgtgcctgc tgcttctaag 2400

gtccaggtcg tggttgacga cgctgctctc gctcgttggc ctgctaccgg taacatccgt 2460

ttcgaggacg tgtggatgca gtaccgtctt gacgctcctt gggctcttaa gggtgtcacc 2520

ttcaagatca acgacggtga gaaggtcggt gctgtgggtc gtaccggttc tggtaagtct 2580

accacgcttc ttgctcttta ccgtatgttc gagcttggta agggtcgtat ccttgtcgac 2640

ggtgtggaca tcgctaccct ttctctcaag cgtcttcgta ccggtctttc tatcattcct 2700

caggagcctg tcatgttcac cggtaccgtg cgttctaacc ttgacccttt cggtgagttc 2760

aaggacgatg ctattctttg ggaggtgctt aagaaggtcg gtctcgagga ccaggctcag 2820

cacgctggtg gtcttgacgg tcaggtcgat ggtaccggtg gtaaggcttg gtctcttggt 2880

cagatgcagc ttgtgtgcct tgctcgtgct gctcttcgtg ctgtgcctat cctttgcctt 2940

gacgaggcta ccgctgctat ggacccgcac actgaggcta tcgtgcagca gaccatcaag 3000

aaggtgttcg acgaccgtac caccatcacc attgctcacc gtcttgacac catcatcgag 3060

tctgacaaga tcatcgtgat ggagcagggt tctcttatgg agtacgagtc tccttctaag 3120

cttctcgcta accgtgactc tatgttctct aagcttgtcg acaagaccgg tcctgctgct 3180

gctgctgctc ttcgtaagat ggctgaggac ttctggtcta ctcgttctgc tcagggtcgt 3240

aaccagtaa 3249

<210> SEQ ID NO 13
<211> LENGTH: 35
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 13

```
Met Ala Ala Ser Thr Met Ala Leu Ser Ser Pro Ala Phe Ala Gly Lys
1               5                   10                  15

Ala Val Asn Leu Ser Pro Ala Ala Ser Glu Val Leu Gly Ser Gly Arg
            20                  25                  30

Val Thr Met
```

```
        35


<210> SEQ ID NO 14
<211> LENGTH: 44
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: PGR5 transit peptide

<400> SEQUENCE: 14

Met Ala Ala Ala Ser Ile Ser Ala Ile Gly Cys Asn Gln Thr Leu Ile
1               5                   10                  15

Gly Thr Ser Phe Tyr Gly Gly Trp Gly Ser Ser Ile Ser Gly Glu Asp
            20                  25                  30

Tyr Gln Thr Met Leu Ser Lys Thr Val Ala Pro Pro
        35                  40


<210> SEQ ID NO 15
<211> LENGTH: 45
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: psaD transit eptide

<400> SEQUENCE: 15

Met Ala Thr Gln Ala Ala Gly Ile Phe Asn Ser Ala Ile Thr Thr Ala
1               5                   10                  15

Ala Thr Ser Gly Val Lys Lys Leu His Phe Phe Ser Thr Thr His Arg
            20                  25                  30

Pro Lys Ser Leu Ser Phe Thr Lys Thr Ala Ile Arg Ala
        35                  40                  45


<210> SEQ ID NO 16
<211> LENGTH: 1011
<212> TYPE: DNA
<213> ORGANISM: Chlamydomonas reinhardtii

<400> SEQUENCE: 16

atgcagacca ctatgactcg cccttgcctt gcccagcccg tgctgcgatc tcgtgtgctc      60

cggtcgccta tgcgggtggt tgcagcgagc gctcctaccg cggtgacgac agtcgtgacc     120

tcgaatggaa atggcaacgg tcatttccaa gctgctacta cgcccgtgcc ccctactccc     180

gctcccgtcg ctgtttccgc gcctgtgcgc gctgtgtcgg tgctgactcc tcctcaagtg     240

tatgagaacg ccattaatgt tggcgcctac aaggccgggc taacgcctct ggcaacgttt     300

gtccagggca tccaagccgg tgcctacatt gcgttcggcg ccttcctcgc catctccgtg     360

ggaggcaaca tccccggcgt cgccgccgcc aaccccggcc tggccaagct gctatttgct     420

ctggtgttcc ccgtgggtct gtccatggtg accaactgcg gcgccgagct gttcacgggc     480

aacaccatga tgctcacatg cgcgctcatc gagaagaagg ccacttgggg gcagcttctg     540

aagaactgga gcgtgtccta cttcggcaac ttcgtgggct ccatcgccat ggtcgccgcc     600

gtggtggcca ccggctgcct gaccaccaac accctgcctg tgcagatggc caccctcaag     660

gccaacctgg gcttcaccga ggtgctgtcg cgctccatcc tgtgcaactg gctggtgtgc     720

tgcgccgtgt ggtccgcctc cgccgccacc tcgctgcccg gccgcatcct ggcgctgtgg     780

ccctgcatca ccgccttcgt ggccatcggc ctggagcact ccgtcgccaa catgttcgtg     840

attcctctgg gcatgatgct gggcgctgag gtcacgtgga gccagttctt tttcaacaac     900
```

```
ctgatccccg tcaccctggg caacaccatt gctggcgttc tcatgatggc catcgcctac    960

tccatctcgt tcggctccct cggcaagtcc gccaagcccg ccaccgcgta a            1011
```

<210> SEQ ID NO 17
<211> LENGTH: 892
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 17

```
atgatatcct cttcagctgt gactacagtc agccgtgctt ctacggtgca atcggccgcg     60

gtggctccat tcggcggcct caaatccatg actggattcc cagttaagaa ggtcaacact    120

gacattactt ccattacaag caatggtgga agagtaaagt gcatgcaggt ggagctctct    180

catcattggg gttatggtaa acacaatggt cctgaacact ggcataaaga ctttccaatt    240

gcaaaaggtg aacgtcaatc acctgttgat attgacactc atacagctaa atatgaccct    300

tctttaaaac cattatctgt ttcatatgat caagcaactt ctttacgtat tttaaacaat    360

ggtcatgctt ttaatgtaga atttgatgac tctcaagata aagcagtatt aaaaggtggt    420

ccattagatg gtacttaccg tttaattcaa tttcactttc actggggttc attagatggt    480

caaggttcag aacatactgt agataaaaaa aaatatgctg cagaattaca cttagttcac    540

tggaacacaa aatatggtga ttttggtaaa gctgtacaac aacctgatgg tttagctgtt    600

ttaggtattt ttttaaaagt tggtagtgct aaaccaggtc ttcaaaaagt tgttgatgta    660

ttagattcaa ttaaaacaaa aggtaaaagt gctgacttta ctaatttcga tcctcgtggt    720

ttacttcctg aatctttaga ttactggaca tatccaggtt cattaacaac acctcctctt    780

ttagaatgtg taacatggat tgtattaaaa gaaccaatta gtgtaagtag tgaacaagta    840

ttaaaattcc gtaaacttaa tttcaatggt gaaggtgaac cagaagaatt aa            892
```

<210> SEQ ID NO 18
<211> LENGTH: 336
<212> TYPE: PRT
<213> ORGANISM: Chlamydomonas reinhardtii

<400> SEQUENCE: 18

```
Met Gln Thr Thr Met Thr Arg Pro Cys Leu Ala Gln Pro Val Leu Arg
1               5                   10                  15

Ser Arg Val Leu Arg Ser Pro Met Arg Val Val Ala Ala Ser Ala Pro
            20                  25                  30

Thr Ala Val Thr Thr Val Val Thr Ser Asn Gly Asn Gly Asn Gly His
        35                  40                  45

Phe Gln Ala Ala Thr Thr Pro Val Pro Pro Thr Pro Ala Pro Val Ala
    50                  55                  60

Val Ser Ala Pro Val Arg Ala Val Ser Val Leu Thr Pro Pro Gln Val
65                  70                  75                  80

Tyr Glu Asn Ala Ile Asn Val Gly Ala Tyr Lys Ala Gly Leu Thr Pro
                85                  90                  95

Leu Ala Thr Phe Val Gln Gly Ile Gln Ala Gly Ala Tyr Ile Ala Phe
            100                 105                 110

Gly Ala Phe Leu Ala Ile Ser Val Gly Gly Asn Ile Pro Gly Val Ala
        115                 120                 125

Ala Ala Asn Pro Gly Leu Ala Lys Leu Leu Phe Ala Leu Val Phe Pro
    130                 135                 140

Val Gly Leu Ser Met Val Thr Asn Cys Gly Ala Glu Leu Phe Thr Gly
```

```
145                 150                 155                 160

Asn Thr Met Met Leu Thr Cys Ala Leu Ile Glu Lys Lys Ala Thr Trp
                165                 170                 175

Gly Gln Leu Leu Lys Asn Trp Ser Val Ser Tyr Phe Gly Asn Phe Val
            180                 185                 190

Gly Ser Ile Ala Met Val Ala Ala Val Val Ala Thr Gly Cys Leu Thr
        195                 200                 205

Thr Asn Thr Leu Pro Val Gln Met Ala Thr Leu Lys Ala Asn Leu Gly
    210                 215                 220

Phe Thr Glu Val Leu Ser Arg Ser Ile Leu Cys Asn Trp Leu Val Cys
225                 230                 235                 240

Cys Ala Val Trp Ser Ala Ser Ala Ala Thr Ser Leu Pro Gly Arg Ile
                245                 250                 255

Leu Ala Leu Trp Pro Cys Ile Thr Ala Phe Val Ala Ile Gly Leu Glu
            260                 265                 270

His Ser Val Ala Asn Met Phe Val Ile Pro Leu Gly Met Met Leu Gly
        275                 280                 285

Ala Glu Val Thr Trp Ser Gln Phe Phe Phe Asn Asn Leu Ile Pro Val
    290                 295                 300

Thr Leu Gly Asn Thr Ile Ala Gly Val Leu Met Met Ala Ile Ala Tyr
305                 310                 315                 320

Ser Ile Ser Phe Gly Ser Leu Gly Lys Ser Ala Lys Pro Ala Thr Ala
                325                 330                 335


<210> SEQ ID NO 19
<211> LENGTH: 260
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 19

Met Ser His His Trp Gly Tyr Gly Lys His Asn Gly Pro Glu His Trp
1               5                   10                  15

His Lys Asp Phe Pro Ile Ala Lys Gly Glu Arg Gln Ser Pro Val Asp
            20                  25                  30

Ile Asp Thr His Thr Ala Lys Tyr Asp Pro Ser Leu Lys Pro Leu Ser
        35                  40                  45

Val Ser Tyr Asp Gln Ala Thr Ser Leu Arg Ile Leu Asn Asn Gly His
    50                  55                  60

Ala Phe Asn Val Glu Phe Asp Asp Ser Gln Asp Lys Ala Val Leu Lys
65                  70                  75                  80

Gly Gly Pro Leu Asp Gly Thr Tyr Arg Leu Ile Gln Phe His Phe His
                85                  90                  95

Trp Gly Ser Leu Asp Gly Gln Gly Ser Glu His Thr Val Asp Lys Lys
            100                 105                 110

Lys Tyr Ala Ala Glu Leu His Leu Val His Trp Asn Thr Lys Tyr Gly
        115                 120                 125

Asp Phe Gly Lys Ala Val Gln Gln Pro Asp Gly Leu Ala Val Leu Gly
    130                 135                 140

Ile Phe Leu Lys Val Gly Ser Ala Lys Pro Gly Leu Gln Lys Val Val
145                 150                 155                 160

Asp Val Leu Asp Ser Ile Lys Thr Lys Gly Lys Ser Ala Asp Phe Thr
                165                 170                 175

Asn Phe Asp Pro Arg Gly Leu Leu Pro Glu Ser Leu Asp Tyr Trp Thr
            180                 185                 190
```

-continued

```
Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Leu Glu Cys Val Thr Trp
        195                 200                 205

Ile Val Leu Lys Glu Pro Ile Ser Val Ser Ser Glu Gln Val Leu Lys
    210                 215                 220

Phe Arg Lys Leu Asn Phe Asn Gly Glu Gly Glu Pro Glu Glu Leu Met
225                 230                 235                 240

Val Asp Asn Trp Arg Pro Ala Gln Pro Leu Lys Asn Arg Gln Ile Lys
                245                 250                 255

Ala Ser Phe Lys
            260


<210> SEQ ID NO 20
<211> LENGTH: 159
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 20

Met Val Met Leu Ser Thr Trp Ser Leu Met Thr Leu Arg Thr Lys Gln
1               5                   10                  15

Leu His Leu Val His Trp Asn Thr Lys Tyr Gly Asp Phe Gly Lys Ala
            20                  25                  30

Val Gln Gln Pro Asp Gly Leu Ala Val Leu Gly Ile Phe Leu Lys Val
        35                  40                  45

Gly Ser Ala Lys Pro Gly Leu Gln Lys Val Val Asp Val Leu Asp Ser
    50                  55                  60

Ile Lys Thr Lys Gly Lys Ser Ala Asp Phe Thr Asn Phe Asp Pro Arg
65                  70                  75                  80

Gly Leu Leu Pro Glu Ser Leu Asp Tyr Trp Thr Tyr Pro Gly Ser Leu
                85                  90                  95

Thr Thr Pro Pro Leu Leu Glu Cys Val Thr Trp Ile Val Leu Lys Glu
            100                 105                 110

Pro Ile Ser Val Ser Ser Glu Gln Val Leu Lys Phe Arg Lys Leu Asn
        115                 120                 125

Phe Asn Gly Glu Gly Glu Pro Glu Glu Leu Met Val Asp Asn Trp Arg
    130                 135                 140

Pro Ala Gln Pro Leu Lys Asn Arg Gln Ile Lys Ala Ser Phe Lys
145                 150                 155


<210> SEQ ID NO 21
<211> LENGTH: 252
<212> TYPE: PRT
<213> ORGANISM: Neisseria gonorrhoeae

<400> SEQUENCE: 21

Met Pro Arg Phe Pro Arg Thr Leu Pro Arg Leu Thr Ala Val Leu Leu
1               5                   10                  15

Leu Ala Cys Thr Ala Phe Ser Ala Ala Ala His Gly Asn His Thr His
            20                  25                  30

Trp Gly Tyr Thr Gly His Asp Ser Pro Glu Ser Trp Gly Asn Leu Ser
        35                  40                  45

Glu Glu Phe Arg Leu Cys Ser Thr Gly Lys Asn Gln Ser Pro Val Asn
    50                  55                  60

Ile Thr Glu Thr Val Ser Gly Lys Leu Pro Ala Ile Lys Val Asn Tyr
65                  70                  75                  80

Lys Pro Ser Met Val Asp Val Glu Asn Asn Gly His Thr Ile Gln Val
                85                  90                  95
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Asn Tyr Pro Glu Gly Gly Asn Thr Leu Thr Val Asn Gly Arg Thr Tyr
            100                 105                 110

Thr Leu Lys Gln Phe His Phe His Val Pro Ser Glu Asn Gln Ile Lys
        115                 120                 125

Gly Arg Thr Phe Pro Met Glu Ala His Phe Val His Leu Asp Glu Asn
    130                 135                 140

Lys Gln Pro Leu Val Leu Ala Val Leu Tyr Glu Ala Gly Lys Thr Asn
145                 150                 155                 160

Gly Arg Leu Ser Ser Ile Trp Asn Val Met Pro Met Thr Ala Gly Lys
                165                 170                 175

Val Lys Leu Asn Gln Pro Phe Asp Ala Ser Thr Leu Leu Pro Lys Arg
            180                 185                 190

Leu Lys Tyr Tyr Arg Phe Ala Gly Ser Leu Thr Thr Pro Pro Cys Thr
        195                 200                 205

Glu Gly Val Ser Trp Leu Val Leu Lys Thr Tyr Asp His Ile Asp Gln
    210                 215                 220

Ala Gln Ala Glu Lys Phe Thr Arg Ala Val Gly Ser Glu Asn Asn Arg
225                 230                 235                 240

Pro Val Gln Pro Leu Asn Ala Arg Val Val Ile Glu
                245                 250


<210> SEQ ID NO 22
<211> LENGTH: 217
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: DNAJ transit peptide

<400> SEQUENCE: 22

Met Ala Ser Leu Ser Thr Ile Thr Gln Pro Ser Leu Val His Ile Pro
1               5                   10                  15

Gly Glu Ser Val Leu His His Val Pro Ser Thr Cys Ser Phe Pro Trp
            20                  25                  30

Lys Pro Thr Ile Asn Thr Lys Arg Ile Ile Cys Ser Pro Ala Arg Asn
        35                  40                  45

Ser Ser Glu Val Ser Ala Glu Ala Glu Thr Glu Gly Gly Ser Ser Thr
    50                  55                  60

Ala Val Asp Glu Ala Pro Lys Glu Ser Pro Ser Leu Ile Ser Ala Leu
65                  70                  75                  80

Asn Val Glu Arg Ala Leu Arg Gly Leu Pro Ile Thr Asp Val Asp His
                85                  90                  95

Tyr Gly Arg Leu Gly Ile Phe Arg Asn Cys Ser Tyr Asp Gln Val Thr
            100                 105                 110

Ile Gly Tyr Lys Glu Arg Val Lys Glu Leu Lys Glu Gln Gly Leu Asp
        115                 120                 125

Glu Glu Gln Leu Lys Thr Lys Met Asp Leu Ile Lys Ser Tyr Thr Ile
    130                 135                 140

Leu Ser Thr Val Glu Glu Arg Arg Met Tyr Asp Trp Ser Leu Ala Arg
145                 150                 155                 160

Ser Glu Lys Ala Glu Arg Tyr Val Trp Pro Phe Glu Val Asp Ile Met
                165                 170                 175

Glu Pro Ser Arg Glu Glu Pro Pro Pro Gln Glu Pro Glu Asp Val Gly
            180                 185                 190

Pro Thr Arg Ile Leu Gly Tyr Phe Ile Gly Ala Trp Leu Val Leu Gly
        195                 200                 205
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Val Ala Leu Ser Val Ala Phe Asn Arg
    210                 215


<210> SEQ ID NO 23
<211> LENGTH: 67
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 23

Met Asp Lys Ala Leu Thr Gly Ile Ser Ala Ala Ala Leu Thr Ala Ser
1               5                   10                  15

Met Val Ile Pro Glu Ile Ala Glu Ala Ala Gly Ser Gly Ile Ser Pro
            20                  25                  30

Ser Leu Lys Asn Phe Leu Leu Ser Ile Ala Ser Gly Gly Leu Val Leu
        35                  40                  45

Thr Val Ile Ile Gly Val Val Val Gly Val Ser Asn Phe Asp Pro Val
    50                  55                  60

Lys Arg Thr
65


<210> SEQ ID NO 24
<211> LENGTH: 260
<212> TYPE: PRT
<213> ORGANISM: Macaca fascicularis

<400> SEQUENCE: 24

Met Ser His His Trp Gly Tyr Gly Lys His Asn Gly Pro Glu His Trp
1               5                   10                  15

His Lys Asp Phe Pro Ile Ala Lys Gly Gln Arg Gln Ser Pro Val Asp
            20                  25                  30

Ile Asp Thr His Thr Ala Lys Tyr Asp Pro Ser Leu Lys Pro Leu Ser
        35                  40                  45

Val Ser Tyr Asp Gln Ala Thr Ser Leu Arg Ile Leu Asn Asn Gly His
    50                  55                  60

Ser Phe Asn Val Glu Phe Asp Asp Ser Gln Asp Lys Ala Val Ile Lys
65                  70                  75                  80

Gly Gly Pro Leu Asp Gly Thr Tyr Arg Leu Ile Gln Phe His Phe His
                85                  90                  95

Trp Gly Ser Leu Asp Gly Gln Gly Ser Glu His Thr Val Asp Lys Lys
            100                 105                 110

Lys Tyr Ala Ala Glu Leu His Leu Val His Trp Asn Thr Lys Tyr Gly
        115                 120                 125

Asp Phe Gly Lys Ala Val Gln Gln Pro Asp Gly Leu Ala Val Leu Gly
    130                 135                 140

Ile Phe Leu Lys Val Gly Ser Ala Lys Pro Gly Leu Gln Lys Val Val
145                 150                 155                 160

Asp Val Leu Asp Ser Ile Lys Thr Lys Gly Lys Ser Ala Asp Phe Thr
                165                 170                 175

Asn Phe Asp Pro Arg Gly Leu Leu Pro Glu Ser Leu Asp Tyr Trp Thr
            180                 185                 190

Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Leu Glu Cys Val Thr Trp
        195                 200                 205

Ile Val Leu Lys Glu Pro Ile Ser Val Ser Ser Glu Gln Met Ser Lys
    210                 215                 220

Phe Arg Lys Leu Asn Phe Asn Gly Glu Gly Glu Pro Glu Glu Leu Met
225                 230                 235                 240
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Val Asp Asn Trp Arg Pro Ala Gln Pro Leu Lys Asn Arg Gln Ile Lys
                245                 250                 255

Ala Ser Phe Lys
            260


<210> SEQ ID NO 25
<211> LENGTH: 260
<212> TYPE: PRT
<213> ORGANISM: Pan troglodytes

<400> SEQUENCE: 25

Met Ser His His Trp Gly Tyr Gly Lys His Asn Gly Pro Glu His Trp
1               5                   10                  15

His Lys Asp Phe Pro Ile Ala Lys Gly Glu Arg Gln Ser Pro Val Asp
            20                  25                  30

Ile Asp Thr His Thr Ala Lys Tyr Asp Pro Ser Leu Lys Pro Leu Ser
        35                  40                  45

Val Ser Tyr Gly Gln Ala Thr Ser Leu Arg Ile Leu Asn Asn Gly His
    50                  55                  60

Ala Phe Asn Val Glu Phe Asp Asp Ser Gln Asp Lys Ala Val Leu Lys
65                  70                  75                  80

Gly Gly Pro Leu Asp Gly Thr Tyr Arg Leu Ile Gln Phe His Phe His
                85                  90                  95

Trp Gly Ser Leu Asp Gly Gln Gly Ser Glu His Thr Val Asp Lys Lys
            100                 105                 110

Lys Tyr Ala Ala Glu Leu His Leu Val His Trp Asn Thr Lys Tyr Gly
        115                 120                 125

Asp Phe Gly Lys Ala Val Gln Gln Pro Asp Gly Leu Ala Val Leu Gly
    130                 135                 140

Ile Phe Leu Lys Val Gly Ser Ala Lys Pro Gly Leu Gln Lys Val Val
145                 150                 155                 160

Asp Val Leu Asp Ser Ile Lys Thr Lys Gly Lys Ser Ala Asp Phe Thr
                165                 170                 175

Asn Phe Asp Pro His Gly Leu Leu Pro Glu Ser Leu Asp Tyr Trp Thr
            180                 185                 190

Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Leu Glu Cys Val Thr Trp
        195                 200                 205

Ile Val Leu Lys Glu Pro Ile Ser Val Ser Ser Glu Gln Met Leu Lys
    210                 215                 220

Phe Arg Lys Leu Asn Phe Asn Gly Glu Gly Glu Pro Glu Glu Leu Met
225                 230                 235                 240

Val Asp Asn Trp Arg Pro Ala Gln Pro Leu Lys Asn Arg Gln Ile Lys
                245                 250                 255

Ala Ser Phe Lys
            260


<210> SEQ ID NO 26
<211> LENGTH: 260
<212> TYPE: PRT
<213> ORGANISM: Pongo abelii

<400> SEQUENCE: 26

Met Ser His His Trp Gly Tyr Gly Lys His Asn Gly Pro Glu His Trp
1               5                   10                  15

His Lys Asp Phe Pro Ile Ala Lys Gly Glu Arg Gln Ser Pro Val Asp
            20                  25                  30
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Ile Asp Thr His Thr Ala Lys Tyr Asp Pro Ser Leu Lys Pro Leu Ser
        35                  40                  45

Val Cys Tyr Asp Gln Ala Thr Ser Leu Arg Ile Leu Asn Asn Gly His
    50                  55                  60

Ser Phe Asn Val Glu Phe Asp Asp Ser Gln Asp Lys Ala Val Leu Lys
65                  70                  75                  80

Gly Gly Pro Leu Asp Gly Thr Tyr Arg Leu Ile Gln Phe His Phe His
                85                  90                  95

Trp Gly Ser Leu Asp Gly Gln Gly Ser Glu His Thr Val Asp Lys Lys
            100                 105                 110

Lys Tyr Ala Ala Glu Leu His Leu Val His Trp Asn Thr Lys Tyr Gly
        115                 120                 125

Asp Phe Gly Lys Ala Val Gln Gln Pro Asp Gly Leu Ala Val Leu Gly
    130                 135                 140

Ile Phe Leu Lys Val Gly Ser Ala Lys Pro Gly Leu Gln Lys Val Val
145                 150                 155                 160

Asp Val Leu Asp Ser Ile Lys Thr Lys Gly Lys Cys Ala Asp Phe Thr
                165                 170                 175

Asn Phe Asp Pro Arg Gly Leu Leu Pro Ala Ser Leu Asp Tyr Trp Thr
            180                 185                 190

Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Leu Glu Cys Val Thr Trp
        195                 200                 205

Ile Val Leu Lys Glu Pro Ile Ser Val Ser Ser Glu Gln Met Leu Lys
    210                 215                 220

Phe Arg Lys Leu Asn Phe Asn Gly Glu Gly Glu Pro Glu Glu Leu Met
225                 230                 235                 240

Val Asp Asn Trp Arg Pro Ala Gln Pro Leu Lys Lys Arg Gln Ile Lys
                245                 250                 255

Ala Ser Phe Lys
            260


<210> SEQ ID NO 27
<211> LENGTH: 260
<212> TYPE: PRT
<213> ORGANISM: Pongo abelii

<400> SEQUENCE: 27

Met Ser His His Trp Gly Tyr Gly Lys His Asn Gly Pro Glu His Trp
1               5                   10                  15

His Lys Asp Phe Pro Ile Ala Lys Gly Glu Arg Gln Ser Pro Val Asp
            20                  25                  30

Ile Asp Thr His Thr Ala Lys Tyr Asp Pro Ser Leu Lys Pro Leu Ser
        35                  40                  45

Val Cys Tyr Asp Gln Ala Thr Ser Leu Arg Ile Leu Asn Asn Gly His
    50                  55                  60

Ser Phe Asn Val Glu Phe Asp Asp Ser Gln Asp Lys Ala Val Leu Lys
65                  70                  75                  80

Gly Gly Pro Leu Asp Gly Thr Tyr Arg Leu Ile Gln Phe His Phe His
                85                  90                  95

Trp Gly Ser Leu Asp Gly Gln Gly Ser Glu His Thr Val Asp Lys Lys
            100                 105                 110

Lys Tyr Ala Ala Glu Leu His Leu Val His Trp Asn Thr Lys Tyr Gly
        115                 120                 125

Asp Phe Gly Lys Ala Val Gln Gln Pro Asp Gly Leu Ala Val Leu Gly
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    130                 135                 140

Ile Phe Leu Lys Val Gly Ser Ala Lys Pro Gly Leu Gln Lys Val Val
145                 150                 155                 160

Asp Val Leu Asp Ser Ile Lys Thr Lys Gly Lys Cys Ala Asp Phe Thr
                165                 170                 175

Asn Phe Asp Pro Arg Gly Leu Leu Pro Ala Ser Leu Asp Tyr Trp Thr
            180                 185                 190

Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Leu Glu Cys Val Thr Trp
        195                 200                 205

Ile Val Leu Lys Glu Pro Ile Ser Val Ser Ser Glu Gln Met Leu Lys
    210                 215                 220

Phe Arg Lys Leu Asn Phe Asn Gly Glu Gly Glu Pro Glu Glu Leu Met
225                 230                 235                 240

Val Asp Asn Trp Arg Pro Ala Gln Pro Leu Lys Lys Arg Gln Ile Lys
                245                 250                 255

Ala Ser Phe Lys
            260


<210> SEQ ID NO 28
<211> LENGTH: 260
<212> TYPE: PRT
<213> ORGANISM: Callithrix jacchus

<400> SEQUENCE: 28

Met Ser His His Trp Gly Tyr Gly Lys His Asn Gly Pro Glu His Trp
1               5                   10                  15

His Lys Asp Phe Pro Ile Ala Lys Gly Glu Arg Gln Ser Pro Val Asp
            20                  25                  30

Ile Asp Thr His Thr Ala Lys Tyr Asp Pro Ser Leu Lys Pro Leu Ser
        35                  40                  45

Val Ser Tyr Asp Gln Ala Thr Ser Trp Arg Ile Leu Asn Asn Gly His
    50                  55                  60

Ser Phe Asn Val Glu Phe Asp Asp Ser Gln Asp Lys Ala Val Leu Lys
65                  70                  75                  80

Gly Gly Pro Leu Asp Gly Thr Tyr Arg Leu Ile Gln Phe His Phe His
                85                  90                  95

Trp Gly Ser Thr Asp Gly Gln Gly Ser Glu His Thr Val Asp Lys Lys
            100                 105                 110

Lys Tyr Ala Ala Glu Leu His Leu Val His Trp Asn Thr Lys Tyr Gly
        115                 120                 125

Asp Phe Gly Lys Ala Ala Gln Gln Pro Asp Gly Leu Ala Val Leu Gly
    130                 135                 140

Ile Phe Leu Lys Val Gly Ser Ala Lys Pro Gly Leu Gln Lys Val Val
145                 150                 155                 160

Asp Val Leu Asp Ser Ile Lys Thr Lys Gly Lys Ser Ala Asp Phe Thr
                165                 170                 175

Asn Phe Asp Pro Arg Gly Leu Leu Pro Glu Ser Leu Asp Tyr Trp Thr
            180                 185                 190

Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Leu Glu Ser Val Thr Trp
        195                 200                 205

Ile Val Leu Lys Glu Pro Ile Ser Val Ser Ser Glu Gln Ile Leu Lys
    210                 215                 220

Phe Arg Lys Leu Asn Phe Ser Gly Glu Gly Glu Pro Glu Glu Leu Met
225                 230                 235                 240
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Val Asp Asn Trp Arg Pro Ala Gln Pro Leu Lys Asn Arg Gln Ile Lys
            245                 250                 255

Ala Ser Phe Lys
            260


<210> SEQ ID NO 29
<211> LENGTH: 260
<212> TYPE: PRT
<213> ORGANISM: Lemur catta

<400> SEQUENCE: 29

Met Ser His His Trp Gly Tyr Gly Lys His Asn Gly Pro Glu His Trp
1               5                   10                  15

His Lys Asp Phe Pro Ile Ala Lys Gly Glu Arg Gln Ser Pro Val Asp
            20                  25                  30

Ile Asn Thr Gly Ala Ala Lys His Asp Pro Ser Leu Lys Pro Leu Ser
        35                  40                  45

Val Tyr Tyr Glu Gln Ala Thr Ser Arg Arg Ile Leu Asn Asn Gly His
    50                  55                  60

Ser Phe Asn Val Glu Phe Asp Asp Ser Gln Asp Lys Ala Val Leu Lys
65                  70                  75                  80

Gly Gly Pro Leu Asp Gly Thr Tyr Arg Leu Ile Gln Phe His Phe His
                85                  90                  95

Trp Gly Ser Leu Asp Gly Gln Gly Ser Glu His Thr Val Asp Lys Lys
            100                 105                 110

Lys Tyr Ala Ala Glu Leu His Leu Val His Trp Asn Thr Lys Tyr Gly
        115                 120                 125

Asp Phe Gly Lys Ala Val Gln Gln Pro Asp Gly Leu Ala Val Leu Gly
    130                 135                 140

Ile Phe Leu Lys Val Gly Ser Ala Lys Pro Gly Leu Gln Lys Val Val
145                 150                 155                 160

Asp Val Leu Asp Ser Ile Lys Thr Lys Gly Lys Ser Ala Asp Phe Thr
                165                 170                 175

Asn Phe Asp Pro Arg Gly Leu Leu Pro Glu Ser Leu Asp Tyr Trp Thr
            180                 185                 190

Tyr Leu Gly Ser Leu Thr Thr Pro Pro Leu Leu Glu Cys Val Thr Trp
        195                 200                 205

Ile Val Leu Lys Glu Pro Ile Ser Val Ser Ser Glu Gln Met Met Lys
    210                 215                 220

Phe Arg Lys Leu Ser Phe Ser Gly Glu Gly Glu Pro Glu Glu Leu Met
225                 230                 235                 240

Val Asp Asn Trp Arg Pro Ala Gln Pro Leu Lys Asn Arg Gln Ile Lys
                245                 250                 255

Ala Ser Phe Lys
            260


<210> SEQ ID NO 30
<211> LENGTH: 260
<212> TYPE: PRT
<213> ORGANISM: Ailuropoda melanoleuca

<400> SEQUENCE: 30

Met Ala His His Trp Gly Tyr Gly Lys His Asn Gly Pro Glu His Trp
1               5                   10                  15

Tyr Lys Asp Phe Pro Ile Ala Lys Gly Gln Arg Gln Ser Pro Val Asp
            20                  25                  30
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Ile Asp Thr Lys Ala Ala Ile His Asp Pro Ala Leu Lys Ala Leu Cys
        35                  40                  45

Pro Thr Tyr Glu Gln Ala Val Ser Gln Arg Val Ile Asn Asn Gly His
    50                  55                  60

Ser Phe Asn Val Glu Phe Asp Asp Ser Gln Asp Asn Ala Val Leu Lys
65                  70                  75                  80

Gly Gly Pro Leu Thr Gly Thr Tyr Arg Leu Ile Gln Phe His Phe His
                85                  90                  95

Trp Gly Ser Ser Asp Gly Gln Gly Ser Glu His Thr Val Asp Lys Lys
            100                 105                 110

Lys Tyr Ala Ala Glu Leu His Leu Val His Trp Asn Thr Lys Tyr Gly
        115                 120                 125

Asp Phe Gly Lys Ala Val Gln Gln Pro Asp Gly Leu Ala Val Leu Gly
    130                 135                 140

Ile Phe Leu Lys Ile Gly Asp Ala Arg Pro Gly Leu Gln Lys Val Leu
145                 150                 155                 160

Asp Ala Leu Asp Ser Ile Lys Thr Lys Gly Lys Ser Ala Asp Phe Thr
                165                 170                 175

Asn Phe Asp Pro Arg Gly Leu Leu Pro Glu Ser Leu Asp Tyr Trp Thr
            180                 185                 190

Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Leu Glu Cys Val Thr Trp
        195                 200                 205

Ile Val Leu Lys Glu Pro Ile Ser Val Ser Ser Glu Gln Met Leu Lys
    210                 215                 220

Phe Arg Arg Leu Asn Phe Asn Lys Glu Gly Glu Pro Glu Glu Leu Met
225                 230                 235                 240

Val Asp Asn Trp Arg Pro Ala Gln Pro Leu His Asn Arg Gln Ile Asn
                245                 250                 255

Ala Ser Phe Lys
            260


<210> SEQ ID NO 31
<211> LENGTH: 260
<212> TYPE: PRT
<213> ORGANISM: Equus caballus

<400> SEQUENCE: 31

Met Ser His His Trp Gly Tyr Gly Gln His Asn Gly Pro Lys His Trp
1               5                   10                  15

His Lys Asp Phe Pro Ile Ala Lys Gly Gln Arg Gln Ser Pro Val Asp
            20                  25                  30

Ile Asp Thr Lys Ala Ala Val His Asp Ala Ala Leu Lys Pro Leu Ala
        35                  40                  45

Val His Tyr Glu Gln Ala Thr Ser Arg Arg Ile Val Asn Asn Gly His
    50                  55                  60

Ser Phe Asn Val Glu Phe Asp Asp Ser Gln Asp Lys Ala Val Leu Gln
65                  70                  75                  80

Gly Gly Pro Leu Thr Gly Thr Tyr Arg Leu Ile Gln Phe His Phe His
                85                  90                  95

Trp Gly Ser Ser Asp Gly Gln Gly Ser Glu His Thr Val Asp Lys Lys
            100                 105                 110

Lys Tyr Ala Ala Glu Leu His Leu Val His Trp Asn Thr Lys Tyr Gly
        115                 120                 125

Asp Phe Gly Lys Ala Val Gln Gln Pro Asp Gly Leu Ala Val Val Gly
    130                 135                 140
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Val Phe Leu Lys Val Gly Gly Ala Lys Pro Gly Leu Gln Lys Val Leu
145                 150                 155                 160

Asp Val Leu Asp Ser Ile Lys Thr Lys Gly Lys Ser Ala Asp Phe Thr
                165                 170                 175

Asn Phe Asp Pro Arg Gly Leu Leu Pro Glu Ser Leu Asp Tyr Trp Thr
            180                 185                 190

Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Leu Glu Cys Val Thr Trp
        195                 200                 205

Ile Val Leu Arg Glu Pro Ile Ser Val Ser Ser Glu Gln Leu Leu Lys
    210                 215                 220

Phe Arg Ser Leu Asn Phe Asn Ala Glu Gly Lys Pro Glu Asp Pro Met
225                 230                 235                 240

Val Asp Asn Trp Arg Pro Ala Gln Pro Leu Asn Ser Arg Gln Ile Arg
                245                 250                 255

Ala Ser Phe Lys
            260


<210> SEQ ID NO 32
<211> LENGTH: 260
<212> TYPE: PRT
<213> ORGANISM: Canis lupus

<400> SEQUENCE: 32

Met Ala His His Trp Gly Tyr Ala Lys His Asn Gly Pro Glu His Trp
1               5                   10                  15

His Lys Asp Phe Pro Ile Ala Lys Gly Glu Arg Gln Ser Pro Val Asp
            20                  25                  30

Ile Asp Thr Lys Ala Ala Val His Asp Pro Ala Leu Lys Ser Leu Cys
        35                  40                  45

Pro Cys Tyr Asp Gln Ala Val Ser Gln Arg Ile Ile Asn Asn Gly His
    50                  55                  60

Ser Phe Asn Val Glu Phe Asp Asp Ser Gln Asp Lys Thr Val Leu Lys
65                  70                  75                  80

Gly Gly Pro Leu Thr Gly Thr Tyr Arg Leu Ile Gln Phe His Phe His
                85                  90                  95

Trp Gly Ser Ser Asp Gly Gln Gly Ser Glu His Thr Val Asp Lys Lys
            100                 105                 110

Lys Tyr Ala Ala Glu Leu His Leu Val His Trp Asn Thr Lys Tyr Gly
        115                 120                 125

Glu Phe Gly Lys Ala Val Gln Gln Pro Asp Gly Leu Ala Val Leu Gly
    130                 135                 140

Ile Phe Leu Lys Ile Gly Gly Ala Asn Pro Gly Leu Gln Lys Ile Leu
145                 150                 155                 160

Asp Ala Leu Asp Ser Ile Lys Thr Lys Gly Lys Ser Ala Asp Phe Thr
                165                 170                 175

Asn Phe Asp Pro Arg Gly Leu Leu Pro Glu Ser Leu Asp Tyr Trp Thr
            180                 185                 190

Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Leu Glu Cys Val Thr Trp
        195                 200                 205

Ile Val Leu Lys Glu Pro Ile Ser Val Ser Ser Glu Gln Met Leu Lys
    210                 215                 220

Phe Arg Lys Leu Asn Phe Asn Lys Glu Gly Glu Pro Glu Glu Leu Met
225                 230                 235                 240

Met Asp Asn Trp Arg Pro Ala Gln Pro Leu His Ser Arg Gln Ile Asn
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                245                 250                 255

Ala Ser Phe Lys
            260


<210> SEQ ID NO 33
<211> LENGTH: 260
<212> TYPE: PRT
<213> ORGANISM: Oryctolagus cuniculus

<400> SEQUENCE: 33

Met Ser His His Trp Gly Tyr Gly Lys His Asn Gly Pro Glu His Trp
1               5                   10                  15

His Lys Asp Phe Pro Ile Ala Asn Gly Glu Arg Gln Ser Pro Ile Asp
            20                  25                  30

Ile Asp Thr Asn Ala Ala Lys His Asp Pro Ser Leu Lys Pro Leu Arg
        35                  40                  45

Val Cys Tyr Glu His Pro Ile Ser Arg Arg Ile Ile Asn Asn Gly His
    50                  55                  60

Ser Phe Asn Val Glu Phe Asp Asp Ser His Asp Lys Thr Val Leu Lys
65                  70                  75                  80

Glu Gly Pro Leu Glu Gly Thr Tyr Arg Leu Ile Gln Phe His Phe His
                85                  90                  95

Trp Gly Ser Ser Asp Gly Gln Gly Ser Glu His Thr Val Asn Lys Lys
            100                 105                 110

Lys Tyr Ala Ala Glu Leu His Leu Val His Trp Asn Thr Lys Tyr Gly
        115                 120                 125

Asp Phe Gly Lys Ala Val Lys His Pro Asp Gly Leu Ala Val Leu Gly
    130                 135                 140

Ile Phe Leu Lys Ile Gly Ser Ala Thr Pro Gly Leu Gln Lys Val Val
145                 150                 155                 160

Asp Thr Leu Ser Ser Ile Lys Thr Lys Gly Lys Ser Val Asp Phe Thr
                165                 170                 175

Asp Phe Asp Pro Arg Gly Leu Leu Pro Glu Ser Leu Asp Tyr Trp Thr
            180                 185                 190

Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Leu Glu Cys Val Thr Trp
        195                 200                 205

Ile Val Leu Lys Glu Pro Ile Thr Val Ser Ser Glu Gln Met Leu Lys
    210                 215                 220

Phe Arg Asn Leu Asn Phe Asn Lys Glu Ala Glu Pro Glu Glu Pro Met
225                 230                 235                 240

Val Asp Asn Trp Arg Pro Thr Gln Pro Leu Lys Gly Arg Gln Val Lys
                245                 250                 255

Ala Ser Phe Val
            260


<210> SEQ ID NO 34
<211> LENGTH: 249
<212> TYPE: PRT
<213> ORGANISM: Ailuropoda melanoleuca

<400> SEQUENCE: 34

Gly Pro Glu His Trp Tyr Lys Asp Phe Pro Ile Ala Lys Gly Gln Arg
1               5                   10                  15

Gln Ser Pro Val Asp Ile Asp Thr Lys Ala Ala Ile His Asp Pro Ala
            20                  25                  30

Leu Lys Ala Leu Cys Pro Thr Tyr Glu Gln Ala Val Ser Gln Arg Val
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        35                  40                  45

Ile Asn Asn Gly His Ser Phe Asn Val Glu Phe Asp Asp Ser Gln Asp
    50                  55                  60

Asn Ala Val Leu Lys Gly Gly Pro Leu Thr Gly Thr Tyr Arg Leu Ile
65                  70                  75                  80

Gln Phe His Phe His Trp Gly Ser Ser Asp Gly Gln Gly Ser Glu His
                85                  90                  95

Thr Val Asp Lys Lys Lys Tyr Ala Ala Glu Leu His Leu Val His Trp
            100                 105                 110

Asn Thr Lys Tyr Gly Asp Phe Gly Lys Ala Val Gln Gln Pro Asp Gly
        115                 120                 125

Leu Ala Val Leu Gly Ile Phe Leu Lys Ile Gly Asp Ala Arg Pro Gly
    130                 135                 140

Leu Gln Lys Val Leu Asp Ala Leu Asp Ser Ile Lys Thr Lys Gly Lys
145                 150                 155                 160

Ser Ala Asp Phe Thr Asn Phe Asp Pro Arg Gly Leu Leu Pro Glu Ser
                165                 170                 175

Leu Asp Tyr Trp Thr Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Leu
            180                 185                 190

Glu Cys Val Thr Trp Ile Val Leu Lys Glu Pro Ile Ser Val Ser Ser
        195                 200                 205

Glu Gln Met Leu Lys Phe Arg Arg Leu Asn Phe Asn Lys Glu Gly Glu
    210                 215                 220

Pro Glu Glu Leu Met Val Asp Asn Trp Arg Pro Ala Gln Pro Leu His
225                 230                 235                 240

Asn Arg Gln Ile Asn Ala Ser Phe Lys
                245


<210> SEQ ID NO 35
<211> LENGTH: 260
<212> TYPE: PRT
<213> ORGANISM: Sus scrofa

<400> SEQUENCE: 35

Met Ser His His Trp Gly Tyr Asp Lys His Asn Gly Pro Glu His Trp
1               5                   10                  15

His Lys Asp Phe Pro Ile Ala Lys Gly Asp Arg Gln Ser Pro Val Asp
            20                  25                  30

Ile Asn Thr Ser Thr Ala Val His Asp Pro Ala Leu Lys Pro Leu Ser
        35                  40                  45

Leu Cys Tyr Glu Gln Ala Thr Ser Gln Arg Ile Val Asn Asn Gly His
    50                  55                  60

Ser Phe Asn Val Glu Phe Asp Ser Ser Gln Asp Lys Gly Val Leu Glu
65                  70                  75                  80

Gly Gly Pro Leu Ala Gly Thr Tyr Arg Leu Ile Gln Phe His Phe His
                85                  90                  95

Trp Gly Ser Ser Asp Gly Gln Gly Ser Glu His Thr Val Asp Lys Lys
            100                 105                 110

Lys Tyr Ala Ala Glu Leu His Leu Val His Trp Asn Thr Lys Tyr Lys
        115                 120                 125

Asp Phe Gly Glu Ala Ala Gln Gln Pro Asp Gly Leu Ala Val Leu Gly
    130                 135                 140

Val Phe Leu Lys Ile Gly Asn Ala Gln Pro Gly Leu Gln Lys Ile Val
145                 150                 155                 160
```

```
Asp Val Leu Asp Ser Ile Lys Thr Lys Gly Lys Ser Val Glu Phe Thr
                165                 170                 175

Gly Phe Asp Pro Arg Asp Leu Leu Pro Gly Ser Leu Asp Tyr Trp Thr
            180                 185                 190

Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Leu Glu Ser Val Thr Trp
        195                 200                 205

Ile Val Leu Arg Glu Pro Ile Ser Val Ser Ser Gly Gln Met Met Lys
    210                 215                 220

Phe Arg Thr Leu Asn Phe Asn Lys Glu Gly Glu Pro Glu His Pro Met
225                 230                 235                 240

Val Asp Asn Trp Arg Pro Thr Gln Pro Leu Lys Asn Arg Gln Ile Arg
                245                 250                 255

Ala Ser Phe Gln
            260
```

<210> SEQ ID NO 36
<211> LENGTH: 235
<212> TYPE: PRT
<213> ORGANISM: Callithrix jacchus

<400> SEQUENCE: 36

```
Met Ser His His Trp Gly Tyr Gly Lys His Asn Gly Pro Glu His Trp
1               5                   10                  15

His Lys Asp Phe Pro Ile Ala Lys Gly Glu Arg Gln Ser Pro Val Asp
            20                  25                  30

Ile Asp Thr His Thr Ala Lys Tyr Asp Pro Ser Leu Lys Pro Leu Ser
        35                  40                  45

Val Ser Tyr Asp Gln Ala Thr Ser Trp Arg Ile Leu Asn Asn Gly His
    50                  55                  60

Ser Phe Asn Val Glu Phe Asp Asp Ser Gln Asp Lys Ala Val Leu Lys
65                  70                  75                  80

Gly Gly Pro Leu Asp Gly Thr Tyr Arg Leu Ile Gln Leu His Leu Val
                85                  90                  95

His Trp Asn Thr Lys Tyr Gly Asp Phe Gly Lys Ala Ala Gln Gln Pro
            100                 105                 110

Asp Gly Leu Ala Val Leu Gly Ile Phe Leu Lys Val Gly Ser Ala Lys
        115                 120                 125

Pro Gly Leu Gln Lys Val Val Asp Val Leu Asp Ser Ile Lys Thr Lys
    130                 135                 140

Gly Lys Ser Ala Asp Phe Thr Asn Phe Asp Pro Arg Gly Leu Leu Pro
145                 150                 155                 160

Glu Ser Leu Asp Tyr Trp Thr Tyr Pro Gly Ser Leu Thr Thr Pro Pro
                165                 170                 175

Leu Leu Glu Ser Val Thr Trp Ile Val Leu Lys Glu Pro Ile Ser Val
            180                 185                 190

Ser Ser Glu Gln Ile Leu Lys Phe Arg Lys Leu Asn Phe Ser Gly Glu
        195                 200                 205

Gly Glu Pro Glu Glu Leu Met Val Asp Asn Trp Arg Pro Ala Gln Pro
    210                 215                 220

Leu Lys Asn Arg Gln Ile Lys Ala Ser Phe Lys
225                 230                 235
```

<210> SEQ ID NO 37
<211> LENGTH: 260
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

```
<400> SEQUENCE: 37

Met Ser His His Trp Gly Tyr Ser Lys His Asn Gly Pro Glu Asn Trp
1               5                   10                  15

His Lys Asp Phe Pro Ile Ala Asn Gly Asp Arg Gln Ser Pro Val Asp
            20                  25                  30

Ile Asp Thr Ala Thr Ala Gln His Asp Pro Ala Leu Gln Pro Leu Leu
        35                  40                  45

Ile Ser Tyr Asp Lys Ala Ala Ser Lys Ser Ile Val Asn Asn Gly His
    50                  55                  60

Ser Phe Asn Val Glu Phe Asp Asp Ser Gln Asp Asn Ala Val Leu Lys
65                  70                  75                  80

Gly Gly Pro Leu Ser Asp Ser Tyr Arg Leu Ile Gln Phe His Phe His
                85                  90                  95

Trp Gly Ser Ser Asp Gly Gln Gly Ser Glu His Thr Val Asn Lys Lys
            100                 105                 110

Lys Tyr Ala Ala Glu Leu His Leu Val His Trp Asn Thr Lys Tyr Gly
        115                 120                 125

Asp Phe Gly Lys Ala Val Gln Gln Pro Asp Gly Leu Ala Val Leu Gly
    130                 135                 140

Ile Phe Leu Lys Ile Gly Pro Ala Ser Gln Gly Leu Gln Lys Val Leu
145                 150                 155                 160

Glu Ala Leu His Ser Ile Lys Thr Lys Gly Lys Arg Ala Ala Phe Ala
                165                 170                 175

Asn Phe Asp Pro Cys Ser Leu Leu Pro Gly Asn Leu Asp Tyr Trp Thr
            180                 185                 190

Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Leu Glu Cys Val Thr Trp
        195                 200                 205

Ile Val Leu Arg Glu Pro Ile Thr Val Ser Ser Glu Gln Met Ser His
    210                 215                 220

Phe Arg Thr Leu Asn Phe Asn Glu Glu Gly Asp Ala Glu Glu Ala Met
225                 230                 235                 240

Val Asp Asn Trp Arg Pro Ala Gln Pro Leu Lys Asn Arg Lys Ile Lys
                245                 250                 255

Ala Ser Phe Lys
            260


<210> SEQ ID NO 38
<211> LENGTH: 260
<212> TYPE: PRT
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 38

Met Ser His His Trp Gly Tyr Gly Lys His Asn Gly Pro Glu His Trp
1               5                   10                  15

His Lys Asp Phe Pro Ile Ala Asn Gly Glu Arg Gln Ser Pro Val Asp
            20                  25                  30

Ile Asp Thr Lys Ala Val Val Gln Asp Pro Ala Leu Lys Pro Leu Ala
        35                  40                  45

Leu Val Tyr Gly Glu Ala Thr Ser Arg Arg Met Val Asn Asn Gly His
    50                  55                  60

Ser Phe Asn Val Glu Tyr Asp Asp Ser Gln Asp Lys Ala Val Leu Lys
65                  70                  75                  80

Asp Gly Pro Leu Thr Gly Thr Tyr Arg Leu Val Gln Phe His Phe His
                85                  90                  95
```

```
Trp Gly Ser Ser Asp Asp Gln Gly Ser Glu His Thr Val Asp Arg Lys
            100                 105                 110

Lys Tyr Ala Ala Glu Leu His Leu Val His Trp Asn Thr Lys Tyr Gly
        115                 120                 125

Asp Phe Gly Thr Ala Ala Gln Gln Pro Asp Gly Leu Ala Val Val Gly
    130                 135                 140

Val Phe Leu Lys Val Gly Asp Ala Asn Pro Ala Leu Gln Lys Val Leu
145                 150                 155                 160

Asp Ala Leu Asp Ser Ile Lys Thr Lys Gly Lys Ser Thr Asp Phe Pro
                165                 170                 175

Asn Phe Asp Pro Gly Ser Leu Leu Pro Asn Val Leu Asp Tyr Trp Thr
            180                 185                 190

Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Leu Glu Ser Val Thr Trp
        195                 200                 205

Ile Val Leu Lys Glu Pro Ile Ser Val Ser Ser Gln Gln Met Leu Lys
    210                 215                 220

Phe Arg Thr Leu Asn Phe Asn Ala Glu Gly Glu Pro Glu Leu Leu Met
225                 230                 235                 240

Leu Ala Asn Trp Arg Pro Ala Gln Pro Leu Lys Asn Arg Gln Val Arg
                245                 250                 255

Gly Phe Pro Lys
            260


<210> SEQ ID NO 39
<211> LENGTH: 232
<212> TYPE: PRT
<213> ORGANISM: Oryctolagus cuniculus

<400> SEQUENCE: 39

Gly Lys His Asn Gly Pro Glu His Trp His Lys Asp Phe Pro Ile Ala
1               5                   10                  15

Asn Gly Glu Arg Gln Ser Pro Ile Asp Ile Asp Thr Asn Ala Ala Lys
            20                  25                  30

His Asp Pro Ser Leu Lys Pro Leu Arg Val Cys Tyr Glu His Pro Ile
        35                  40                  45

Ser Arg Arg Ile Ile Asn Asn Gly His Ser Phe Asn Val Glu Phe Asp
    50                  55                  60

Asp Ser His Asp Lys Thr Val Leu Lys Glu Gly Pro Leu Glu Gly Thr
65                  70                  75                  80

Tyr Arg Leu Ile Gln Phe His Phe His Trp Gly Ser Ser Asp Gly Gln
                85                  90                  95

Gly Ser Glu His Thr Val Asn Lys Lys Lys Tyr Ala Ala Glu Leu His
            100                 105                 110

Leu Val His Trp Asn Thr Lys Tyr Gly Asp Phe Gly Lys Ala Val Lys
        115                 120                 125

His Pro Asp Gly Leu Ala Val Leu Gly Ile Phe Leu Lys Ile Gly Ser
    130                 135                 140

Ala Thr Pro Gly Leu Gln Lys Val Val Asp Thr Leu Ser Ser Ile Lys
145                 150                 155                 160

Thr Lys Gly Lys Ser Val Asp Phe Thr Asp Phe Asp Pro Arg Gly Leu
                165                 170                 175

Leu Pro Glu Ser Leu Asp Tyr Trp Thr Tyr Pro Gly Ser Leu Thr Thr
            180                 185                 190

Pro Pro Leu Leu Glu Cys Val Thr Trp Ile Val Leu Lys Glu Pro Ile
```

```
        195                 200                 205

Thr Val Ser Ser Glu Gln Met Leu Lys Phe Arg Asn Leu Asn Phe Asn
    210                 215                 220

Lys Glu Ala Glu Pro Glu Glu Pro
225                 230


<210> SEQ ID NO 40
<211> LENGTH: 260
<212> TYPE: PRT
<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 40

Met Ser His His Trp Gly Tyr Ser Lys Ser Asn Gly Pro Glu Asn Trp
1               5                   10                  15

His Lys Glu Phe Pro Ile Ala Asn Gly Asp Arg Gln Ser Pro Val Asp
            20                  25                  30

Ile Asp Thr Gly Thr Ala Gln His Asp Pro Ser Leu Gln Pro Leu Leu
        35                  40                  45

Ile Cys Tyr Asp Lys Val Ala Ser Lys Ser Ile Val Asn Asn Gly His
    50                  55                  60

Ser Phe Asn Val Glu Phe Asp Asp Ser Gln Asp Phe Ala Val Leu Lys
65                  70                  75                  80

Glu Gly Pro Leu Ser Gly Ser Tyr Arg Leu Ile Gln Phe His Phe His
                85                  90                  95

Trp Gly Ser Ser Asp Gly Gln Gly Ser Glu His Thr Val Asn Lys Lys
            100                 105                 110

Lys Tyr Ala Ala Glu Leu His Leu Val His Trp Asn Thr Lys Tyr Gly
        115                 120                 125

Asp Phe Gly Lys Ala Val Gln His Pro Asp Gly Leu Ala Val Leu Gly
    130                 135                 140

Ile Phe Leu Lys Ile Gly Pro Ala Ser Gln Gly Leu Gln Lys Ile Thr
145                 150                 155                 160

Glu Ala Leu His Ser Ile Lys Thr Lys Gly Lys Arg Ala Ala Phe Ala
                165                 170                 175

Asn Phe Asp Pro Cys Ser Leu Leu Pro Gly Asn Leu Asp Tyr Trp Thr
            180                 185                 190

Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Leu Glu Cys Val Thr Trp
        195                 200                 205

Ile Val Leu Lys Glu Pro Ile Thr Val Ser Ser Glu Gln Met Ser His
    210                 215                 220

Phe Arg Lys Leu Asn Phe Asn Ser Glu Gly Glu Ala Glu Glu Leu Met
225                 230                 235                 240

Val Asp Asn Trp Arg Pro Ala Gln Pro Leu Lys Asn Arg Lys Ile Lys
                245                 250                 255

Ala Ser Phe Lys
            260


<210> SEQ ID NO 41
<211> LENGTH: 208
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 41

Met Ser Leu Ser Ile Thr Asn Asn Gly His Ser Val Gln Val Asp Phe
1               5                   10                  15

Asn Asp Ser Asp Asp Arg Thr Val Val Thr Gly Gly Pro Leu Glu Gly
```

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            20                  25                  30

Pro Tyr Arg Leu Lys Gln Phe His Phe His Trp Gly Lys Lys His Asp
        35                  40                  45

Val Gly Ser Glu His Thr Val Asp Gly Lys Ser Phe Pro Ser Glu Leu
    50                  55                  60

His Leu Val His Trp Asn Ala Lys Lys Tyr Ser Thr Phe Gly Glu Ala
65                  70                  75                  80

Ala Ser Ala Pro Asp Gly Leu Ala Val Val Gly Val Phe Leu Glu Thr
                85                  90                  95

Gly Asp Glu His Pro Ser Met Asn Arg Leu Thr Asp Ala Leu Tyr Met
            100                 105                 110

Val Arg Phe Lys Gly Thr Lys Ala Gln Phe Ser Cys Phe Asn Pro Lys
        115                 120                 125

Cys Leu Leu Pro Ala Ser Arg His Tyr Trp Thr Tyr Pro Gly Ser Leu
    130                 135                 140

Thr Thr Pro Pro Leu Ser Glu Ser Val Thr Trp Ile Val Leu Arg Glu
145                 150                 155                 160

Pro Ile Cys Ile Ser Glu Arg Gln Met Gly Lys Phe Arg Ser Leu Leu
                165                 170                 175

Phe Thr Ser Glu Asp Asp Glu Arg Ile His Met Val Asn Asn Phe Arg
            180                 185                 190

Pro Pro Gln Pro Leu Lys Gly Arg Val Val Lys Ala Ser Phe Arg Ala
        195                 200                 205


<210> SEQ ID NO 42
<211> LENGTH: 264
<212> TYPE: PRT
<213> ORGANISM: Pongo abelii

<400> SEQUENCE: 42

Met Thr Gly His His Gly Trp Gly Tyr Gly Gln Asp Asp Gly Pro Ser
1               5                   10                  15

His Trp His Lys Leu Tyr Pro Ile Ala Gln Gly Asp Arg Gln Ser Pro
            20                  25                  30

Ile Asn Ile Ile Ser Ser Gln Ala Val Tyr Ser Pro Ser Leu Gln Pro
        35                  40                  45

Leu Glu Leu Ser Tyr Glu Ala Cys Met Ser Leu Ser Ile Thr Asn Asn
    50                  55                  60

Gly His Ser Val Gln Val Asp Phe Asn Asp Ser Asp Asp Arg Thr Val
65                  70                  75                  80

Val Thr Gly Gly Pro Leu Glu Gly Pro Tyr Arg Leu Lys Gln Phe His
                85                  90                  95

Phe His Trp Gly Lys Lys His Asp Val Gly Ser Glu His Thr Val Asp
            100                 105                 110

Gly Lys Ser Phe Pro Ser Glu Leu His Leu Val His Trp Asn Ala Lys
        115                 120                 125

Lys Tyr Ser Thr Phe Gly Glu Ala Ala Ser Ala Pro Asp Gly Leu Ala
    130                 135                 140

Val Val Gly Val Phe Leu Glu Thr Gly Asp Glu His Pro Ser Met Asn
145                 150                 155                 160

Arg Leu Thr Asp Ala Leu Tyr Met Val Arg Phe Lys Gly Thr Lys Ala
                165                 170                 175

Gln Phe Ser Cys Phe Asn Pro Lys Ser Leu Leu Pro Ala Ser Arg His
            180                 185                 190
```

```
Tyr Trp Thr Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Ser Glu Ser
        195                 200                 205

Val Thr Trp Ile Val Leu Arg Glu Pro Ile Cys Ile Ser Glu Arg Gln
    210                 215                 220

Met Gly Lys Phe Arg Ser Leu Leu Phe Thr Ser Glu Asp Asp Glu Arg
225                 230                 235                 240

Ile His Met Val Asn Asn Phe Arg Pro Pro Gln Pro Leu Lys Gly Arg
                245                 250                 255

Val Val Lys Ala Ser Phe Arg Ala
            260
```

<210> SEQ ID NO 43
<211> LENGTH: 264
<212> TYPE: PRT
<213> ORGANISM: Pan troglodytes

<400> SEQUENCE: 43

```
Met Thr Gly His His Gly Trp Gly Tyr Gly Gln Asp Asp Gly Pro Ser
1               5                   10                  15

His Trp His Lys Leu Tyr Pro Ile Ala Gln Gly Asp Arg Gln Ser Pro
            20                  25                  30

Ile Asn Ile Ile Ser Ser Gln Ala Val Tyr Ser Pro Ser Leu Gln Pro
        35                  40                  45

Leu Glu Leu Ser Tyr Glu Ala Cys Met Ser Leu Ser Ile Thr Asn Asn
    50                  55                  60

Gly His Ser Val Gln Val Asp Phe Asn Asp Ser Asp Asp Arg Thr Val
65                  70                  75                  80

Val Thr Gly Gly Pro Leu Glu Gly Pro Tyr Arg Leu Lys Gln Phe His
                85                  90                  95

Phe His Trp Gly Lys Lys His Asp Val Gly Ser Glu His Thr Val Asp
            100                 105                 110

Gly Lys Ser Phe Pro Ser Glu Leu His Leu Val His Trp Asn Ala Lys
        115                 120                 125

Lys Tyr Ser Thr Phe Gly Glu Ala Ala Ser Ala Pro Asp Gly Leu Ala
    130                 135                 140

Val Val Gly Val Phe Leu Glu Thr Gly Asp Glu His Pro Ser Met Asn
145                 150                 155                 160

Arg Leu Thr Asp Ala Leu Tyr Met Val Arg Phe Lys Gly Thr Lys Ala
                165                 170                 175

Gln Phe Ser Cys Phe Asn Pro Lys Cys Leu Leu Pro Ala Ser Arg His
            180                 185                 190

Tyr Trp Thr Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Ser Glu Ser
        195                 200                 205

Val Thr Trp Ile Val Leu Arg Glu Pro Ile Cys Ile Ser Glu Arg Gln
    210                 215                 220

Met Arg Lys Phe Arg Ser Leu Leu Phe Thr Ser Glu Asp Asp Glu Arg
225                 230                 235                 240

Ile His Met Val Asn Asn Phe Arg Pro Pro Gln Pro Leu Lys Gly Arg
                245                 250                 255

Val Val Lys Ala Ser Phe Arg Ala
            260
```

<210> SEQ ID NO 44
<211> LENGTH: 264
<212> TYPE: PRT
<213> ORGANISM: Callithrix jacchus

```
<400> SEQUENCE: 44

Met Thr Gly His His Gly Trp Gly Tyr Gly Gln Asp Asp Gly Pro Ser
1               5                   10                  15

His Trp His Lys Leu Tyr Pro Ile Ala Gln Gly Asp Arg Gln Ser Pro
            20                  25                  30

Ile Asn Ile Ile Ser Ser Gln Ala Val Tyr Ser Pro Ser Leu Gln Pro
        35                  40                  45

Leu Glu Leu Ser Tyr Glu Ala Cys Met Ser Leu Ser Ile Thr Asn Asn
    50                  55                  60

Gly His Ser Val Gln Val Asp Phe Asn Asp Ser Asp Asp Arg Thr Val
65                  70                  75                  80

Val Thr Gly Gly Pro Leu Glu Gly Pro Tyr Arg Leu Lys Gln Phe His
                85                  90                  95

Phe His Trp Gly Lys Lys His Asp Val Gly Ser Glu His Thr Val Asp
            100                 105                 110

Gly Lys Ser Phe Pro Ser Glu Leu His Leu Val His Trp Asn Ala Lys
        115                 120                 125

Lys Tyr Ser Thr Phe Gly Glu Ala Ala Ser Ala Pro Asp Gly Leu Ala
    130                 135                 140

Val Val Gly Val Phe Leu Glu Thr Gly Asp Glu His Pro Ser Met Asn
145                 150                 155                 160

Arg Leu Thr Asp Ala Leu Tyr Met Val Arg Phe Lys Gly Thr Lys Ala
                165                 170                 175

Gln Phe Ser Cys Phe Asn Pro Lys Cys Leu Leu Pro Ala Ser Trp His
            180                 185                 190

Tyr Trp Thr Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Ser Glu Ser
        195                 200                 205

Val Thr Trp Ile Val Leu Arg Glu Pro Ile Cys Ile Ser Glu Arg Gln
    210                 215                 220

Met Gly Lys Phe Arg Ser Leu Leu Phe Thr Ser Glu Asp Asp Glu Arg
225                 230                 235                 240

Val His Met Val Asn Asn Phe Arg Pro Pro Gln Pro Leu Lys Gly Arg
                245                 250                 255

Val Val Lys Ala Ser Phe Arg Ala
            260


<210> SEQ ID NO 45
<211> LENGTH: 251
<212> TYPE: PRT
<213> ORGANISM: Ailuropoda melanoleuca

<400> SEQUENCE: 45

Gly Pro Ser Gln Trp His Lys Leu Tyr Pro Ile Ala Gln Gly Asp Arg
1               5                   10                  15

Gln Ser Pro Ile Asn Ile Val Ser Ser Gln Ala Val Tyr Ser Pro Ser
            20                  25                  30

Leu Lys Pro Leu Glu Leu Ser Tyr Glu Ala Cys Ile Ser Leu Ser Ile
        35                  40                  45

Ala Asn Asn Gly His Ser Val Gln Val Asp Phe Asn Asp Ser Asp Asp
    50                  55                  60

Arg Thr Val Val Thr Gly Gly Pro Leu Asp Gly Pro Tyr Arg Leu Lys
65                  70                  75                  80

Gln Phe His Phe His Trp Gly Lys Lys His Ser Val Gly Ser Glu His
                85                  90                  95
```

Thr Val Asp Gly Lys Ser Phe Pro Ser Glu Leu His Leu Val His Trp
100 105 110

Asn Ala Lys Lys Tyr Ser Thr Phe Gly Glu Ala Ala Ser Ala Pro Asp
115 120 125

Gly Leu Ala Val Val Gly Val Phe Leu Glu Thr Gly Asp Glu His Pro
130 135 140

Ser Met Asn Arg Leu Thr Asp Ala Leu Tyr Met Val Arg Phe Lys Gly
145 150 155 160

Thr Lys Ala Gln Phe Ser Cys Phe Asn Pro Lys Cys Leu Leu Pro Ala
165 170 175

Ser Arg His Tyr Trp Thr Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu
180 185 190

Ser Glu Ser Val Thr Trp Ile Val Leu Arg Glu Pro Ile Ser Ile Ser
195 200 205

Glu Arg Gln Met Glu Lys Phe Arg Ser Leu Leu Phe Thr Ser Glu Asp
210 215 220

Asp Glu Arg Ile His Met Val Asn Asn Phe Arg Pro Pro Gln Pro Leu
225 230 235 240

Lys Gly Arg Val Val Lys Ala Ser Phe Arg Ala
245 250

<210> SEQ ID NO 46
<211> LENGTH: 264
<212> TYPE: PRT
<213> ORGANISM: Canis familiaris

<400> SEQUENCE: 46

Met Thr Gly His His Cys Trp Gly Tyr Gly Gln Asn Asp Gly Pro Ser
1 5 10 15

Gln Trp His Lys Leu Tyr Pro Ile Ala Gln Gly Asp Arg Gln Ser Pro
20 25 30

Ile Asn Ile Val Ser Ser Gln Ala Val Tyr Ser Pro Ser Leu Lys Pro
35 40 45

Leu Glu Leu Ser Tyr Glu Ala Cys Ile Ser Leu Ser Ile Thr Asn Asn
50 55 60

Gly His Ser Val Gln Val Asp Phe Asn Asp Ser Asp Asp Arg Thr Ala
65 70 75 80

Val Thr Gly Gly Pro Leu Asp Gly Pro Tyr Arg Leu Lys Gln Leu His
85 90 95

Phe His Trp Gly Lys Lys His Ser Val Gly Ser Glu His Thr Val Asp
100 105 110

Gly Lys Ser Phe Pro Ser Glu Leu His Leu Val His Trp Asn Ala Lys
115 120 125

Lys Tyr Ser Thr Phe Gly Glu Ala Ala Ser Ala Pro Asp Gly Leu Ala
130 135 140

Val Val Gly Ile Phe Leu Glu Thr Gly Asp Glu His Pro Ser Met Asn
145 150 155 160

Arg Leu Thr Asp Ala Leu Tyr Met Val Arg Phe Lys Gly Thr Lys Ala
165 170 175

Gln Phe Ser Cys Phe Asn Pro Lys Cys Leu Leu Pro Ala Ser Arg His
180 185 190

Tyr Trp Thr Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Ser Glu Ser
195 200 205

Val Thr Trp Ile Val Leu Arg Glu Pro Ile Ser Ile Ser Glu Arg Gln

```
    210                 215                 220

Met Glu Lys Phe Arg Ser Leu Leu Phe Thr Ser Glu Glu Asp Glu Arg
225                 230                 235                 240

Ile His Met Val Asn Asn Phe Arg Pro Pro Gln Pro Leu Lys Gly Arg
                245                 250                 255

Val Val Lys Ala Ser Phe Arg Ala
            260


<210> SEQ ID NO 47
<211> LENGTH: 264
<212> TYPE: PRT
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 47

Met Thr Gly His His Gly Trp Gly Tyr Gly Gln Asn Asp Gly Pro Ser
1               5                   10                  15

His Trp His Lys Leu Tyr Pro Ile Ala Gln Gly Asp Arg Gln Ser Pro
            20                  25                  30

Ile Asn Ile Val Ser Ser Gln Ala Val Tyr Ser Pro Ser Leu Lys Pro
        35                  40                  45

Leu Glu Ile Ser Tyr Glu Ser Cys Thr Ser Leu Ser Ile Ala Asn Asn
    50                  55                  60

Gly His Ser Val Gln Val Asp Phe Asn Asp Ser Asp Asp Arg Thr Val
65                  70                  75                  80

Val Ser Gly Gly Pro Leu Asp Gly Pro Tyr Arg Leu Lys Gln Phe His
                85                  90                  95

Phe His Trp Gly Lys Lys His Gly Val Gly Ser Glu His Thr Val Asp
            100                 105                 110

Gly Lys Ser Phe Pro Ser Glu Leu His Leu Val His Trp Asn Ala Lys
        115                 120                 125

Lys Tyr Ser Thr Phe Gly Glu Ala Ala Ser Ala Pro Asp Gly Leu Ala
    130                 135                 140

Val Val Gly Val Phe Leu Glu Thr Gly Asp Glu His Pro Ser Met Asn
145                 150                 155                 160

Arg Leu Thr Asp Ala Leu Tyr Met Val Arg Phe Lys Gly Thr Lys Ala
                165                 170                 175

Gln Phe Ser Cys Phe Asn Pro Lys Cys Leu Leu Pro Ala Ser Arg His
            180                 185                 190

Tyr Trp Thr Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Ser Glu Ser
        195                 200                 205

Val Thr Trp Ile Val Leu Arg Glu Pro Ile Arg Ile Ser Glu Arg Gln
    210                 215                 220

Met Glu Lys Phe Arg Ser Leu Leu Phe Thr Ser Glu Glu Asp Glu Arg
225                 230                 235                 240

Ile His Met Val Asn Asn Phe Arg Pro Pro Gln Pro Leu Lys Gly Arg
                245                 250                 255

Val Val Lys Ala Ser Phe Arg Ala
            260


<210> SEQ ID NO 48
<211> LENGTH: 271
<212> TYPE: PRT
<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 48

Met Thr Val Leu Trp Trp Pro Met Leu Arg Glu Glu Leu Met Ser Lys
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1               5                   10                  15

Leu Arg Thr Gly Gly Pro Ser Asn Trp His Lys Leu Tyr Pro Ile Ala
            20                  25                  30

Gln Gly Asp Arg Gln Ser Pro Ile Asn Ile Ile Ser Ser Gln Ala Val
        35                  40                  45

Tyr Ser Pro Ser Leu Gln Pro Leu Glu Leu Phe Tyr Glu Ala Cys Met
    50                  55                  60

Ser Leu Ser Ile Thr Asn Asn Gly His Ser Val Gln Val Asp Phe Asn
65                  70                  75                  80

Asp Ser Asp Asp Arg Thr Val Val Ala Gly Gly Pro Leu Glu Gly Pro
                85                  90                  95

Tyr Arg Leu Lys Gln Leu His Phe His Trp Gly Lys Lys Arg Asp Val
            100                 105                 110

Gly Ser Glu His Thr Val Asp Gly Lys Ser Phe Pro Ser Glu Leu His
        115                 120                 125

Leu Val His Trp Asn Ala Lys Lys Tyr Ser Thr Phe Gly Glu Ala Ala
    130                 135                 140

Ala Ala Pro Asp Gly Leu Ala Val Val Gly Ile Phe Leu Glu Thr Gly
145                 150                 155                 160

Asp Glu His Pro Ser Met Asn Arg Leu Thr Asp Ala Leu Tyr Met Val
                165                 170                 175

Arg Phe Lys Asp Thr Lys Ala Gln Phe Ser Cys Phe Asn Pro Lys Cys
            180                 185                 190

Leu Leu Pro Thr Ser Arg His Tyr Trp Thr Tyr Pro Gly Ser Leu Thr
        195                 200                 205

Thr Pro Pro Leu Ser Glu Ser Val Thr Trp Ile Val Leu Arg Glu Pro
    210                 215                 220

Ile Arg Ile Ser Glu Arg Gln Met Glu Lys Phe Arg Ser Leu Leu Phe
225                 230                 235                 240

Thr Ser Glu Asp Asp Glu Arg Ile His Met Val Asn Asn Phe Arg Pro
                245                 250                 255

Pro Gln Pro Leu Lys Gly Arg Val Val Lys Ala Ser Phe Gln Ser
            260                 265                 270


<210> SEQ ID NO 49
<211> LENGTH: 266
<212> TYPE: PRT
<213> ORGANISM: Oryctolagus cuniculus

<400> SEQUENCE: 49

Met Thr Gly His His Gly Trp Gly Tyr Gly Gln Asp Asp Gly Gly Arg
1               5                   10                  15

Pro Ser His Trp His Lys Leu Tyr Pro Ile Ala Gln Gly Asp Arg Gln
            20                  25                  30

Ser Pro Ile Asn Ile Val Ser Ser Gln Ala Val Tyr Ser Pro Gly Leu
        35                  40                  45

Gln Pro Leu Glu Leu Ser Tyr Glu Ala Cys Thr Ser Leu Ser Ile Ala
    50                  55                  60

Asn Asn Gly His Ser Val Gln Val Asp Phe Asn Asp Ser Asp Asp Arg
65                  70                  75                  80

Thr Val Val Thr Gly Gly Pro Leu Glu Gly Pro Tyr Arg Leu Lys Gln
                85                  90                  95

Phe His Phe His Trp Gly Lys Arg Arg Asp Ala Gly Ser Glu His Thr
            100                 105                 110
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Val Asp Gly Lys Ser Phe Pro Ser Glu Leu His Leu Val His Trp Asn
        115                 120                 125

Ala Arg Lys Tyr Ser Thr Phe Gly Glu Ala Ala Ser Ala Pro Asp Gly
    130                 135                 140

Leu Ala Val Val Gly Val Phe Leu Glu Thr Gly Asn Glu His Pro Ser
145                 150                 155                 160

Met Asn Arg Leu Thr Asp Ala Leu Tyr Met Val Arg Phe Lys Gly Thr
                165                 170                 175

Lys Ala Gln Phe Ser Cys Phe Asn Pro Lys Cys Leu Leu Pro Ser Ser
            180                 185                 190

Arg His Tyr Trp Thr Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Ser
        195                 200                 205

Glu Ser Val Thr Trp Ile Val Leu Arg Glu Pro Ile Ser Ile Ser Glu
    210                 215                 220

Arg Gln Met Glu Lys Phe Arg Ser Leu Leu Phe Thr Ser Glu Asp Asp
225                 230                 235                 240

Glu Arg Val His Met Val Asn Asn Phe Arg Pro Pro Gln Pro Leu Arg
                245                 250                 255

Gly Arg Val Val Lys Ala Ser Phe Arg Ala
            260                 265


<210> SEQ ID NO 50
<211> LENGTH: 255
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 50

Gly Gln Asp Asp Gly Pro Ser Asn Trp His Lys Leu Tyr Pro Ile Ala
1               5                   10                  15

Gln Gly Asp Arg Gln Ser Pro Ile Asn Ile Ile Ser Ser Gln Ala Val
            20                  25                  30

Tyr Ser Pro Ser Leu Gln Pro Leu Glu Leu Phe Tyr Glu Ala Cys Met
        35                  40                  45

Ser Leu Ser Ile Thr Asn Asn Gly His Ser Val Gln Val Asp Phe Asn
    50                  55                  60

Asp Ser Asp Asp Arg Thr Val Val Ser Gly Gly Pro Leu Glu Gly Pro
65                  70                  75                  80

Tyr Arg Leu Lys Gln Leu His Phe His Trp Gly Lys Lys Arg Asp Met
                85                  90                  95

Gly Ser Glu His Thr Val Asp Gly Lys Ser Phe Pro Ser Glu Leu His
            100                 105                 110

Leu Val His Trp Asn Ala Lys Lys Tyr Ser Thr Phe Gly Glu Ala Ala
        115                 120                 125

Ala Ala Pro Asp Gly Leu Ala Val Val Gly Val Phe Leu Glu Thr Gly
    130                 135                 140

Asp Glu His Pro Ser Met Asn Arg Leu Thr Asp Ala Leu Tyr Met Val
145                 150                 155                 160

Arg Phe Lys Asp Thr Lys Ala Gln Phe Ser Cys Phe Asn Pro Lys Cys
                165                 170                 175

Leu Leu Pro Thr Ser Arg His Tyr Trp Thr Tyr Pro Gly Ser Leu Thr
            180                 185                 190

Thr Pro Pro Leu Ser Glu Ser Val Thr Trp Ile Val Leu Arg Glu Pro
        195                 200                 205

Ile Arg Ile Ser Glu Arg Gln Met Glu Lys Phe Arg Ser Leu Leu Phe
    210                 215                 220
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Thr Ser Glu Asp Asp Glu Arg Ile His Met Val Asp Asn Phe Arg Pro
225                 230                 235                 240

Pro Gln Pro Leu Lys Gly Arg Val Val Lys Ala Ser Phe Gln Ala
                245                 250                 255


<210> SEQ ID NO 51
<211> LENGTH: 264
<212> TYPE: PRT
<213> ORGANISM: Monodelphis domestica

<400> SEQUENCE: 51

Met Thr Gly His His Gly Trp Gly Tyr Gly Gln Glu Asp Gly Pro Ser
1               5                   10                  15

Glu Trp His Lys Leu Tyr Pro Ile Ala Gln Gly Asp Arg Gln Ser Pro
            20                  25                  30

Ile Asp Ile Val Ser Ser Gln Ala Val Tyr Asp Pro Thr Leu Lys Pro
        35                  40                  45

Leu Val Leu Ala Tyr Glu Ser Cys Met Ser Leu Ser Ile Ala Asn Asn
    50                  55                  60

Gly His Ser Val Met Val Glu Phe Asp Asp Val Asp Asp Arg Thr Val
65                  70                  75                  80

Val Asn Gly Gly Pro Leu Asp Gly Pro Tyr Arg Leu Lys Gln Phe His
                85                  90                  95

Phe His Trp Gly Lys Lys His Ser Leu Gly Ser Glu His Thr Val Asp
            100                 105                 110

Gly Lys Ser Phe Ser Ser Glu Leu His Leu Val His Trp Asn Gly Lys
        115                 120                 125

Lys Tyr Lys Thr Phe Ala Glu Ala Ala Ala Ala Pro Asp Gly Leu Ala
    130                 135                 140

Val Val Gly Ile Phe Leu Glu Thr Gly Asp Glu His Ala Ser Met Asn
145                 150                 155                 160

Arg Leu Thr Asp Ala Leu Tyr Met Val Arg Phe Lys Gly Thr Lys Ala
                165                 170                 175

Gln Phe Asn Ser Phe Asn Pro Lys Cys Leu Leu Pro Met Asn Leu Ser
            180                 185                 190

Tyr Trp Thr Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Ser Glu Ser
        195                 200                 205

Val Thr Trp Ile Val Leu Lys Glu Pro Ile Thr Ile Ser Glu Lys Gln
    210                 215                 220

Met Glu Lys Phe Arg Ser Leu Leu Phe Thr Ala Glu Glu Asp Glu Lys
225                 230                 235                 240

Val Arg Met Val Asn Asn Phe Arg Pro Pro Gln Pro Leu Lys Gly Arg
                245                 250                 255

Val Val Gln Ala Ser Phe Arg Ser
            260


<210> SEQ ID NO 52
<211> LENGTH: 264
<212> TYPE: PRT
<213> ORGANISM: Gallus gallus

<400> SEQUENCE: 52

Met Thr Gly His His Ser Trp Gly Tyr Gly Gln Asp Asp Gly Pro Ser
1               5                   10                  15

Glu Trp His Lys Ser Tyr Pro Ile Ala Gln Gly Asn Arg Gln Ser Pro
            20                  25                  30
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Ile Asp Ile Ile Ser Ala Lys Ala Val Tyr Asp Pro Lys Leu Met Pro
        35                  40                  45

Leu Val Ile Ser Tyr Glu Ser Cys Thr Ser Leu Asn Ile Ser Asn Asn
    50                  55                  60

Gly His Ser Val Met Val Glu Phe Glu Asp Ile Asp Asp Lys Thr Val
65                  70                  75                  80

Ile Ser Gly Gly Pro Phe Glu Ser Pro Phe Arg Leu Lys Gln Phe His
                85                  90                  95

Phe His Trp Gly Ala Lys His Ser Glu Gly Ser Glu His Thr Ile Asp
            100                 105                 110

Gly Lys Pro Phe Pro Cys Glu Leu His Leu Val His Trp Asn Ala Lys
        115                 120                 125

Lys Tyr Ala Thr Phe Gly Glu Ala Ala Ala Ala Pro Asp Gly Leu Ala
    130                 135                 140

Val Val Gly Val Phe Leu Glu Ile Gly Lys Glu His Ala Asn Met Asn
145                 150                 155                 160

Arg Leu Thr Asp Ala Leu Tyr Met Val Lys Phe Lys Gly Thr Lys Ala
                165                 170                 175

Gln Phe Arg Ser Phe Asn Pro Lys Cys Leu Leu Pro Leu Ser Leu Asp
            180                 185                 190

Tyr Trp Thr Tyr Leu Gly Ser Leu Thr Thr Pro Pro Leu Asn Glu Ser
        195                 200                 205

Val Ile Trp Val Val Leu Lys Glu Pro Ile Ser Ile Ser Glu Lys Gln
    210                 215                 220

Leu Glu Lys Phe Arg Met Leu Leu Phe Thr Ser Glu Glu Asp Gln Lys
225                 230                 235                 240

Val Gln Met Val Asn Asn Phe Arg Pro Pro Gln Pro Leu Lys Gly Arg
                245                 250                 255

Thr Val Arg Ala Ser Phe Lys Ala
            260


<210> SEQ ID NO 53
<211> LENGTH: 264
<212> TYPE: PRT
<213> ORGANISM: Taeniopygia guttata

<400> SEQUENCE: 53

Met Thr Gly Gln His Ser Trp Gly Tyr Gly Gln Ala Asp Gly Pro Ser
1               5                   10                  15

Glu Trp His Lys Ala Tyr Pro Ile Ala Gln Gly Asn Arg Gln Ser Pro
            20                  25                  30

Ile Asp Ile Asp Ser Ala Arg Ala Val Tyr Asp Pro Ser Leu Gln Pro
        35                  40                  45

Leu Leu Ile Ser Tyr Glu Ser Cys Ser Ser Leu Ser Ile Ser Asn Thr
    50                  55                  60

Gly His Ser Val Met Val Glu Phe Glu Asp Thr Asp Asp Arg Thr Ala
65                  70                  75                  80

Ile Ser Gly Gly Pro Phe Gln Asn Pro Phe Arg Leu Lys Gln Phe His
                85                  90                  95

Phe His Trp Gly Thr Thr His Ser Gln Gly Ser Glu His Thr Ile Asp
            100                 105                 110

Gly Lys Pro Phe Pro Cys Glu Leu His Leu Val His Trp Asn Ala Arg
        115                 120                 125

Lys Tyr Thr Thr Phe Gly Glu Ala Ala Ala Ala Pro Asp Gly Leu Ala
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    130                 135                 140

Val Val Gly Val Phe Leu Glu Ile Gly Lys Glu His Ala Ser Met Asn
145                 150                 155                 160

Arg Leu Thr Asp Ala Leu Tyr Met Val Lys Phe Lys Gly Thr Lys Ala
                165                 170                 175

Gln Phe Arg Gly Phe Asn Pro Lys Cys Leu Leu Pro Leu Ser Leu Asp
            180                 185                 190

Tyr Trp Thr Tyr Leu Gly Ser Leu Thr Thr Pro Pro Leu Asn Glu Ser
        195                 200                 205

Val Thr Trp Ile Val Leu Lys Glu Pro Ile Arg Ile Ser Val Lys Gln
    210                 215                 220

Leu Glu Lys Phe Arg Met Leu Leu Phe Thr Gly Glu Glu Asp Gln Arg
225                 230                 235                 240

Ile Gln Met Ala Asn Asn Phe Arg Pro Pro Gln Pro Leu Lys Gly Arg
                245                 250                 255

Ile Val Arg Ala Ser Phe Lys Ala
            260


<210> SEQ ID NO 54
<211> LENGTH: 262
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 54

Met Ser Arg Leu Ser Trp Gly Tyr Arg Glu His Asn Gly Pro Ile His
1               5                   10                  15

Trp Lys Glu Phe Phe Pro Ile Ala Asp Gly Asp Gln Gln Ser Pro Ile
            20                  25                  30

Glu Ile Lys Thr Lys Glu Val Lys Tyr Asp Ser Ser Leu Arg Pro Leu
        35                  40                  45

Ser Ile Lys Tyr Asp Pro Ser Ser Ala Lys Ile Ile Ser Asn Ser Gly
    50                  55                  60

His Ser Phe Asn Val Asp Phe Asp Asp Thr Glu Asn Lys Ser Val Leu
65                  70                  75                  80

Arg Gly Gly Pro Leu Thr Gly Ser Tyr Arg Leu Arg Gln Val His Leu
                85                  90                  95

His Trp Gly Ser Ala Asp Asp His Gly Ser Glu His Ile Val Asp Gly
            100                 105                 110

Val Ser Tyr Ala Ala Glu Leu His Val Val His Trp Asn Ser Asp Lys
        115                 120                 125

Tyr Pro Ser Phe Val Glu Ala Ala His Glu Pro Asp Gly Leu Ala Val
    130                 135                 140

Leu Gly Val Phe Leu Gln Ile Gly Glu Pro Asn Ser Gln Leu Gln Lys
145                 150                 155                 160

Ile Thr Asp Thr Leu Asp Ser Ile Lys Glu Lys Gly Lys Gln Thr Arg
                165                 170                 175

Phe Thr Asn Phe Asp Leu Leu Ser Leu Leu Pro Pro Ser Trp Asp Tyr
            180                 185                 190

Trp Thr Tyr Pro Gly Ser Leu Thr Val Pro Pro Leu Leu Glu Ser Val
        195                 200                 205

Thr Trp Ile Val Leu Lys Gln Pro Ile Asn Ile Ser Ser Gln Gln Leu
    210                 215                 220

Ala Lys Phe Arg Ser Leu Leu Cys Thr Ala Glu Gly Glu Ala Ala Ala
225                 230                 235                 240
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Phe Leu Val Ser Asn His Arg Pro Pro Gln Pro Leu Lys Gly Arg Lys
                245                 250                 255

Val Arg Ala Ser Phe His
            260


<210> SEQ ID NO 55
<211> LENGTH: 262
<212> TYPE: PRT
<213> ORGANISM: Pan troglodytes

<400> SEQUENCE: 55

Met Ser Arg Leu Ser Trp Gly Tyr Arg Glu His Asn Gly Pro Ile His
1               5                   10                  15

Trp Lys Glu Phe Phe Pro Ile Ala Asp Gly Asp Gln Gln Ser Pro Ile
            20                  25                  30

Glu Ile Lys Thr Lys Glu Val Lys Tyr Asp Ser Ser Leu Arg Pro Leu
        35                  40                  45

Ser Ile Lys Tyr Asp Pro Ser Ser Ala Lys Ile Ile Ser Asn Ser Gly
    50                  55                  60

His Ser Phe Asn Val Asp Phe Asp Asp Thr Glu Asn Lys Ser Val Leu
65                  70                  75                  80

Arg Gly Gly Pro Leu Thr Gly Ser Tyr Arg Leu Arg Gln Phe His Leu
                85                  90                  95

His Trp Gly Ser Ala Asp Asp His Gly Ser Glu His Ile Val Asp Gly
            100                 105                 110

Val Ser Tyr Ala Ala Glu Leu His Val Val His Trp Asn Ser Asp Lys
        115                 120                 125

Tyr Pro Ser Phe Val Glu Ala Ala His Glu Pro Asp Gly Leu Ala Val
    130                 135                 140

Leu Gly Val Phe Leu Gln Ile Gly Glu Pro Asn Ser Gln Leu Gln Lys
145                 150                 155                 160

Ile Thr Asp Thr Leu Asp Ser Ile Lys Glu Lys Gly Lys Gln Thr Arg
                165                 170                 175

Phe Thr Asn Phe Asp Pro Leu Ser Leu Leu Pro Pro Ser Trp Asp Tyr
            180                 185                 190

Trp Thr Tyr Pro Gly Ser Leu Thr Val Pro Pro Leu Leu Glu Ser Val
        195                 200                 205

Thr Trp Ile Val Leu Lys Gln Pro Ile Asn Ile Ser Ser Gln Gln Leu
    210                 215                 220

Ala Lys Phe Arg Ser Leu Leu Cys Thr Ala Glu Gly Glu Ala Ala Ala
225                 230                 235                 240

Phe Leu Val Ser Asn His Arg Pro Pro Gln Pro Leu Lys Gly Arg Lys
                245                 250                 255

Val Arg Ala Ser Phe His
            260


<210> SEQ ID NO 56
<211> LENGTH: 262
<212> TYPE: PRT
<213> ORGANISM: Macaca mulatta

<400> SEQUENCE: 56

Met Ser Arg Leu Ser Trp Gly Tyr Arg Glu His Asn Gly Pro Ile His
1               5                   10                  15

Trp Lys Glu Phe Phe Pro Ile Ala Asp Gly Asp Gln Gln Ser Pro Ile
            20                  25                  30
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Glu Ile Lys Thr Gln Glu Val Lys Tyr Asp Ser Ser Leu Arg Pro Leu
        35                  40                  45

Ser Ile Lys Tyr Asp Pro Ser Ser Ala Lys Ile Ile Ser Asn Ser Gly
    50                  55                  60

His Ser Phe Asn Val Asp Phe Asp Asp Thr Glu Asp Lys Ser Val Leu
65                  70                  75                  80

Arg Gly Gly Pro Leu Ala Gly Ser Tyr Arg Leu Arg Gln Phe His Leu
                85                  90                  95

His Trp Gly Ser Ala Asp Asp His Gly Ser Glu His Ile Val Asp Gly
            100                 105                 110

Val Ser Tyr Ala Ala Glu Leu His Val Val His Trp Asn Ser Asp Lys
        115                 120                 125

Tyr Pro Ser Phe Val Glu Ala Ala His Glu Pro Asp Gly Leu Ala Val
    130                 135                 140

Leu Gly Val Phe Leu Gln Ile Gly Glu Pro Asn Ser Gln Leu Gln Lys
145                 150                 155                 160

Ile Thr Asp Ile Leu Asp Ser Ile Lys Glu Lys Gly Lys Gln Thr Arg
                165                 170                 175

Phe Thr Asn Phe Asp Pro Leu Ser Leu Leu Pro Pro Ser Trp Asp Tyr
            180                 185                 190

Trp Thr Tyr Pro Gly Ser Leu Thr Val Pro Pro Leu Leu Glu Ser Val
        195                 200                 205

Ile Trp Ile Val Leu Lys Gln Pro Ile Asn Val Ser Ser Gln Gln Leu
    210                 215                 220

Ala Lys Phe Arg Ser Leu Leu Cys Thr Ala Glu Gly Glu Ala Ala Ala
225                 230                 235                 240

Phe Leu Leu Ser Asn His Arg Pro Pro Gln Pro Leu Lys Gly Arg Lys
                245                 250                 255

Val Arg Ala Ser Phe Arg
            260


<210> SEQ ID NO 57
<211> LENGTH: 262
<212> TYPE: PRT
<213> ORGANISM: Oryctolagus cuniculus

<400> SEQUENCE: 57

Met Ser Arg Ile Ser Trp Gly Tyr Gly Glu His Asn Gly Pro Ile His
1               5                   10                  15

Trp Asn Gln Phe Phe Pro Ile Ala Asp Gly Asp Gln Gln Ser Pro Ile
            20                  25                  30

Glu Ile Lys Thr Lys Glu Val Lys Tyr Asp Ser Ser Leu Arg Pro Leu
        35                  40                  45

Ser Ile Lys Tyr Asp Pro Ser Ser Ala Lys Ile Ile Ser Asn Ser Gly
    50                  55                  60

His Ser Phe Asn Val Asp Phe Asp Asp Thr Glu Asp Lys Ser Val Leu
65                  70                  75                  80

Arg Gly Gly Pro Leu Thr Gly Asn Tyr Arg Leu Arg Gln Phe His Leu
                85                  90                  95

His Trp Gly Ser Ala Asp Asp His Gly Ser Glu His Val Val Asp Gly
            100                 105                 110

Val Arg Tyr Ala Ala Glu Leu His Val Val His Trp Asn Ser Asp Lys
        115                 120                 125

Tyr Pro Ser Phe Val Glu Ala Ala His Glu Pro Asp Gly Leu Ala Val
    130                 135                 140
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Leu Gly Val Phe Leu Gln Ile Gly Glu Tyr Asn Ser Gln Leu Gln Lys
145                 150                 155                 160

Ile Thr Asp Ile Leu Asp Ser Ile Lys Glu Lys Gly Lys Gln Thr Arg
                165                 170                 175

Phe Thr Asn Phe Asp Pro Leu Ser Leu Leu Pro Ser Ser Trp Asp Tyr
            180                 185                 190

Trp Thr Tyr Pro Gly Ser Leu Thr Val Pro Pro Leu Leu Glu Ser Val
        195                 200                 205

Thr Trp Ile Val Leu Lys Gln Pro Ile Asn Ile Ser Ser Gln Gln Leu
    210                 215                 220

Ala Lys Phe Arg Ser Leu Leu Cys Ser Ala Glu Gly Glu Ser Ala Ala
225                 230                 235                 240

Phe Leu Leu Ser Asn His Arg Pro Pro Gln Pro Leu Lys Gly Arg Lys
                245                 250                 255

Val Arg Ala Ser Phe His
            260


<210> SEQ ID NO 58
<211> LENGTH: 262
<212> TYPE: PRT
<213> ORGANISM: Ailuropoda melanoleuca

<400> SEQUENCE: 58

Met Ser Arg Leu Ser Trp Gly Tyr Gly Glu His Asn Gly Pro Ile His
1               5                   10                  15

Trp Asn Lys Phe Phe Pro Ile Ala Asp Gly Asp Gln Gln Ser Pro Ile
            20                  25                  30

Glu Ile Lys Thr Lys Glu Val Lys Tyr Asp Ser Ser Leu Arg Pro Leu
        35                  40                  45

Ser Ile Lys Tyr Asp Ala Asn Ser Ala Lys Ile Ile Ser Asn Ser Gly
    50                  55                  60

His Ser Phe Ser Val Asp Phe Asp Asp Thr Glu Asp Lys Ser Val Leu
65                  70                  75                  80

Arg Gly Gly Pro Leu Thr Gly Ser Tyr Arg Leu Arg Gln Phe His Leu
                85                  90                  95

His Trp Gly Ser Ala Asp Asp His Gly Ser Glu His Val Val Asp Gly
            100                 105                 110

Val Arg Tyr Ala Ala Glu Leu His Val Val His Trp Asn Ser Asp Lys
        115                 120                 125

Tyr Pro Ser Phe Val Glu Ala Ala His Glu Pro Asp Gly Leu Ala Val
    130                 135                 140

Leu Gly Val Phe Leu Gln Ile Gly Glu His Asn Ser Gln Leu Gln Lys
145                 150                 155                 160

Ile Thr Asp Ile Leu Asp Ser Ile Lys Glu Lys Gly Lys Gln Thr Arg
                165                 170                 175

Phe Thr Asn Phe Asp Pro Leu Ser Leu Leu Pro Pro Ser Trp Asp Tyr
            180                 185                 190

Trp Thr Tyr Pro Gly Ser Leu Thr Val Pro Pro Leu Leu Glu Ser Val
        195                 200                 205

Thr Trp Ile Val Leu Lys Gln Pro Ile Asn Ile Ser Ser Glu Gln Leu
    210                 215                 220

Ala Thr Phe Arg Thr Leu Leu Cys Thr Ala Glu Gly Glu Ala Ala Ala
225                 230                 235                 240

Phe Leu Leu Ser Asn His Arg Pro Pro Gln Pro Leu Lys Gly Arg Lys
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                245                 250                 255

Val Arg Ala Ser Phe His
            260


<210> SEQ ID NO 59
<211> LENGTH: 262
<212> TYPE: PRT
<213> ORGANISM: Sus scrofa

<400> SEQUENCE: 59

Met Ser Arg Phe Ser Trp Gly Tyr Gly Glu His Asn Gly Pro Val His
1               5                   10                  15

Trp Asn Glu Phe Phe Pro Ile Ala Asp Gly Asp Gln Gln Ser Pro Ile
            20                  25                  30

Glu Ile Lys Thr Lys Glu Val Lys Tyr Asp Ser Ser Leu Arg Pro Leu
        35                  40                  45

Ser Ile Lys Tyr Asp Pro Ser Ser Ala Lys Ile Ile Ser Asn Ser Gly
    50                  55                  60

His Ser Phe Ser Val Asp Phe Asp Asp Thr Glu Asp Lys Ser Val Leu
65                  70                  75                  80

Arg Gly Gly Pro Leu Thr Gly Ser Tyr Arg Leu Arg Gln Phe His Leu
                85                  90                  95

His Trp Gly Ser Ala Asp Asp His Gly Ser Glu His Val Val Asp Gly
            100                 105                 110

Val Lys Tyr Ala Ala Glu Leu His Val Val His Trp Asn Ser Asp Lys
        115                 120                 125

Tyr Pro Ser Phe Val Glu Ala Ala His Glu Pro Asp Gly Leu Ala Val
    130                 135                 140

Leu Gly Val Phe Leu Gln Ile Gly Glu His Asn Ser Gln Leu Gln Lys
145                 150                 155                 160

Ile Thr Asp Ile Leu Asp Ser Ile Lys Glu Lys Gly Lys Gln Thr Arg
                165                 170                 175

Phe Thr Asn Phe Asp Pro Leu Ser Leu Leu Pro Pro Ser Trp Asp Tyr
            180                 185                 190

Trp Thr Tyr Pro Gly Ser Leu Thr Val Pro Pro Leu Leu Glu Ser Val
        195                 200                 205

Thr Trp Ile Ile Leu Lys Gln Pro Ile Asn Ile Ser Ser Gln Gln Leu
    210                 215                 220

Ala Thr Phe Arg Thr Leu Leu Cys Thr Lys Glu Gly Glu Glu Ala Ala
225                 230                 235                 240

Phe Leu Leu Ser Asn His Arg Pro Leu Gln Pro Leu Lys Gly Arg Lys
                245                 250                 255

Val Arg Ala Ser Phe His
            260


<210> SEQ ID NO 60
<211> LENGTH: 262
<212> TYPE: PRT
<213> ORGANISM: Callithrix jacchus

<400> SEQUENCE: 60

Met Ser Arg Leu Ser Trp Gly Tyr Gly Glu His Asn Gly Pro Ile His
1               5                   10                  15

Trp Asn Glu Phe Phe Pro Ile Ala Asp Gly Asp Arg Gln Ser Pro Ile
            20                  25                  30

Glu Ile Lys Ala Lys Glu Val Lys Tyr Asp Ser Ser Leu Arg Pro Leu
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        35                  40                  45

Ser Ile Lys Tyr Asp Pro Ser Ser Ala Lys Ile Ile Ser Asn Ser Gly
    50                  55                  60

His Ser Phe Asn Val Asp Phe Asp Asp Thr Glu Asp Lys Ser Val Leu
65                  70                  75                  80

His Gly Gly Pro Leu Thr Gly Ser Tyr Arg Leu Arg Gln Phe His Leu
                85                  90                  95

His Trp Gly Ser Ala Asp Asp His Gly Ser Glu His Val Val Asp Gly
            100                 105                 110

Val Arg Tyr Ala Ala Glu Leu His Val Val His Trp Asn Ser Glu Lys
        115                 120                 125

Tyr Pro Ser Phe Val Glu Ala Ala His Glu Pro Asp Gly Leu Ala Val
    130                 135                 140

Leu Gly Val Phe Leu Gln Ile Gly Glu Pro Asn Ser Gln Leu Gln Lys
145                 150                 155                 160

Ile Ile Asp Ile Leu Asp Ser Ile Lys Glu Lys Gly Lys Gln Ile Arg
                165                 170                 175

Phe Thr Asn Phe Asp Pro Leu Ser Leu Phe Pro Pro Ser Trp Asp Tyr
            180                 185                 190

Trp Thr Tyr Ser Gly Ser Leu Thr Val Pro Pro Leu Leu Glu Ser Val
        195                 200                 205

Thr Trp Ile Leu Leu Lys Gln Pro Ile Asn Ile Ser Ser Gln Gln Leu
    210                 215                 220

Ala Lys Phe Arg Ser Leu Leu Cys Thr Ala Glu Gly Glu Ala Ala Ala
225                 230                 235                 240

Phe Leu Leu Ser Asn Tyr Arg Pro Pro Gln Pro Leu Lys Gly Arg Lys
                245                 250                 255

Val Arg Ala Ser Phe Arg
            260


<210> SEQ ID NO 61
<211> LENGTH: 262
<212> TYPE: PRT
<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 61

Met Ala Arg Leu Ser Trp Gly Tyr Asp Glu His Asn Gly Pro Ile His
1               5                   10                  15

Trp Asn Glu Leu Phe Pro Ile Ala Asp Gly Asp Gln Gln Ser Pro Ile
            20                  25                  30

Glu Ile Lys Thr Lys Glu Val Lys Tyr Asp Ser Ser Leu Arg Pro Leu
        35                  40                  45

Ser Ile Lys Tyr Asp Pro Ala Ser Ala Lys Ile Ile Ser Asn Ser Gly
    50                  55                  60

His Ser Phe Asn Val Asp Phe Asp Asp Thr Glu Asp Lys Ser Val Leu
65                  70                  75                  80

Arg Gly Gly Pro Leu Thr Gly Ser Tyr Arg Leu Arg Gln Phe His Leu
                85                  90                  95

His Trp Gly Ser Ala Asp Asp His Gly Ser Glu His Val Val Asp Gly
            100                 105                 110

Val Arg Tyr Ala Ala Glu Leu His Val Val His Trp Asn Ser Asp Lys
        115                 120                 125

Tyr Pro Ser Phe Val Glu Ala Ala His Glu Ser Asp Gly Leu Ala Val
    130                 135                 140
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Leu Gly Val Phe Leu Gln Ile Gly Glu His Asn Pro Gln Leu Gln Lys
145                 150                 155                 160

Ile Thr Asp Ile Leu Asp Ser Ile Lys Glu Lys Gly Lys Gln Thr Arg
                165                 170                 175

Phe Thr Asn Phe Asp Pro Leu Cys Leu Leu Pro Ser Ser Trp Asp Tyr
            180                 185                 190

Trp Thr Tyr Pro Gly Ser Leu Thr Val Pro Pro Leu Leu Glu Ser Val
        195                 200                 205

Thr Trp Ile Val Leu Lys Gln Pro Ile Ser Ile Ser Ser Gln Gln Leu
    210                 215                 220

Ala Arg Phe Arg Ser Leu Leu Cys Thr Ala Glu Gly Glu Ser Ala Ala
225                 230                 235                 240

Phe Leu Leu Ser Asn His Arg Pro Pro Gln Pro Leu Lys Gly Arg Arg
                245                 250                 255

Val Arg Ala Ser Phe Tyr
            260


<210> SEQ ID NO 62
<211> LENGTH: 262
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 62

Met Ala Arg Leu Ser Trp Gly Tyr Gly Glu His Asn Gly Pro Ile His
1               5                   10                  15

Trp Asn Glu Leu Phe Pro Ile Ala Asp Gly Asp Gln Gln Ser Pro Ile
            20                  25                  30

Glu Ile Lys Thr Lys Glu Val Lys Tyr Asp Ser Ser Leu Arg Pro Leu
        35                  40                  45

Ser Ile Lys Tyr Asp Pro Ala Ser Ala Lys Ile Ile Ser Asn Ser Gly
    50                  55                  60

His Ser Phe Asn Val Asp Phe Asp Asp Thr Glu Asp Lys Ser Val Leu
65                  70                  75                  80

Arg Gly Gly Pro Leu Thr Gly Asn Tyr Arg Leu Arg Gln Phe His Leu
                85                  90                  95

His Trp Gly Ser Ala Asp Asp His Gly Ser Glu His Val Val Asp Gly
            100                 105                 110

Val Arg Tyr Ala Ala Glu Leu His Val Val His Trp Asn Ser Asp Lys
        115                 120                 125

Tyr Pro Ser Phe Val Glu Ala Ala His Glu Ser Asp Gly Leu Ala Val
    130                 135                 140

Leu Gly Val Phe Leu Gln Ile Gly Glu His Asn Pro Gln Leu Gln Lys
145                 150                 155                 160

Ile Thr Asp Ile Leu Asp Ser Ile Lys Glu Lys Gly Lys Gln Thr Arg
                165                 170                 175

Phe Thr Asn Phe Asp Pro Leu Cys Leu Leu Pro Ser Ser Trp Asp Tyr
            180                 185                 190

Trp Thr Tyr Pro Gly Ser Leu Thr Val Pro Pro Leu Leu Glu Ser Val
        195                 200                 205

Thr Trp Ile Val Leu Lys Gln Pro Ile Ser Ile Ser Ser Gln Gln Leu
    210                 215                 220

Ala Arg Phe Arg Ser Leu Leu Cys Thr Ala Glu Gly Glu Ser Ala Ala
225                 230                 235                 240

Phe Leu Leu Ser Asn His Arg Pro Pro Gln Pro Leu Lys Gly Arg Arg
                245                 250                 255
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Val Arg Ala Ser Phe Tyr
            260


<210> SEQ ID NO 63
<211> LENGTH: 262
<212> TYPE: PRT
<213> ORGANISM: Canis familiaris

<400> SEQUENCE: 63

Met Ser Arg Leu Ser Trp Gly Tyr Gly Glu His Asn Gly Pro Ile His
1               5                   10                  15

Trp Asn Lys Phe Phe Pro Ile Ala Asp Gly Asp Gln Gln Ser Pro Ile
            20                  25                  30

Glu Ile Lys Thr Lys Glu Val Lys Tyr Asp Ser Ser Leu Arg Pro Leu
        35                  40                  45

Ser Ile Lys Tyr Asp Ala Asn Ser Ala Lys Ile Ile Ser Asn Ser Gly
    50                  55                  60

His Ser Phe Ser Val Asp Phe Asp Asp Thr Glu Asp Lys Ser Val Leu
65                  70                  75                  80

Arg Gly Gly Pro Leu Thr Gly Ser Tyr Arg Leu Arg Gln Phe His Leu
                85                  90                  95

His Trp Gly Ser Ala Asp Asp His Gly Ser Glu His Val Val Asp Gly
            100                 105                 110

Val Arg Tyr Ala Ala Glu Leu His Val Val His Trp Asn Ser Asp Lys
        115                 120                 125

Tyr Pro Ser Phe Val Glu Ala Ala His Glu Pro Asp Gly Leu Ala Val
    130                 135                 140

Leu Gly Val Phe Leu Gln Ile Gly Glu His Asn Ser Gln Leu Gln Lys
145                 150                 155                 160

Ile Thr Asp Ile Leu Asp Ser Ile Lys Glu Lys Gly Lys Gln Thr Arg
                165                 170                 175

Phe Thr Asn Phe Asp Pro Leu Ser Leu Leu Pro Pro Ser Trp Asp Tyr
            180                 185                 190

Trp Thr Tyr Pro Gly Ser Leu Thr Val Pro Pro Leu Leu Glu Ser Val
        195                 200                 205

Thr Trp Ile Val Leu Lys Gln Pro Ile Asn Ile Ser Ser Gln Gln Leu
    210                 215                 220

Ala Thr Phe Arg Thr Leu Leu Cys Thr Ala Glu Gly Glu Ala Ala Ala
225                 230                 235                 240

Phe Leu Leu Ser Asn His Arg Pro Pro Gln Pro Leu Lys Gly Arg Lys
                245                 250                 255

Val Arg Ala Ser Phe His
            260


<210> SEQ ID NO 64
<211> LENGTH: 252
<212> TYPE: PRT
<213> ORGANISM: Equus caballus

<400> SEQUENCE: 64

Met Ser Gly Pro Val His Trp Asn Glu Phe Phe Pro Ile Ala Asp Gly
1               5                   10                  15

Asp Gln Gln Ser Pro Ile Glu Ile Lys Thr Lys Glu Val Lys Tyr Asp
            20                  25                  30

Ser Ser Leu Arg Pro Leu Thr Ile Lys Tyr Asp Pro Ser Ser Ala Lys
        35                  40                  45
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Ile Ile Ser Asn Ser Gly His Ser Phe Ser Val Gly Phe Asp Asp Thr
    50                  55                  60

Glu Asn Lys Ser Val Leu Arg Gly Gly Pro Leu Thr Gly Ser Tyr Arg
65                  70                  75                  80

Leu Arg Gln Phe His Leu His Trp Gly Ser Ala Asp Asp His Gly Ser
                85                  90                  95

Glu His Val Val Asp Gly Val Arg Tyr Ala Ala Glu Leu His Ile Val
            100                 105                 110

His Trp Asn Ser Asp Lys Tyr Pro Ser Phe Val Glu Ala Ala His Glu
        115                 120                 125

Pro Asp Gly Leu Ala Val Leu Gly Val Phe Leu Gln Val Gly Glu His
    130                 135                 140

Asn Ser Gln Leu Gln Lys Ile Thr Asp Thr Leu Asp Ser Ile Lys Glu
145                 150                 155                 160

Lys Gly Lys Gln Thr Leu Phe Thr Asn Phe Asp Pro Leu Ser Leu Leu
                165                 170                 175

Pro Pro Ser Trp Asp Tyr Trp Thr Tyr Pro Gly Ser Leu Thr Val Pro
            180                 185                 190

Pro Leu Leu Glu Ser Val Thr Trp Ile Ile Leu Lys Gln Pro Ile Asn
        195                 200                 205

Ile Ser Ser Gln Gln Leu Val Lys Phe Arg Thr Leu Leu Cys Thr Ala
    210                 215                 220

Glu Gly Glu Thr Ala Ala Phe Leu Leu Ser Asn His Arg Pro Pro Gln
225                 230                 235                 240

Pro Leu Lys Gly Arg Lys Val Arg Ala Ser Phe Arg
                245                 250


<210> SEQ ID NO 65
<211> LENGTH: 262
<212> TYPE: PRT
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 65

Met Ser Gly Phe Ser Trp Gly Tyr Gly Glu Arg Asp Gly Pro Val His
1               5                   10                  15

Trp Asn Glu Phe Phe Pro Ile Ala Asp Gly Asp Gln Gln Ser Pro Ile
            20                  25                  30

Glu Ile Lys Thr Lys Glu Val Arg Tyr Asp Ser Ser Leu Arg Pro Leu
        35                  40                  45

Gly Ile Lys Tyr Asp Ala Ser Ser Ala Lys Ile Ile Ser Asn Ser Gly
    50                  55                  60

His Ser Phe Asn Val Asp Phe Asp Asp Thr Asp Asp Lys Ser Val Leu
65                  70                  75                  80

Arg Gly Gly Pro Leu Thr Gly Ser Tyr Arg Leu Arg Gln Phe His Leu
                85                  90                  95

His Trp Gly Ser Thr Asp Asp His Gly Ser Glu His Val Val Asp Gly
            100                 105                 110

Val Arg Tyr Ala Ala Glu Leu His Val Val His Trp Asn Ser Asp Lys
        115                 120                 125

Tyr Pro Ser Phe Val Glu Ala Ala His Glu Pro Asp Gly Leu Ala Val
    130                 135                 140

Leu Gly Ile Phe Leu Gln Ile Gly Glu His Asn Pro Gln Leu Gln Lys
145                 150                 155                 160

Ile Thr Asp Ile Leu Asp Ser Ile Lys Glu Lys Gly Lys Gln Thr Arg
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                165                 170                 175

Phe Thr Asn Phe Asp Pro Val Cys Leu Leu Pro Pro Cys Arg Asp Tyr
            180                 185                 190

Trp Thr Tyr Pro Gly Ser Leu Thr Val Pro Pro Leu Leu Glu Ser Val
        195                 200                 205

Thr Trp Ile Ile Leu Lys Gln Pro Ile Asn Ile Ser Ser Gln Gln Leu
    210                 215                 220

Ala Ala Phe Arg Thr Leu Leu Cys Ser Arg Glu Gly Glu Thr Ala Ala
225                 230                 235                 240

Phe Leu Leu Ser Asn His Arg Pro Pro Gln Pro Leu Lys Gly Arg Lys
                245                 250                 255

Val Arg Ala Ser Phe Arg
            260


<210> SEQ ID NO 66
<211> LENGTH: 419
<212> TYPE: PRT
<213> ORGANISM: Monodelphis domestica

<400> SEQUENCE: 66

Met Ala Ser Val Phe Ala Gly Trp Gly Pro Gly Arg Thr His Leu Phe
1               5                   10                  15

Phe Arg Phe Phe Pro Gly Pro Phe Ser Ala Leu Pro Ala Gln Thr Ser
            20                  25                  30

Arg Gly Val Leu Val Phe Thr Ala Pro Gly Pro Ser Pro Arg Arg Val
        35                  40                  45

Pro Asp Pro Val His Pro Gly Arg Asp Val Val Arg Pro Ser Gly Ser
    50                  55                  60

Leu Phe Ser Cys Arg Leu Pro Pro Pro Arg Pro Ser Ala Pro Ala Arg
65                  70                  75                  80

Glu Arg Arg Pro Leu Ala Glu Lys Val Gly Arg Ser Ser Ala Pro His
                85                  90                  95

Leu Pro Leu Asp Asn Phe Glu Phe Ile Ala Lys Arg Leu Arg Arg Arg
            100                 105                 110

Val Leu Ser Gly Leu Ala Ala Glu Ser Ala Gly Ala Leu Ala Pro Ser
        115                 120                 125

Leu Pro Arg Ser Leu His Ser Ser Leu Gly Leu Arg Ser Ser Leu Lys
    130                 135                 140

Ser Gln Arg Val Phe Pro Ser Pro His Ser Glu Glu Thr Met Ser Arg
145                 150                 155                 160

Leu Ser Trp Gly Tyr Cys Glu His Asn Gly Pro Val His Trp Ser Glu
                165                 170                 175

Leu Phe Pro Ile Ala Asp Gly Asp Tyr Gln Ser Pro Ile Glu Ile Asn
            180                 185                 190

Thr Lys Glu Val Lys Tyr Asp Ser Ser Leu Arg Pro Leu Ser Ile Lys
        195                 200                 205

Tyr Asp Pro Ala Ser Ala Lys Ile Ile Ser Asn Ser Gly His Ser Phe
    210                 215                 220

Ser Val Asp Phe Asp Asp Ser Glu Asp Lys Ser Val Leu Arg Gly Gly
225                 230                 235                 240

Pro Leu Ile Gly Thr Tyr Arg Leu Arg Gln Phe His Leu His Trp Gly
                245                 250                 255

Ser Thr Asp Asp Gln Gly Ser Glu His Thr Val Asp Gly Met Lys Tyr
            260                 265                 270
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Ala Ala Glu Leu His Val Val His Trp Asn Ser Asp Lys Tyr Pro Ser
        275                 280                 285

Phe Val Glu Ala Ala His Glu Pro Asp Gly Leu Ala Val Leu Gly Ile
    290                 295                 300

Phe Leu Gln Thr Gly Glu His Asn Leu Gln Met Gln Lys Ile Thr Asp
305                 310                 315                 320

Ile Leu Asp Ser Ile Lys Glu Lys Gly Lys Gln Ile Arg Phe Thr Asn
                325                 330                 335

Phe Asp Pro Ala Thr Leu Leu Pro Gln Ser Trp Asp Tyr Trp Thr Tyr
            340                 345                 350

Pro Gly Ser Leu Thr Val Pro Pro Leu Leu Glu Ser Val Thr Trp Ile
        355                 360                 365

Val Leu Lys Gln Pro Ile Thr Ile Ser Ser Gln Gln Leu Ala Lys Phe
    370                 375                 380

Arg Ser Leu Leu Tyr Thr Gly Glu Gly Glu Ala Ala Ala Phe Leu Leu
385                 390                 395                 400

Ser Asn Tyr Arg Pro Pro Gln Pro Leu Lys Gly Arg Lys Val Arg Ala
                405                 410                 415

Ser Phe Arg


<210> SEQ ID NO 67
<211> LENGTH: 428
<212> TYPE: PRT
<213> ORGANISM: Ornithorhynchus anatinus

<400> SEQUENCE: 67

Met Lys Lys Gly Val Gly Ser Phe Tyr Glu Leu Ala Val Asn Arg Trp
1               5                   10                  15

Ser Val Val Asn Arg Val Gln Ile Met Ile Val Glu Ser Ile Thr Glu
            20                  25                  30

Pro Leu Leu Cys Gly Ser Ala Leu Ala Val Ala Pro Ala Leu Ala Leu
        35                  40                  45

Ala Val Val Gln Ala Leu Ala Leu Thr Val Val Gln Ala Leu Ala Leu
    50                  55                  60

Ala Val Ser Pro Ala Leu Ala Leu Ser Val Ala Pro Ala Leu Ala Leu
65                  70                  75                  80

Ala Val Val Gln Ala Leu Ala Leu Ala Val Val Gln Ala Leu Ala Leu
                85                  90                  95

Ala Val Ala Gln Ala Leu Ala Leu Ala Val Ala Gln Ala Leu Ala Leu
            100                 105                 110

Ala Val Ala Gln Ala Leu Ala Leu Ala Leu Pro Gln Ala Leu Ala Leu
        115                 120                 125

Thr Leu Pro Gln Ala Leu Ala Leu Thr Leu Ser Pro Thr Leu Ala Leu
    130                 135                 140

Ser Val Ala Pro Ala Leu Ala Leu Ala Val Ala Pro Ala Leu Ala Leu
145                 150                 155                 160

Ala Asp Ser Pro Ala Leu Ala Leu Ala Leu Ala Arg Pro His Pro Ser
                165                 170                 175

Ser Gly Pro Ile His Trp Asn Glu Leu Phe Pro Ile Ala Asp Gly Asp
            180                 185                 190

Arg Gln Ser Pro Ile Glu Ile Lys Thr Lys Glu Val Lys Tyr Asp Ser
        195                 200                 205

Ser Leu Arg Pro Leu Ser Ile Lys Tyr Asp Pro Thr Ser Ala Lys Ile
    210                 215                 220
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Ile Ser Asn Ser Gly His Ser Phe Ser Val Asp Phe Asp Asp Thr Glu
225                 230                 235                 240

Asp Lys Ser Val Leu Arg Gly Gly Pro Leu Ser Gly Thr Tyr Arg Leu
                245                 250                 255

Arg Gln Phe His Phe His Trp Gly Ser Ala Asp Asp His Gly Ser Glu
            260                 265                 270

His Thr Val Asp Gly Met Glu Tyr Ser Ala Glu Leu His Val Val His
        275                 280                 285

Trp Asn Ser Asp Lys Tyr Ser Ser Phe Val Glu Ala Ala His Glu Pro
    290                 295                 300

Asp Gly Leu Ala Val Leu Gly Ile Phe Leu Lys Arg Gly Glu His Asn
305                 310                 315                 320

Leu Gln Leu Gln Lys Ile Thr Asp Ile Leu Asp Ala Ile Lys Glu Lys
                325                 330                 335

Gly Lys Gln Met Arg Phe Thr Asn Phe Asp Pro Leu Ser Leu Leu Pro
            340                 345                 350

Leu Thr Arg Asp Tyr Trp Thr Tyr Pro Gly Ser Leu Thr Val Pro Pro
        355                 360                 365

Leu Leu Glu Ser Val Ile Trp Ile Ile Phe Lys Gln Pro Ile Ser Ile
    370                 375                 380

Ser Ser Gln Gln Leu Ala Lys Phe Arg Asn Leu Leu Tyr Thr Ala Glu
385                 390                 395                 400

Gly Glu Ala Ala Asp Phe Met Leu Ser Asn His Arg Pro Pro Gln Pro
                405                 410                 415

Leu Lys Gly Arg Lys Val Arg Ala Ser Phe Arg Ser
            420                 425


<210> SEQ ID NO 68
<211> LENGTH: 1082
<212> TYPE: PRT
<213> ORGANISM: Chlamydomonas reinhardtii

<400> SEQUENCE: 68

Met Leu Pro Gly Leu Gly Val Ile Leu Leu Val Leu Pro Met Gln Tyr
1               5                   10                  15

Tyr Phe Gly Tyr Lys Ile Val Gln Ile Lys Leu Gln Asn Ala Lys His
            20                  25                  30

Val Ala Leu Arg Ser Ala Ile Met Gln Glu Val Leu Pro Ala Ile Lys
        35                  40                  45

Leu Val Lys Tyr Tyr Ala Trp Glu Gln Phe Phe Glu Asn Gln Ile Ser
    50                  55                  60

Lys Val Arg Arg Glu Glu Ile Arg Leu Asn Phe Trp Asn Cys Val Met
65                  70                  75                  80

Lys Val Ile Asn Val Ala Cys Val Phe Cys Val Pro Pro Met Thr Ala
                85                  90                  95

Phe Val Ile Phe Thr Thr Tyr Glu Phe Gln Arg Ala Arg Leu Val Ser
            100                 105                 110

Ser Val Ala Phe Thr Thr Leu Ser Leu Phe Asn Ile Leu Arg Phe Pro
        115                 120                 125

Leu Val Val Leu Pro Lys Ala Leu Arg Ala Val Ser Glu Ala Asn Ala
    130                 135                 140

Ser Leu Gln Arg Leu Glu Ala Tyr Leu Leu Glu Glu Val Pro Ser Gly
145                 150                 155                 160

Thr Ala Ala Val Lys Thr Pro Lys Asn Ala Pro Pro Gly Ala Val Ile
                165                 170                 175
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Glu Asn Gly Val Phe His His Pro Ser Asn Pro Asn Trp His Leu His
            180                 185                 190

Val Pro Lys Phe Glu Val Lys Pro Gly Gln Val Val Ala Val Val Gly
        195                 200                 205

Arg Ile Ala Ala Gly Lys Ser Ser Leu Val Gln Ala Ile Leu Gly Asn
    210                 215                 220

Met Val Lys Glu His Gly Ser Phe Asn Val Gly Gly Arg Ile Ser Tyr
225                 230                 235                 240

Val Pro Gln Asn Pro Trp Leu Gln Asn Leu Ser Leu Arg Asp Asn Val
                245                 250                 255

Leu Phe Gly Glu Gln Phe Asp Glu Asn Lys Tyr Thr Asp Val Ile Glu
            260                 265                 270

Ser Cys Ala Leu Thr Leu Asp Leu Gln Ile Leu Ser Asn Gly Asp Gln
        275                 280                 285

Ser Lys Ala Gly Ile Arg Gly Val Asn Phe Ser Gly Gly Gln Arg Gln
    290                 295                 300

Arg Val Asn Leu Ala Arg Cys Ala Tyr Ala Asp Ala Asp Leu Val Leu
305                 310                 315                 320

Leu Asp Asn Ala Leu Ser Ala Val Asp His His Thr Ala His His Ile
                325                 330                 335

Phe Asp Lys Cys Ile Lys Gly Leu Phe Ser Asp Lys Ala Val Val Leu
            340                 345                 350

Val Thr His Gln Ile Glu Phe Met Pro Arg Cys Asp Asn Val Ala Ile
        355                 360                 365

Met Asp Glu Gly Arg Cys Leu Tyr Phe Gly Lys Trp Asn Glu Glu Ala
    370                 375                 380

Gln His Leu Leu Gly Lys Leu Leu Pro Ile Thr His Leu Leu His Ala
385                 390                 395                 400

Ala Gly Ser Gln Glu Ala Pro Pro Ala Pro Lys Lys Lys Ala Glu Asp
                405                 410                 415

Lys Ala Gly Pro Gln Lys Ser Gln Ser Leu Gln Leu Thr Leu Ala Pro
            420                 425                 430

Thr Ser Ile Gly Lys Pro Thr Glu Lys Pro Lys Asp Val Gln Lys Leu
        435                 440                 445

Thr Ala Tyr Gln Ala Ala Leu Ile Tyr Thr Trp Tyr Gly Asn Leu Phe
    450                 455                 460

Leu Val Gly Val Cys Phe Phe Phe Phe Leu Ala Ala Gln Cys Ser Arg
465                 470                 475                 480

Gln Ile Ser Asp Phe Trp Val Arg Trp Trp Val Asn Asp Glu Tyr Lys
                485                 490                 495

Lys Phe Pro Val Lys Gly Glu Gln Asp Ser Ala Ala Thr Thr Phe Tyr
            500                 505                 510

Cys Leu Ile Tyr Leu Leu Leu Val Gly Leu Phe Tyr Ile Phe Met Ile
        515                 520                 525

Phe Arg Gly Ala Thr Phe Leu Trp Trp Val Leu Lys Ser Ser Glu Thr
    530                 535                 540

Ile Arg Arg Lys Ala Leu His Asn Val Leu Asn Ala Pro Met Gly Phe
545                 550                 555                 560

Phe Leu Val Thr Pro Val Gly Asp Leu Leu Leu Asn Phe Thr Lys Asp
                565                 570                 575

Gln Asp Ile Met Asp Glu Asn Leu Pro Asp Ala Val His Phe Met Gly
            580                 585                 590
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Ile Tyr Gly Leu Ile Leu Leu Ala Thr Thr Ile Thr Val Ser Val Thr
        595                 600                 605

Ile Asn Phe Phe Ala Ala Phe Thr Gly Ala Leu Ile Ile Met Thr Leu
    610                 615                 620

Ile Met Leu Ser Ile Tyr Leu Pro Ala Ala Thr Ala Leu Lys Lys Ala
625                 630                 635                 640

Arg Ala Val Ser Gly Gly Met Leu Val Gly Leu Val Ala Glu Val Leu
                645                 650                 655

Glu Gly Leu Gly Val Val Gln Ala Phe Asn Lys Gln Glu Tyr Phe Ile
            660                 665                 670

Glu Glu Ala Ala Arg Arg Thr Asn Ile Thr Asn Ser Ala Val Phe Asn
        675                 680                 685

Ala Glu Ala Leu Asn Leu Trp Leu Ala Phe Trp Cys Asp Phe Ile Gly
    690                 695                 700

Ala Cys Leu Val Gly Val Val Ser Ala Phe Ala Val Gly Met Ala Lys
705                 710                 715                 720

Asp Leu Gly Gly Ala Thr Val Gly Leu Ala Phe Ser Asn Ile Ile Gln
                725                 730                 735

Met Leu Val Phe Tyr Thr Trp Val Val Arg Phe Ile Ser Glu Ser Ile
            740                 745                 750

Ser Leu Phe Asn Ser Val Glu Gly Met Ala Tyr Leu Ala Asp Tyr Val
        755                 760                 765

Pro His Asp Gly Val Phe Tyr Asp Gln Arg Gln Lys Asp Gly Val Ala
    770                 775                 780

Lys Gln Ile Val Leu Pro Asp Gly Asn Ile Val Pro Ala Ala Ser Lys
785                 790                 795                 800

Val Gln Val Val Val Asp Asp Ala Ala Leu Ala Arg Trp Pro Ala Thr
                805                 810                 815

Gly Asn Ile Arg Phe Glu Asp Val Trp Met Gln Tyr Arg Leu Asp Ala
            820                 825                 830

Pro Trp Ala Leu Lys Gly Val Thr Phe Lys Ile Asn Asp Gly Glu Lys
        835                 840                 845

Val Gly Ala Val Gly Arg Thr Gly Ser Gly Lys Ser Thr Thr Leu Leu
    850                 855                 860

Ala Leu Tyr Arg Met Phe Glu Leu Gly Lys Gly Arg Ile Leu Val Asp
865                 870                 875                 880

Gly Val Asp Ile Ala Thr Leu Ser Leu Lys Arg Leu Arg Thr Gly Leu
                885                 890                 895

Ser Ile Ile Pro Gln Glu Pro Val Met Phe Thr Gly Thr Val Arg Ser
            900                 905                 910

Asn Leu Asp Pro Phe Gly Glu Phe Lys Asp Asp Ala Ile Leu Trp Glu
        915                 920                 925

Val Leu Lys Lys Val Gly Leu Glu Asp Gln Ala Gln His Ala Gly Gly
    930                 935                 940

Leu Asp Gly Gln Val Asp Gly Thr Gly Gly Lys Ala Trp Ser Leu Gly
945                 950                 955                 960

Gln Met Gln Leu Val Cys Leu Ala Arg Ala Ala Leu Arg Ala Val Pro
                965                 970                 975

Ile Leu Cys Leu Asp Glu Ala Thr Ala Ala Met Asp Pro His Thr Glu
            980                 985                 990

Ala Ile Val Gln Gln Thr Ile Lys  Lys Val Phe Asp Asp  Arg Thr Thr
        995                 1000                 1005

Ile Thr  Ile Ala His Arg Leu  Asp Thr Ile Ile Glu  Ser Asp Lys
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    1010                 1015                 1020

Ile Ile  Val Met Glu Gln Gly  Ser Leu Met Glu Tyr  Glu Ser Pro
    1025                 1030                 1035

Ser Lys  Leu Leu Ala Asn Arg  Asp Ser Met Phe Ser  Lys Leu Val
    1040                 1045                 1050

Asp Lys  Thr Gly Pro Ala Ala  Ala Ala Ala Leu Arg  Lys Met Ala
    1055                 1060                 1065

Glu Asp  Phe Trp Ser Thr Arg  Ser Ala Gln Gly Arg  Asn Gln
    1070                 1075                 1080


<210> SEQ ID NO 69
<211> LENGTH: 1321
<212> TYPE: PRT
<213> ORGANISM: Volvox carteri

<400> SEQUENCE: 69

Met Gly Thr Ile Ser His Pro Ala Arg Gly Asn Asp Pro Thr Ala Gly
1               5                   10                  15

Phe Phe Asn Lys Phe Ala Phe Gly Trp Met Phe Lys His Val Ser Glu
            20                  25                  30

Ala Arg Lys Asn Gly Asp Ile Asp Leu Asp Lys Met Gly Met Pro Pro
        35                  40                  45

Glu Asn His Ala His Glu Ala Tyr Asp Met Phe Ala Ser Asn Trp Ala
    50                  55                  60

Ala Glu Met Lys Leu Lys Asp Ser Gly Ala Lys Pro Ser Leu Val Arg
65                  70                  75                  80

Ala Leu Arg Lys Ser Phe Gly Leu Val Tyr Leu Leu Gly Gly Val Phe
                85                  90                  95

Lys Cys Phe Trp Ser Thr Phe Val Ile Thr Gly Ala Phe Tyr Phe Val
            100                 105                 110

Arg Ser Leu Leu Ala His Val Asn Gly Ile Lys Asp Gly Arg Leu Tyr
        115                 120                 125

Ser Lys Thr Val Ser Gly Trp Cys Leu Met Ala Gly Phe Thr Leu Asp
    130                 135                 140

Ala Trp Leu Leu Gly Leu Ser Leu Gln Arg Met Gly Tyr Ile Cys Met
145                 150                 155                 160

Ser Val Gly Ile Arg Ala Arg Ala Ala Leu Val Gln Ala Val Thr His
                165                 170                 175

Lys Ala Phe Arg Leu Ser Ser Val Arg Ala Asp Gln Ser Ala Ala Ile
            180                 185                 190

Val Asn Phe Val Ser Ser Asp Ile Gln Lys Ile Tyr Asp Gly Ala Leu
        195                 200                 205

Glu Phe His Tyr Leu Trp Thr Ala Pro Phe Glu Ala Ala Ala Ile Leu
    210                 215                 220

Ala Leu Leu Gly Tyr Leu Thr Asn Asp Ser Met Leu Pro Gly Leu Gly
225                 230                 235                 240

Val Ile Leu Leu Val Leu Pro Leu Gln Tyr Phe Phe Gly Tyr Lys Ile
                245                 250                 255

Ile Gln Ile Lys Leu Gln Asn Ala Lys His Val Ala Leu Arg Ser Ser
            260                 265                 270

Ile Leu Gln Glu Val Leu Pro Ala Ile Lys Leu Val Lys Tyr Tyr Ala
        275                 280                 285

Trp Glu Gln Phe Phe Glu Asp Glu Ile Ser Lys Ile Arg Arg Glu Glu
    290                 295                 300
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Met Arg Leu Ser Phe Trp Asn Ala Met Met Lys Val Ile Asn Val Ala
305                 310                 315                 320

Cys Val Phe Cys Val Pro Pro Met Thr Ala Phe Val Ile Phe Thr Thr
                325                 330                 335

Tyr Glu Phe Gln Lys Ala Arg Leu Val Ser Gly Val Ala Phe Thr Thr
            340                 345                 350

Leu Ser Leu Phe Asn Ile Leu Arg Phe Pro Leu Val Val Leu Pro Lys
        355                 360                 365

Ala Leu Arg Ala Val Ser Glu Ala His Ala Ser Leu Gln Arg Leu Glu
    370                 375                 380

Ser Tyr Leu Leu Glu Asp Val Pro Gln Gly Thr Ala Ser Gly Gly Lys
385                 390                 395                 400

Ser Ser Lys Ser Ser Ala Pro Gly Val His Ile Asp Asn Ala Val Tyr
                405                 410                 415

His His Pro Ser Asn Pro Asn Trp His Leu His Val Pro Arg Phe Asp
            420                 425                 430

Val Arg Pro Gly Gln Val Val Ala Val Val Gly Arg Ile Gly Ala Gly
        435                 440                 445

Lys Ser Ser Leu Val Gln Ala Ile Leu Gly Asn Met Val Lys Glu His
    450                 455                 460

Gly Ser Gln Gln Val Gly Gly Arg Ile Ser Tyr Val Pro Gln Asn Pro
465                 470                 475                 480

Trp Leu Gln Asn Leu Ser Ile Arg Asp Asn Val Thr Phe Gly Glu Gly
                485                 490                 495

Trp Asp Glu Asn Lys Tyr Glu Ala Val Ile Asp Ala Cys Ala Leu Thr
            500                 505                 510

Met Asp Leu Gln Ile Leu Pro Gln Gly Asp Gln Ser Lys Ala Gly Ile
        515                 520                 525

Arg Gly Val Asn Phe Ser Gly Gly Gln Arg Gln Arg Val Asn Leu Ala
    530                 535                 540

Arg Cys Ala Tyr Ala Asp Ala Asp Leu Val Leu Leu Asp Asn Ala Leu
545                 550                 555                 560

Ser Ala Val Asp His His Thr Ala His His Ile Phe Asp Lys Cys Ile
                565                 570                 575

Lys Gly Leu Phe Ser Asp Lys Ala Val Val Leu Ile Thr His Gln Ile
            580                 585                 590

Glu Phe Met Pro Arg Cys Asp Ala Val Ala Ile Met Asp Glu Gly Arg
        595                 600                 605

Cys Leu Tyr Phe Gly Lys Trp Asn Glu Glu Ser Gln His Leu Leu Gly
    610                 615                 620

Lys Leu Leu Pro Ile Thr His Leu Leu His Ala Ala Gly Ser Gln Glu
625                 630                 635                 640

Ala Pro Pro Ala Ala Pro Lys Lys Lys Asp Asp Lys Ala Thr Pro Gln
                645                 650                 655

Lys Ser Gln Ser Leu Gln Leu Thr Leu Ala Pro Thr Ser Ile Gly Lys
            660                 665                 670

Pro Thr Gln Lys Asp Thr Lys Ala Ala Pro Lys Leu Thr Ala Phe Lys
        675                 680                 685

Ala Ala Leu Ile Tyr Thr Tyr Tyr Gly Asn Ile Leu Leu Val Phe Val
    690                 695                 700

Cys Phe Ile Thr Phe Leu Ala Ala Gln Thr Cys Arg Gln Met Ser Asp
705                 710                 715                 720

Phe Trp Val Arg Trp Trp Val Asn Asp Glu Tyr Lys His Phe Pro Lys
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                725                 730                 735

Arg Thr Gly Val Arg Glu Glu Ser Ala Thr Lys Phe Tyr Ala Leu Ile
            740                 745                 750

Tyr Leu Leu Leu Val Gly Leu Phe Tyr Phe Thr Met Val Ala Arg Gly
        755                 760                 765

Ser Thr Phe Leu Trp Trp Val Leu Arg Ser Ser Glu Asn Ile Arg Lys
    770                 775                 780

Lys Ala Leu Asn Asn Val Leu Asn Ala Pro Met Gly Phe Phe Leu Val
785                 790                 795                 800

Thr Pro Val Gly Asp Leu Leu Leu Asn Phe Thr Lys Asp Gln Asp Ile
                805                 810                 815

Met Asp Glu Asn Leu Pro Asp Ala Ile His Phe Met Gly Ile Tyr Gly
            820                 825                 830

Leu Ile Leu Leu Ala Thr Thr Ile Thr Val Ser Val Thr Ile Asn Phe
        835                 840                 845

Phe Gly Ala Phe Thr Gly Phe Leu Ile Ile Met Thr Leu Ile Met Leu
    850                 855                 860

Ala Ile Tyr Leu Pro Ala Ala Thr Ala Leu Lys Lys Ala Arg Ala Val
865                 870                 875                 880

Ser Gly Gly Gln Leu Val Gly Leu Val Ala Glu Val Leu Glu Gly Leu
                885                 890                 895

Asn Val Val Gln Ala Phe Ser Lys Gln Glu Tyr Phe Ile Glu Glu Ala
            900                 905                 910

Ala Arg Arg Thr Asp Val Thr Asn Ala Ala Val Phe Asn Ala Glu Ser
        915                 920                 925

Leu Asn Leu Trp Leu Ala Phe Trp Cys Asp Leu Ile Gly Ala Ser Leu
    930                 935                 940

Val Gly Val Val Ser Ala Phe Ala Val Gly Leu Lys Asp Gln Leu Gly
945                 950                 955                 960

Ala Ala Thr Val Gly Leu Ala Phe Ser Asn Ile Ile Gln Met Leu Val
                965                 970                 975

Phe Tyr Thr Trp Val Val Arg Phe Ile Ala Glu Ser Ile Ser Leu Phe
            980                 985                 990

Asn Ser Val Glu Ala Met Ala Trp  Leu Ala Asp Tyr Val  Pro Lys Asp
        995                 1000                 1005

Gly Ile  Phe Tyr Asp Gln Lys  Gln Leu Asp Gly Val  Ala Lys Ser
    1010                 1015                 1020

Ile Thr  Leu Pro Asp Gly Gln  Ile Val Pro Ala Thr  Ser Lys Val
    1025                 1030                 1035

Gln Val  Val Val Asp Asp Ala  Ala Leu Ala Arg Trp  Pro Ala Thr
    1040                 1045                 1050

Gly Asn  Ile Arg Phe Glu Asp  Val Trp Met Gln Tyr  Arg Leu Asp
    1055                 1060                 1065

Ala Ala  Trp Ala Leu Lys Gly  Val Thr Phe Lys Ile  Asn Asp Gly
    1070                 1075                 1080

Glu Lys  Val Gly Ala Val Gly  Arg Thr Gly Ser Gly  Lys Ser Thr
    1085                 1090                 1095

Thr Leu  Leu Ala Leu Tyr Arg  Met Phe Glu Leu Gly  Lys Gly Arg
    1100                 1105                 1110

Ile Leu  Ile Asp Gly Val Asp  Ile Ala Thr Leu Ser  Leu Lys Arg
    1115                 1120                 1125

Leu Arg  Thr Gly Leu Ser Ile  Ile Pro Gln Glu Pro  Val Met Phe
    1130                 1135                 1140
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Thr Gly  Thr Val Arg Ser Asn  Leu Asp Pro Phe Gly  Glu Phe Lys
    1145                 1150                 1155

Asp Asp  Ser Val Leu Trp Glu  Val Leu Gln Lys Val  Gly Leu Glu
    1160                 1165                 1170

Ala Gln  Ala Gln His Ala Gly  Gly Leu Asp Gly Arg  Val Asp Gly
    1175                 1180                 1185

Thr Gly  Gly Lys Ala Trp Ser  Leu Gly Gln Met Gln  Leu Val Cys
    1190                 1195                 1200

Leu Ala  Arg Ala Ala Leu Arg  Ala Val Pro Ile Leu  Cys Leu Asp
    1205                 1210                 1215

Glu Ala  Thr Ala Ala Met Asp  Pro His Thr Glu Gln  Val Val Gln
    1220                 1225                 1230

Glu Thr  Ile Lys Lys Val Phe  Asp Asp Arg Thr Thr  Ile Thr Ile
    1235                 1240                 1245

Ala His  Arg Leu Asp Thr Ile  Ile Glu Ser Asp Lys  Val Leu Val
    1250                 1255                 1260

Met Glu  Ala Gly Glu Leu Lys  Glu Phe Ala Pro Pro  Ala Gln Leu
    1265                 1270                 1275

Leu Ala  Asn Arg Glu Thr Met  Phe Ser Lys Leu Val  Asp Lys Thr
    1280                 1285                 1290

Gly Pro  Ala Ala Ala Ala Ala  Leu Arg Lys Met Ala  Asp Glu His
    1295                 1300                 1305

Phe Ser  Lys Ser Gln Ala Arg  Ala Ala Ala Gln Arg  His
    1310                 1315                 1320


<210> SEQ ID NO 70
<211> LENGTH: 2297
<212> TYPE: PRT
<213> ORGANISM: Chlorella variabilis

<400> SEQUENCE: 70

Met Val Pro Leu Leu Ala Gln Arg Gly Arg Ile Arg Ser Gln Ala Pro
1               5                   10                  15

Arg Thr Trp His Pro Asp Pro Gln Pro Leu His Ala Glu Arg Ser Arg
            20                  25                  30

Gln Cys Pro Gly Arg Gly Val Arg Ala Ala Ala Lys Arg Gly Gly Gly
        35                  40                  45

Ser Gly Gly Ala Thr His Lys Ser Lys Lys Ser Lys Glu Leu Asp Glu
    50                  55                  60

Val Ala Ala Phe Glu Gln Leu Met Cys Asp Trp Asp Asp Ala Phe Ala
65                  70                  75                  80

Ala Asp Cys Tyr Asp Asn Glu Arg Ala Ala Arg Met Ala Arg Leu Ala
                85                  90                  95

Glu Glu Gly Tyr Gln His His Gly Arg Gly Phe Val Phe Val Arg Ser
            100                 105                 110

Arg Leu Asp Lys Arg Ser Arg Lys Ala Arg Asn Asp Ser Gly Ala Ser
        115                 120                 125

Lys Gly Phe Gly Ala Ala Ala Lys Ala Leu Ser Val Glu Gln Gly Thr
    130                 135                 140

Pro Leu Glu Asn Asn Pro Gln Leu His Leu Leu Ser Trp Thr Ala Cys
145                 150                 155                 160

Tyr Ile Ala Ser Ser Gln Leu Asp Ser Leu Gly Gly Leu Phe Ser Thr
                165                 170                 175

Gln Glu Gly Val Leu Leu Pro Asp Ser Gly Ser Leu Leu Thr Asp Gly
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            180                 185                 190

Gly Ser Gly Ala Ser Gly Ser Asn Ala Ala Asp Ala Val Gly Glu Leu
        195                 200                 205

Gln Arg Val Leu Arg Gly Gln Asp Leu Ser Gln Leu Arg Gly Tyr Val
    210                 215                 220

Gly Ala Pro Pro Gln Ala Arg Pro Ala Ser Gly Ser Asp Asp Asp Gly
225                 230                 235                 240

Ser Ser Thr Thr Gly Ser Asn Asn Gly Ala Ala Gly Glu Gly Ser Glu
                245                 250                 255

Val Glu Glu Gly Thr Ala Met Gly Gly Ile Arg Arg Tyr Glu Pro Glu
            260                 265                 270

Ser Gly Glu Leu Val Val Leu Leu Ser Cys Lys Ile Gly Gly Lys Pro
        275                 280                 285

Ala Val Gly Ala Glu Leu Leu Ala Val Ala Gln Ala Glu Asp Gly Lys
    290                 295                 300

His Ala Pro Gly Ala Ser Pro Asp Thr Arg Leu Cys Lys Glu Pro Ser
305                 310                 315                 320

Gln Ser Ala Phe Asp Leu Trp Ser Phe Gly Trp Met Asn Lys Ile Val
                325                 330                 335

Pro Ala Ala Arg Arg Gly Glu Val Glu Val Ala Asp Leu Pro Leu Pro
            340                 345                 350

Glu Ala Gln Gln Ala Glu Pro Cys Tyr Glu Glu Leu Asn Thr Asn Trp
        355                 360                 365

Glu Ala Ala Val Gln Glu Ala Lys Lys Ala Gly Lys Glu Pro Lys Leu
    370                 375                 380

Met Lys Val Leu Trp Lys Thr Tyr Gly Lys Asp Ile Val Leu Ala Gly
385                 390                 395                 400

Ile Phe Lys Leu Met Trp Ser Val Phe Val Ile Leu Gly Ala Tyr Tyr
                405                 410                 415

Phe Thr Arg Ser Ile Leu Met Cys Ile Arg Thr Leu Glu Gly Lys Asp
            420                 425                 430

Asp Ser Ile Tyr Asp Thr Glu Trp Lys Gly Trp Val Leu Thr Gly Phe
        435                 440                 445

Phe Phe Leu Asp Ala Trp Leu Leu Gly Met Met Leu Gln Arg Met Ala
    450                 455                 460

Phe Asn Cys Leu Lys Val Gly Ile Lys Ala Arg Ala Ala Leu Thr Thr
465                 470                 475                 480

Met Ile Ala Arg Lys Cys Tyr Asn Met Ala His Leu Thr Lys Asp Thr
                485                 490                 495

Ala Ala Glu Ala Val Gly Phe Val Ala Ser Asp Ile Asn Lys Val Phe
            500                 505                 510

Glu Gly Ile Gln Glu Val His Tyr Leu Trp Gly Ala Pro Val Glu Ala
        515                 520                 525

Gly Ala Ile Leu Ala Leu Leu Gly Thr Leu Val Gly Val Tyr Cys Ile
    530                 535                 540

Gly Gly Val Ile Ile Val Cys Met Val Val Pro Leu Gln Tyr Tyr Phe
545                 550                 555                 560

Gly Tyr Lys Ile Ile Lys Asn Lys Ile Lys Asn Ala Pro Asn Val Thr
                565                 570                 575

Glu Arg Trp Ser Ile Ile Gln Glu Ile Leu Pro Ala Met Lys Leu Val
            580                 585                 590

Lys Tyr Tyr Ala Trp Glu Arg Phe Phe Glu Lys His Val Ala Asp Met
        595                 600                 605
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Arg Thr Arg Glu Arg His Tyr Met Phe Trp Asn Ala Val Val Lys Thr
    610                 615                 620

Val Asn Val Thr Met Val Phe Gly Val Pro Pro Met Val Thr Phe Ala
625                 630                 635                 640

Val Leu Val Pro Tyr Glu Leu Trp His Val Asp Ser Ser Thr Ser Glu
                645                 650                 655

Pro Tyr Ile Lys Pro Gln Thr Ala Phe Thr Met Leu Ser Leu Phe Asn
            660                 665                 670

Val Leu Arg Phe Pro Leu Val Val Leu Pro Lys Ala Met Arg Cys Val
        675                 680                 685

Ser Glu Ala Leu Arg Ser Val Gly Asn Leu Glu Lys Phe Leu Ala Glu
    690                 695                 700

Pro Val Ala Pro Arg Gln Asp Leu Glu Gly Lys Pro Gly Ala Gln Leu
705                 710                 715                 720

Ser Lys Ala Val Leu Arg His Glu Met Asp Thr Ser Gly Phe Thr Leu
                725                 730                 735

Arg Val Pro Glu Phe Ser Val Lys Ala Gly Glu Leu Val Ala Val Val
            740                 745                 750

Gly Arg Val Gly Ala Gly Lys Ser Ser Ile Leu Gln Ala Met Leu Gly
        755                 760                 765

Asn Met Gln Thr Ala Ser Gly Leu Ala Lys Cys Gln His Ser Ala Ser
    770                 775                 780

Ser Cys Leu Pro Phe Leu Val Glu Gly Thr Ala His Ser Gly Gly Arg
785                 790                 795                 800

Ile Ala Tyr Val Pro Gln Thr Ala Trp Cys Gln Asn Leu Ser Leu Arg
                805                 810                 815

Asp Asn Ile Thr Phe Gly Gln Pro Trp Asp Glu Ala Lys Tyr Lys Gln
            820                 825                 830

Val Ile His Ala Cys Ala Leu Glu Leu Asp Leu Ala Ile Leu Ala Ala
        835                 840                 845

Gly Asp Gln Ser Lys Ala Gly Leu Arg Gly Ile Asn Leu Ser Gly Gly
    850                 855                 860

Gln Arg Gln Arg Leu Asn Leu Ala Arg Cys Ala Tyr Phe Asp Gly Asp
865                 870                 875                 880

Leu Val Leu Leu Asp Asn Ala Leu Ser Ala Val Asp His His Thr Ala
                885                 890                 895

His His Ile Phe Glu His Cys Val Arg Gly Met Phe Arg Asp Lys Ala
            900                 905                 910

Thr Val Leu Val Thr His Gln Val Glu Phe Leu Pro Gln Cys Asp Lys
        915                 920                 925

Val Ala Ile Met Asp Asp Gly Thr Cys Val Tyr Phe Gly Pro Trp Asn
    930                 935                 940

Ala Ala Ala Gln Gln Leu Leu Ser Lys Tyr Leu Pro Ala Ser His Leu
945                 950                 955                 960

Leu Ala Ala Gly Gly Asn Ala Glu Gln Pro Arg Asp Thr Lys Lys Lys
                965                 970                 975

Val Val Lys Lys Glu Glu Thr Lys Lys Thr Glu Asp Ala Gly Lys Ala
            980                 985                 990

Lys Arg Val His Ser Ala Ser Leu  Thr Leu Lys Ser Ala  Leu Trp Glu
        995                 1000                 1005

Tyr Cys  Trp Asp Ala Arg Trp  Ile Ile Phe Cys Leu  Ser Leu Phe
    1010                 1015                 1020
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Phe Phe  Leu Thr Ala Gln Ala  Ser Arg Gln Leu Ala  Asp Tyr Phe
    1025                 1030                 1035

Ile Arg  Trp Trp Thr Arg Asp  His Tyr Asn Lys Tyr  Gly Val Leu
    1040                 1045                 1050

Cys Ile  Asp Glu Gly Asp Asn  Pro Cys Gly Pro Leu  Phe Tyr Val
    1055                 1060                 1065

Gln Tyr  Tyr Gly Ile Leu Gly  Leu Leu Cys Phe Ile  Val Leu Met
    1070                 1075                 1080

Ala Phe  Arg Gly Ala Phe Leu  Tyr Thr Trp Ser Leu  Gly Ala Ser
    1085                 1090                 1095

Tyr Arg  Gln His Glu Lys Ser  Ile His Arg Val Leu  Tyr Ala Pro
    1100                 1105                 1110

Leu Gly  Phe Phe Leu Thr Thr  Pro Val Gly Asp Leu  Leu Val Ser
    1115                 1120                 1125

Phe Thr  Lys Asp Gln Asp Val  Met Asp Asp Ala Leu  Pro Asp Ala
    1130                 1135                 1140

Leu Tyr  Tyr Ala Gly Ile Tyr  Gly Leu Ile Leu Leu  Ala Thr Ala
    1145                 1150                 1155

Ile Thr  Val Ser Val Thr Ile  Pro Leu Phe Ser Ala  Leu Ala Gly
    1160                 1165                 1170

Gly Leu  Phe Val Val Ser Gly  Ile Met Leu Ala Ile  Tyr Leu Pro
    1175                 1180                 1185

Ala Ala  Thr His Leu Lys Lys  Leu Arg Met Gly Thr  Ser Gly Asp
    1190                 1195                 1200

Val Val  Thr Leu Ile Ala Glu  Ala Leu Asp Gly Leu  Gly Val Ile
    1205                 1210                 1215

Gln Ala  Tyr Gly Lys Gln Ala  Tyr Phe Thr Thr Ile  Thr Ser Gln
    1220                 1225                 1230

Tyr Val  Asn Asp Ala His Arg  Ala Leu Phe Gly Ala  Glu Ser Leu
    1235                 1240                 1245

Asn Leu  Trp Leu Ala Phe Ile  Cys Asp Phe Phe Gly  Ala Cys Met
    1250                 1255                 1260

Val Leu  Ser Val Ala Cys Phe  Gly Ile Gly Gln Trp  Ser Thr Leu
    1265                 1270                 1275

Gly Ser  Ser Ser Val Gly Leu  Ala Phe Ser Gln Ser  Ile Gln Met
    1280                 1285                 1290

Leu Val  Phe Tyr Thr Trp Ser  Ile Arg Leu Val Ala  Glu Cys Ile
    1295                 1300                 1305

Gly Leu  Phe Gly Ser Ala Glu  Lys Ile Ala Trp Leu  Ala Asn His
    1310                 1315                 1320

Thr Pro  Gln Glu Ala Gly Ser  Leu Asp Pro Pro Ser  Leu Pro Gly
    1325                 1330                 1335

Ser Gly  Glu Thr Lys Ala Ala  Pro Lys Lys Arg Gly  Thr Ala Gly
    1340                 1345                 1350

Lys Phe  Leu Pro Pro Leu Lys  Asp Glu Asp Leu Ala  Ile Val Pro
    1355                 1360                 1365

Thr Gly  Gly Pro Lys Leu Pro  Ser Gly Trp Pro Arg  Thr Gly Val
    1370                 1375                 1380

Leu Glu  Phe Asn Gln Val Val  Met Lys Tyr Ala Pro  His Leu Pro
    1385                 1390                 1395

Pro Ala  Leu Arg Gly Val Ser  Phe Lys Val Lys Ser  Gly Asp Lys
    1400                 1405                 1410

Val Gly  Val Val Gly Arg Thr  Gly Ser Gly Lys Ser  Thr Leu Leu
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    1415                1420                1425

Leu Ala  Leu Tyr Arg Met Phe  Asn Leu Glu Ser Gly  Ala Ile Thr
    1430                1435                1440

Leu Asp  Gly Ile Asp Ile Ser  Thr Leu Thr Leu Glu  Gln Leu Arg
    1445                1450                1455

Arg Gly  Leu Ser Val Ile Pro  Gln Glu Pro Thr Val  Phe Ser Gly
    1460                1465                1470

Thr Val  Arg Thr Asn Leu Asp  Pro Phe Gly Glu Phe  Gly Ala Asp
    1475                1480                1485

Ala Ile  Leu Trp Glu Ala Leu  Arg Asp Cys Gly Leu  Glu Glu Gln
    1490                1495                1500

Val Lys  Ala Cys Gly Gly Leu  Asp Ala Lys Leu Asp  Gly Thr Gly
    1505                1510                1515

Gly Asn  Ala Trp Ser Ile Gly  Gln Gln Gln Leu Met  Cys Leu Ala
    1520                1525                1530

Arg Ala  Ala Leu Lys Lys Val  Pro Val Leu Cys Leu  Asp Glu Ala
    1535                1540                1545

Thr Ala  Ala Met Asp Pro His  Thr Glu Ala His Val  Leu Glu Ile
    1550                1555                1560

Ile Glu  Arg Ile Phe Ser Asp  Arg Thr Met Leu Thr  Ile Ala His
    1565                1570                1575

Arg Leu  Asp Asn Val Ile Arg  Ser Asp Leu Val Val  Val Met Asp
    1580                1585                1590

Ala Gly  Gln Val Cys Glu Met  Gly Thr Pro Asp Glu  Leu Leu Ala
    1595                1600                1605

Asn Pro  Gln Ser Ala Phe Ser  Gln Leu Val Asp Lys  Thr Gly Ala
    1610                1615                1620

Ala Ser  Ala Ala Ala Leu Arg  Lys Met Ala Ala Asp  Phe Leu Asp
    1625                1630                1635

Glu Arg  Ala Arg Gly Gln Lys  Leu Gly Phe Lys Pro  Arg Pro Ser
    1640                1645                1650

Leu Glu  Glu Ser His Ile Cys  Val Ala Pro Ser Pro  Ser Leu Ile
    1655                1660                1665

Leu Ser  Thr Leu Leu Phe Pro  Pro Ala Phe Met Ala  Asn Val Thr
    1670                1675                1680

Ala Leu  Leu Leu Pro Lys Pro  Val Leu Ser His Ala  Pro Val Ser
    1685                1690                1695

Ser Gln  Thr Val Asn Thr Tyr  Ile Arg Leu Asn Ile  Ile Gln Leu
    1700                1705                1710

Gln Cys  Asn Val Leu His Pro  Ala Thr Lys Glu Ala  Thr Trp Ser
    1715                1720                1725

Ser Arg  Arg Ile Thr Phe Thr  Ala His Leu Ser Ser  Ser Gly Ser
    1730                1735                1740

Lys Pro  Pro Pro Pro Leu Pro  Pro Leu Thr Glu Leu  Pro Glu Gly
    1745                1750                1755

Arg Gly  Leu Asp Trp Ser Ser  Ala Gly Tyr Arg Asp  Gly Arg Glu
    1760                1765                1770

Ala Ile  Pro Ser Pro Ser Ala  Lys Tyr Ser Ala Ala  Asp Tyr Gly
    1775                1780                1785

Ala Ala  Gly Asp Gly Val Thr  Asp Asp Thr Gln Ala  Leu Gln Val
    1790                1795                1800

Ala Val  Ala Ala Ala His Glu  Asp Asp Glu Gly Gly  Val Val Tyr
    1805                1810                1815
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Leu Gly  Ala Gly Thr Phe Val  Leu Thr Gln Pro Leu  Ser Ile Ala
    1820                 1825                 1830

Gly Ser  Asn Val Val Ile Arg  Gly Ala Gly Glu Asp  Ala Thr Thr
    1835                 1840                 1845

Ile Phe  Val Pro Leu Pro Leu  Ser Asp Val Phe Pro  Gly Thr Trp
    1850                 1855                 1860

Ser Met  Asp Ala Ser Gly Lys  Val Thr Ser Pro Trp  Ile Thr Arg
    1865                 1870                 1875

Gly Gly  Phe Leu Ala Phe Ser  Gly Arg Arg Thr Lys  Ser Ser Asp
    1880                 1885                 1890

Ser Ser  Thr Leu Leu Ala Thr  Val Ala Gly Ser Val  Glu Gln Gly
    1895                 1900                 1905

Ala Ser  Val Ile Pro Val Asp  Ser Thr Ala Glu Phe  Arg Leu Gly
    1910                 1915                 1920

Gln Trp  Val Arg Ile Ile Ile  Asn Asp Ala Ser Thr  Asp Ala Ser
    1925                 1930                 1935

Ala Gly  Gly Gly Thr Leu Glu  Arg Gly Ser Ser Glu  Val Gln Glu
    1940                 1945                 1950

Ser Glu  Thr Met Ile Ala Glu  Gly Ala Thr Gly Gly  Gly Ala Gly
    1955                 1960                 1965

Val Arg  Ala Gln Trp Thr Gly  Val Leu His Ala Phe  Glu Pro Thr
    1970                 1975                 1980

Val Gln  Cys Ser Gly Val Glu  Gln Leu Thr Ile Arg  Phe Asn His
    1985                 1990                 1995

Ser Met  Met Ala Ala His Leu  Ala Glu Arg Gly Tyr  Asn Ala Ile
    2000                 2005                 2010

Glu Leu  Glu Asp Val Val Asp  Cys Trp Ile Arg Gln  Val Thr Ile
    2015                 2020                 2025

Leu Asn  Ala Asp Asn Ala Ile  Arg Leu Arg Gly Thr  Asp His Ser
    2030                 2035                 2040

Thr Leu  Ser Gly Gln Ala Cys  Ser Gly Gly Gly Val  Val Ala Val
    2045                 2050                 2055

Val Pro  Val Trp Cys Arg Arg  Gly Leu Pro Ser Pro  Ala Asp Val
    2060                 2065                 2070

Thr Val  Gly Val Thr Glu Leu  Arg Trp Glu Pro Asp  Thr Arg Glu
    2075                 2080                 2085

Val Asn  Gly His His Ala Ile  Thr Val Ser Lys Gly  His Ala Asn
    2090                 2095                 2100

Leu Val  Thr Arg Phe Arg Ile  Thr Ala Pro Phe Tyr  His Asp Ile
    2105                 2110                 2115

Ser Leu  Glu Gly Gly Ala Leu  Leu Asn Val Ile Ser  Ser Gly Gly
    2120                 2125                 2130

Gly Ala  Asn Leu Asn Leu Asp  Leu His Arg Ser Gly  Pro Trp Gly
    2135                 2140                 2145

Asn Leu  Phe Ser Gln Leu Gly  Met Gly Leu Ala Ala  Arg Pro Phe
    2150                 2155                 2160

Asp Ala  Gly Gly Arg Asp Gly  Arg Gly Ala His Ala  Gly Arg Gln
    2165                 2170                 2175

Asn Thr  Phe Trp Asn Leu Gln  Pro Gly Asp Val Ala  Ala Ala Ala
    2180                 2185                 2190

Pro Ala  Leu Gln Pro Ser Ala  Ala Ala Gly Asp Ala  Arg Arg Leu
    2195                 2200                 2205
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Leu Val  Asp Gly Asp Ser Leu  Leu His Ala Gly Thr  Gly Gln Ala
    2210                 2215                 2220

Arg Leu  Leu Arg Gln Leu Glu  Ala Asp Asp Ser Ala  Glu Pro Leu
    2225                 2230                 2235

Leu Leu  Pro Ser Cys Glu Phe  Gly Pro Leu Leu Asn  Phe Val Gly
    2240                 2245                 2250

Gly Phe  Ala Gly Glu Leu Cys  Lys Ser Ser Gly Trp  Leu Val Ala
    2255                 2260                 2265

Gly Leu  Pro Asp Asp Arg Pro  Asp Leu His Ala Ser  Gln Val Thr
    2270                 2275                 2280

Ala Arg  Leu Gln His Gly Ala  Ala Asp Asn Lys Thr  His Ala
    2285                 2290                 2295


<210> SEQ ID NO 71
<211> LENGTH: 373
<212> TYPE: PRT
<213> ORGANISM: Synechocystis PCC6803

<400> SEQUENCE: 71

Met Asp Phe Leu Ser Asn Phe Leu Met Asp Phe Val Lys Gln Leu Gln
1               5                   10                  15

Ser Pro Thr Leu Ser Phe Leu Ile Gly Gly Met Val Ile Ala Ala Cys
            20                  25                  30

Gly Ser Gln Leu Gln Ile Pro Glu Ser Ile Cys Lys Ile Ile Val Phe
        35                  40                  45

Met Leu Leu Thr Lys Ile Gly Leu Thr Gly Gly Met Ala Ile Arg Asn
    50                  55                  60

Ser Asn Leu Thr Glu Met Val Leu Pro Ala Leu Phe Ser Val Ala Ile
65                  70                  75                  80

Gly Ile Leu Ile Val Phe Ile Ala Arg Tyr Thr Leu Ala Arg Met Pro
                85                  90                  95

Lys Val Lys Thr Val Asp Ala Ile Ala Thr Gly Gly Leu Phe Gly Ala
            100                 105                 110

Val Ser Gly Ser Thr Met Ala Ala Ala Leu Thr Leu Leu Glu Glu Gln
        115                 120                 125

Lys Ile Pro Tyr Glu Ala Trp Ala Gly Ala Leu Tyr Pro Phe Met Asp
    130                 135                 140

Ile Pro Ala Leu Val Thr Ala Ile Val Val Ala Asn Ile Tyr Leu Asn
145                 150                 155                 160

Lys Lys Lys Arg Lys Glu Ala Ala Phe Ala Ser Ala Gln Gly Ala Tyr
                165                 170                 175

Ser Lys Gln Pro Val Ala Ala Gly Asp Tyr Ser Ser Ser Ser Asp Tyr
            180                 185                 190

Pro Ser Ser Arg Arg Glu Tyr Ala Gln Gln Glu Ser Gly Asp His Arg
        195                 200                 205

Val Lys Ile Trp Pro Ile Val Glu Glu Ser Leu Gln Gly Pro Ala Leu
    210                 215                 220

Ser Ala Met Leu Leu Gly Val Ala Leu Gly Leu Phe Ala Arg Pro Glu
225                 230                 235                 240

Ser Val Tyr Glu Gly Phe Tyr Asp Pro Leu Phe Arg Gly Leu Leu Ser
                245                 250                 255

Ile Leu Met Leu Val Met Gly Met Glu Ala Trp Ser Arg Ile Ser Glu
            260                 265                 270

Leu Arg Lys Val Ala Gln Trp Tyr Val Val Tyr Ser Ile Val Ala Pro
        275                 280                 285
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Leu Ala His Gly Phe Ile Ala Phe Gly Leu Gly Met Ile Ala His Tyr
    290                 295                 300

Ala Thr Gly Phe Ser Met Gly Gly Val Val Val Leu Ala Val Ile Ala
305                 310                 315                 320

Ala Ser Ser Ser Asp Ile Ser Gly Pro Pro Thr Leu Arg Ala Gly Ile
                325                 330                 335

Pro Ser Ala Asn Pro Ser Ala Tyr Ile Gly Ala Ser Thr Ala Ile Gly
            340                 345                 350

Thr Pro Val Ala Ile Gly Ile Ala Ile Pro Leu Phe Leu Gly Leu Ala
        355                 360                 365

Gln Thr Ile Gly Gly
    370


<210> SEQ ID NO 72
<211> LENGTH: 374
<212> TYPE: PRT
<213> ORGANISM: Synechocystis PCC 6803

<400> SEQUENCE: 72

Met Asp Phe Leu Ser Asn Phe Leu Thr Asp Phe Val Gly Gln Leu Gln
1               5                   10                  15

Ser Pro Thr Leu Ala Phe Leu Ile Gly Gly Met Val Ile Ala Ala Leu
            20                  25                  30

Gly Thr Gln Leu Val Ile Pro Glu Ala Ile Ser Thr Ile Ile Val Phe
        35                  40                  45

Met Leu Leu Thr Lys Ile Gly Leu Thr Gly Gly Met Ala Ile Arg Asn
    50                  55                  60

Ser Asn Leu Thr Glu Met Leu Leu Pro Val Ala Phe Ser Val Ile Leu
65                  70                  75                  80

Gly Ile Leu Ile Val Phe Ile Ala Arg Phe Thr Leu Ala Lys Leu Pro
                85                  90                  95

Asn Val Arg Thr Val Asp Ala Leu Ala Thr Gly Gly Leu Phe Gly Ala
            100                 105                 110

Val Ser Gly Ser Thr Met Ala Ala Ala Leu Thr Thr Leu Glu Glu Ser
        115                 120                 125

Lys Ile Ser Tyr Glu Ala Trp Ala Gly Ala Leu Tyr Pro Phe Met Asp
    130                 135                 140

Ile Pro Ala Leu Val Thr Ala Ile Val Val Ala Asn Ile Tyr Leu Asn
145                 150                 155                 160

Lys Arg Lys Arg Lys Ser Ala Ala Ala Ser Ile Glu Glu Ser Phe Ser
                165                 170                 175

Lys Gln Pro Val Ala Ala Gly Asp Tyr Gly Asp Gln Thr Asp Tyr Pro
            180                 185                 190

Arg Thr Arg Gln Glu Tyr Leu Ser Gln Gln Glu Pro Glu Asp Asn Arg
        195                 200                 205

Val Lys Ile Trp Pro Ile Ile Glu Glu Ser Leu Gln Gly Pro Ala Leu
    210                 215                 220

Ser Ala Met Leu Leu Gly Leu Ala Leu Gly Ile Phe Thr Lys Pro Glu
225                 230                 235                 240

Ser Val Tyr Glu Gly Phe Tyr Asp Pro Leu Phe Arg Gly Leu Leu Ser
                245                 250                 255

Ile Leu Met Leu Ile Met Gly Met Glu Ala Trp Ser Arg Ile Gly Glu
            260                 265                 270

Leu Arg Lys Val Ala Gln Trp Tyr Val Val Tyr Ser Leu Ile Ala Pro
```

```
        275                 280                 285

Ile Val His Gly Phe Ile Ala Phe Gly Leu Gly Met Ile Ala His Tyr
    290                 295                 300

Ala Thr Gly Phe Ser Leu Gly Gly Val Val Val Leu Ala Val Ile Ala
305                 310                 315                 320

Ala Ser Ser Ser Asp Ile Ser Gly Pro Pro Thr Leu Arg Ala Gly Ile
                325                 330                 335

Pro Ser Ala Asn Pro Ser Ala Tyr Ile Gly Ser Ser Thr Ala Ile Gly
            340                 345                 350

Thr Pro Ile Ala Ile Gly Val Cys Ile Pro Leu Phe Ile Gly Leu Ala
        355                 360                 365

Gln Thr Leu Gly Ala Gly
    370


<210> SEQ ID NO 73
<211> LENGTH: 370
<212> TYPE: PRT
<213> ORGANISM: Nostoc PCC 7120
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Anabaena

<400> SEQUENCE: 73

Met Asp Phe Phe Ser Leu Phe Leu Met Asp Phe Val Lys Gln Leu Gln
1               5                   10                  15

Ser Pro Thr Leu Gly Phe Leu Ile Gly Gly Met Val Ile Ala Ala Leu
            20                  25                  30

Gly Ser Glu Leu Ile Ile Pro Glu Ala Ile Cys Gln Ile Ile Val Phe
        35                  40                  45

Met Leu Leu Thr Lys Ile Gly Leu Thr Gly Gly Ile Ala Ile Arg Asn
    50                  55                  60

Ser Asn Leu Thr Glu Met Val Leu Pro Ala Ala Ser Ala Val Ala Val
65                  70                  75                  80

Gly Val Leu Val Val Phe Ile Ala Arg Tyr Thr Leu Ala Lys Leu Pro
                85                  90                  95

Lys Val Asn Thr Val Asp Ala Ile Ala Thr Gly Gly Leu Phe Gly Ala
            100                 105                 110

Val Ser Gly Ser Thr Met Ala Ala Ala Leu Thr Leu Leu Glu Glu Gln
        115                 120                 125

Lys Ile Gln Tyr Glu Ala Trp Ala Ala Ala Leu Tyr Pro Phe Met Asp
    130                 135                 140

Ile Pro Ala Leu Val Thr Ala Ile Val Val Ala Asn Ile Tyr Leu Asn
145                 150                 155                 160

Lys Lys Lys Arg Ser Ala Ala Gly Glu Tyr Leu Ser Lys Gln Ser Val
                165                 170                 175

Ala Ala Gly Glu Tyr Pro Asp Gln Gln Asp Tyr Pro Ser Ser Arg Gln
            180                 185                 190

Glu Tyr Leu Arg Lys Gln Gln Ser Ala Asp Asn Arg Val Lys Ile Trp
        195                 200                 205

Pro Ile Val Lys Glu Ser Leu Gln Gly Pro Ala Leu Ser Ala Met Leu
    210                 215                 220

Leu Gly Ile Ala Leu Gly Leu Phe Thr Gln Pro Glu Ser Val Tyr Lys
225                 230                 235                 240

Ser Phe Tyr Asp Pro Leu Phe Arg Gly Leu Leu Ser Ile Leu Met Leu
                245                 250                 255
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```
Val Met Gly Met Glu Ala Trp Ser Arg Ile Gly Glu Leu Arg Lys Val
            260                 265                 270

Ala Gln Trp Tyr Val Val Tyr Ser Val Val Ala Pro Leu Val His Gly
        275                 280                 285

Phe Ile Ala Phe Gly Leu Gly Met Ile Ala His Tyr Ala Thr Gly Phe
    290                 295                 300

Ser Leu Gly Gly Val Val Ile Leu Ala Val Ile Ala Ala Ser Ser Ser
305                 310                 315                 320

Asp Ile Ser Gly Pro Pro Thr Leu Arg Ala Gly Ile Pro Ser Ala Asn
                325                 330                 335

Pro Ser Ala Tyr Ile Gly Ala Ser Thr Ala Ile Gly Thr Pro Ile Ala
            340                 345                 350

Ile Gly Leu Ala Ile Pro Leu Phe Leu Gly Leu Ala Gln Ala Ile Gly
        355                 360                 365

Gly Arg
    370


<210> SEQ ID NO 74
<211> LENGTH: 377
<212> TYPE: PRT
<213> ORGANISM: Cyanothece sp. PCC 7425

<400> SEQUENCE: 74

Met Asp Phe Trp Ser Tyr Phe Leu Met Asp Phe Val Lys Gln Leu Gln
1               5                   10                  15

Ser Pro Thr Leu Gly Phe Leu Ile Gly Gly Met Val Ile Ala Ala Leu
            20                  25                  30

Gly Ser Gln Leu Val Ile Pro Glu Ala Ile Cys Gln Ile Ile Val Phe
        35                  40                  45

Met Leu Leu Thr Lys Ile Gly Leu Thr Gly Gly Met Ala Ile Arg Asn
    50                  55                  60

Ser Asn Leu Thr Glu Met Val Leu Pro Ala Ala Phe Ser Val Ile Ser
65                  70                  75                  80

Gly Ile Leu Ile Val Phe Ile Ala Arg Tyr Thr Leu Ala Lys Leu Pro
                85                  90                  95

Lys Val Arg Thr Val Asp Ala Ile Ala Thr Gly Gly Leu Phe Gly Ala
            100                 105                 110

Val Ser Gly Ser Thr Met Ala Ala Ala Leu Thr Leu Leu Glu Glu Glu
        115                 120                 125

Lys Ile Pro Tyr Glu Ala Trp Ala Gly Ala Leu Tyr Pro Phe Met Asp
    130                 135                 140

Ile Pro Ala Leu Val Thr Ala Ile Val Ile Ala Asn Ile Tyr Leu Asn
145                 150                 155                 160

Lys Lys Lys Arg Arg Ala Glu Ser Glu Ala Leu Ser Lys Gln Glu Tyr
                165                 170                 175

Leu Gly Lys Gln Ser Ile Val Ala Gly Asp Tyr Pro Ala Gln Gln Asp
            180                 185                 190

Tyr Pro Ser Thr Arg Gln Glu Tyr Leu Ser Lys Gln Gln Gly Pro Glu
        195                 200                 205

Asn Asn Arg Val Lys Ile Trp Pro Ile Val Gln Glu Ser Leu Gln Gly
    210                 215                 220

Pro Ala Leu Ser Ala Met Leu Leu Gly Val Ala Leu Gly Ile Leu Thr
225                 230                 235                 240

Lys Pro Glu Ser Val Tyr Glu Ser Phe Tyr Asp Pro Leu Phe Arg Gly
                245                 250                 255
```

```
Leu Leu Ser Ile Leu Met Leu Val Met Gly Met Glu Ala Trp Ser Arg
            260                 265                 270

Ile Gly Glu Leu Arg Lys Val Ala Gln Trp Tyr Val Val Tyr Ser Val
        275                 280                 285

Val Ala Pro Phe Val His Gly Leu Ile Ala Phe Gly Leu Gly Met Phe
    290                 295                 300

Ala His Tyr Thr Met Gly Phe Ser Met Gly Gly Val Val Val Leu Ala
305                 310                 315                 320

Val Ile Ala Ser Ser Ser Ser Asp Ile Ser Gly Pro Pro Thr Leu Arg
                325                 330                 335

Ala Gly Ile Pro Ser Ala Asn Pro Ser Ala Tyr Ile Gly Ala Ser Thr
            340                 345                 350

Ala Ile Gly Thr Pro Ile Ala Ile Gly Leu Cys Ile Pro Phe Phe Ile
        355                 360                 365

Gly Leu Ala Gln Thr Leu Gly Gly Gly
    370                 375


<210> SEQ ID NO 75
<211> LENGTH: 373
<212> TYPE: PRT
<213> ORGANISM: Microcystis aeruginosa

<400> SEQUENCE: 75

Met Asp Phe Phe Ser Leu Phe Val Met Asp Phe Ile Gln Gln Leu Gln
1               5                   10                  15

Ser Pro Thr Leu Ala Phe Leu Ile Gly Gly Met Ile Ile Ala Ala Leu
            20                  25                  30

Gly Ser Glu Leu Val Ile Pro Glu Ser Ile Cys Thr Ile Ile Val Phe
        35                  40                  45

Met Leu Leu Thr Lys Ile Gly Leu Thr Gly Gly Ile Ala Ile Arg Asn
    50                  55                  60

Ser Asn Leu Thr Glu Met Val Leu Pro Met Ile Phe Ala Val Ile Val
65                  70                  75                  80

Gly Ile Ile Val Val Phe Val Ala Arg Tyr Thr Leu Ala Asn Leu Pro
                85                  90                  95

Lys Val Lys Val Val Asp Ala Ile Ala Thr Gly Gly Leu Phe Gly Ala
            100                 105                 110

Val Ser Gly Ser Thr Met Ala Ala Gly Leu Thr Val Leu Glu Glu Gln
        115                 120                 125

Lys Ile Pro Tyr Glu Ala Trp Ala Gly Ala Leu Tyr Pro Phe Met Asp
    130                 135                 140

Ile Pro Ala Leu Val Thr Ala Ile Val Val Ala Asn Ile Tyr Leu Asn
145                 150                 155                 160

Lys Lys Lys Gln Lys Glu Ala Ala Tyr Asp Gln Glu Ser Phe Ser Lys
                165                 170                 175

Gln Pro Val Ala Ala Gly Asn Tyr Ser Asp Gln Gln Asp Tyr Pro Ser
            180                 185                 190

Ser Arg Gln Glu Tyr Leu Ser Gln Gln Gln Pro Ala Asp Asn Arg Val
        195                 200                 205

Lys Ile Trp Pro Ile Ile Glu Glu Ser Leu Arg Gly Pro Ala Leu Ser
    210                 215                 220

Ala Met Leu Leu Gly Leu Ala Leu Gly Ile Phe Thr Gln Pro Glu Ser
225                 230                 235                 240

Val Tyr Lys Ser Phe Tyr Asp Pro Leu Phe Arg Gly Leu Leu Ser Val
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                245                 250                 255

Leu Met Leu Val Met Gly Met Glu Ala Trp Ser Arg Val Gly Glu Leu
            260                 265                 270

Arg Lys Val Ala Gln Trp Tyr Val Val Tyr Ser Val Ile Ala Pro Phe
        275                 280                 285

Val His Gly Leu Ile Ala Phe Gly Leu Gly Met Ile Ala His Tyr Ala
    290                 295                 300

Thr Gly Phe Ser Trp Gly Gly Val Val Met Leu Ala Val Ile Ala Ser
305                 310                 315                 320

Ser Ser Ser Asp Ile Ser Gly Pro Pro Thr Leu Arg Ala Gly Ile Pro
                325                 330                 335

Ser Ala Asn Pro Ser Ala Tyr Ile Gly Ala Ser Thr Ala Ile Gly Thr
            340                 345                 350

Pro Val Ala Ile Gly Leu Cys Ile Pro Phe Phe Val Gly Leu Ala Gln
        355                 360                 365

Ala Leu Ser Gly Gly
    370


<210> SEQ ID NO 76
<211> LENGTH: 369
<212> TYPE: PRT
<213> ORGANISM: Anabaena variabilis

<400> SEQUENCE: 76

Met Asp Phe Val Ser Leu Phe Val Lys Asp Phe Ile Ala Gln Leu Gln
1               5                   10                  15

Ser Pro Thr Leu Ala Phe Leu Ile Gly Gly Met Ile Ile Ala Ala Leu
            20                  25                  30

Gly Ser Glu Leu Val Ile Pro Glu Ser Ile Cys Thr Ile Ile Val Phe
        35                  40                  45

Met Leu Leu Thr Lys Ile Gly Leu Thr Gly Gly Ile Ala Ile Arg Asn
    50                  55                  60

Ser Asn Leu Thr Glu Met Val Leu Pro Met Ile Phe Ala Val Ile Thr
65                  70                  75                  80

Gly Ile Thr Ile Val Phe Ile Ser Arg Tyr Thr Leu Ala Lys Leu Pro
                85                  90                  95

Lys Val Lys Val Val Asp Ala Ile Ala Thr Gly Gly Leu Phe Gly Ala
            100                 105                 110

Val Ser Gly Ser Thr Met Ala Ala Gly Leu Thr Val Leu Glu Glu Gln
        115                 120                 125

Lys Met Ala Tyr Glu Ala Trp Ala Gly Ala Leu Tyr Pro Phe Met Asp
    130                 135                 140

Ile Pro Ala Leu Val Thr Ala Ile Val Ile Ala Asn Ile Tyr Leu Asn
145                 150                 155                 160

Lys Lys Lys Arg Lys Glu Ala Val Tyr Ser Thr Glu Gln Pro Val Ala
                165                 170                 175

Ala Gly Asp Tyr Pro Asp Gln Lys Asp Tyr Pro Ser Ser Arg Gln Glu
            180                 185                 190

Tyr Leu Ser Gln Gln Lys Gly Asp Glu Asp Asn Arg Val Lys Ile Trp
        195                 200                 205

Pro Ile Ile Glu Glu Ser Leu Arg Gly Pro Ala Leu Ser Ala Met Leu
    210                 215                 220

Leu Gly Leu Ala Leu Gly Leu Phe Thr Gln Pro Glu Ser Val Tyr Lys
225                 230                 235                 240
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Ser Phe Tyr Asp Pro Ala Phe Arg Gly Leu Leu Ser Ile Leu Met Leu
            245                 250                 255

Val Met Gly Met Glu Ala Trp Ser Arg Ile Gly Glu Leu Arg Lys Val
        260                 265                 270

Ala Gln Trp Tyr Val Val Tyr Ser Val Val Ala Pro Phe Val His Gly
        275                 280                 285

Leu Ile Ala Phe Gly Leu Gly Met Ile Ala His Tyr Thr Met Asn Phe
    290                 295                 300

Ser Met Gly Gly Val Val Ile Leu Ala Val Ile Ala Ser Ser Ser Ser
305                 310                 315                 320

Asp Ile Ser Gly Pro Pro Thr Leu Arg Ala Gly Ile Pro Ser Ala Asn
            325                 330                 335

Pro Ser Ala Tyr Ile Gly Ala Ser Thr Ala Val Gly Thr Pro Val Ala
        340                 345                 350

Ile Gly Leu Cys Ile Pro Phe Phe Leu Gly Leu Ala Gln Ala Ile Gly
        355                 360                 365

Gly


<210> SEQ ID NO 77
<211> LENGTH: 1082
<212> TYPE: PRT
<213> ORGANISM: Chlamydomonas reinhardtii

<400> SEQUENCE: 77

Met Leu Pro Gly Leu Gly Val Ile Leu Leu Val Leu Pro Met Gln Tyr
1               5                   10                  15

Tyr Phe Gly Tyr Lys Ile Val Gln Ile Lys Leu Gln Asn Ala Lys His
            20                  25                  30

Val Ala Leu Arg Ser Ala Ile Met Gln Glu Val Leu Pro Ala Ile Lys
        35                  40                  45

Leu Val Lys Tyr Tyr Ala Trp Glu Gln Phe Phe Glu Asn Gln Ile Ser
    50                  55                  60

Lys Val Arg Arg Glu Glu Ile Arg Leu Asn Phe Trp Asn Cys Val Met
65                  70                  75                  80

Lys Val Ile Asn Val Ala Cys Val Phe Cys Val Pro Pro Met Thr Ala
                85                  90                  95

Phe Val Ile Phe Thr Thr Tyr Glu Phe Gln Arg Ala Arg Leu Val Ser
            100                 105                 110

Ser Val Ala Phe Thr Thr Leu Ser Leu Phe Asn Ile Leu Arg Phe Pro
        115                 120                 125

Leu Val Val Leu Pro Lys Ala Leu Arg Ala Val Ser Glu Ala Asn Ala
    130                 135                 140

Ser Leu Gln Arg Leu Glu Ala Tyr Leu Leu Glu Glu Val Pro Ser Gly
145                 150                 155                 160

Thr Ala Ala Val Lys Thr Pro Lys Asn Ala Pro Pro Gly Ala Val Ile
                165                 170                 175

Glu Asn Gly Val Phe His His Pro Ser Asn Pro Asn Trp His Leu His
            180                 185                 190

Val Pro Lys Phe Glu Val Lys Pro Gly Gln Val Val Ala Val Val Gly
        195                 200                 205

Arg Ile Ala Ala Gly Lys Ser Ser Leu Val Gln Ala Ile Leu Gly Asn
    210                 215                 220

Met Val Lys Glu His Gly Ser Phe Asn Val Gly Gly Arg Ile Ser Tyr
225                 230                 235                 240
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Val Pro Gln Asn Pro Trp Leu Gln Asn Leu Ser Leu Arg Asp Asn Val
                245                 250                 255

Leu Phe Gly Glu Gln Phe Asp Glu Asn Lys Tyr Thr Asp Val Ile Glu
            260                 265                 270

Ser Cys Ala Leu Thr Leu Asp Leu Gln Ile Leu Ser Asn Gly Asp Gln
        275                 280                 285

Ser Lys Ala Gly Ile Arg Gly Val Asn Phe Ser Gly Gly Gln Arg Gln
    290                 295                 300

Arg Val Asn Leu Ala Arg Cys Ala Tyr Ala Asp Ala Asp Leu Val Leu
305                 310                 315                 320

Leu Asp Asn Ala Leu Ser Ala Val Asp His His Thr Ala His His Ile
                325                 330                 335

Phe Asp Lys Cys Ile Lys Gly Leu Phe Ser Asp Lys Ala Val Val Leu
            340                 345                 350

Val Thr His Gln Ile Glu Phe Met Pro Arg Cys Asp Asn Val Ala Ile
        355                 360                 365

Met Asp Glu Gly Arg Cys Leu Tyr Phe Gly Lys Trp Asn Glu Glu Ala
    370                 375                 380

Gln His Leu Leu Gly Lys Leu Leu Pro Ile Thr His Leu Leu His Ala
385                 390                 395                 400

Ala Gly Ser Gln Glu Ala Pro Pro Ala Pro Lys Lys Lys Ala Glu Asp
                405                 410                 415

Lys Ala Gly Pro Gln Lys Ser Gln Ser Leu Gln Leu Thr Leu Ala Pro
            420                 425                 430

Thr Ser Ile Gly Lys Pro Thr Glu Lys Pro Lys Asp Val Gln Lys Leu
        435                 440                 445

Thr Ala Tyr Gln Ala Ala Leu Ile Tyr Thr Trp Tyr Gly Asn Leu Phe
    450                 455                 460

Leu Val Gly Val Cys Phe Phe Phe Phe Leu Ala Ala Gln Cys Ser Arg
465                 470                 475                 480

Gln Ile Ser Asp Phe Trp Val Arg Trp Trp Val Asn Asp Glu Tyr Lys
                485                 490                 495

Lys Phe Pro Val Lys Gly Glu Gln Asp Ser Ala Ala Thr Thr Phe Tyr
            500                 505                 510

Cys Leu Ile Tyr Leu Leu Leu Val Gly Leu Phe Tyr Ile Phe Met Ile
        515                 520                 525

Phe Arg Gly Ala Thr Phe Leu Trp Trp Val Leu Lys Ser Ser Glu Thr
    530                 535                 540

Ile Arg Arg Lys Ala Leu His Asn Val Leu Asn Ala Pro Met Gly Phe
545                 550                 555                 560

Phe Leu Val Thr Pro Val Gly Asp Leu Leu Leu Asn Phe Thr Lys Asp
                565                 570                 575

Gln Asp Ile Met Asp Glu Asn Leu Pro Asp Ala Val His Phe Met Gly
            580                 585                 590

Ile Tyr Gly Leu Ile Leu Leu Ala Thr Thr Ile Thr Val Ser Val Thr
        595                 600                 605

Ile Asn Phe Phe Ala Ala Phe Thr Gly Ala Leu Ile Ile Met Thr Leu
    610                 615                 620

Ile Met Leu Ser Ile Tyr Leu Pro Ala Ala Thr Ala Leu Lys Lys Ala
625                 630                 635                 640

Arg Ala Val Ser Gly Gly Met Leu Val Gly Leu Val Ala Glu Val Leu
                645                 650                 655

Glu Gly Leu Gly Val Val Gln Ala Phe Asn Lys Gln Glu Tyr Phe Ile
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            660                 665                 670

Glu Glu Ala Ala Arg Arg Thr Asn Ile Thr Asn Ser Ala Val Phe Asn
        675                 680                 685

Ala Glu Ala Leu Asn Leu Trp Leu Ala Phe Trp Cys Asp Phe Ile Gly
    690                 695                 700

Ala Cys Leu Val Gly Val Val Ser Ala Phe Ala Val Gly Met Ala Lys
705                 710                 715                 720

Asp Leu Gly Gly Ala Thr Val Gly Leu Ala Phe Ser Asn Ile Ile Gln
                725                 730                 735

Met Leu Val Phe Tyr Thr Trp Val Val Arg Phe Ile Ser Glu Ser Ile
            740                 745                 750

Ser Leu Phe Asn Ser Val Glu Gly Met Ala Tyr Leu Ala Asp Tyr Val
        755                 760                 765

Pro His Asp Gly Val Phe Tyr Asp Gln Arg Gln Lys Asp Gly Val Ala
    770                 775                 780

Lys Gln Ile Val Leu Pro Asp Gly Asn Ile Val Pro Ala Ala Ser Lys
785                 790                 795                 800

Val Gln Val Val Val Asp Asp Ala Ala Leu Ala Arg Trp Pro Ala Thr
                805                 810                 815

Gly Asn Ile Arg Phe Glu Asp Val Trp Met Gln Tyr Arg Leu Asp Ala
            820                 825                 830

Pro Trp Ala Leu Lys Gly Val Thr Phe Lys Ile Asn Asp Gly Glu Lys
        835                 840                 845

Val Gly Ala Val Gly Arg Thr Gly Ser Gly Lys Ser Thr Thr Leu Leu
    850                 855                 860

Ala Leu Tyr Arg Met Phe Glu Leu Gly Lys Gly Arg Ile Leu Val Asp
865                 870                 875                 880

Gly Val Asp Ile Ala Thr Leu Ser Leu Lys Arg Leu Arg Thr Gly Leu
                885                 890                 895

Ser Ile Ile Pro Gln Glu Pro Val Met Phe Thr Gly Thr Val Arg Ser
            900                 905                 910

Asn Leu Asp Pro Phe Gly Glu Phe Lys Asp Asp Ala Ile Leu Trp Glu
        915                 920                 925

Val Leu Lys Lys Val Gly Leu Glu Asp Gln Ala Gln His Ala Gly Gly
    930                 935                 940

Leu Asp Gly Gln Val Asp Gly Thr Gly Gly Lys Ala Trp Ser Leu Gly
945                 950                 955                 960

Gln Met Gln Leu Val Cys Leu Ala Arg Ala Ala Leu Arg Ala Val Pro
                965                 970                 975

Ile Leu Cys Leu Asp Glu Ala Thr Ala Ala Met Asp Pro His Thr Glu
            980                 985                 990

Ala Ile Val Gln Gln Thr Ile Lys  Lys Val Phe Asp Asp  Arg Thr Thr
        995                 1000                 1005

Ile Thr  Ile Ala His Arg Leu  Asp Thr Ile Ile Glu  Ser Asp Lys
    1010                 1015                 1020

Ile Ile  Val Met Glu Gln Gly  Ser Leu Met Glu Tyr  Glu Ser Pro
    1025                 1030                 1035

Ser Lys  Leu Leu Ala Asn Arg  Asp Ser Met Phe Ser  Lys Leu Val
    1040                 1045                 1050

Asp Lys  Thr Gly Pro Ala Ala  Ala Ala Ala Leu Arg  Lys Met Ala
    1055                 1060                 1065

Glu Asp  Phe Trp Ser Thr Arg  Ser Ala Gln Gly Arg  Asn Gln
    1070                 1075                 1080
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<210> SEQ ID NO 78
<211> LENGTH: 366
<212> TYPE: PRT
<213> ORGANISM: Cyanothece

<400> SEQUENCE: 78

Met Asp Phe Leu Ser Leu Phe Val Lys Asp Phe Ile Ile Gln Leu Gln
1               5                   10                  15

Ser Pro Thr Leu Ala Phe Leu Ile Gly Gly Met Val Ile Ala Ala Leu
            20                  25                  30

Gly Ser Glu Leu Val Ile Pro Glu Ser Ile Cys Thr Ile Ile Val Phe
        35                  40                  45

Met Leu Leu Thr Lys Ile Gly Leu Thr Gly Gly Ile Ala Ile Arg Asn
    50                  55                  60

Ser Asn Leu Thr Glu Met Val Leu Pro Met Ile Cys Ala Val Ile Val
65                  70                  75                  80

Gly Ile Val Val Val Phe Ile Ala Arg Tyr Thr Leu Ala Lys Leu Pro
                85                  90                  95

Lys Val Asn Val Val Asp Ala Ile Ala Thr Gly Gly Leu Phe Gly Ala
            100                 105                 110

Val Ser Gly Ser Thr Met Ala Ala Gly Leu Thr Val Leu Glu Glu Gln
        115                 120                 125

Lys Ile Pro Tyr Glu Ala Trp Ala Gly Ala Leu Tyr Pro Phe Met Asp
    130                 135                 140

Ile Pro Ala Leu Val Thr Ala Ile Val Val Ala Asn Ile Tyr Leu Asn
145                 150                 155                 160

Lys Lys Lys Arg Lys Ala Thr Val Met Gln Glu Ser Leu Ser Lys Gln
                165                 170                 175

Pro Val Ala Ala Gly Asp Tyr Pro Ser Ser Arg Gln Glu Tyr Val Ser
            180                 185                 190

Gln Gln Gln Pro Glu Asp Asn Arg Val Lys Ile Trp Pro Ile Ile Glu
        195                 200                 205

Glu Ser Leu Arg Gly Pro Ala Leu Ser Ala Met Leu Leu Gly Leu Ala
    210                 215                 220

Leu Gly Ile Leu Thr Gln Pro Glu Ser Val Tyr Lys Gly Phe Tyr Asp
225                 230                 235                 240

Pro Pro Phe Arg Gly Leu Leu Ser Ile Leu Met Leu Val Met Gly Met
                245                 250                 255

Glu Ala Trp Ser Arg Ile Gly Glu Leu Arg Lys Val Ala Gln Trp Tyr
            260                 265                 270

Val Val Tyr Ser Val Ala Ala Pro Phe Ile His Gly Leu Leu Ala Phe
        275                 280                 285

Gly Leu Gly Met Ile Ala His Tyr Thr Met Gly Phe Ser Met Gly Gly
    290                 295                 300

Val Val Ile Leu Ala Val Ile Ala Ser Ser Ser Ser Asp Ile Ser Gly
305                 310                 315                 320

Pro Pro Thr Leu Arg Ala Gly Ile Pro Ser Ala Asn Pro Ser Ala Tyr
                325                 330                 335

Ile Gly Ala Ser Thr Ala Ile Gly Thr Pro Val Ala Ile Gly Leu Cys
            340                 345                 350

Ile Pro Phe Phe Val Gly Leu Ala Gln Ala Ile Gly Gly Phe
        355                 360                 365
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<210> SEQ ID NO 79
<211> LENGTH: 337
<212> TYPE: PRT
<213> ORGANISM: Volvox carteri
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: f. nagariensis

<400> SEQUENCE: 79

Met Gln Thr Thr Met Ser Val Thr Arg Pro Cys Val Gly Leu Arg Pro
1               5                   10                  15

Leu Pro Val Arg Asn Val Arg Ser Leu Ile Arg Ala Gln Ala Ala Pro
            20                  25                  30

Gln Gln Val Ser Thr Ala Val Ser Thr Asn Gly Asn Gly Asn Gly Val
        35                  40                  45

Ala Ala Ala Ser Leu Ser Val Pro Ala Pro Val Ala Ala Pro Ala Gln
    50                  55                  60

Ala Val Ser Thr Pro Val Arg Ala Val Ser Val Leu Thr Pro Pro Gln
65                  70                  75                  80

Val Tyr Glu Asn Ala Ala Asn Val Gly Ala Tyr Lys Ala Ser Leu Gly
                85                  90                  95

Val Leu Ala Thr Phe Val Gln Gly Ile Gln Ala Gly Ala Tyr Ile Ala
            100                 105                 110

Phe Gly Ala Phe Leu Ala Cys Ser Val Gly Gly Asn Ile Pro Gly Ile
        115                 120                 125

Thr Ala Ser Asn Pro Gly Leu Ala Lys Leu Leu Phe Ala Leu Val Phe
    130                 135                 140

Pro Val Gly Leu Ser Met Val Thr Asn Cys Gly Ala Glu Leu Tyr Thr
145                 150                 155                 160

Gly Asn Thr Met Met Leu Thr Cys Ala Ile Phe Glu Lys Lys Ala Thr
                165                 170                 175

Trp Ala Gln Leu Val Lys Asn Trp Val Val Ser Tyr Ala Gly Asn Phe
            180                 185                 190

Val Gly Ser Ile Ala Met Val Ala Ala Val Val Ala Thr Gly Leu Met
        195                 200                 205

Ala Ser Asn Gln Leu Pro Val Asn Met Ala Thr Ala Lys Ser Ser Leu
    210                 215                 220

Gly Phe Thr Glu Val Leu Ser Arg Ser Ile Leu Cys Asn Trp Leu Val
225                 230                 235                 240

Cys Cys Ala Val Trp Ser Ala Ser Ala Ala Thr Ser Leu Pro Gly Arg
                245                 250                 255

Ile Leu Gly Leu Trp Pro Pro Ile Thr Ala Phe Val Ala Ile Gly Leu
            260                 265                 270

Glu His Ser Val Ala Asn Met Phe Val Ile Pro Leu Gly Met Met Leu
        275                 280                 285

Gly Ala Asp Val Thr Trp Ser Gln Phe Phe Phe Asn Asn Leu Val Pro
    290                 295                 300

Val Thr Leu Gly Asn Thr Ile Ala Gly Val Val Met Met Ala Val Ala
305                 310                 315                 320

Tyr Ser Val Ser Tyr Gly Ser Leu Gly Lys Thr Pro Lys Pro Ala Thr
                325                 330                 335

Ala


<210> SEQ ID NO 80
<211> LENGTH: 2297
<212> TYPE: PRT
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<213> ORGANISM: Chlorella variabilis

<400> SEQUENCE: 80

Met Val Pro Leu Leu Ala Gln Arg Gly Arg Ile Arg Ser Gln Ala Pro
1               5                   10                  15

Arg Thr Trp His Pro Asp Pro Gln Pro Leu His Ala Glu Arg Ser Arg
            20                  25                  30

Gln Cys Pro Gly Arg Gly Val Arg Ala Ala Ala Lys Arg Gly Gly Gly
        35                  40                  45

Ser Gly Gly Ala Thr His Lys Ser Lys Lys Ser Lys Glu Leu Asp Glu
    50                  55                  60

Val Ala Ala Phe Glu Gln Leu Met Cys Asp Trp Asp Asp Ala Phe Ala
65                  70                  75                  80

Ala Asp Cys Tyr Asp Asn Glu Arg Ala Ala Arg Met Ala Arg Leu Ala
                85                  90                  95

Glu Glu Gly Tyr Gln His His Gly Arg Gly Phe Val Phe Val Arg Ser
            100                 105                 110

Arg Leu Asp Lys Arg Ser Arg Lys Ala Arg Asn Asp Ser Gly Ala Ser
        115                 120                 125

Lys Gly Phe Gly Ala Ala Ala Lys Ala Leu Ser Val Glu Gln Gly Thr
    130                 135                 140

Pro Leu Glu Asn Asn Pro Gln Leu His Leu Leu Ser Trp Thr Ala Cys
145                 150                 155                 160

Tyr Ile Ala Ser Ser Gln Leu Asp Ser Leu Gly Gly Leu Phe Ser Thr
                165                 170                 175

Gln Glu Gly Val Leu Leu Pro Asp Ser Gly Ser Leu Leu Thr Asp Gly
            180                 185                 190

Gly Ser Gly Ala Ser Gly Ser Asn Ala Ala Asp Ala Val Gly Glu Leu
        195                 200                 205

Gln Arg Val Leu Arg Gly Gln Asp Leu Ser Gln Leu Arg Gly Tyr Val
    210                 215                 220

Gly Ala Pro Pro Gln Ala Arg Pro Ala Ser Gly Ser Asp Asp Asp Gly
225                 230                 235                 240

Ser Ser Thr Thr Gly Ser Asn Asn Gly Ala Ala Gly Glu Gly Ser Glu
                245                 250                 255

Val Glu Glu Gly Thr Ala Met Gly Gly Ile Arg Arg Tyr Glu Pro Glu
            260                 265                 270

Ser Gly Glu Leu Val Val Leu Leu Ser Cys Lys Ile Gly Gly Lys Pro
        275                 280                 285

Ala Val Gly Ala Glu Leu Leu Ala Val Ala Gln Ala Glu Asp Gly Lys
    290                 295                 300

His Ala Pro Gly Ala Ser Pro Asp Thr Arg Leu Cys Lys Glu Pro Ser
305                 310                 315                 320

Gln Ser Ala Phe Asp Leu Trp Ser Phe Gly Trp Met Asn Lys Ile Val
                325                 330                 335

Pro Ala Ala Arg Arg Gly Glu Val Glu Val Ala Asp Leu Pro Leu Pro
            340                 345                 350

Glu Ala Gln Gln Ala Glu Pro Cys Tyr Glu Glu Leu Asn Thr Asn Trp
        355                 360                 365

Glu Ala Ala Val Gln Glu Ala Lys Lys Ala Gly Lys Glu Pro Lys Leu
    370                 375                 380

Met Lys Val Leu Trp Lys Thr Tyr Gly Lys Asp Ile Val Leu Ala Gly
385                 390                 395                 400
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Ile Phe Lys Leu Met Trp Ser Val Phe Val Ile Leu Gly Ala Tyr Tyr
                405                 410                 415

Phe Thr Arg Ser Ile Leu Met Cys Ile Arg Thr Leu Glu Gly Lys Asp
            420                 425                 430

Asp Ser Ile Tyr Asp Thr Glu Trp Lys Gly Trp Val Leu Thr Gly Phe
        435                 440                 445

Phe Phe Leu Asp Ala Trp Leu Leu Gly Met Met Leu Gln Arg Met Ala
    450                 455                 460

Phe Asn Cys Leu Lys Val Gly Ile Lys Ala Arg Ala Ala Leu Thr Thr
465                 470                 475                 480

Met Ile Ala Arg Lys Cys Tyr Asn Met Ala His Leu Thr Lys Asp Thr
                485                 490                 495

Ala Ala Glu Ala Val Gly Phe Val Ala Ser Asp Ile Asn Lys Val Phe
            500                 505                 510

Glu Gly Ile Gln Glu Val His Tyr Leu Trp Gly Ala Pro Val Glu Ala
        515                 520                 525

Gly Ala Ile Leu Ala Leu Leu Gly Thr Leu Val Gly Val Tyr Cys Ile
    530                 535                 540

Gly Gly Val Ile Ile Val Cys Met Val Val Pro Leu Gln Tyr Tyr Phe
545                 550                 555                 560

Gly Tyr Lys Ile Ile Lys Asn Lys Ile Lys Asn Ala Pro Asn Val Thr
                565                 570                 575

Glu Arg Trp Ser Ile Ile Gln Glu Ile Leu Pro Ala Met Lys Leu Val
            580                 585                 590

Lys Tyr Tyr Ala Trp Glu Arg Phe Phe Glu Lys His Val Ala Asp Met
        595                 600                 605

Arg Thr Arg Glu Arg His Tyr Met Phe Trp Asn Ala Val Val Lys Thr
    610                 615                 620

Val Asn Val Thr Met Val Phe Gly Val Pro Pro Met Val Thr Phe Ala
625                 630                 635                 640

Val Leu Val Pro Tyr Glu Leu Trp His Val Asp Ser Ser Thr Ser Glu
                645                 650                 655

Pro Tyr Ile Lys Pro Gln Thr Ala Phe Thr Met Leu Ser Leu Phe Asn
            660                 665                 670

Val Leu Arg Phe Pro Leu Val Val Leu Pro Lys Ala Met Arg Cys Val
        675                 680                 685

Ser Glu Ala Leu Arg Ser Val Gly Asn Leu Glu Lys Phe Leu Ala Glu
    690                 695                 700

Pro Val Ala Pro Arg Gln Asp Leu Glu Gly Lys Pro Gly Ala Gln Leu
705                 710                 715                 720

Ser Lys Ala Val Leu Arg His Glu Met Asp Thr Ser Gly Phe Thr Leu
                725                 730                 735

Arg Val Pro Glu Phe Ser Val Lys Ala Gly Glu Leu Val Ala Val Val
            740                 745                 750

Gly Arg Val Gly Ala Gly Lys Ser Ser Ile Leu Gln Ala Met Leu Gly
        755                 760                 765

Asn Met Gln Thr Ala Ser Gly Leu Ala Lys Cys Gln His Ser Ala Ser
    770                 775                 780

Ser Cys Leu Pro Phe Leu Val Glu Gly Thr Ala His Ser Gly Gly Arg
785                 790                 795                 800

Ile Ala Tyr Val Pro Gln Thr Ala Trp Cys Gln Asn Leu Ser Leu Arg
                805                 810                 815

Asp Asn Ile Thr Phe Gly Gln Pro Trp Asp Glu Ala Lys Tyr Lys Gln
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            820                 825                 830

Val Ile His Ala Cys Ala Leu Glu Leu Asp Leu Ala Ile Leu Ala Ala
        835                 840                 845

Gly Asp Gln Ser Lys Ala Gly Leu Arg Gly Ile Asn Leu Ser Gly Gly
    850                 855                 860

Gln Arg Gln Arg Leu Asn Leu Ala Arg Cys Ala Tyr Phe Asp Gly Asp
865                 870                 875                 880

Leu Val Leu Leu Asp Asn Ala Leu Ser Ala Val Asp His His Thr Ala
                885                 890                 895

His His Ile Phe Glu His Cys Val Arg Gly Met Phe Arg Asp Lys Ala
            900                 905                 910

Thr Val Leu Val Thr His Gln Val Glu Phe Leu Pro Gln Cys Asp Lys
        915                 920                 925

Val Ala Ile Met Asp Asp Gly Thr Cys Val Tyr Phe Gly Pro Trp Asn
    930                 935                 940

Ala Ala Ala Gln Gln Leu Leu Ser Lys Tyr Leu Pro Ala Ser His Leu
945                 950                 955                 960

Leu Ala Ala Gly Gly Asn Ala Glu Gln Pro Arg Asp Thr Lys Lys Lys
                965                 970                 975

Val Val Lys Lys Glu Glu Thr Lys Lys Thr Glu Asp Ala Gly Lys Ala
            980                 985                 990

Lys Arg Val His Ser Ala Ser Leu  Thr Leu Lys Ser Ala  Leu Trp Glu
        995                 1000                 1005

Tyr Cys  Trp Asp Ala Arg Trp  Ile Ile Phe Cys Leu  Ser Leu Phe
    1010                 1015                 1020

Phe Phe  Leu Thr Ala Gln Ala  Ser Arg Gln Leu Ala  Asp Tyr Phe
    1025                 1030                 1035

Ile Arg  Trp Trp Thr Arg Asp  His Tyr Asn Lys Tyr  Gly Val Leu
    1040                 1045                 1050

Cys Ile  Asp Glu Gly Asp Asn  Pro Cys Gly Pro Leu  Phe Tyr Val
    1055                 1060                 1065

Gln Tyr  Tyr Gly Ile Leu Gly  Leu Leu Cys Phe Ile  Val Leu Met
    1070                 1075                 1080

Ala Phe  Arg Gly Ala Phe Leu  Tyr Thr Trp Ser Leu  Gly Ala Ser
    1085                 1090                 1095

Tyr Arg  Gln His Glu Lys Ser  Ile His Arg Val Leu  Tyr Ala Pro
    1100                 1105                 1110

Leu Gly  Phe Phe Leu Thr Thr  Pro Val Gly Asp Leu  Leu Val Ser
    1115                 1120                 1125

Phe Thr  Lys Asp Gln Asp Val  Met Asp Asp Ala Leu  Pro Asp Ala
    1130                 1135                 1140

Leu Tyr  Tyr Ala Gly Ile Tyr  Gly Leu Ile Leu Leu  Ala Thr Ala
    1145                 1150                 1155

Ile Thr  Val Ser Val Thr Ile  Pro Leu Phe Ser Ala  Leu Ala Gly
    1160                 1165                 1170

Gly Leu  Phe Val Val Ser Gly  Ile Met Leu Ala Ile  Tyr Leu Pro
    1175                 1180                 1185

Ala Ala  Thr His Leu Lys Lys  Leu Arg Met Gly Thr  Ser Gly Asp
    1190                 1195                 1200

Val Val  Thr Leu Ile Ala Glu  Ala Leu Asp Gly Leu  Gly Val Ile
    1205                 1210                 1215

Gln Ala  Tyr Gly Lys Gln Ala  Tyr Phe Thr Thr Ile  Thr Ser Gln
    1220                 1225                 1230
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Tyr Val  Asn Asp Ala His Arg  Ala Leu Phe Gly Ala  Glu Ser Leu
    1235                 1240                 1245

Asn Leu  Trp Leu Ala Phe Ile  Cys Asp Phe Phe Gly  Ala Cys Met
    1250                 1255                 1260

Val Leu  Ser Val Ala Cys Phe  Gly Ile Gly Gln Trp  Ser Thr Leu
    1265                 1270                 1275

Gly Ser  Ser Ser Val Gly Leu  Ala Phe Ser Gln Ser  Ile Gln Met
    1280                 1285                 1290

Leu Val  Phe Tyr Thr Trp Ser  Ile Arg Leu Val Ala  Glu Cys Ile
    1295                 1300                 1305

Gly Leu  Phe Gly Ser Ala Glu  Lys Ile Ala Trp Leu  Ala Asn His
    1310                 1315                 1320

Thr Pro  Gln Glu Ala Gly Ser  Leu Asp Pro Pro Ser  Leu Pro Gly
    1325                 1330                 1335

Ser Gly  Glu Thr Lys Ala Ala  Pro Lys Lys Arg Gly  Thr Ala Gly
    1340                 1345                 1350

Lys Phe  Leu Pro Pro Leu Lys  Asp Glu Asp Leu Ala  Ile Val Pro
    1355                 1360                 1365

Thr Gly  Gly Pro Lys Leu Pro  Ser Gly Trp Pro Arg  Thr Gly Val
    1370                 1375                 1380

Leu Glu  Phe Asn Gln Val Val  Met Lys Tyr Ala Pro  His Leu Pro
    1385                 1390                 1395

Pro Ala  Leu Arg Gly Val Ser  Phe Lys Val Lys Ser  Gly Asp Lys
    1400                 1405                 1410

Val Gly  Val Val Gly Arg Thr  Gly Ser Gly Lys Ser  Thr Leu Leu
    1415                 1420                 1425

Leu Ala  Leu Tyr Arg Met Phe  Asn Leu Glu Ser Gly  Ala Ile Thr
    1430                 1435                 1440

Leu Asp  Gly Ile Asp Ile Ser  Thr Leu Thr Leu Glu  Gln Leu Arg
    1445                 1450                 1455

Arg Gly  Leu Ser Val Ile Pro  Gln Glu Pro Thr Val  Phe Ser Gly
    1460                 1465                 1470

Thr Val  Arg Thr Asn Leu Asp  Pro Phe Gly Glu Phe  Gly Ala Asp
    1475                 1480                 1485

Ala Ile  Leu Trp Glu Ala Leu  Arg Asp Cys Gly Leu  Glu Glu Gln
    1490                 1495                 1500

Val Lys  Ala Cys Gly Gly Leu  Asp Ala Lys Leu Asp  Gly Thr Gly
    1505                 1510                 1515

Gly Asn  Ala Trp Ser Ile Gly  Gln Gln Gln Leu Met  Cys Leu Ala
    1520                 1525                 1530

Arg Ala  Ala Leu Lys Lys Val  Pro Val Leu Cys Leu  Asp Glu Ala
    1535                 1540                 1545

Thr Ala  Ala Met Asp Pro His  Thr Glu Ala His Val  Leu Glu Ile
    1550                 1555                 1560

Ile Glu  Arg Ile Phe Ser Asp  Arg Thr Met Leu Thr  Ile Ala His
    1565                 1570                 1575

Arg Leu  Asp Asn Val Ile Arg  Ser Asp Leu Val Val  Val Met Asp
    1580                 1585                 1590

Ala Gly  Gln Val Cys Glu Met  Gly Thr Pro Asp Glu  Leu Leu Ala
    1595                 1600                 1605

Asn Pro  Gln Ser Ala Phe Ser  Gln Leu Val Asp Lys  Thr Gly Ala
    1610                 1615                 1620
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Ala Ser  Ala Ala Ala Leu Arg  Lys Met Ala Ala Asp  Phe Leu Asp
    1625                 1630                 1635

Glu Arg  Ala Arg Gly Gln Lys  Leu Gly Phe Lys Pro  Arg Pro Ser
    1640                 1645                 1650

Leu Glu  Glu Ser His Ile Cys  Val Ala Pro Ser Pro  Ser Leu Ile
    1655                 1660                 1665

Leu Ser  Thr Leu Leu Phe Pro  Pro Ala Phe Met Ala  Asn Val Thr
    1670                 1675                 1680

Ala Leu  Leu Leu Pro Lys Pro  Val Leu Ser His Ala  Pro Val Ser
    1685                 1690                 1695

Ser Gln  Thr Val Asn Thr Tyr  Ile Arg Leu Asn Ile  Ile Gln Leu
    1700                 1705                 1710

Gln Cys  Asn Val Leu His Pro  Ala Thr Lys Glu Ala  Thr Trp Ser
    1715                 1720                 1725

Ser Arg  Arg Ile Thr Phe Thr  Ala His Leu Ser Ser  Ser Gly Ser
    1730                 1735                 1740

Lys Pro  Pro Pro Pro Leu Pro  Pro Leu Thr Glu Leu  Pro Glu Gly
    1745                 1750                 1755

Arg Gly  Leu Asp Trp Ser Ser  Ala Gly Tyr Arg Asp  Gly Arg Glu
    1760                 1765                 1770

Ala Ile  Pro Ser Pro Ser Ala  Lys Tyr Ser Ala Ala  Asp Tyr Gly
    1775                 1780                 1785

Ala Ala  Gly Asp Gly Val Thr  Asp Asp Thr Gln Ala  Leu Gln Val
    1790                 1795                 1800

Ala Val  Ala Ala Ala His Glu  Asp Asp Glu Gly Gly  Val Val Tyr
    1805                 1810                 1815

Leu Gly  Ala Gly Thr Phe Val  Leu Thr Gln Pro Leu  Ser Ile Ala
    1820                 1825                 1830

Gly Ser  Asn Val Val Ile Arg  Gly Ala Gly Glu Asp  Ala Thr Thr
    1835                 1840                 1845

Ile Phe  Val Pro Leu Pro Leu  Ser Asp Val Phe Pro  Gly Thr Trp
    1850                 1855                 1860

Ser Met  Asp Ala Ser Gly Lys  Val Thr Ser Pro Trp  Ile Thr Arg
    1865                 1870                 1875

Gly Gly  Phe Leu Ala Phe Ser  Gly Arg Arg Thr Lys  Ser Ser Asp
    1880                 1885                 1890

Ser Ser  Thr Leu Leu Ala Thr  Val Ala Gly Ser Val  Glu Gln Gly
    1895                 1900                 1905

Ala Ser  Val Ile Pro Val Asp  Ser Thr Ala Glu Phe  Arg Leu Gly
    1910                 1915                 1920

Gln Trp  Val Arg Ile Ile Ile  Asn Asp Ala Ser Thr  Asp Ala Ser
    1925                 1930                 1935

Ala Gly  Gly Gly Thr Leu Glu  Arg Gly Ser Ser Glu  Val Gln Glu
    1940                 1945                 1950

Ser Glu  Thr Met Ile Ala Glu  Gly Ala Thr Gly Gly  Gly Ala Gly
    1955                 1960                 1965

Val Arg  Ala Gln Trp Thr Gly  Val Leu His Ala Phe  Glu Pro Thr
    1970                 1975                 1980

Val Gln  Cys Ser Gly Val Glu  Gln Leu Thr Ile Arg  Phe Asn His
    1985                 1990                 1995

Ser Met  Met Ala Ala His Leu  Ala Glu Arg Gly Tyr  Asn Ala Ile
    2000                 2005                 2010

Glu Leu  Glu Asp Val Val Asp  Cys Trp Ile Arg Gln  Val Thr Ile
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    2015                 2020                 2025

Leu Asn  Ala Asp Asn Ala Ile  Arg Leu Arg Gly Thr  Asp His Ser
    2030                 2035                 2040

Thr Leu  Ser Gly Gln Ala Cys  Ser Gly Gly Gly Val  Val Ala Val
    2045                 2050                 2055

Val Pro  Val Trp Cys Arg Arg  Gly Leu Pro Ser Pro  Ala Asp Val
    2060                 2065                 2070

Thr Val  Gly Val Thr Glu Leu  Arg Trp Glu Pro Asp  Thr Arg Glu
    2075                 2080                 2085

Val Asn  Gly His His Ala Ile  Thr Val Ser Lys Gly  His Ala Asn
    2090                 2095                 2100

Leu Val  Thr Arg Phe Arg Ile  Thr Ala Pro Phe Tyr  His Asp Ile
    2105                 2110                 2115

Ser Leu  Glu Gly Gly Ala Leu  Leu Asn Val Ile Ser  Ser Gly Gly
    2120                 2125                 2130

Gly Ala  Asn Leu Asn Leu Asp  Leu His Arg Ser Gly  Pro Trp Gly
    2135                 2140                 2145

Asn Leu  Phe Ser Gln Leu Gly  Met Gly Leu Ala Ala  Arg Pro Phe
    2150                 2155                 2160

Asp Ala  Gly Gly Arg Asp Gly  Arg Gly Ala His Ala  Gly Arg Gln
    2165                 2170                 2175

Asn Thr  Phe Trp Asn Leu Gln  Pro Gly Asp Val Ala  Ala Ala Ala
    2180                 2185                 2190

Pro Ala  Leu Gln Pro Ser Ala  Ala Ala Gly Asp Ala  Arg Arg Leu
    2195                 2200                 2205

Leu Val  Asp Gly Asp Ser Leu  Leu His Ala Gly Thr  Gly Gln Ala
    2210                 2215                 2220

Arg Leu  Leu Arg Gln Leu Glu  Ala Asp Asp Ser Ala  Glu Pro Leu
    2225                 2230                 2235

Leu Leu  Pro Ser Cys Glu Phe  Gly Pro Leu Leu Asn  Phe Val Gly
    2240                 2245                 2250

Gly Phe  Ala Gly Glu Leu Cys  Lys Ser Ser Gly Trp  Leu Val Ala
    2255                 2260                 2265

Gly Leu  Pro Asp Asp Arg Pro  Asp Leu His Ala Ser  Gln Val Thr
    2270                 2275                 2280

Ala Arg  Leu Gln His Gly Ala  Ala Asp Asn Lys Thr  His Ala
    2285                 2290                 2295


<210> SEQ ID NO 81
<211> LENGTH: 373
<212> TYPE: PRT
<213> ORGANISM: Synechococcus PCC7942
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: PCC 7942

<400> SEQUENCE: 81

Met Asp Phe Leu Ser Asn Phe Leu Met Asp Phe Val Lys Gln Leu Gln
1               5                   10                  15

Ser Pro Thr Leu Ser Phe Leu Ile Gly Gly Met Val Ile Ala Ala Cys
            20                  25                  30

Gly Ser Gln Leu Gln Ile Pro Glu Ser Ile Cys Lys Ile Ile Val Phe
        35                  40                  45

Met Leu Leu Thr Lys Ile Gly Leu Thr Gly Gly Met Ala Ile Arg Asn
    50                  55                  60
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Ser Asn Leu Thr Glu Met Val Leu Pro Ala Leu Phe Ser Val Ala Ile
65                  70                  75                  80

Gly Ile Leu Ile Val Phe Ile Ala Arg Tyr Thr Leu Ala Arg Met Pro
                85                  90                  95

Lys Val Lys Thr Val Asp Ala Ile Ala Thr Gly Gly Leu Phe Gly Ala
            100                 105                 110

Val Ser Gly Ser Thr Met Ala Ala Ala Leu Thr Leu Leu Glu Glu Gln
        115                 120                 125

Lys Ile Pro Tyr Glu Ala Trp Ala Gly Ala Leu Tyr Pro Phe Met Asp
    130                 135                 140

Ile Pro Ala Leu Val Thr Ala Ile Val Val Ala Asn Ile Tyr Leu Asn
145                 150                 155                 160

Lys Lys Lys Arg Lys Glu Ala Ala Phe Ala Ser Ala Gln Gly Ala Tyr
                165                 170                 175

Ser Lys Gln Pro Val Ala Ala Gly Asp Tyr Ser Ser Ser Ser Asp Tyr
            180                 185                 190

Pro Ser Ser Arg Arg Glu Tyr Ala Gln Gln Glu Ser Gly Asp His Arg
        195                 200                 205

Val Lys Ile Trp Pro Ile Val Glu Glu Ser Leu Gln Gly Pro Ala Leu
    210                 215                 220

Ser Ala Met Leu Leu Gly Val Ala Leu Gly Leu Phe Ala Arg Pro Glu
225                 230                 235                 240

Ser Val Tyr Glu Gly Phe Tyr Asp Pro Leu Phe Arg Gly Leu Leu Ser
                245                 250                 255

Ile Leu Met Leu Val Met Gly Met Glu Ala Trp Ser Arg Ile Ser Glu
            260                 265                 270

Leu Arg Lys Val Ala Gln Trp Tyr Val Val Tyr Ser Ile Val Ala Pro
        275                 280                 285

Leu Ala His Gly Phe Ile Ala Phe Gly Leu Gly Met Ile Ala His Tyr
    290                 295                 300

Ala Thr Gly Phe Ser Met Gly Gly Val Val Val Leu Ala Val Ile Ala
305                 310                 315                 320

Ala Ser Ser Ser Asp Ile Ser Gly Pro Pro Thr Leu Arg Ala Gly Ile
                325                 330                 335

Pro Ser Ala Asn Pro Ser Ala Tyr Ile Gly Ala Ser Thr Ala Ile Gly
            340                 345                 350

Thr Pro Val Ala Ile Gly Ile Ala Ile Pro Leu Phe Leu Gly Leu Ala
        355                 360                 365

Gln Thr Ile Gly Gly
    370


<210> SEQ ID NO 82
<211> LENGTH: 374
<212> TYPE: PRT
<213> ORGANISM: Synechocystis PCC6803

<400> SEQUENCE: 82

Met Asp Phe Leu Ser Asn Phe Leu Thr Asp Phe Val Gly Gln Leu Gln
1               5                   10                  15

Ser Pro Thr Leu Ala Phe Leu Ile Gly Gly Met Val Ile Ala Ala Leu
            20                  25                  30

Gly Thr Gln Leu Val Ile Pro Glu Ala Ile Ser Thr Ile Ile Val Phe
        35                  40                  45

Met Leu Leu Thr Lys Ile Gly Leu Thr Gly Gly Met Ala Ile Arg Asn
    50                  55                  60
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Ser Asn Leu Thr Glu Met Leu Leu Pro Val Ala Phe Ser Val Ile Leu
65                  70                  75                  80

Gly Ile Leu Ile Val Phe Ile Ala Arg Phe Thr Leu Ala Lys Leu Pro
                85                  90                  95

Asn Val Arg Thr Val Asp Ala Leu Ala Thr Gly Gly Leu Phe Gly Ala
            100                 105                 110

Val Ser Gly Ser Thr Met Ala Ala Ala Leu Thr Thr Leu Glu Glu Ser
        115                 120                 125

Lys Ile Ser Tyr Glu Ala Trp Ala Gly Ala Leu Tyr Pro Phe Met Asp
    130                 135                 140

Ile Pro Ala Leu Val Thr Ala Ile Val Val Ala Asn Ile Tyr Leu Asn
145                 150                 155                 160

Lys Arg Lys Arg Lys Ser Ala Ala Ala Ser Ile Glu Glu Ser Phe Ser
                165                 170                 175

Lys Gln Pro Val Ala Ala Gly Asp Tyr Gly Asp Gln Thr Asp Tyr Pro
            180                 185                 190

Arg Thr Arg Gln Glu Tyr Leu Ser Gln Gln Glu Pro Glu Asp Asn Arg
        195                 200                 205

Val Lys Ile Trp Pro Ile Ile Glu Glu Ser Leu Gln Gly Pro Ala Leu
    210                 215                 220

Ser Ala Met Leu Leu Gly Leu Ala Leu Gly Ile Phe Thr Lys Pro Glu
225                 230                 235                 240

Ser Val Tyr Glu Gly Phe Tyr Asp Pro Leu Phe Arg Gly Leu Leu Ser
                245                 250                 255

Ile Leu Met Leu Ile Met Gly Met Glu Ala Trp Ser Arg Ile Gly Glu
            260                 265                 270

Leu Arg Lys Val Ala Gln Trp Tyr Val Val Tyr Ser Leu Ile Ala Pro
        275                 280                 285

Ile Val His Gly Phe Ile Ala Phe Gly Leu Gly Met Ile Ala His Tyr
    290                 295                 300

Ala Thr Gly Phe Ser Leu Gly Gly Val Val Val Leu Ala Val Ile Ala
305                 310                 315                 320

Ala Ser Ser Ser Asp Ile Ser Gly Pro Pro Thr Leu Arg Ala Gly Ile
                325                 330                 335

Pro Ser Ala Asn Pro Ser Ala Tyr Ile Gly Ser Ser Thr Ala Ile Gly
            340                 345                 350

Thr Pro Ile Ala Ile Gly Val Cys Ile Pro Leu Phe Ile Gly Leu Ala
        355                 360                 365

Gln Thr Leu Gly Ala Gly
    370


<210> SEQ ID NO 83
<211> LENGTH: 370
<212> TYPE: PRT
<213> ORGANISM: Nostoc sp. PCC 7120 (Anabaena sp. PCC 7120)

<400> SEQUENCE: 83

Met Asp Phe Phe Ser Leu Phe Leu Met Asp Phe Val Lys Gln Leu Gln
1               5                   10                  15

Ser Pro Thr Leu Gly Phe Leu Ile Gly Gly Met Val Ile Ala Ala Leu
            20                  25                  30

Gly Ser Glu Leu Ile Ile Pro Glu Ala Ile Cys Gln Ile Ile Val Phe
        35                  40                  45

Met Leu Leu Thr Lys Ile Gly Leu Thr Gly Gly Ile Ala Ile Arg Asn
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    50                  55                  60

Ser Asn Leu Thr Glu Met Val Leu Pro Ala Ala Ser Ala Val Ala Val
65                  70                  75                  80

Gly Val Leu Val Val Phe Ile Ala Arg Tyr Thr Leu Ala Lys Leu Pro
                85                  90                  95

Lys Val Asn Thr Val Asp Ala Ile Ala Thr Gly Gly Leu Phe Gly Ala
            100                 105                 110

Val Ser Gly Ser Thr Met Ala Ala Ala Leu Thr Leu Leu Glu Glu Gln
        115                 120                 125

Lys Ile Gln Tyr Glu Ala Trp Ala Ala Ala Leu Tyr Pro Phe Met Asp
    130                 135                 140

Ile Pro Ala Leu Val Thr Ala Ile Val Val Ala Asn Ile Tyr Leu Asn
145                 150                 155                 160

Lys Lys Lys Arg Ser Ala Ala Gly Glu Tyr Leu Ser Lys Gln Ser Val
                165                 170                 175

Ala Ala Gly Glu Tyr Pro Asp Gln Gln Asp Tyr Pro Ser Ser Arg Gln
            180                 185                 190

Glu Tyr Leu Arg Lys Gln Gln Ser Ala Asp Asn Arg Val Lys Ile Trp
        195                 200                 205

Pro Ile Val Lys Glu Ser Leu Gln Gly Pro Ala Leu Ser Ala Met Leu
    210                 215                 220

Leu Gly Ile Ala Leu Gly Leu Phe Thr Gln Pro Glu Ser Val Tyr Lys
225                 230                 235                 240

Ser Phe Tyr Asp Pro Leu Phe Arg Gly Leu Leu Ser Ile Leu Met Leu
                245                 250                 255

Val Met Gly Met Glu Ala Trp Ser Arg Ile Gly Glu Leu Arg Lys Val
            260                 265                 270

Ala Gln Trp Tyr Val Val Tyr Ser Val Val Ala Pro Leu Val His Gly
        275                 280                 285

Phe Ile Ala Phe Gly Leu Gly Met Ile Ala His Tyr Ala Thr Gly Phe
    290                 295                 300

Ser Leu Gly Gly Val Val Ile Leu Ala Val Ile Ala Ala Ser Ser Ser
305                 310                 315                 320

Asp Ile Ser Gly Pro Pro Thr Leu Arg Ala Gly Ile Pro Ser Ala Asn
                325                 330                 335

Pro Ser Ala Tyr Ile Gly Ala Ser Thr Ala Ile Gly Thr Pro Ile Ala
            340                 345                 350

Ile Gly Leu Ala Ile Pro Leu Phe Leu Gly Leu Ala Gln Ala Ile Gly
        355                 360                 365

Gly Arg
    370


<210> SEQ ID NO 84
<211> LENGTH: 377
<212> TYPE: PRT
<213> ORGANISM: Cyanothece PCC 7425

<400> SEQUENCE: 84

Met Asp Phe Trp Ser Tyr Phe Leu Met Asp Phe Val Lys Gln Leu Gln
1               5                   10                  15

Ser Pro Thr Leu Gly Phe Leu Ile Gly Gly Met Val Ile Ala Ala Leu
            20                  25                  30

Gly Ser Gln Leu Val Ile Pro Glu Ala Ile Cys Gln Ile Ile Val Phe
        35                  40                  45
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Met Leu Leu Thr Lys Ile Gly Leu Thr Gly Gly Met Ala Ile Arg Asn
    50                  55                  60

Ser Asn Leu Thr Glu Met Val Leu Pro Ala Ala Phe Ser Val Ile Ser
65                  70                  75                  80

Gly Ile Leu Ile Val Phe Ile Ala Arg Tyr Thr Leu Ala Lys Leu Pro
                85                  90                  95

Lys Val Arg Thr Val Asp Ala Ile Ala Thr Gly Gly Leu Phe Gly Ala
            100                 105                 110

Val Ser Gly Ser Thr Met Ala Ala Ala Leu Thr Leu Leu Glu Glu Glu
        115                 120                 125

Lys Ile Pro Tyr Glu Ala Trp Ala Gly Ala Leu Tyr Pro Phe Met Asp
    130                 135                 140

Ile Pro Ala Leu Val Thr Ala Ile Val Ile Ala Asn Ile Tyr Leu Asn
145                 150                 155                 160

Lys Lys Lys Arg Arg Ala Glu Ser Glu Ala Leu Ser Lys Gln Glu Tyr
                165                 170                 175

Leu Gly Lys Gln Ser Ile Val Ala Gly Asp Tyr Pro Ala Gln Gln Asp
            180                 185                 190

Tyr Pro Ser Thr Arg Gln Glu Tyr Leu Ser Lys Gln Gln Gly Pro Glu
        195                 200                 205

Asn Asn Arg Val Lys Ile Trp Pro Ile Val Gln Glu Ser Leu Gln Gly
    210                 215                 220

Pro Ala Leu Ser Ala Met Leu Leu Gly Val Ala Leu Gly Ile Leu Thr
225                 230                 235                 240

Lys Pro Glu Ser Val Tyr Glu Ser Phe Tyr Asp Pro Leu Phe Arg Gly
                245                 250                 255

Leu Leu Ser Ile Leu Met Leu Val Met Gly Met Glu Ala Trp Ser Arg
            260                 265                 270

Ile Gly Glu Leu Arg Lys Val Ala Gln Trp Tyr Val Val Tyr Ser Val
        275                 280                 285

Val Ala Pro Phe Val His Gly Leu Ile Ala Phe Gly Leu Gly Met Phe
    290                 295                 300

Ala His Tyr Thr Met Gly Phe Ser Met Gly Gly Val Val Val Leu Ala
305                 310                 315                 320

Val Ile Ala Ser Ser Ser Ser Asp Ile Ser Gly Pro Pro Thr Leu Arg
                325                 330                 335

Ala Gly Ile Pro Ser Ala Asn Pro Ser Ala Tyr Ile Gly Ala Ser Thr
            340                 345                 350

Ala Ile Gly Thr Pro Ile Ala Ile Gly Leu Cys Ile Pro Phe Phe Ile
        355                 360                 365

Gly Leu Ala Gln Thr Leu Gly Gly Gly
    370                 375


<210> SEQ ID NO 85
<211> LENGTH: 373
<212> TYPE: PRT
<213> ORGANISM: Microcystis aeruginosa

<400> SEQUENCE: 85

Met Asp Phe Phe Ser Leu Phe Val Met Asp Phe Ile Gln Gln Leu Gln
1               5                   10                  15

Ser Pro Thr Leu Ala Phe Leu Ile Gly Gly Met Ile Ile Ala Ala Leu
            20                  25                  30

Gly Ser Glu Leu Val Ile Pro Glu Ser Ile Cys Thr Ile Ile Val Phe
        35                  40                  45
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Met Leu Leu Thr Lys Ile Gly Leu Thr Gly Gly Ile Ala Ile Arg Asn
    50                  55                  60

Ser Asn Leu Thr Glu Met Val Leu Pro Met Ile Phe Ala Val Ile Val
65                  70                  75                  80

Gly Ile Ile Val Val Phe Val Ala Arg Tyr Thr Leu Ala Asn Leu Pro
                85                  90                  95

Lys Val Lys Val Val Asp Ala Ile Ala Thr Gly Gly Leu Phe Gly Ala
            100                 105                 110

Val Ser Gly Ser Thr Met Ala Ala Gly Leu Thr Val Leu Glu Glu Gln
        115                 120                 125

Lys Ile Pro Tyr Glu Ala Trp Ala Gly Ala Leu Tyr Pro Phe Met Asp
    130                 135                 140

Ile Pro Ala Leu Val Thr Ala Ile Val Val Ala Asn Ile Tyr Leu Asn
145                 150                 155                 160

Lys Lys Lys Gln Lys Glu Ala Ala Tyr Asp Gln Glu Ser Phe Ser Lys
                165                 170                 175

Gln Pro Val Ala Ala Gly Asn Tyr Ser Asp Gln Gln Asp Tyr Pro Ser
            180                 185                 190

Ser Arg Gln Glu Tyr Leu Ser Gln Gln Gln Pro Ala Asp Asn Arg Val
        195                 200                 205

Lys Ile Trp Pro Ile Ile Glu Glu Ser Leu Arg Gly Pro Ala Leu Ser
    210                 215                 220

Ala Met Leu Leu Gly Leu Ala Leu Gly Ile Phe Thr Gln Pro Glu Ser
225                 230                 235                 240

Val Tyr Lys Ser Phe Tyr Asp Pro Leu Phe Arg Gly Leu Leu Ser Val
                245                 250                 255

Leu Met Leu Val Met Gly Met Glu Ala Trp Ser Arg Val Gly Glu Leu
            260                 265                 270

Arg Lys Val Ala Gln Trp Tyr Val Val Tyr Ser Val Ile Ala Pro Phe
        275                 280                 285

Val His Gly Leu Ile Ala Phe Gly Leu Gly Met Ile Ala His Tyr Ala
    290                 295                 300

Thr Gly Phe Ser Trp Gly Gly Val Val Met Leu Ala Val Ile Ala Ser
305                 310                 315                 320

Ser Ser Ser Asp Ile Ser Gly Pro Pro Thr Leu Arg Ala Gly Ile Pro
                325                 330                 335

Ser Ala Asn Pro Ser Ala Tyr Ile Gly Ala Ser Thr Ala Ile Gly Thr
            340                 345                 350

Pro Val Ala Ile Gly Leu Cys Ile Pro Phe Phe Val Gly Leu Ala Gln
        355                 360                 365

Ala Leu Ser Gly Gly
    370


<210> SEQ ID NO 86
<211> LENGTH: 369
<212> TYPE: PRT
<213> ORGANISM: Anabaena variabilis

<400> SEQUENCE: 86

Met Asp Phe Val Ser Leu Phe Val Lys Asp Phe Ile Ala Gln Leu Gln
1               5                   10                  15

Ser Pro Thr Leu Ala Phe Leu Ile Gly Gly Met Ile Ile Ala Ala Leu
            20                  25                  30

Gly Ser Glu Leu Val Ile Pro Glu Ser Ile Cys Thr Ile Ile Val Phe
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        35                  40                  45

Met Leu Leu Thr Lys Ile Gly Leu Thr Gly Gly Ile Ala Ile Arg Asn
    50                  55                  60

Ser Asn Leu Thr Glu Met Val Leu Pro Met Ile Phe Ala Val Ile Thr
65                  70                  75                  80

Gly Ile Thr Ile Val Phe Ile Ser Arg Tyr Thr Leu Ala Lys Leu Pro
                85                  90                  95

Lys Val Lys Val Val Asp Ala Ile Ala Thr Gly Gly Leu Phe Gly Ala
            100                 105                 110

Val Ser Gly Ser Thr Met Ala Ala Gly Leu Thr Val Leu Glu Glu Gln
        115                 120                 125

Lys Met Ala Tyr Glu Ala Trp Ala Gly Ala Leu Tyr Pro Phe Met Asp
    130                 135                 140

Ile Pro Ala Leu Val Thr Ala Ile Val Ile Ala Asn Ile Tyr Leu Asn
145                 150                 155                 160

Lys Lys Lys Arg Lys Glu Ala Val Tyr Ser Thr Glu Gln Pro Val Ala
                165                 170                 175

Ala Gly Asp Tyr Pro Asp Gln Lys Asp Tyr Pro Ser Ser Arg Gln Glu
            180                 185                 190

Tyr Leu Ser Gln Gln Lys Gly Asp Glu Asp Asn Arg Val Lys Ile Trp
        195                 200                 205

Pro Ile Ile Glu Glu Ser Leu Arg Gly Pro Ala Leu Ser Ala Met Leu
    210                 215                 220

Leu Gly Leu Ala Leu Gly Leu Phe Thr Gln Pro Glu Ser Val Tyr Lys
225                 230                 235                 240

Ser Phe Tyr Asp Pro Ala Phe Arg Gly Leu Leu Ser Ile Leu Met Leu
                245                 250                 255

Val Met Gly Met Glu Ala Trp Ser Arg Ile Gly Glu Leu Arg Lys Val
            260                 265                 270

Ala Gln Trp Tyr Val Val Tyr Ser Val Val Ala Pro Phe Val His Gly
        275                 280                 285

Leu Ile Ala Phe Gly Leu Gly Met Ile Ala His Tyr Thr Met Asn Phe
    290                 295                 300

Ser Met Gly Gly Val Val Ile Leu Ala Val Ile Ala Ser Ser Ser Ser
305                 310                 315                 320

Asp Ile Ser Gly Pro Pro Thr Leu Arg Ala Gly Ile Pro Ser Ala Asn
                325                 330                 335

Pro Ser Ala Tyr Ile Gly Ala Ser Thr Ala Val Gly Thr Pro Val Ala
            340                 345                 350

Ile Gly Leu Cys Ile Pro Phe Phe Leu Gly Leu Ala Gln Ala Ile Gly
        355                 360                 365

Gly


<210> SEQ ID NO 87
<211> LENGTH: 366
<212> TYPE: PRT
<213> ORGANISM: Cyanothece

<400> SEQUENCE: 87

Met Asp Phe Leu Ser Leu Phe Val Lys Asp Phe Ile Ile Gln Leu Gln
1               5                   10                  15

Ser Pro Thr Leu Ala Phe Leu Ile Gly Gly Met Val Ile Ala Ala Leu
            20                  25                  30

Gly Ser Glu Leu Val Ile Pro Glu Ser Ile Cys Thr Ile Ile Val Phe
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        35                  40                  45

Met Leu Leu Thr Lys Ile Gly Leu Thr Gly Gly Ile Ala Ile Arg Asn
    50                  55                  60

Ser Asn Leu Thr Glu Met Val Leu Pro Met Ile Cys Ala Val Ile Val
65                  70                  75                  80

Gly Ile Val Val Val Phe Ile Ala Arg Tyr Thr Leu Ala Lys Leu Pro
                85                  90                  95

Lys Val Asn Val Val Asp Ala Ile Ala Thr Gly Gly Leu Phe Gly Ala
            100                 105                 110

Val Ser Gly Ser Thr Met Ala Ala Gly Leu Thr Val Leu Glu Glu Gln
        115                 120                 125

Lys Ile Pro Tyr Glu Ala Trp Ala Gly Ala Leu Tyr Pro Phe Met Asp
    130                 135                 140

Ile Pro Ala Leu Val Thr Ala Ile Val Val Ala Asn Ile Tyr Leu Asn
145                 150                 155                 160

Lys Lys Lys Arg Lys Ala Thr Val Met Gln Glu Ser Leu Ser Lys Gln
                165                 170                 175

Pro Val Ala Ala Gly Asp Tyr Pro Ser Ser Arg Gln Glu Tyr Val Ser
            180                 185                 190

Gln Gln Gln Pro Glu Asp Asn Arg Val Lys Ile Trp Pro Ile Ile Glu
        195                 200                 205

Glu Ser Leu Arg Gly Pro Ala Leu Ser Ala Met Leu Leu Gly Leu Ala
    210                 215                 220

Leu Gly Ile Leu Thr Gln Pro Glu Ser Val Tyr Lys Gly Phe Tyr Asp
225                 230                 235                 240

Pro Pro Phe Arg Gly Leu Leu Ser Ile Leu Met Leu Val Met Gly Met
                245                 250                 255

Glu Ala Trp Ser Arg Ile Gly Glu Leu Arg Lys Val Ala Gln Trp Tyr
            260                 265                 270

Val Val Tyr Ser Val Ala Ala Pro Phe Ile His Gly Leu Leu Ala Phe
        275                 280                 285

Gly Leu Gly Met Ile Ala His Tyr Thr Met Gly Phe Ser Met Gly Gly
    290                 295                 300

Val Val Ile Leu Ala Val Ile Ala Ser Ser Ser Ser Asp Ile Ser Gly
305                 310                 315                 320

Pro Pro Thr Leu Arg Ala Gly Ile Pro Ser Ala Asn Pro Ser Ala Tyr
                325                 330                 335

Ile Gly Ala Ser Thr Ala Ile Gly Thr Pro Val Ala Ile Gly Leu Cys
            340                 345                 350

Ile Pro Phe Phe Val Gly Leu Ala Gln Ala Ile Gly Gly Phe
        355                 360                 365


<210> SEQ ID NO 88
<211> LENGTH: 378
<212> TYPE: PRT
<213> ORGANISM: Arthrospira platensis str. Paraca

<400> SEQUENCE: 88

Met Asp Phe Leu Ser Gly Phe Leu Thr Arg Phe Leu Ala Gln Leu Gln
1               5                   10                  15

Ser Pro Thr Leu Gly Phe Leu Ile Gly Gly Met Val Ile Ala Ala Val
            20                  25                  30

Asn Ser Gln Leu Gln Ile Pro Asp Ala Ile Tyr Lys Phe Val Val Phe
        35                  40                  45
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Met Leu Leu Met Lys Val Gly Leu Ser Gly Gly Ile Ala Ile Arg Gly
    50                  55                  60

Ser Asn Leu Thr Glu Met Leu Leu Pro Ala Val Phe Ala Leu Val Thr
65                  70                  75                  80

Gly Ile Val Ile Val Phe Ile Gly Arg Tyr Thr Leu Ala Lys Leu Pro
                85                  90                  95

Asn Val Lys Thr Val Asp Ala Ile Ala Thr Ala Gly Leu Phe Gly Ala
            100                 105                 110

Val Ser Gly Ser Thr Met Ala Ala Ala Leu Thr Leu Leu Glu Glu Gln
        115                 120                 125

Gly Met Glu Tyr Glu Ala Trp Ala Ala Ala Leu Tyr Pro Phe Met Asp
    130                 135                 140

Ile Pro Ala Leu Val Ser Ala Ile Val Leu Ala Ser Ile Tyr Val Ser
145                 150                 155                 160

Lys Gln Lys His Ser Asp Met Ala Asp Glu Ser Leu Ser Lys His Glu
                165                 170                 175

Ser Leu Ser Lys Gln Pro Val Ala Ala Gly Asp Tyr Pro Ser Lys Pro
            180                 185                 190

Glu Tyr Pro Thr Thr Arg Gln Glu Tyr Leu Ser Gln Gln Arg Gly Ser
        195                 200                 205

Ala Asn Gln Gly Val Glu Ile Trp Pro Ile Ile Lys Glu Ser Leu Gln
    210                 215                 220

Gly Ser Ala Leu Ser Ala Leu Leu Leu Gly Leu Ala Leu Gly Leu Leu
225                 230                 235                 240

Thr Arg Pro Glu Ser Val Phe Gln Ser Phe Tyr Glu Pro Leu Phe Arg
                245                 250                 255

Gly Leu Leu Ser Ile Leu Met Leu Val Met Gly Met Glu Ala Thr Ala
            260                 265                 270

Arg Leu Gly Glu Leu Arg Lys Val Ala Gln Trp Tyr Ala Val Tyr Ala
        275                 280                 285

Phe Ile Ala Pro Leu Leu His Gly Leu Ile Ala Phe Gly Leu Gly Met
    290                 295                 300

Ile Ala His Val Val Thr Gly Phe Ser Leu Gly Gly Val Val Ile Leu
305                 310                 315                 320

Ala Val Ile Ala Ser Ser Ser Ser Asp Ile Ser Gly Pro Pro Thr Leu
                325                 330                 335

Arg Ala Gly Ile Pro Ser Ala Asn Pro Ser Ala Tyr Ile Gly Ser Ser
            340                 345                 350

Thr Ala Val Gly Thr Pro Val Ala Ile Ala Leu Gly Ile Pro Leu Tyr
        355                 360                 365

Ile Gly Leu Ala Gln Ala Leu Met Gly Gly
    370                 375


<210> SEQ ID NO 89
<211> LENGTH: 336
<212> TYPE: PRT
<213> ORGANISM: Chlamydomonas reinhardtii

<400> SEQUENCE: 89

Met Gln Thr Thr Met Thr Arg Pro Cys Leu Ala Gln Pro Val Leu Arg
1               5                   10                  15

Ser Arg Val Leu Arg Ser Pro Met Arg Val Val Ala Ala Ser Ala Pro
            20                  25                  30

Thr Ala Val Thr Thr Val Val Thr Ser Asn Gly Asn Gly Asn Gly His
        35                  40                  45
```

```
Phe Gln Ala Ala Thr Thr Pro Val Pro Pro Thr Pro Ala Pro Val Ala
    50                  55                  60

Val Ser Ala Pro Val Arg Ala Val Ser Val Leu Thr Pro Pro Gln Val
65                  70                  75                  80

Tyr Glu Asn Ala Ile Asn Val Gly Ala Tyr Lys Ala Gly Leu Thr Pro
                85                  90                  95

Leu Ala Thr Phe Val Gln Gly Ile Gln Ala Gly Ala Tyr Ile Ala Phe
            100                 105                 110

Gly Ala Phe Leu Ala Ile Ser Val Gly Gly Asn Ile Pro Gly Val Ala
        115                 120                 125

Ala Ala Asn Pro Gly Leu Ala Lys Leu Leu Phe Ala Leu Val Phe Pro
    130                 135                 140

Val Gly Leu Ser Met Val Thr Asn Cys Gly Ala Glu Leu Phe Thr Gly
145                 150                 155                 160

Asn Thr Met Met Leu Thr Cys Ala Leu Ile Glu Lys Lys Ala Thr Trp
                165                 170                 175

Gly Gln Leu Leu Lys Asn Trp Ser Val Ser Tyr Phe Gly Asn Phe Val
            180                 185                 190

Gly Ser Ile Ala Met Val Ala Ala Val Val Ala Thr Gly Cys Leu Thr
        195                 200                 205

Thr Asn Thr Leu Pro Val Gln Met Ala Thr Leu Lys Ala Asn Leu Gly
    210                 215                 220

Phe Thr Glu Val Leu Ser Arg Ser Ile Leu Cys Asn Trp Leu Val Cys
225                 230                 235                 240

Cys Ala Val Trp Ser Ala Ser Ala Ala Thr Ser Leu Pro Gly Arg Ile
                245                 250                 255

Leu Ala Leu Trp Pro Cys Ile Thr Ala Phe Val Ala Ile Gly Leu Glu
            260                 265                 270

His Ser Val Ala Asn Met Phe Val Ile Pro Leu Gly Met Met Leu Gly
        275                 280                 285

Ala Glu Val Thr Trp Ser Gln Phe Phe Phe Asn Asn Leu Ile Pro Val
    290                 295                 300

Thr Leu Gly Asn Thr Ile Ala Gly Val Leu Met Met Ala Ile Ala Tyr
305                 310                 315                 320

Ser Ile Ser Phe Gly Ser Leu Gly Lys Ser Ala Lys Pro Ala Thr Ala
                325                 330                 335


<210> SEQ ID NO 90
<211> LENGTH: 337
<212> TYPE: PRT
<213> ORGANISM: Volvox carteri
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: f. nagariensis

<400> SEQUENCE: 90

Met Gln Thr Thr Met Ser Val Thr Arg Pro Cys Val Gly Leu Arg Pro
1               5                   10                  15

Leu Pro Val Arg Asn Val Arg Ser Leu Ile Arg Ala Gln Ala Ala Pro
            20                  25                  30

Gln Gln Val Ser Thr Ala Val Ser Thr Asn Gly Asn Gly Asn Gly Val
        35                  40                  45

Ala Ala Ala Ser Leu Ser Val Pro Ala Pro Val Ala Ala Pro Ala Gln
    50                  55                  60

Ala Val Ser Thr Pro Val Arg Ala Val Ser Val Leu Thr Pro Pro Gln
```

```
65                  70                  75                  80

Val Tyr Glu Asn Ala Ala Asn Val Gly Ala Tyr Lys Ala Ser Leu Gly
                85                  90                  95

Val Leu Ala Thr Phe Val Gln Gly Ile Gln Ala Gly Ala Tyr Ile Ala
            100                 105                 110

Phe Gly Ala Phe Leu Ala Cys Ser Val Gly Gly Asn Ile Pro Gly Ile
        115                 120                 125

Thr Ala Ser Asn Pro Gly Leu Ala Lys Leu Leu Phe Ala Leu Val Phe
    130                 135                 140

Pro Val Gly Leu Ser Met Val Thr Asn Cys Gly Ala Glu Leu Tyr Thr
145                 150                 155                 160

Gly Asn Thr Met Met Leu Thr Cys Ala Ile Phe Glu Lys Lys Ala Thr
                165                 170                 175

Trp Ala Gln Leu Val Lys Asn Trp Val Val Ser Tyr Ala Gly Asn Phe
            180                 185                 190

Val Gly Ser Ile Ala Met Val Ala Ala Val Val Ala Thr Gly Leu Met
        195                 200                 205

Ala Ser Asn Gln Leu Pro Val Asn Met Ala Thr Ala Lys Ser Ser Leu
    210                 215                 220

Gly Phe Thr Glu Val Leu Ser Arg Ser Ile Leu Cys Asn Trp Leu Val
225                 230                 235                 240

Cys Cys Ala Val Trp Ser Ala Ser Ala Ala Thr Ser Leu Pro Gly Arg
                245                 250                 255

Ile Leu Gly Leu Trp Pro Pro Ile Thr Ala Phe Val Ala Ile Gly Leu
            260                 265                 270

Glu His Ser Val Ala Asn Met Phe Val Ile Pro Leu Gly Met Met Leu
        275                 280                 285

Gly Ala Asp Val Thr Trp Ser Gln Phe Phe Phe Asn Asn Leu Val Pro
    290                 295                 300

Val Thr Leu Gly Asn Thr Ile Ala Gly Val Val Met Met Ala Val Ala
305                 310                 315                 320

Tyr Ser Val Ser Tyr Gly Ser Leu Gly Lys Thr Pro Lys Pro Ala Thr
                325                 330                 335

Ala


<210> SEQ ID NO 91
<211> LENGTH: 3249
<212> TYPE: DNA
<213> ORGANISM: Engineered construct (codon optimized gene)

<400> SEQUENCE: 91

atgctgcccg gcctgggcgt catcctgctg gtgctgccca tgcagtacta cttcggctac      60

aagatcgtgc agatcaagct gcagaacgcc aagcacgtcg ccctgcgctc cgccatcatg     120

caggaggtgc tgcccgccat caagctggtc aagtactacg cctgggagca gttctttgag     180

aaccagatca gcaaggtccg ccgcgaggag atccgcctca acttctggaa ctgcgtgatg     240

aaggtcatca acgtggcctg cgtgttctgc gtgccgccca tgaccgcctt cgtcatcttc     300

accacctacg agttccagcg cgcccgcctg gtgtccagcg tcgccttcac caccctgtcg     360

ctgttcaaca ttctgcgctt ccccctggtc gtgctgccca aggccctgcg tgccgtgtcc     420

gaggccaacg cgtctctcca gcgcctggag gcctacctgc tggaggaggt gccctcgggc     480

actgccgccg tcaagacccc caagaacgct ccccccggcg ccgtcatcga gaacggtgtg     540

ttccaccacc cctccaaccc caactggcac ctgcacgtgc ccaagttcga ggtcaagccc     600
```

-continued

```
ggccaggtcg ttgctgtggt gggccgcatc gccgccggca agtcgtccct ggtgcaggcc    660

atcctcggca acatggtcaa ggagcacggc agcttcaacg tgggcggccg catctcctac    720

gtgccgcaga accccctggct gcagaacctg tccctgcgtg acaacgtgct gtttggcgag    780

cagttcgatg agaacaagta caccgacgtc atcgagtcct gcgccctgac cctggacctg    840

cagatcctgt ccaacggtga ccagtccaag gccggcatcc gcggtgtcaa cttctccggt    900

ggccagcgcc agcgcgtgaa cctggcccgc tgcgcctacg ccgacgccga cctggtgctg    960

ctcgacaacg ccctgtccgc cgtggaccac cacaccgccc accacatctt cgacaagtgc   1020

atcaagggcc tgttctccga caaggccgtg gtgctggtca cccaccagat cgagttcatg   1080

ccccgctgcg acaacgtggc catcatggac gagggccgct gcctgtactt cggcaagtgg   1140

aacgaggagg cccagcacct gctcggcaag ctgctgccca tcacccacct gctgcacgcc   1200

gccggctccc aggaggctcc ccccgccccc aagaagaagg ccgaggacaa ggccggcccc   1260

cagaagtcgc agtcgctgca gctgaccctg gcccccacct ccatcggcaa gcccaccgag   1320

aagcccaagg acgtccagaa gctgactgcc taccaggccg ccctcatcta cacctggtac   1380

ggcaacctgt tcctggttgg cgtgtgcttc ttcttcttcc tggcggctca gtgctctcgc   1440

cagatctccg atttctgggt gcgctggtgg gtgaacgacg agtacaagaa gttccccgtg   1500

aagggcgagc aggactcggc cgccaccacc ttctactgcc tcatctacct gctgctggtg   1560

ggcctgttct acatcttcat gatcttccgc ggcgccactt tcctgtggtg ggtgctcaag   1620

tcctcggaga ccatccgcag gaaggccctg cacaacgtcc tcaacgcgcc catgggcttc   1680

ttcctggtca cgccggtcgg cgacctgctg ctcaacttca ccaaggacca ggacattatg   1740

gatgagaacc tgcccgatgc cgttcacttc atgggcatct acggcctgat tctgctggcg   1800

accaccatca ccgtgtccgt caccatcaac ttcttcgccg ccttcaccgg cgcgctgatc   1860

atcatgaccc tcatcatgct ctccatctac ctgcccgccg ccactgccct gaagaaggcg   1920

cgcgccgtgt ctggcggcat gctggtcggc ctggttgccg aggttctgga gggccttggc   1980

gtggttcagg ccttcaacaa gcaggagtac ttcattgagg aggccgcccg ccgcaccaac   2040

atcaccaact ccgccgtctt caacgccgag gcgctgaacc tgtggctggc tttctggtgc   2100

gacttcatcg gcgcctgcct ggtgggcgtg gtgtccgcct tcgccgtggg catggccaag   2160

gacctgggcg gcgcgaccgt cggcctggcc ttctccaaca tcattcagat gcttgtgttc   2220

tacacctggg tggtccgctt catctccgag tccatctccc tcttcaactc cgtcgagggc   2280

atggcctacc tcgccgacta cgtgccccac gatggtgtct tctatgacca gcgccagaag   2340

gacggcgtcg ccaagcaaat cgtcctgccc gacggcaaca tcgtgcccgc cgcctccaag   2400

gtccaggtcg tggttgacga cgccgccctc gcccgctggc ctgccaccgg caacatccgc   2460

ttcgaggacg tgtggatgca gtaccgcctg gacgctcctt gggctctgaa gggcgtcacc   2520

ttcaagatca acgacggcga gaaggtcggc gccgtgggcc gcaccggctc cggcaagtcc   2580

accacgctgc tggcgctgta ccgcatgttc gagctgggca agggccgcat cctggtcgac   2640

ggcgtggaca tcgccaccct gtcgctcaag cgcctgcgca ccggcctgtc catcattccc   2700

caggagcccg tcatgttcac cggcaccgtg cgctccaacc tggacccctt cggcgagttc   2760

aaggacgatg ccattctgtg ggaggtgctg aagaaggtcg gcctcgagga ccaggcgcag   2820

cacgccggcg gcctggacgg ccaggtcgat ggcaccggcg gcaaggcctg gtctctgggc   2880

cagatgcagc tggtgtgcct ggctcgcgcc gccctgcgcg ccgtgcccat cctgtgcctg   2940
```

```
gacgaggcta ccgccgccat ggacccgcac actgaggcca tcgtgcagca gaccatcaag   3000

aaggtgttcg acgaccgcac caccatcacc attgcccacc gcctggacac catcatcgag   3060

tccgacaaga tcatcgtgat ggagcagggc tcgctgatgg agtacgagtc gccctcgaag   3120

ctgctcgcca accgcgactc catgttctcc aagctggtcg acaagaccgg ccccgccgcc   3180

gccgctgcgc tgcgcaagat ggccgaggac ttctggtcca ctcgctccgc gcagggccgc   3240

aaccagtaa                                                           3249
```

<210> SEQ ID NO 92
<211> LENGTH: 1008
<212> TYPE: DNA
<213> ORGANISM: Engineered construct (codon optimized gene)

<400> SEQUENCE: 92

```
atgcagacca ctatgactcg cccttgcctt gcccagcccg tgctgcgatc tcgtgtgctc     60

cggtcgccta tgcgggtggt tgcagcgagc gctcctaccg cggtgacgac agtcgtgacc    120

tcgaatggaa atggcaacgg tcatttccaa gctgctacta cgcccgtgcc ccctactccc    180

gctcccgtcg ctgtttccgc gcctgtgcgc gctgtgtcgg tgctgactcc tcctcaagtg    240

tatgagaacg ccattaatgt tggcgcctac aaggccgggc taacgcctct ggcaacgttt    300

gtccagggca tccaagccgg tgcctacatt gcgttcggcg ccttcctcgc catctccgtg    360

ggaggcaaca tccccggcgt cgccgccgcc aaccccggcc tggccaagct gctatttgct    420

ctggtgttcc ccgtgggtct gtccatggtg accaactgcg gcgccgagct gttcacgggc    480

aacaccatga tgctcacatg cgcgctcatc gagaagaagg ccacttgggg gcagcttctg    540

aagaactgga gcgtgtccta cttcggcaac ttcgtgggct ccatcgccat ggtcgccgcc    600

gtggtggcca ccggctgcct gaccaccaac accctgcctg tgcagatggc caccctcaag    660

gccaacctgg gcttcaccga ggtgctgtcg cgctccatcc tgtgcaactg gctggtgtgc    720

tgcgccgtgt ggtccgcctc cgccgccacc tcgctgcccg gccgcatcct ggcgctgtgg    780

ccctgcatca ccgccttcgt ggccatcggc ctggagcact ccgtcgccaa catgttcgtg    840

attcctctgg gcatgatgct gggcgctgag gtcacgtgga gccagttctt tttcaacaac    900

ctgatccccg tcaccctggg caacaccatt gctggcgttc tcatgatggc catcgcctac    960

tccatctcgt tcggctccct cggcaagtcc gccaagcccg ccaccgcg                1008
```

<210> SEQ ID NO 93
<211> LENGTH: 148
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Ferredoxin1

<400> SEQUENCE: 93

```
Met Ala Ser Thr Ala Leu Ser Ser Ala Ile Val Ser Thr Ser Phe Leu
1               5                   10                  15

Arg Arg Gln Gln Thr Pro Ile Ser Leu Arg Ser Leu Pro Phe Ala Asn
            20                  25                  30

Thr Gln Ser Leu Phe Gly Leu Lys Ser Ser Thr Ala Arg Gly Gly Arg
        35                  40                  45

Val Thr Ala Met Ala Thr Tyr Lys Val Lys Phe Ile Thr Pro Glu Gly
    50                  55                  60

Glu Gln Glu Val Glu Cys Glu Glu Asp Val Tyr Val Leu Asp Ala Ala
65                  70                  75                  80
```

```
Glu Glu Ala Gly Leu Asp Leu Pro Tyr Ser Cys Arg Ala Gly Ser Cys
                85                  90                  95

Ser Ser Cys Ala Gly Lys Val Val Ser Gly Ser Ile Asp Gln Ser Asp
            100                 105                 110

Gln Ser Phe Leu Asp Asp Glu Gln Met Ser Glu Gly Tyr Val Leu Thr
        115                 120                 125

Cys Val Ala Tyr Pro Thr Ser Asp Val Val Ile Glu Thr His Lys Glu
    130                 135                 140

Glu Ala Ile Met
145
```

<210> SEQ ID NO 94
<211> LENGTH: 783
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 94

```
atgtcccatc actgggggta cggcaaacac aacggacctg agcactggca taaggacttc      60

cccattgcca agggagagcg ccagtcccct gttgacatcg acactcatac agccaagtat     120

gacccttccc tgaagcccct gtctgtttcc tatgatcaag caacttccct gaggatcctc     180

aacaatggtc atgctttcaa cgtggagttt gatgactctc aggacaaagc agtgctcaag     240

ggaggacccc tggatggcac ttacagattg attcagtttc actttcactg ggttcactt      300

gatggacaag gttcagagca tactgtggat aaaaagaaat atgctgcaga acttcacttg     360

gttcactgga acaccaaata tggggatttt gggaaagctg tgcagcaacc tgatggactg     420

gccgttctag gtatttttt gaaggttggc agcgctaaac cgggccttca gaaagttgtt      480

gatgtgctgg attccattaa aacaaagggc aagagtgctg acttcactaa cttcgatcct     540

cgtggcctcc ttcctgaatc cttggattac tggacctacc caggctcact gaccacccct     600

cctcttctgg aatgtgtgac ctggattgtg ctcaaggaac ccatcagcgt cagcagcgag     660

caggtgttga aattccgtaa acttaacttc aatggggagg gtgaacccga agaactgatg     720

gtggacaact ggcgcccagc tcagccactg aagaacaggc aaatcaaagc ttccttcaaa     780

taa                                                                   783
```

<210> SEQ ID NO 95
<211> LENGTH: 148
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Ferredoxin2(thale cress)

<400> SEQUENCE: 95

```
Met Ala Ser Thr Ala Leu Ser Ser Ala Ile Val Gly Thr Ser Phe Ile
1               5                   10                  15

Arg Arg Ser Pro Ala Pro Ile Ser Leu Arg Ser Leu Pro Ser Ala Asn
            20                  25                  30

Thr Gln Ser Leu Phe Gly Leu Lys Ser Gly Thr Ala Arg Gly Gly Arg
        35                  40                  45

Val Thr Ala Met Ala Thr Tyr Lys Val Lys Phe Ile Thr Pro Glu Gly
    50                  55                  60

Glu Leu Glu Val Glu Cys Asp Asp Asp Val Tyr Val Leu Asp Ala Ala
65                  70                  75                  80

Glu Glu Ala Gly Ile Asp Leu Pro Tyr Ser Cys Arg Ala Gly Ser Cys
```

```
                85                  90                  95

Ser Ser Cys Ala Gly Lys Val Val Ser Gly Ser Val Asp Gln Ser Asp
            100                 105                 110

Gln Ser Phe Leu Asp Asp Glu Gln Ile Gly Glu Gly Phe Val Leu Thr
        115                 120                 125

Cys Ala Ala Tyr Pro Thr Ser Asp Val Thr Ile Glu Thr His Lys Glu
    130                 135                 140

Glu Asp Ile Val
145


<210> SEQ ID NO 96
<211> LENGTH: 253
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana (thale cress)
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: ferredoxin-NADP(+)oxidoreductase(FNR1)

<400> SEQUENCE: 96

Phe Thr Thr Glu Gly Glu Val Pro Tyr Arg Glu Gly Gln Ser Ile Gly
1               5                   10                  15

Val Ile Pro Glu Gly Ile Asp Lys Asn Gly Lys Pro His Lys Leu Arg
            20                  25                  30

Leu Tyr Ser Ile Ala Ser Ser Ala Ile Gly Asp Phe Gly Asp Ser Lys
        35                  40                  45

Thr Val Ser Leu Cys Val Lys Arg Leu Val Tyr Thr Asn Asp Gly Gly
    50                  55                  60

Glu Ile Val Lys Gly Val Cys Ser Asn Phe Leu Cys Asp Leu Lys Pro
65                  70                  75                  80

Gly Asp Glu Ala Lys Ile Thr Gly Pro Val Gly Lys Glu Met Leu Met
                85                  90                  95

Pro Lys Asp Pro Asn Ala Thr Ile Ile Met Leu Gly Thr Gly Thr Gly
            100                 105                 110

Ile Ala Pro Phe Arg Ser Phe Leu Trp Lys Met Phe Phe Glu Glu His
        115                 120                 125

Glu Asp Tyr Lys Phe Asn Gly Leu Ala Trp Leu Phe Leu Gly Val Pro
    130                 135                 140

Thr Ser Ser Ser Leu Leu Tyr Lys Glu Glu Phe Glu Lys Met Lys Glu
145                 150                 155                 160

Lys Asn Pro Asp Asn Phe Arg Leu Asp Phe Ala Val Ser Arg Glu Gln
                165                 170                 175

Thr Asn Glu Lys Gly Glu Lys Met Tyr Ile Gln Thr Arg Met Ala Glu
            180                 185                 190

Tyr Ala Glu Glu Leu Trp Glu Leu Leu Lys Lys Asp Asn Thr Phe Val
        195                 200                 205

Tyr Met Cys Gly Leu Lys Gly Met Glu Lys Gly Ile Asp Asp Ile Met
    210                 215                 220

Val Ser Leu Ala Ala Lys Asp Gly Ile Asp Trp Leu Glu Tyr Lys Lys
225                 230                 235                 240

Gln Leu Lys Arg Ser Glu Gln Trp Asn Val Glu Val Tyr
                245                 250


<210> SEQ ID NO 97
<211> LENGTH: 294
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana (thale cress)
<220> FEATURE:
```

-continued

```
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: ferredoxin-NADP(+)oxidoreductase(FNR2)

<400> SEQUENCE: 97

Met Ala Thr Thr Met Asn Ala Ala Val Ser Leu Thr Ser Ser Asn Ser
1               5                   10                  15

Ser Ser Phe Pro Ala Thr Ser Cys Ala Ile Ala Pro Glu Arg Ile Arg
            20                  25                  30

Phe Thr Lys Gly Ala Phe Tyr Tyr Lys Ser Asn Asn Val Val Thr Gly
        35                  40                  45

Lys Arg Val Phe Ser Ile Lys Ala Gln Ile Thr Thr Glu Thr Asp Thr
    50                  55                  60

Pro Thr Pro Ala Lys Lys Val Glu Lys Val Ser Lys Lys Asn Glu Glu
65                  70                  75                  80

Gly Val Ile Val Asn Arg Tyr Arg Pro Lys Glu Pro Tyr Thr Gly Lys
                85                  90                  95

Cys Leu Leu Asn Thr Lys Ile Thr Ala Asp Asp Ala Pro Gly Glu Thr
            100                 105                 110

Trp His Met Val Phe Ser His Gln Gly Glu Ile Pro Tyr Arg Glu Gly
        115                 120                 125

Gln Ser Val Gly Val Ile Ala Asp Gly Ile Asp Lys Asn Gly Lys Pro
    130                 135                 140

His Lys Val Arg Leu Tyr Ser Ile Ala Ser Ser Ala Leu Gly Asp Leu
145                 150                 155                 160

Gly Asn Ser Glu Thr Val Ser Leu Cys Val Lys Arg Leu Val Tyr Thr
                165                 170                 175

Asn Asp Gln Gly Glu Thr Val Lys Gly Val Cys Ser Asn Phe Leu Cys
            180                 185                 190

Asp Leu Ala Pro Gly Ser Asp Val Lys Leu Thr Gly Pro Val Gly Lys
        195                 200                 205

Glu Met Leu Met Pro Lys Asp Pro Asn Ala Thr Val Ile Met Leu Ala
    210                 215                 220

Thr Gly Thr Gly Ile Ala Pro Phe Arg Ser Phe Leu Trp Lys Met Phe
225                 230                 235                 240

Phe Glu Lys His Asp Asp Tyr Lys Phe Asn Gly Leu Ala Trp Leu Phe
                245                 250                 255

Leu Gly Val Pro Thr Thr Ser Ser Leu Leu Tyr Gln Glu Glu Phe Asp
            260                 265                 270

Lys Met Lys Ala Lys Ala Pro Glu Asn Phe Arg Val Asp Tyr Ala Ile
        275                 280                 285

Ser Arg Glu Gln Ala Asn
    290


<210> SEQ ID NO 98
<211> LENGTH: 249
<212> TYPE: PRT
<213> ORGANISM: Proteobacteria

<400> SEQUENCE: 98

Met Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr Phe
1               5                   10                  15

Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val Ser
            20                  25                  30

Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe Phe
        35                  40                  45
```

```
Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr Val
    50                  55                  60

Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met Arg
65                  70                  75                  80

Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr Ile
                85                  90                  95

Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu Ile
            100                 105                 110

Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu Leu
        115                 120                 125

Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala Gly
    130                 135                 140

Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp Val
145                 150                 155                 160

Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys Asn
                165                 170                 175

Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr Ile
            180                 185                 190

Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly Tyr
        195                 200                 205

Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr Asn
    210                 215                 220

Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp Asn
225                 230                 235                 240

Val Ala Val Lys Glu Ser Ser Asn Ala
                245
```

<210> SEQ ID NO 99
<211> LENGTH: 446
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana (thale cress)

<400> SEQUENCE: 99

```
atttcgaaag agaatctcag aaagatcaat ctagagagac ccgttcgtct cctttcctta      60

agccattacc tctgaaacca tccaaggctt tggttgcaac tggaggcaga gcacagaggc     120

ttcaagttaa ggccctcaag atggacaagg ctttgaccgg tatctccgcg gctgctctta     180

ctgcttcgat ggtgattccg gagatagctg aagctgctgg ttctggaatc tctccttccc     240

tcaagaattt cttgctcagc attgcttctg gtggcctcgt cctcactgtc atcattggtg     300

tcgtcgtcgg cgtctccaac tttgaccctg tcaagagaac ctaagaccta tatatctttc     360

ttacatcatt attgtaatct gttctccttc tgtgtattcg tttcaatgtt gcagcaatga     420

acttttggat aaaaaaaaaa aaaaaa                                          446
```

<210> SEQ ID NO 100
<211> LENGTH: 642
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 100

```
aaggcagaag caccggtcag ctgggggaag ggacacagag gaagagacgg agtgtacagg      60

gaccaaggtt gtatgtcaag gagcaaagag caggaagaca ggaggctttg agcacacacg     120

gctttgtcta ttccagtaac aacccccttg ctgccgctca ccggttccat ggagataata     180

tttggccaga ataagaaaga acagctggag ccagttcagg ccaaagtgac aggcagcatt     240
```

```
ccagcatggc tgcaggggac cctgctccga aacgggcccg ggatgcacac agtgggagag    300

agcaagtaca accattggtt tgatggcctg gcccttctcc acagtttctc catcagagat    360

ggggaggtct tctacaggag caaatacctg cagagtgaca cctacatcgc caacattgag    420

gccaacagaa tcgtggtgtc tgagttcgga accatggcct acccggaccc ctgcaaaaac    480

atcttttcca aagctttctc ctacttgtct cacaccatcc ccgacttcac agacaactgt    540

ctgatcaaca tcatgaaatg tggagaagac ttctatgcaa ccacggagac caactacatc    600

aggaaaatcg acccccagac cctagagacc ttggagaagg tg                       642


<210> SEQ ID NO 101
<211> LENGTH: 217
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: (thale cress)

<400> SEQUENCE: 101

Met Ala Ser Leu Ser Thr Ile Thr Gln Pro Ser Leu Val His Ile Pro
1               5                   10                  15

Gly Glu Ser Val Leu His His Val Pro Ser Thr Cys Ser Phe Pro Trp
            20                  25                  30

Lys Pro Thr Ile Asn Thr Lys Arg Ile Ile Cys Ser Pro Ala Arg Asn
        35                  40                  45

Ser Ser Glu Val Ser Ala Glu Ala Glu Thr Glu Gly Gly Ser Ser Thr
    50                  55                  60

Ala Val Asp Glu Ala Pro Lys Glu Ser Pro Ser Leu Ile Ser Ala Leu
65                  70                  75                  80

Asn Val Glu Arg Ala Leu Arg Gly Leu Pro Ile Thr Asp Val Asp His
                85                  90                  95

Tyr Gly Arg Leu Gly Ile Phe Arg Asn Cys Ser Tyr Asp Gln Val Thr
            100                 105                 110

Ile Gly Tyr Lys Glu Arg Val Lys Glu Leu Lys Glu Gln Gly Leu Asp
        115                 120                 125

Glu Glu Gln Leu Lys Thr Lys Met Asp Leu Ile Lys Ser Tyr Thr Ile
    130                 135                 140

Leu Ser Thr Val Glu Glu Arg Arg Met Tyr Asp Trp Ser Leu Ala Arg
145                 150                 155                 160

Ser Glu Lys Ala Glu Arg Tyr Val Trp Pro Phe Glu Val Asp Ile Met
                165                 170                 175

Glu Pro Ser Arg Glu Glu Pro Pro Pro Gln Glu Pro Glu Asp Val Gly
            180                 185                 190

Pro Thr Arg Ile Leu Gly Tyr Phe Ile Gly Ala Trp Leu Val Leu Gly
        195                 200                 205

Val Ala Leu Ser Val Ala Phe Asn Arg
    210                 215


<210> SEQ ID NO 102
<211> LENGTH: 53
<212> TYPE: PRT
<213> ORGANISM: Cyanophora paradoxa

<400> SEQUENCE: 102

Met Asn Ala Phe Val Ala Ser Val Ala Pro Ile Ala Val Ala Gly Ser
1               5                   10                  15

Ala Thr Leu Ser Ser Ala Val Cys Ala Gln Lys Lys Ala Phe Phe Gly
```

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            20                  25                  30

Ala Gln Val Ala Ala Lys Lys Thr Thr Phe Glu Ala Ala Pro Ala Arg
        35                  40                  45

Phe Ile Val Arg Ala
    50


<210> SEQ ID NO 103
<211> LENGTH: 45
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 103

Met Ala Thr Gln Ala Ala Gly Ile Phe Asn Ser Ala Ile Thr Thr Ala
1               5                   10                  15

Ala Thr Ser Gly Val Lys Lys Leu His Phe Phe Ser Thr Thr His Arg
            20                  25                  30

Pro Lys Ser Leu Ser Phe Thr Lys Thr Ala Ile Arg Ala
        35                  40                  45


<210> SEQ ID NO 104
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: (thale cress)
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: CAB transit peptide(thale cress)

<400> SEQUENCE: 104

Met Gln Ser Ser Ala Val Phe Ser Leu Ser Pro Ser Leu Pro Leu Leu
1               5                   10                  15

Lys Pro Arg Arg Leu Ser Leu Arg His His Pro Ile Thr Thr
            20                  25                  30


<210> SEQ ID NO 105
<211> LENGTH: 44
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: (thale cress)
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: PGR5 transit peptide(thale cress)

<400> SEQUENCE: 105

Met Ala Ala Ala Ser Ile Ser Ala Ile Gly Cys Asn Gln Thr Leu Ile
1               5                   10                  15

Gly Thr Ser Phe Tyr Gly Gly Trp Gly Ser Ser Ile Ser Gly Glu Asp
            20                  25                  30

Tyr Gln Thr Met Leu Ser Lys Thr Val Ala Pro Pro
        35                  40


<210> SEQ ID NO 106
<211> LENGTH: 2955
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: PCRL1 gene
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: PCRL1 gene(thale cress)
```

<400> SEQUENCE: 106

catatttgat tttcacatgg attaacgaaa ctatattatg gaacacattc aaaattataa 60

caacaaaaaa aatacaagta ttatttcaaa actacacaag gttgtgctta tttcttgaat 120

tattttactt tcctaatgag agcaaagttt ctcaaagaag taatcatatg atgtttttct 180

ttgaatgtgc ctcacactta cttacaaaca caacacaagc caatgagagc tacatgaaaa 240

gatctgaaga ttatacaaaa cagcatacaa actttggttt ttctccttct tcttcaattt 300

ctccaccttc ttcatttgtt agtattaatt ttacatacac ttctacataa ccctgagaaa 360

aagaaaaccc taaaattttg aattttccat tgaatcaaga aagatttcat cagaaatcaa 420

agttgagata agaattaaac cttggctctt agatttaagc tttccctcct tctggtaatg 480

tgatcaaacg agaacctgag tcatagacca tctccgttcc acagctaaaa accagaagaa 540

tcataagact tcaagaaacg ttgtagacaa tttgtgtgat cgattcgagt ctacagctga 600

gaagcttacc ctgagcattt gacattgttg gtgttactat cattggggat ggatagtatc 660

gttccaaaga aagatacatt ctctgttcca cagtttgggc aagggccctg tgaaagatat 720

gttccacgaa aattaaaagc atttcataat aatcgcataa aactcgtagg atttggcact 780

ataccaatcc aaatttgtag cgtttagcac aaaatagatt attatctcaa gtctaatctc 840

ttgtttaagc atttttgata ctgagaaaac aagatttagt tctataactt ttatttttcc 900

acttcatgaa ctgatcttgg aagatgatta atgtttttac cttcaagatc aagaagtctt 960

tgaggatcag tttggtgagt gataacgcca gatatacaat tgcaggcacc gcagcgaacc 1020

atgtgaaaat gaaactgaat ggttccggaa gctgcagatt tttgtttttg tttttaatc 1080

agttgcatga atactggaac aattactacg agtatatatt ctccaaacca tagtagaata 1140

gtcgaaagag gttttacctc gagcaggtac gtgatttcaa aaccagtaat gtcatcaaga 1200

aagaaaaatc tggagaacaa ttgaagaaaa caacaatttt aaactaacta acataagcta 1260

agatcatgtg atttgaaagt tgagagagga acagaaccgg aggtactcac agtccgagag 1320

caacaacagt tgctggtaca ttcaacaaga acattttgaa gtaatcaatg gcaagatcac 1380

tataaacctg cataatcaag gaggtccaca agtctataac atctctagag tttgtcccaa 1440

acaatgaatc taatgttatg ttctgtaatg tccaaagaat atatgagcta tccgaacaat 1500

taagagtttt taccttttta ctacgaagac tgcatcttgg accctcacac acaatctcac 1560

tgccgtccat ctacagaaac caaagaaaca atcataacgt ttgtccaaat tacacatgta 1620

acaagatgga tgaaactaag aaatagtatt tgtaagtata aatagattaa gaacctttag 1680

tttcattttg agcttatcat actcttcatc actcaagatt ggatttccag agacataagc 1740

cattgaagct tcaaggaatc tttgttcatc agaacctaca atacatagat aaaattagat 1800

caagaatcaa gaacctaggc gaatggatta ttgacaaaac tataaatcat aagtgttcat 1860

tacttagcat gacaacactg cttccttccc acatcaactc ttctttaagg ttatcaaact 1920

cttcattaga cataatcgct ttgccttcgt aataaaacga ctgcaaaaga aaagaaacag 1980

aaacaatcct cgattatata gagataaacc catactaatg ataaaaacac tttatttgat 2040

gtgttacttg catcgcttgg aggaactctt gttccatttc accgatagtt ctcttctcat 2100

tcttgttgat gctacaataa ggtaaaatct tgctatcaac ttcttcccca cccacctgac 2160

ctgaagacaa gtcataaaaa tgattttaag aagtaaggaa actctcaagg agcaatcttt 2220

tagtggatta gagtataaaa actaaaaatc cacagaggaa aaaagttcca tataacaact 2280 tttcttaact agaattaaag cttgagtgat tttattctat gattgaataa aatcaaaact 2340

ttctcaaaag ccactgtgtt cccaaacaat gatcagagac aaaatcaaag ctacaataca 2400

acagcttttc tcaactaaat ttgaagattg agtgcttttt tgtttcgatc acataacgat 2460

gagttaataa cttaagaacc ttaagctaca cacaaatttt aatcctaaaa aggctacaaa 2520

ttggaaatca tttatctaat tatcttctat gatcataaaa atctcaactt ttcacaccaa 2580

tttcgttccc aaagaaagat cagaggcaaa aacaaataaa aaaatcgaaa ctttaaagag 2640

gcaaataaaa atcgagacct gattgatcag tagaagcttt aaggggcaat aaggtaagtc 2700

ttcgtctgag agaaatcgat cgtccatggg taaagggagc aggacactgt gtcctcgaag 2760

aagaacaagt gatgggtttg cgagaaattg cagaaaatct agggattgtt agagtaaaag 2820

ccatcgtctt tatccctcac gccgatgatt gagtgagatc gttgttttct cttgtccggg 2880

acgaagaaca aaaaaaaaag ttagaagctt tggatttgtg tggttgagaa ttgagatggt 2940

gatgtttttt actgt 2955

<210> SEQ ID NO 107
<211> LENGTH: 55
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana (thale cress)
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Rubisco
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Rubisco(thale cress)

<400> SEQUENCE: 107

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1               5                   10                  15

Gln Ala Thr Met Val Ala Pro Phe Asn Gly Leu Lys Ser Ser Ala Ala
            20                  25                  30

Phe Pro Ala Thr Arg Lys Ala Asn Asn Asp Ile Thr Ser Ile Thr Ser
        35                  40                  45

Asn Gly Gly Arg Val Asn Cys
    50                  55
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<210> SEQ ID NO 108
<211> LENGTH: 795
<212> TYPE: DNA
<213> ORGANISM: homo sapien

<400> SEQUENCE: 108

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gactttccaa ttgcaaaagg tgaacgtcaa tcacctgttg atattgacac tcatacagct 120

aaatatgacc cttctttaaa accattatct gtttcatatg atcaagcaac ttctttacgt 180

attttaaaca atggtcatgc ttttaatgta gaatttgatg actctcaaga taaagcagta 240

ttaaaaggtg gtccattaga tggtacttac cgtttaattc aatttcactt tcactggggt 300

tcattagatg gtcaaggttc agaacatact gtagataaaa aaaaatatgc tgcagaatta 360

cacttagttc actggaacac aaaatatggt gattttggta aagctgtaca acaacctgat 420

ggtttagctg ttttaggtat ttttttaaaa gttggtagtg ctaaaccagg tcttcaaaaa 480

gttgttgatg tattagattc aattaaaaca aaaggtaaaa gtgctgactt tactaatttc 540

gatcctcgtg gtttacttcc tgaatcttta gattactgga catatccagg ttcattaaca 600

acacctcctc ttttagaatg tgtaacatgg attgtattaa aagaaccaat tagtgtaagt 660

-continued

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agtgaacaag tattaaaatt ccgtaaactt aatttcaatg gtgaaggtga accagaagaa    720

ttaatggttg ataactggcg tccagctcaa ccattaaaaa atcgtcaaat taaagcttca    780

ttcaaataag catgc                                                     795
```

What is claimed is:

1. A construct comprising:

i) a first heterologous nucleic acid sequence comprising a first heterologous polynucleotide sequence encoding a cyclic electron modulator gene wherein the cyclic electron modulator is operatively linked to at least one regulatory element wherein the first heterologous nucleic acid sequence encodes a protein having a sequence selected from PRG5 of SEQ ID NO: 1 or PGRL1 of SEQ ID NO: 3 or a sequence with at least 80% sequence homology thereto; and

ii) a second heterologous nucleic acid sequence comprising a second heterologous polynucleotide sequence encoding an ATP dependent bicarbonate anion transporter localized to the plasma membrane wherein the ATP dependent bicarbonate anion transporter localized to the plasma membrane is operatively coupled to the at least one regulatory element wherein the second heterologous nucleic acid sequence encodes a protein having a sequence selected from HLA3 (SEQ ID NO:77) or a sequence with at least 80% sequence homology thereto.

2. The construct of claim **1** wherein the HLA3 is codon optimized for plant expression.

3. The construct of claim **1** wherein the at least one regulatory element includes a promoter.

4. The construct of claim **1** wherein the at least one regulatory element is a tissue specific promoter.

5. The construct of claim **1** wherein the at least one regulatory element includes a promoter that is a green tissue/leaf-specific promoter.

6. The construct of claim **1** wherein the promoter is selected from among CAB and rbcS.

7. The construct of claim **1** wherein the first nucleic acid sequence and the second nucleic acid sequence encode:

i) the PGR5 protein, and the HLA3 protein; or

ii) the PGRL1 protein, and the HLA3 protein.

8. The construct of claim **1** further comprising iii) a third heterologous nucleic acid sequence comprising a third heterologous polynucleotide sequence encoding a bicarbonate anion transporter protein localized to the chloroplast envelope wherein the bicarbonate anion transporter protein localized to the chloroplast envelope is operatively coupled to the regulatory element wherein the third heterologous nucleic acid sequence i-encodes a sequence selected from LCIA of SEQ ID NO: 18 or a sequence with at least 80% sequence homology thereto.

9. The construct of claim **8** wherein the at least one regulatory element is a green tissue/leaf-specific promoter.

10. The construct of claim **8** wherein the at least one regulatory element includes a promoter selected from among CAB and rbcS.

11. The construct of claim **1** further comprising iii) a third heterologous nucleic acid sequence comprising a third heterologous polynucleotide sequence encoding a carbonic anhydrase wherein the carbonic anhydrase is operatively coupled to the at least one regulatory element wherein the third heterologous nucleic acid sequence encodes a protein selected from a human carbonic anhydrase-2 (HCA2) of SEQ ID NO: 18, bacterial *Neisseria gonorrhoeae* carbonic anhydrase (BCA) of SEQ ID NO: 5 or a sequence with at least 80% sequence homology thereto.

12. The construct of claim **11** wherein the at least one regulatory element includes a green tissue/leaf-specific promoter.

13. The construct of claim **11** wherein the at least one regulatory element includes a promoter selected from among CAB and rbcS.

14. The construct of claim **11** wherein the third heterologous nucleic acid sequence encodes the BCA protein of SEQ ID NO: 5 protein or a sequence with at least 80% sequence homology thereto.

15. The construct of claim **8** wherein the heterologous nucleotide sequences encode the PGR5 protein, the HLA3 protein, and the LCIA protein or sequences with at least 80% homology thereto.

16. The construct of claim **11** wherein the heterologous nucleotide sequences encode the PGR5 protein, the HLA3 protein, and the BCA protein or sequences with at least 80% homology thereto.

17. The construct of claim **11**, wherein

a) the PGR5 protein has an amino acid sequence at least 80% identical to SEQ ID NO:1;

b) the HLA 3 protein has an amino acid sequence at least 80% identical to SEQ ID NO:77; and

c) the BCA protein has an amino acid sequence at least 80% identical to SEQ ID NO:21.

18. The construct of claim **1** wherein the at least one regulatory element of the first heterologous nucleic acid sequence and the at least one regulatory element of the second heterologous nucleic acid sequence includes a promoter which can be the same or different for the first heterologous nucleic acid and the second heterologous nucleic acid.

19. A seed comprising the construct of claim **1**.

20. A vector comprising the construct of claim **1**.

* * * * *