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Donohue et al.

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(54) **OLEAGINOUS MICROORGANISMS AND USES OF SAME**

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(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 350 days.

(21) Appl. No.: **15/901,676**

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Related U.S. Application Data

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(51) **Int. Cl.**

C12N 1/20	(2006.01)
C12P 7/64	(2006.01)
C12N 15/74	(2006.01)

(52) **U.S. Cl.**
CPC ***C12N 15/74*** (2013.01); ***C12N 1/20*** (2013.01); ***C12P 7/6409*** (2013.01)

(58) **Field of Classification Search**
None
See application file for complete search history.

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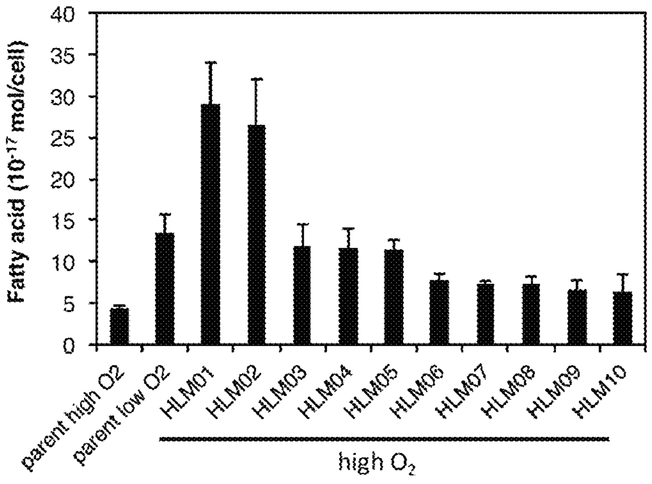
(57) **ABSTRACT**

Recombinant microorganisms including one or more modifications that enhance lipid production and uses of same for producing lipid. The modifications alter cell surface functions, envelope functions, and other functions. The modifications are capable of converting non-oleaginous microorganisms into oleaginous microorganisms. The lipids produced by some of the recombinant microorganisms are excreted.

16 Claims, 14 Drawing Sheets
(1 of 14 Drawing Sheet(s) Filed in Color)
Specification includes a Sequence Listing.



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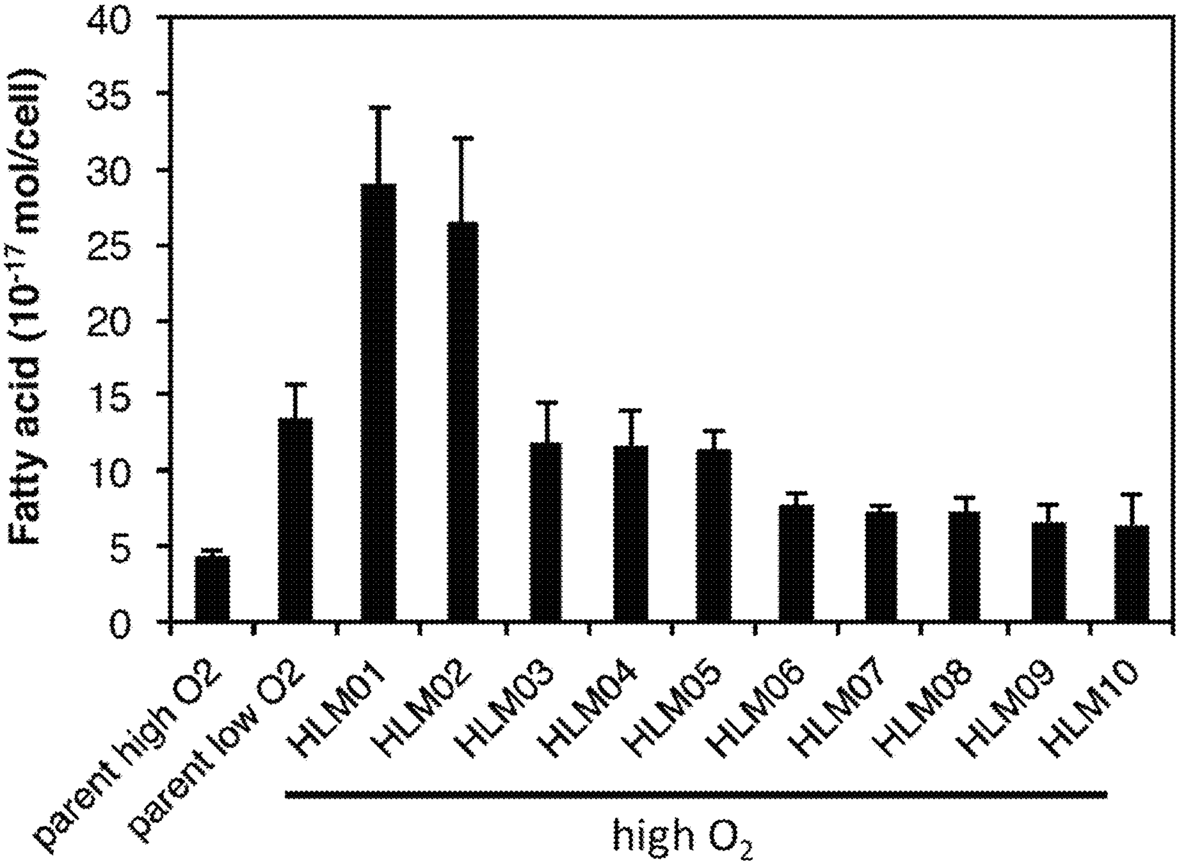
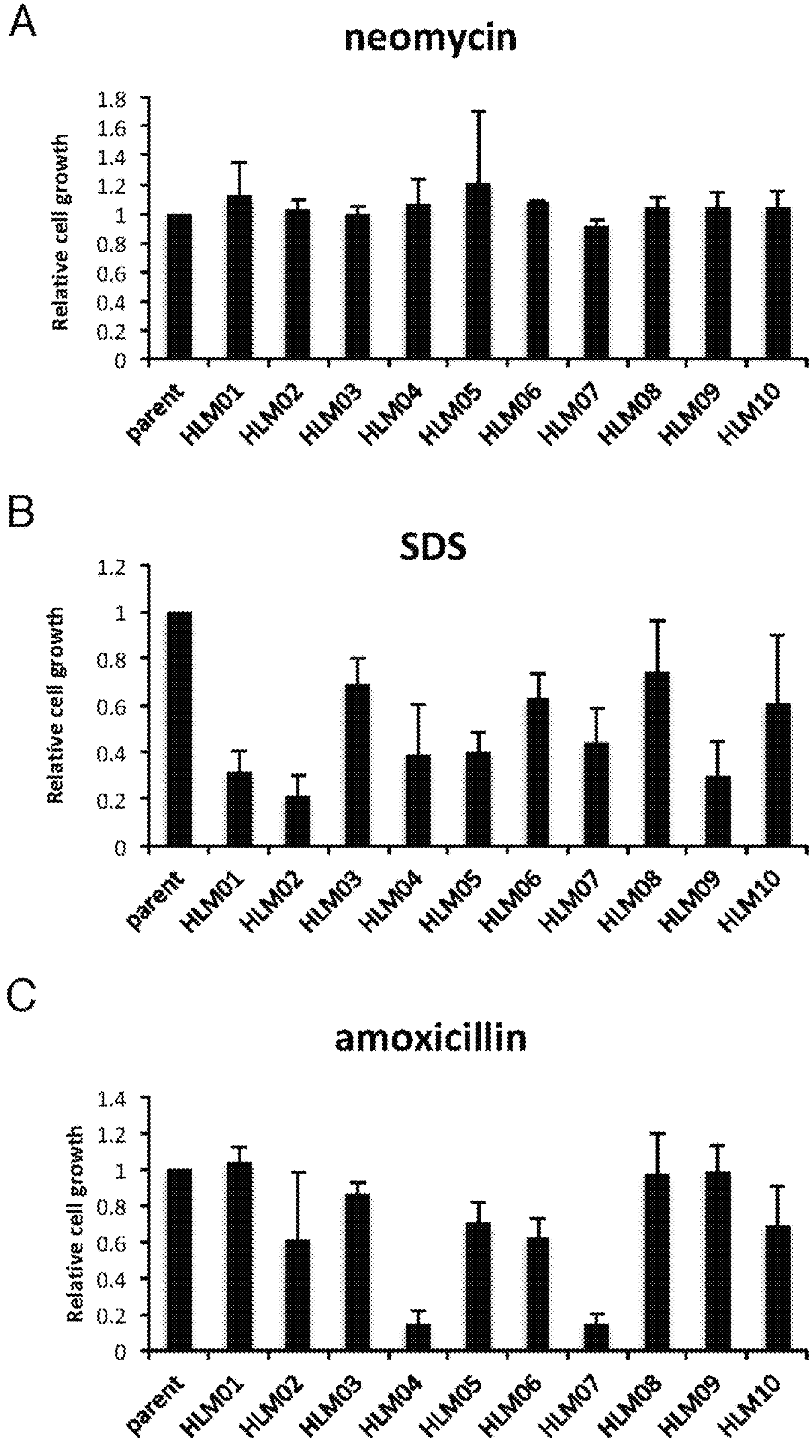

Fatty acid (10^{-17} mol/cell)
40
35
30
25
20
15
10
5
0
parent high O2
parent low O2
HLM01
HLM02
HLM03
HLM04
HLM05
HLM06
HLM07
HLM08
HLM09
HLM10
high O_2

FIG. 1


A
neomycin
Relative cell growth
0
0.2
0.4
0.6
0.8
1
1.2
1.4
1.6
1.8
parent
HLM01
HLM02
HLM03
HLM04
HLM05
HLM06
HLM07
HLM08
HLM09
HLM10
B
SDS
Relative cell growth
0
0.2
0.4
0.6
0.8
1
1.2
parent
HLM01
HLM02
HLM03
HLM04
HLM05
HLM06
HLM07
HLM08
HLM09
HLM10
C
amoxicillin
Relative cell growth
0
0.2
0.4
0.6
0.8
1
1.2
1.4
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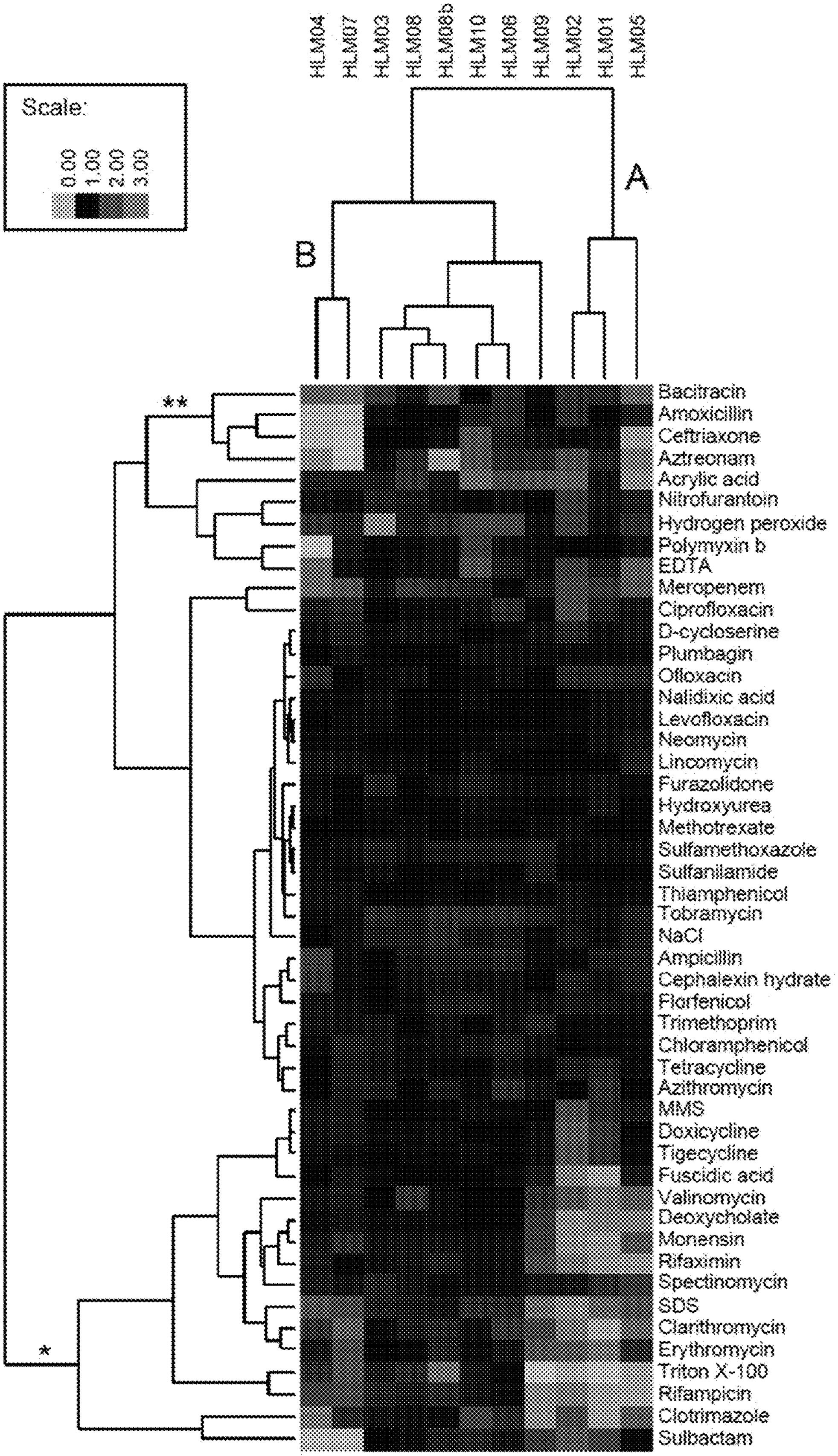
HLM10

FIG. 2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HLM02
HLM01
HLM05
A
B
**
*
Bacitracin
Amoxicillin
Ceftriaxone
Aztreonam
Acrylic acid
Nitrofurantoin
Hydrogen peroxide
Polymyxin b
EDTA
Meropenem
Ciprofloxacin
D-cycloserine
Plumbagin
Ofloxacin
Nalidixic acid
Levofloxacin
Neomycin
Lincomycin
Furazolidone
Hydroxyurea
Methotrexate
Sulfamethoxazole
Sulfanilamide
Thiamphenicol
Tobramycin
NaCl
Ampicillin
Cephalexin hydrate
Florfenicol
Trimethoprim
Chloramphenicol
Tetracycline
Azithromycin
MMS
Doxicycline
Tigecycline
Fuscidic acid
Valinomycin
Deoxycholate
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Clotrimazole
Sulbactam

FIG. 3

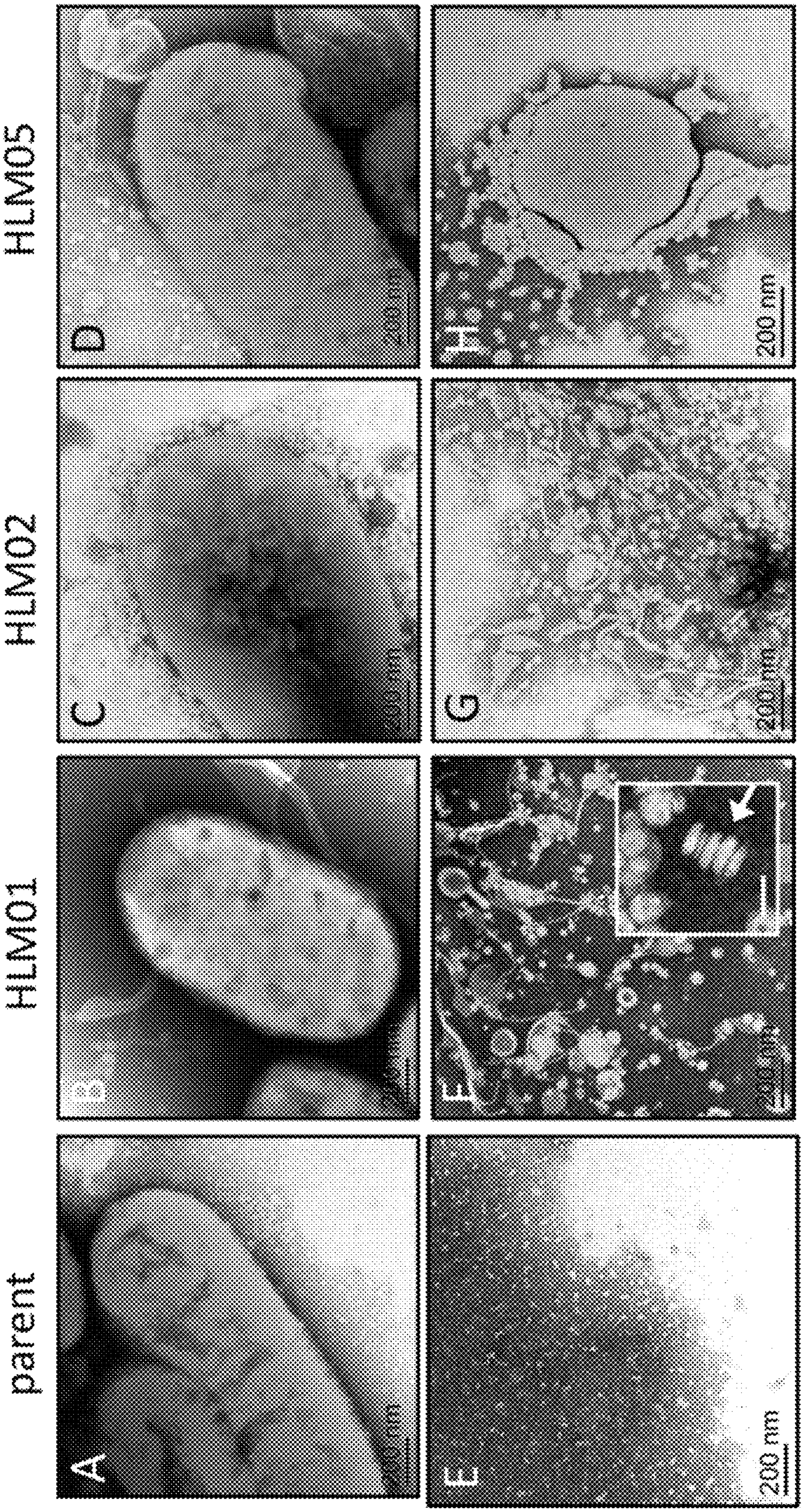


FIG. 4

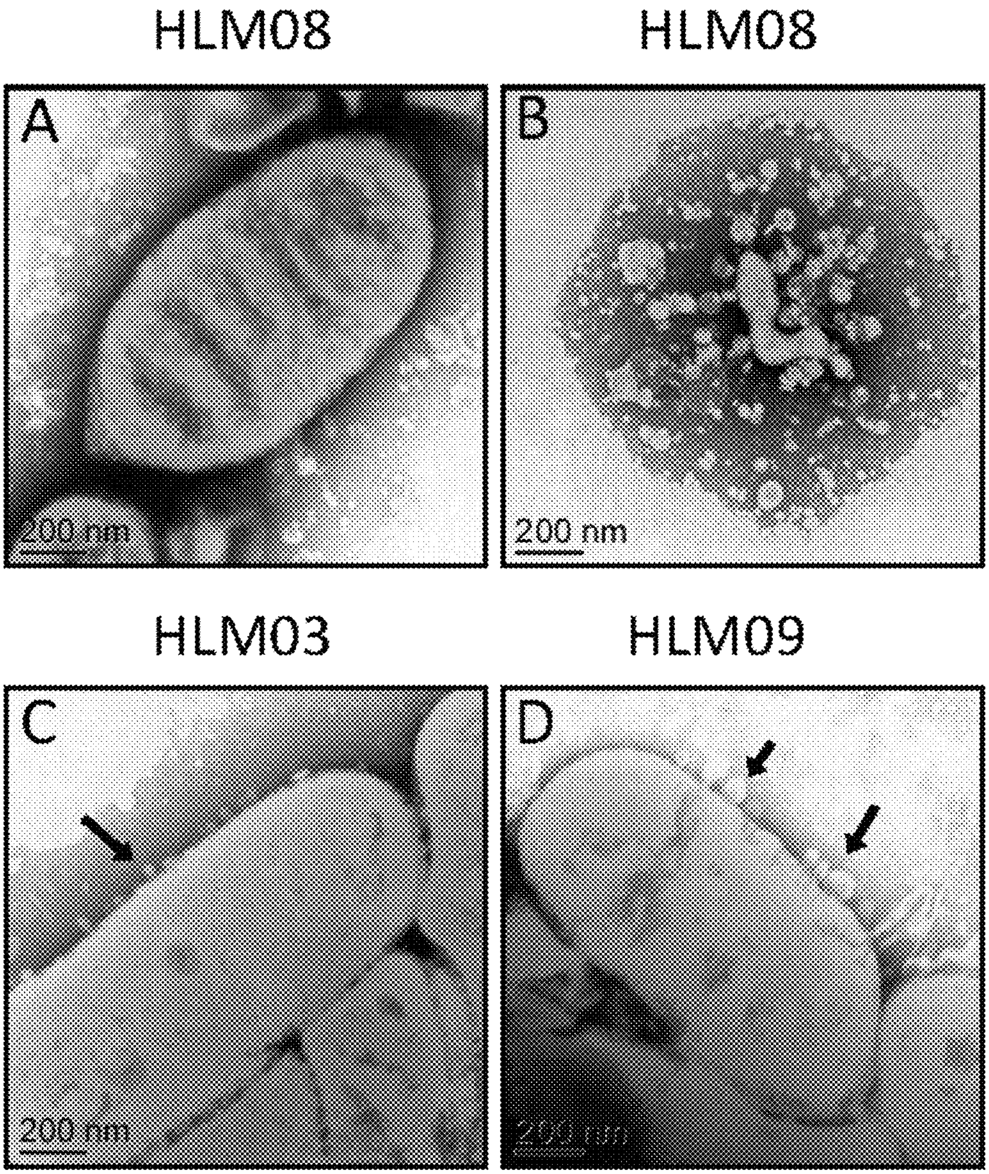


FIG. 5

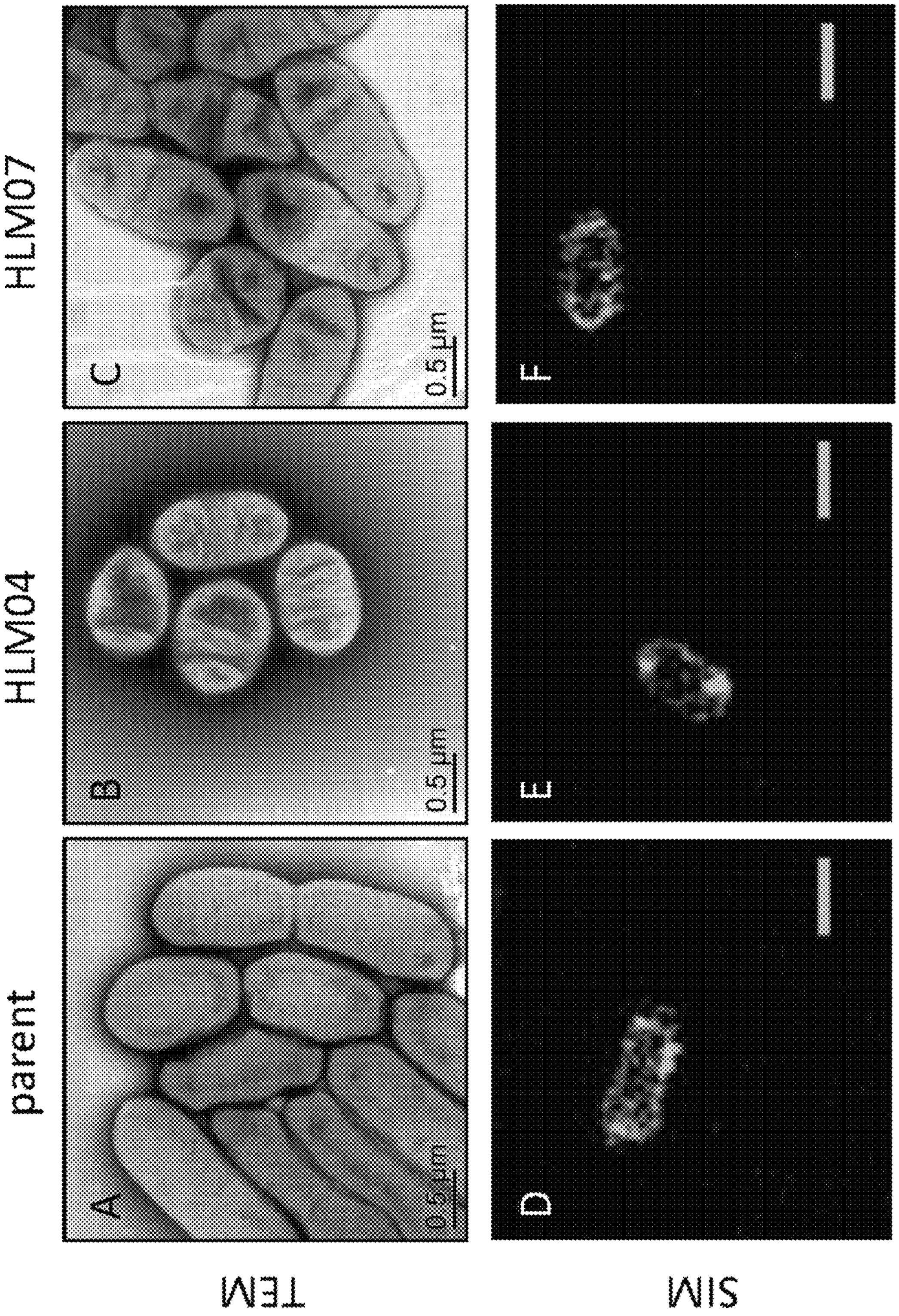
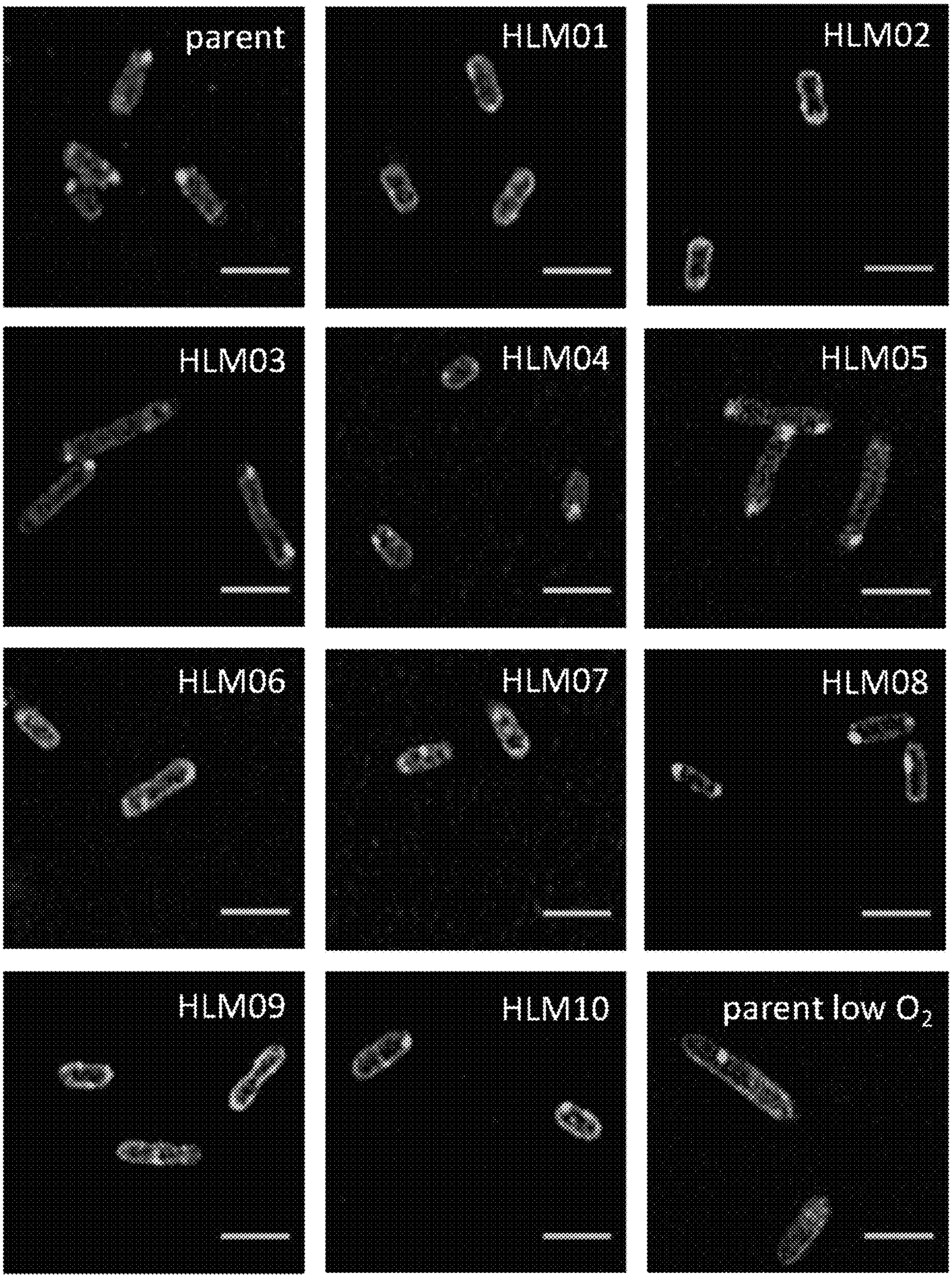


FIG. 6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HLM09
HLM10
parent low O_2

FIG. 7

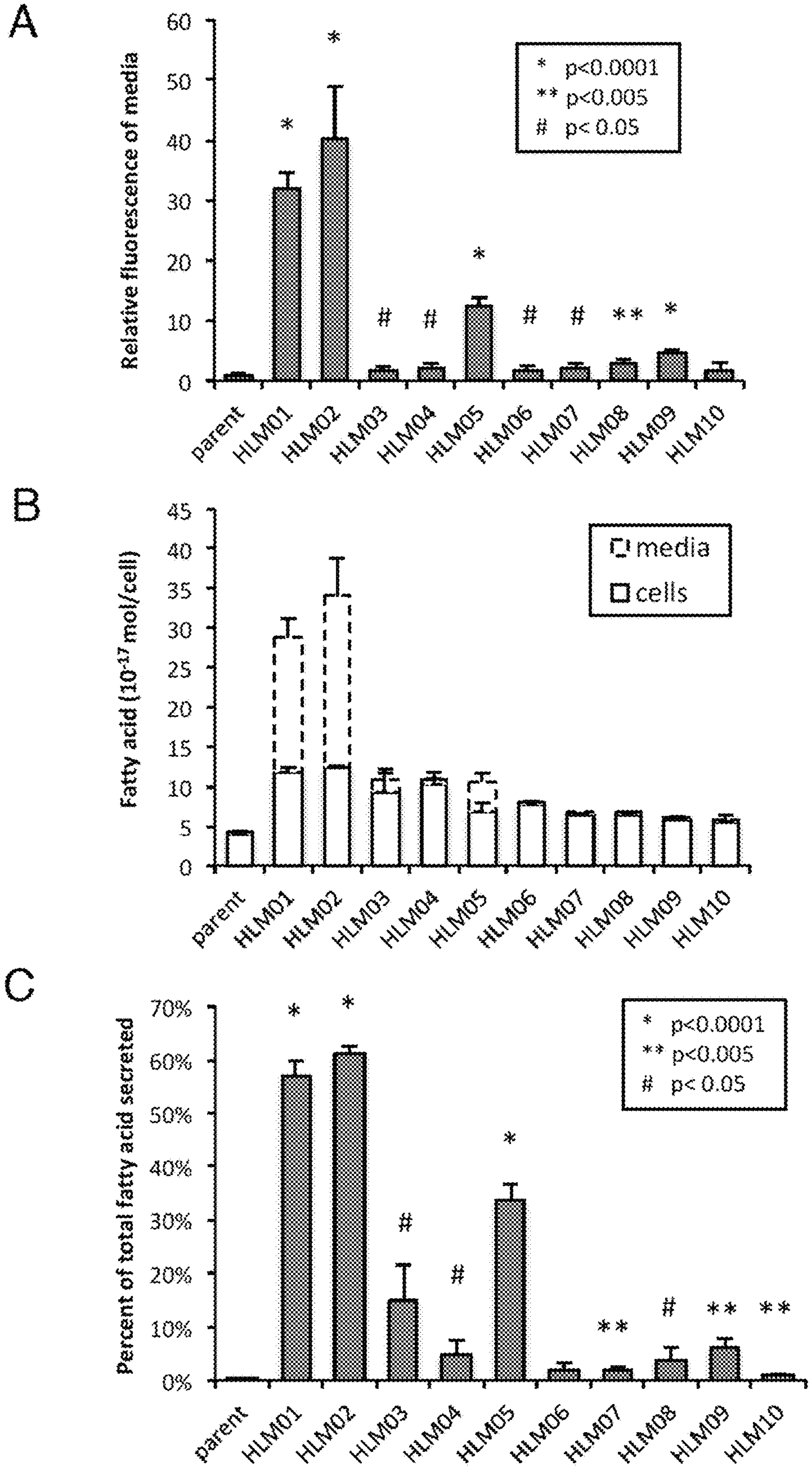

A
Relative fluorescence of media
0
10
20
30
40
50
60
* p<0.0001
** p<0.005
# p< 0.05
parent
HLM01
HLM02
HLM03
HLM04
HLM05
HLM06
HLM07
HLM08
HLM09
HLM10
B
Fatty acid (10^{-17} mol/cell)
0
5
10
15
20
25
30
35
40
45
media
cells
C
Percent of total fatty acid secreted
0%
10%
20%
30%
40%
50%
60%
70%

FIG. 8

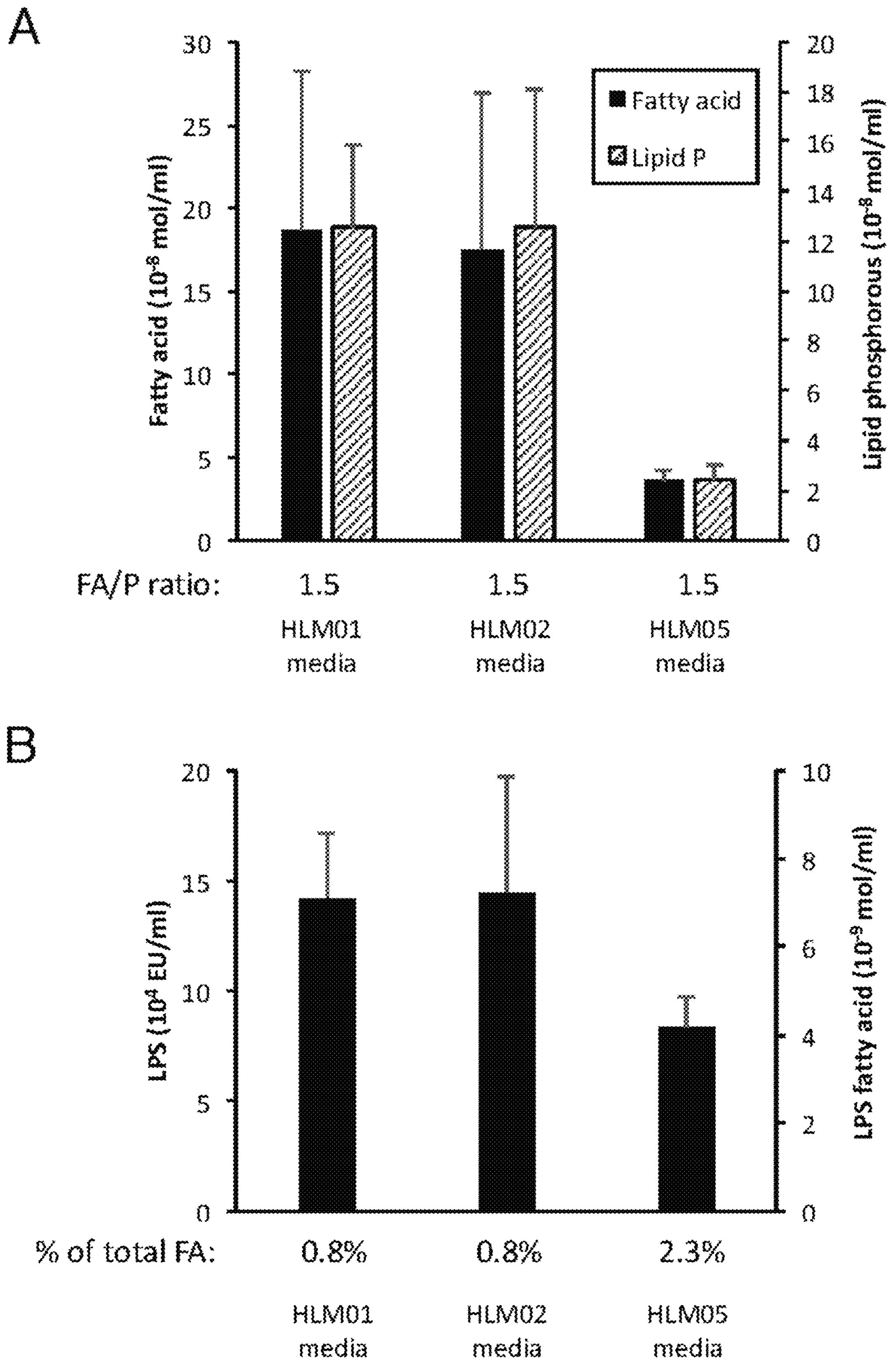

A
Fatty acid (10^-8 mol/ml)
0
5
10
15
20
25
30
Lipid phosphorous (10^-8 mol/ml)
0
2
4
6
8
10
12
14
16
18
20
■ Fatty acid
▨ Lipid P
FA/P ratio:
1.5
1.5
1.5
HLM01 media
HLM02 media
HLM05 media
B
LPS (10^4 EU/ml)
0
5
10
15
20
LPS fatty acid (10^-9 mol/ml)
0
2
4
6
8
10
% of total FA:
0.8%
0.8%
2.3%
HLM01 media
HLM02 media
HLM05 media

FIG. 9

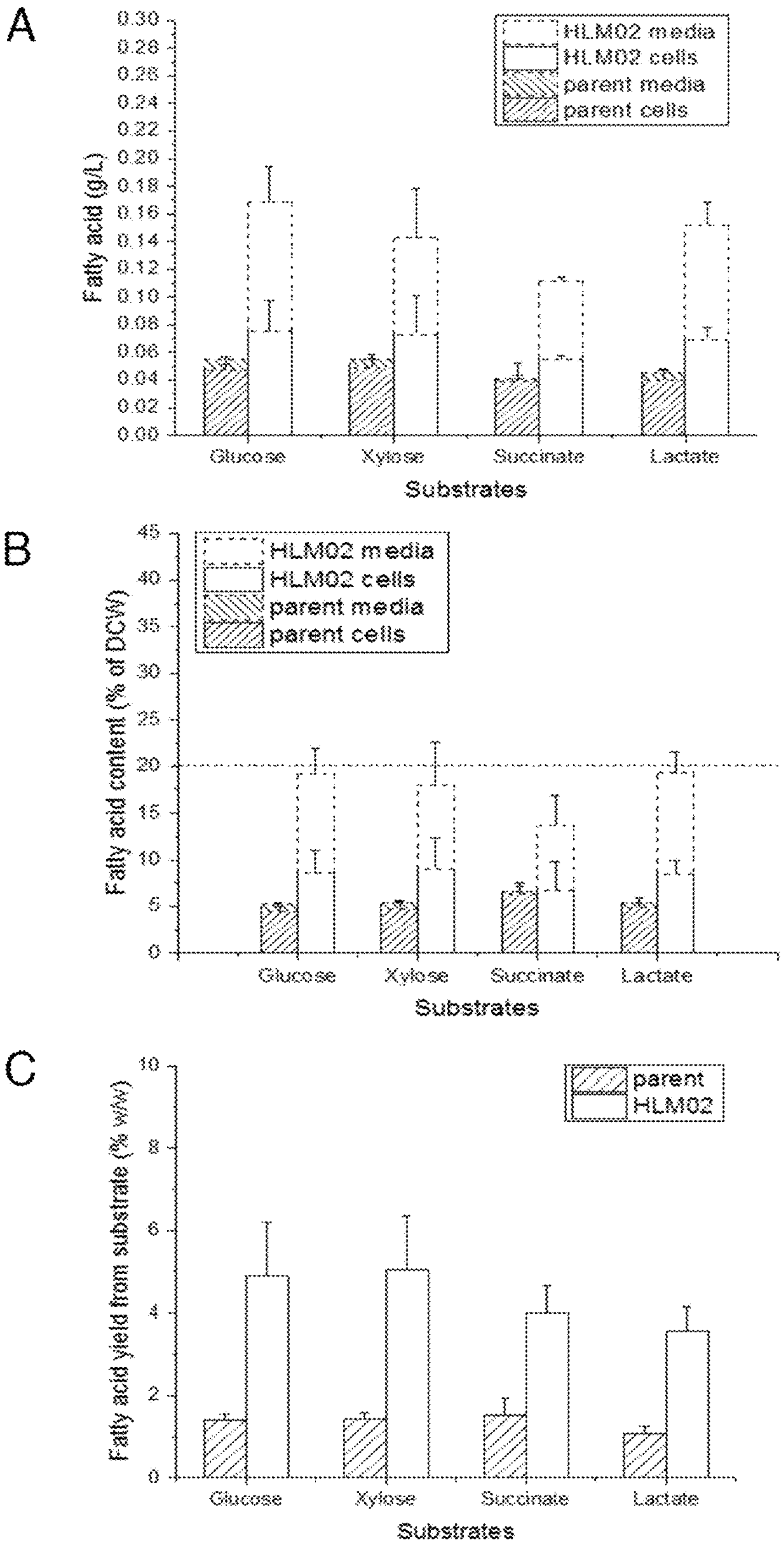

A
Fatty acid (g/L)
0.30
0.28
0.26
0.24
0.22
0.20
0.18
0.16
0.14
0.12
0.10
0.08
0.06
0.04
0.02
0.00
HLM02 media
HLM02 cells
parent media
parent cells
Glucose
Xylose
Succinate
Lactate
Substrates
B
Fatty acid content (% of DCW)
45
40
35
30
25
20
15
10
5
0
HLM02 media
HLM02 cells
parent media
parent cells
Glucose
Xylose
Succinate
Lactate
Substrates
C
Fatty acid yield from substrate (% w/w)
10
8
6
4
2
0
parent
HLM02
Glucose
Xylose
Succinate
Lactate
Substrates

FIG. 10

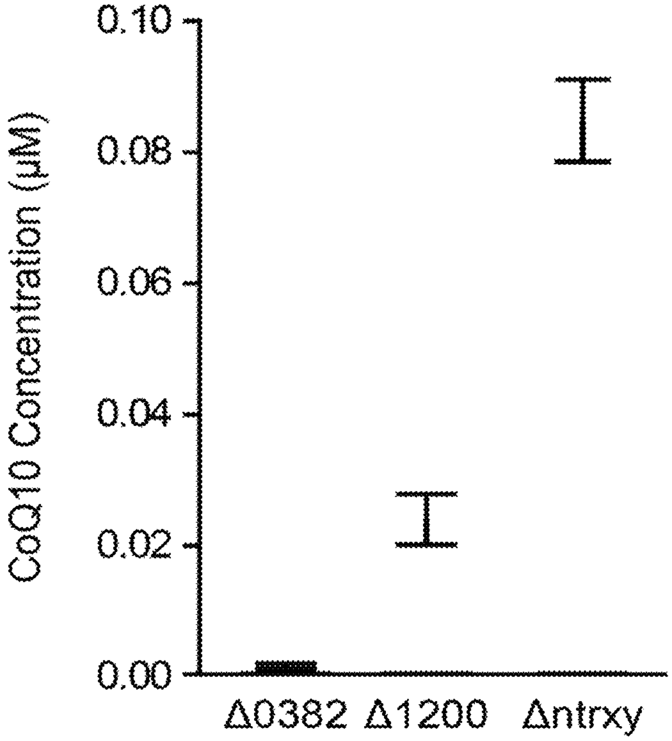
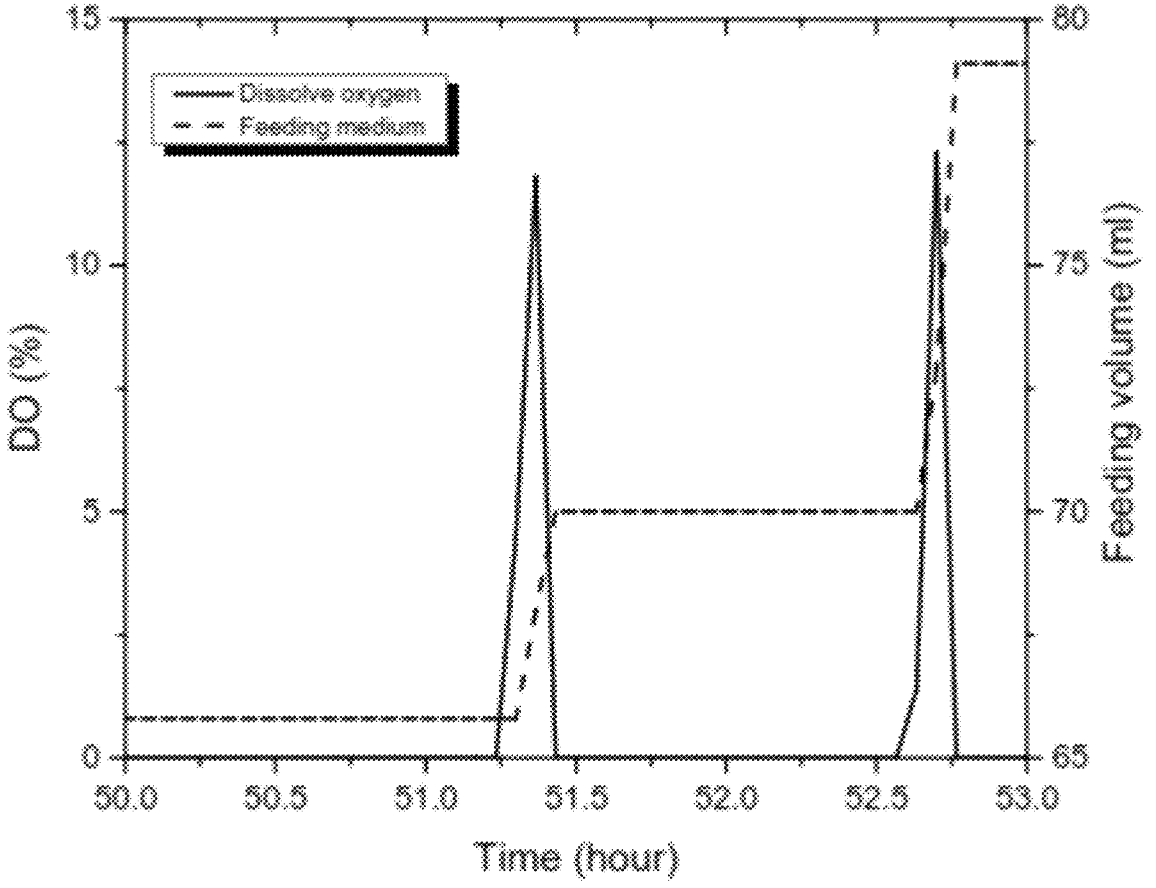

CoQ10 Concentration (µM)
0.10
0.08
0.06
0.04
0.02
0.00
Δ0382
Δ1200
Δntrxy

FIG. 11



Dissolve oxygen
Feeding medium
DO (%)
Feeding volume (ml)
Time (hour)
0
5
10
15
65
70
75
80
50.0
50.5
51.0
51.5
52.0
52.5
53.0

FIG. 12

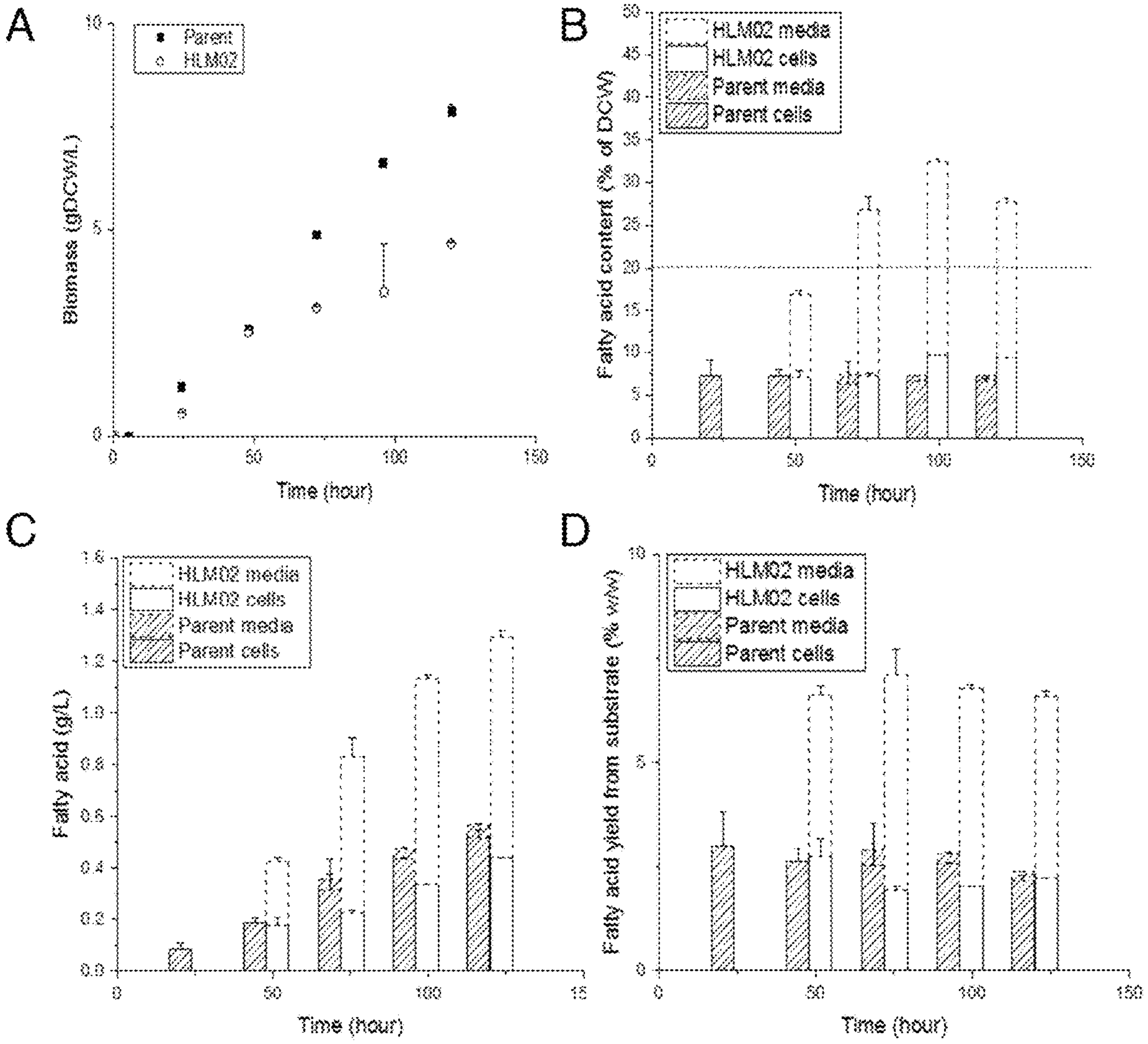

A
Parent
HLM02
Biomass (gDCW/L)
Time (hour)
0
5
10
0
50
100
150
B
HLM02 media
HLM02 cells
Parent media
Parent cells
Fatty acid content (% of DCW)
Time (hour)
0
5
10
15
20
25
30
35
40
45
50
0
50
100
150
C
HLM02 media
HLM02 cells
Parent media
Parent cells
Fatty acid (g/L)
Time (hour)
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
1.6
0
50
100
15
D
HLM02 media
HLM02 cells
Parent media
Parent cells
Fatty acid yield from substrate (% w/w)
Time (hour)
0
5
10
0
50
100
150

FIG. 13

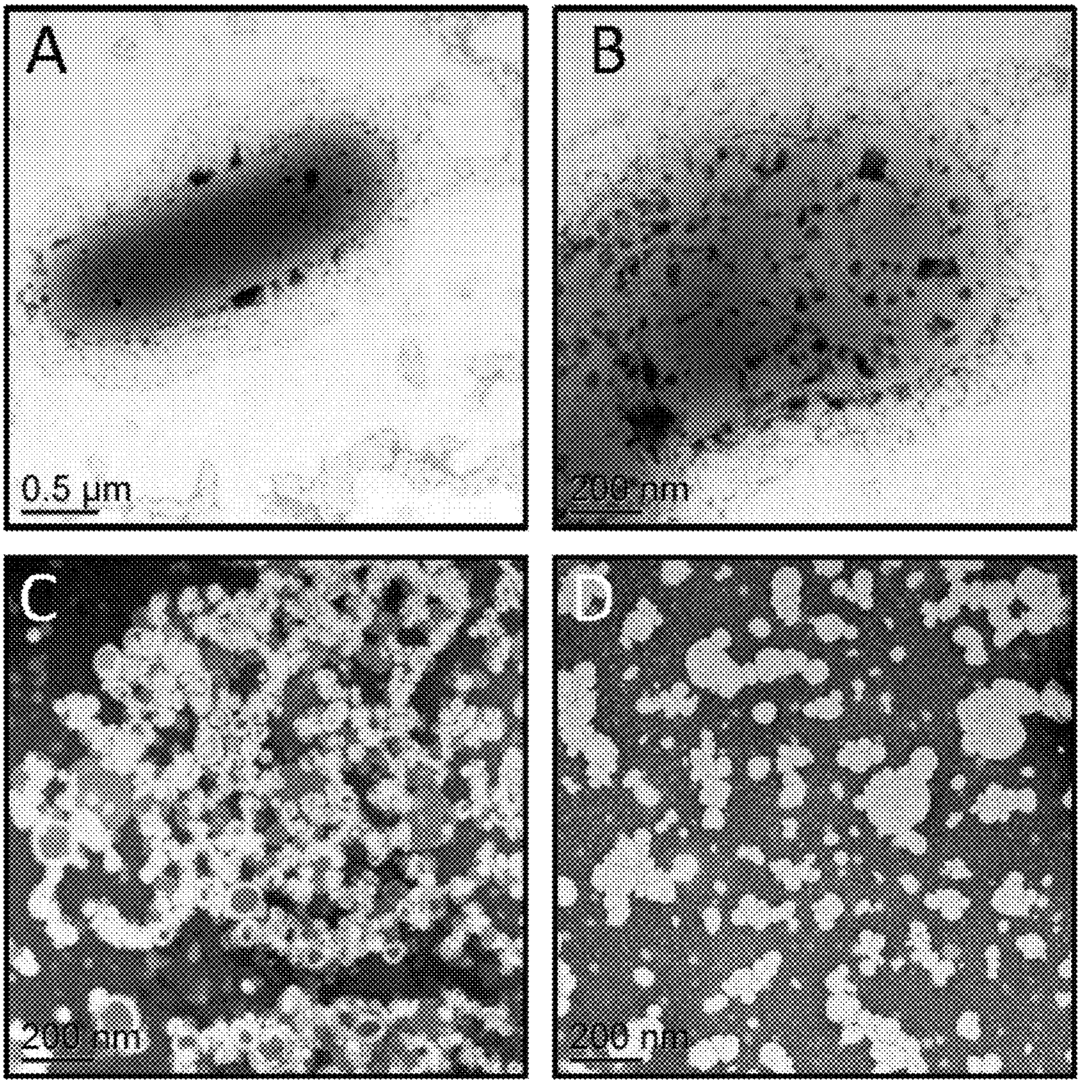


FIG. 14

OLEAGINOUS MICROORGANISMS AND USES OF SAME

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

This invention was made with government support under DE-FC02-07ER64494 awarded by the U.S. Department of Energy. The government has certain rights in the invention.

FIELD OF THE INVENTION

The invention is directed to modified microorganisms configured for enhanced production of lipid and lipid-associated bioproducts and methods of using same.

BACKGROUND

Lipids derived from bacteria, yeast, and microalgae offer a promising source of renewable fuels and chemicals. These sources can offset petroleum usage and reduce CO_2 emissions (Liang et al. 2013, Sawangkeaw et al. 2013). A major challenge to producing microbial replacements for oils that are cost-competitive with petroleum products is increasing the yield of these lipids, which are energetically expensive for cells to produce and thus tightly regulated (Zhang et al. 2010, Levering et al. 2015). One approach for microbial oil production is the use of oleaginous microorganisms, defined as those accumulating over 20% of their dry cell weight (DCW) as lipid (Liang et al. 2013). However, even though very high oil content (up to 90%) can be observed under some experimental conditions, lipid content is usually not high under nutrient replete conditions (Levering et al. 2015, Kosa et al. 2011). Genetic and process engineering strategies are being investigated to further increase the biomass lipid content and yield of oleaginous microorganisms (Liang et al. 2013, Kosa et al. 2011). However, although biosynthetic pathways for fatty acids and lipids are well understood in some microorganisms, identifying and bypassing the mechanisms regulating lipid accumulation in oleaginous strains remains a challenge (Blatti et al. 2013, Levering et al. 2015, Liang et al. 2013).

An alternative approach to increasing lipid production in microorganisms is transgenically engineering lipogenic pathways into non-oleaginous, but robust and genetically tractable hosts (d'Espaux et al. 2015). Many enzymes that convert fatty acids, or pathway intermediates, into products with desirable fuel properties have been investigated for their potential use in non-oleaginous microorganisms (Steen et al. 2010, Schirmer et al. 2010, Goh et al. 2012, Kalscheuer et al. 2006, Choi et al. 2013, Feng et al. 2015). However, achieving industrially relevant lipid production levels and yields can require genetic and metabolic engineering steps that are not feasible in many hosts (d'Espaux et al. 2015).

Mechanisms for increasing production of lipids and lipid-associated bioproducts in microorganisms, particularly in non-oleaginous microorganisms, are needed.

SUMMARY OF THE INVENTION

One aspect of the invention is directed to microorganisms with modifications that exhibit enhanced lipid production with respect to corresponding microorganisms that do not contain the modifications.

Some versions are directed to a recombinant microorganism. The recombinant microorganism comprises one or more modifications with respect to a corresponding microorganism not comprising the one or more modifications. The one or more modifications are selected from the group consisting of: a modification that reduces the activity of RSP2839 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP2840 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP3218 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP1056 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP1200 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP1422 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP0355 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP2545 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP2544 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP2543 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP2745 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP2293 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP2839 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP0334 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP0333 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP0332 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP0331 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP0330 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP0335 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP3540 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP3539 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP3538 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP2095 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP6038 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP2097 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP2098 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP2099 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP2100 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP2101 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP2111 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP2112 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP2113 or a homolog thereof with respect to the corresponding microorganism; a modification that reduces the activity of RSP2916 or a homolog thereof with respect to the corresponding microorganism; and a modification that increases the activity of RSP1860 or a homolog thereof with respect to with respect to the corresponding microorganism. The microorganism may comprise two or more of the one or more modifications. The microorganism may comprise three or more of the one or more modifications. The one or more modifications can be combined in any combination.

In some versions, the homolog of each of RSP2839, RSP2840, RSP3218, RSP1056, RSP1200, RSP1422, RSP0355, RSP2545, RSP2544, RSP2543, RSP2745, RSP2293, RSP2839, RSP0334, RSP0333, RSP0332, RSP0331, RSP0330, RSP0335, RSP3540, RSP3539, RSP3538, RSP2095, RSP6038, RSP2097, RSP2098, RSP2099, RSP2100, RSP2101, RSP2111, RSP2112, RSP2113, RSP2916, and RSP1860 is an ortholog thereof, and the homolog of RSP1860 is an ortholog of RSP1860, comprises or encodes a sequence at least 95% identical to the amino acid sequence of RSP1860, or comprises or encodes a sequence at least 95% identical to the amino acid sequence of the ortholog of RSP1860.

In some versions, the recombinant microorganism exhibits enhanced lipid secretion with respect to the corresponding microorganism.

In some versions, the one or more modifications comprise a modification selected from the group consisting of the modification that reduces the activity of the RSP2839 or homolog thereof, the modification that reduces the activity of the RSP2840 or homolog thereof, and the modification that reduces the activity of the RSP1200 or homolog thereof.

In some versions, the one or more modifications comprise the modification that reduces the activity of the RSP2839 or homolog thereof and the modification that reduces the activity of the RSP2840 or homolog thereof.

In some versions, the homolog of RSP2839 is an NtrY and the homolog of RSP2840 is an NtrX.

In some versions, the recombinant microorganism further comprises one or more modifications that reduce the activity of one or more of an acyl-CoA dehydrogenase, an enoyl-CoA hydratase, a 3-hydroxyacyl-CoA dehydrogenase, and a 3-ketoacyl-CoA thiolase and/or increase the activity of one or more of an acyl-CoA synthetase, an acetyl-CoA carboxylase, an acetyl CoA:ACP transacylase, a malonyl CoA:ACP transacylase, a (3-ketoacyl-ACP synthase, a 3-ketoacyl-ACP reductase, a 3-hydroxyacyl-ACP dehydrase, an enoyl-ACP reductase, a glycerol-3-phosphate acyltransferase, and a 1-acylglycerol-3-phosphate acyltransferase with respect to the corresponding microorganism.

In some versions, the recombinant microorganism comprises one or more modifications that reduce the activity of RSP0382 or a homolog thereof with respect to the corresponding microorganism.

In some versions, the recombinant microorganism further comprises a recombinant gene configured to express a lipid-associated protein.

In some versions, the one or more modifications comprises one or more recombinant genes configured to express one or more of RSP2144 or a homolog thereof, RSP1091 or a homolog thereof, and RSP1090 or a homolog thereof; a modification that disrupts binding between ChrR and σ^E or homologs thereof; a modification that increases expression of σ^E or a homolog thereof; and/or a modification that eliminates from the microorganism a native ChrR or homolog thereof.

In some versions, the corresponding microorganism is a non-oleaginous microorganism.

In some versions, the recombinant microorganism is a bacterium, such as a microorganism from the genus *Rhodobacter.*

In some versions, the recombinant microorganism exhibits at least a 2-fold enhanced lipid production with respect to the corresponding microorganism when the recombinant microorganism and the corresponding organism are grown under aerobic conditions, is capable of producing at least 1 g/L lipid, and/or is capable of producing lipids in an amount of at least 20% (w/w) dry cell weight.

Another aspect of the invention is directed to methods for producing bioproducts such as lipids, proteins, or other classes of lipid-associated organic compounds.

Some methods comprise culturing a recombinant microorganism of the invention in a medium for a time sufficient to consume nutrients present in the medium and produce the bioproduct.

In some versions, the culturing comprises periodically adding fresh nutrients to the medium during the culturing.

In some versions, the culturing comprises culturing the microorganism at a first level of dissolved oxygen in the medium and adding nutrients to the medium upon detecting an increase in the dissolved oxygen from the first level to a second level in an amount sufficient to reduce the dissolved oxygen from the second level to a third level.

In some versions, the medium comprises biomass hydrolysate.

In some versions, the nutrients comprise at least one of glucose, xylose, succinate, lactate, and acetate.

In some versions, the bioproduct is selected from the group consisting of a lipid, a protein, and an organic compound.

In some versions, the organic compound comprises a quinone.

In some versions, the culturing is conducted at least until the microorganism produces 1 g/L lipid.

In some versions, the culturing is conducted at least until the microorganism produces lipids in an amount of at least 20% (w/w) dry cell weight.

In some versions, the culturing is conducted under aerobic conditions.

The objects and advantages of the invention will appear more fully from the following detailed description of the preferred embodiment of the invention made in conjunction with the accompanying drawings.

BRIEF DESCRIPTION OF THE DRAWINGS

The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

FIG. **1**. Fatty acid content of parent *Rhodobacter sphaeroides* strain grown at high and low O_2 compared to high-lipid (HL) mutants grown at high O_2. Data shown represents the mean of three or more independent cultures ±standard deviation.

FIG. **2**. Relative fitness of high-lipid (HL) mutants in the presence of indicated compounds (A, neomycin; B, sodium dodecyl sulfate (SDS); C, amoxicillin) compared to the parent strain. Data shown represents the mean of three cultures ±standard deviation.

FIG. **3**. Chemical sensitivity analysis of high-lipid (HL) mutants. Cluster A shows increased sensitivity to a group of compounds that report on membrane integrity (*). Cluster B shows increased sensitivity to a group of peptidoglycan active compounds (**). The color scale indicates relative fitness compared to the parent strain. A value of 1 (black) indicates no change relative to the parent, <1 (blue) indicates increased sensitivity to the compound, >1 (yellow) indicates increased resistance to the compound.

FIG. **4**. Transmission electron microscopy micrographs of whole mounts of the parent strain (A, E) and high-lipid (HL) mutants (B-D, F-H). The lower row of panels (E-H) shows views of extracellular material from these strains. Similar micrographs of the parent strain and other HL mutants are shown in FIGS. **5** and **6**. Arrow in the inset (F) indicates a stacked structure typical of liposomes; scale bar for this inset panel is 50 nm.

FIG. **5**. Transmission electron microscopy micrographs of whole mounts of indicated high-lipid (HL) mutants. A and B) HLM08 has extracellular material, irregular shaped particles of varied sizes as well as stacked structures. C) HLM03 and D) HLM09 have structures extending off the cell surface (arrows).

FIG. **6**. Cell shape of high-lipid (HL) mutants HLM04 and HLM07 compared to the parent strain. A-C) Transmission electron microscopy micrographs of cell whole mounts. D-F) Super-resolution structured illumination microscopy images of Nile Red-stained cells. Scale bars for (D-F) measure 1 μm.

FIG. **7**. Super-resolution structured illumination microscopy images of Nile Red-stained parent and high-lipid (HL) mutant cells. Representative fields are shown from images used to measure cell dimensions. Scale bar length=2 μm.

FIG. **8**. Analysis of the extracellular material of parent and high-lipid (HL) mutant strains. A) Nile red staining of the media from parent and HL mutant cultures. B) Fatty acid content of cell and media fractions of parent and HL mutant cultures. C) Percent of total fatty acids found in media fraction for data shown in (B). Data shown represents the mean of three or more independent cultures ±standard deviation. P values are for the difference of each HL mutant compared to the parent strain.

FIG. **9**. Analysis of extracellular material of HLM01, HLM02, and HLM05 for phospholipid and lipopolysaccharide (LPS) content. A) Fatty acid and lipid phosphorous levels in the media with molar ratios listed below the graph. B) LPS content of the media, with conversion to estimated LPS-associated fatty acids on the secondary vertical axis. The relative contribution of LPS-associated fatty acids to the total amount of secreted fatty acids is shown below the graph. Data shown represents the mean of four or more independent cultures ±standard deviation.

FIG. **10**. Fatty acid production by parent and HLM02 strains in batch cultures with one of four different carbon sources. A) Fatty acid productivity per culture volume and B) fatty acid content as a percent of dry cell weight (DCW). C) Fatty acid yield per carbon substrate consumed. Data shown represents the mean of three or more independent cultures ±standard deviation.

FIG. **11**. Coenzyme Q10 (CoQ10) levels in the supernatants from the parent strain (Δ0382), a strain lacking the genes disrupted in HLM05 (Δ1200Δ0382, shown as Δ1200), and a strain lacking the genes disrupted in HLM01 and HLM02 (ΔNtrXYΔ0382, shown as Δntrxy).

FIG. **12**. Feeding protocol for fed-batch high-density cultures. The solid line shows culture dissolved oxygen (DO), which is maintained at a low baseline level by bubbling the reactor with saturated air. Increases in DO (seen at ~51.2 and 52.6 hours) indicate reduced metabolic activity in the reactor, and at these times a bolus of feeding medium is added increasing the total feeding volume (dotted line). After feeding, the culture DO drops to baseline as cellular respiration increases. A three hour period is shown from a 120 hour reactor run, the illustrated process repeats iteratively throughout the reactor incubation.

FIG. **13**. Fed-batch reactor production of fatty acids by HLM02 mutant compared to the parent strain, grown with xylose as a carbon source. A) Total biomass and B) fatty acid content in the fed-batch reactor. C) Productivity of fatty acids and D) yield of fatty acids per xylose consumed. Data are shown from a representative bioreactor run for each strain; error bars represent standard deviation between technical replicates.

FIG. **14**. Transmission electron microscopy of whole mounts of the HLM02 mutant grown in the fed-batch bioreactor. Views are shown of cells surrounded by extracellular structures (A,B), and of extracellular structures only (C,D).

DETAILED DESCRIPTION OF THE INVENTION

One aspect of the invention is directed to recombinant microorganisms configured for enhanced lipid production. The recombinant microorganisms of the invention comprise one or more modifications that reduce the activity of one or more genes or gene products, increase the activity of one or more genes or gene products, or reduce the activity of one or more genes or gene products and increase the activity of one or more genes or gene products. The recombinant microorganisms with the modifications exhibit enhanced lipid production with respect to corresponding microorganisms not comprising the modifications.

"Modifications that reduce the activity of one or more genes or gene products" refers to any modification to a microorganism that decreases or ablates expression of the gene and thus production of the gene product or decreases or ablates the functioning of the gene product. Decreasing or ablating the functioning of a gene product may comprise decreasing or ablating the specific activity of a gene product. Exemplary modifications that reduce the activity of one or more genes or gene products include genetic modifications. The genetic modifications include mutations to a gene that decrease or ablate expression of the gene in producing the gene product. Such mutations may include mutations to the coding sequence, the promoter, an enhancer, or any other part of the gene. The genetic mutations also include mutations to the coding sequence of a gene that decrease or ablate the functioning of a gene product expressed from the gene. The genetic mutations also include recombinant nucleotide sequences configured to express antisense RNAs or other molecules that decrease or ablate production of a gene product. The genetic modifications also include mutations to a first gene (such as a transcription factor or an inhibitor of a transcription factor) that affects the expression of a second gene. Other genetic modifications are described elsewhere herein.

"Modifications that increase the activity of one or more genes or gene products" refers to any modification to microorganism that increases expression of a gene in producing its gene product or increases the functioning of the gene product. "Increase" in this context refers to increasing beyond a positive baseline activity or increasing beyond null activity and thereby introducing a new activity. Exemplary modifications that increase the activity of one or more genes or gene products include genetic modifications. The genetic modifications include genetic modifications to a gene in a manner that increases expression of the gene in producing the gene product. Such modifications include operationally connecting the coding sequence to a stronger promoter or enhancer, etc., and/or introducing additional copies of the gene (whether the native gene or a recombinant version). The genetic modifications also include mutations to a first gene (such as a transcription factor or an inhibitor of a transcription factor) that affects the expression of a second gene. The genetic modifications also include one or more copies of a gene introduced into the microorganism. Other genetic modifications are described herein. Any modifications described herein can comprise recombinant genes.

"Corresponding microorganism" refers to a microorganism of the same species having the same or substantially same genetic and proteomic composition as a recombinant microorganism of the invention, with the exception of genetic and proteomic differences resulting from the modifications described herein for the recombinant microorganisms of the invention. In some versions, the corresponding microorganism is the native version of the recombinant microorganism of the invention, i.e., the unmodified microorganism as found in nature. The terms "microorganism" and "microbe" are used interchangeably herein.

Unless explicitly stated otherwise or indicated from the context, the designations beginning with the prefix "RSP" (e.g., "RSP2839," "RSP2840," "RSP3218," "RSP1056," etc.) and the term "homologs" are used herein to refer to both a gene coding sequence and products (such as proteins) encoded by the coding sequence. The gene coding sequences and products encoded thereby are collectively referred herein to "molecular elements." The sequences corresponding to the designations beginning with the prefix "RSP" are all publicly available and readily accessible. See Kontur 2012. An exemplary database in which the sequences can be found is accessible via the web at img.jgi.doe.gov. The following SEQ ID NOS correspond to the following molecular elements in which "NT" refers to the DNA coding sequence and "PRT" refers to the protein sequence:

SEQ ID NO:1: RSP0190—NT;
SEQ ID NO:2: RSP0190—PRT;
SEQ ID NO:3: RSP0191—NT;
SEQ ID NO:4: RSP0191—PRT;
SEQ ID NO:5: RSP0330—NT;
SEQ ID NO:6: RSP0330—PRT;
SEQ ID NO:7: RSP0331—NT;
SEQ ID NO:8: RSP0331—PRT;
SEQ ID NO:9: RSP0332—NT;
SEQ ID NO:10: RSP0332—PRT;
SEQ ID NO:11: RSP0333—NT;
SEQ ID NO:12: RSP0333—PRT;
SEQ ID NO:13: RSP0334—NT;
SEQ ID NO:14: RSP0334—PRT;
SEQ ID NO:15: RSP0335—NT;
SEQ ID NO:16: RSP0335—PRT;
SEQ ID NO:17: RSP0339—NT;
SEQ ID NO:18: RSP0339—PRT;
SEQ ID NO:19: RSP0355—NT;
SEQ ID NO:20: RSP0355—PRT;
SEQ ID NO:21: RSP0382—NT;
SEQ ID NO:22: RSP0382—PRT;
SEQ ID NO:23: RSP0579—NT;
SEQ ID NO:24: RSP0579—PRT;
SEQ ID NO:25: RSP0735—NT;
SEQ ID NO:26: RSP0735—PRT;
SEQ ID NO:27: RSP0747—NT;
SEQ ID NO:28: RSP0747—PRT;
SEQ ID NO:29: RSP0892—NT;
SEQ ID NO:30: RSP0892—PRT;
SEQ ID NO:31: RSP1004—NT;
SEQ ID NO:32: RSP1004—PRT;
SEQ ID NO:33: RSP1056—NT;
SEQ ID NO:34: RSP1056—PRT;
SEQ ID NO:35: RSP1090—NT;
SEQ ID NO:36: RSP1090—PRT;
SEQ ID NO:37: RSP1091—NT;
SEQ ID NO:38: RSP1091—PRT;
SEQ ID NO:39: RSP1200—NT;
SEQ ID NO:40: RSP1200—PRT;
SEQ ID NO:41: RSP1256—NT;
SEQ ID NO:42: RSP1256—PRT;
SEQ ID NO:43: RSP1293—NT;
SEQ ID NO:44: RSP1293—PRT;
SEQ ID NO:45: RSP1354—NT;
SEQ ID NO:46: RSP1354—PRT;
SEQ ID NO:47: RSP1422—NT;
SEQ ID NO:48: RSP1422—PRT;
SEQ ID NO:49: RSP1687—NT;
SEQ ID NO:50: RSP1687—PRT;
SEQ ID NO:51: RSP1772—NT;
SEQ ID NO:52: RSP1772—PRT;
SEQ ID NO:53: RSP1860—NT;
SEQ ID NO:54: RSP1860—PRT;
SEQ ID NO:55: RSP2095—NT;
SEQ ID NO:56: RSP2095—PRT;
SEQ ID NO:57: RSP2097—NT;
SEQ ID NO:58: RSP2097—PRT;
SEQ ID NO:59: RSP2098—NT;
SEQ ID NO:60: RSP2098—PRT;
SEQ ID NO:61: RSP2099—NT;
SEQ ID NO:62: RSP2099—PRT;
SEQ ID NO:63: RSP2100—NT;
SEQ ID NO:64: RSP2100—PRT;
SEQ ID NO:65: RSP2101—NT;
SEQ ID NO:66: RSP2101—PRT;
SEQ ID NO:67: RSP2111—NT;
SEQ ID NO:68: RSP2111—PRT;
SEQ ID NO:69: RSP2112—NT;
SEQ ID NO:70: RSP2112—PRT;
SEQ ID NO:71: RSP2113—NT;
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SEQ ID NO:73: RSP2144—NT;
SEQ ID NO:74: RSP2144—PRT;
SEQ ID NO:75: RSP2196—NT;
SEQ ID NO:76: RSP2196—PRT;
SEQ ID NO:77: RSP2197—NT;
SEQ ID NO:78: RSP2197—PRT;
SEQ ID NO:79: RSP2293—NT;
SEQ ID NO:80: RSP2293—PRT;
SEQ ID NO:81: RSP2344—NT;
SEQ ID NO:82: RSP2344—PRT;
SEQ ID NO:83: RSP2371—NT;
SEQ ID NO:84: RSP2371—PRT;
SEQ ID NO:85: RSP2461—NT;
SEQ ID NO:86: RSP2461—PRT;
SEQ ID NO:87: RSP2464—NT;
SEQ ID NO:88: RSP2464—PRT;
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SEQ ID NO:90: RSP2538—PRT;
SEQ ID NO:91: RSP2543—NT;
SEQ ID NO:92: RSP2543—PRT;
SEQ ID NO:93: RSP2544—NT;

SEQ ID NO:94: RSP2544—PRT;
SEQ ID NO:95: RSP2545—NT;
SEQ ID NO:96: RSP2545—PRT;
SEQ ID NO:97: RSP2612—NT;
SEQ ID NO:98: RSP2612—PRT;
SEQ ID NO:99: RSP2712—NT;
SEQ ID NO:100: RSP2712—PRT;
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SEQ ID NO:106: RSP2840—PRT;
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SEQ ID NO:108: RSP2915—PRT;
SEQ ID NO:109: RSP2916—NT;
SEQ ID NO:110: RSP2916—PRT;
SEQ ID NO:111: RSP2974—NT;
SEQ ID NO:112: RSP2974—PRT;
SEQ ID NO:113: RSP3018—NT;
SEQ ID NO:114: RSP3018—PRT;
SEQ ID NO:115: RSP3062—NT;
SEQ ID NO:116: RSP3062—PRT;
SEQ ID NO:117: RSP3177—NT;
SEQ ID NO:118: RSP3177—PRT;
SEQ ID NO:119: RSP3178—NT;
SEQ ID NO:120: RSP3178—PRT;
SEQ ID NO:121: RSP3184—NT;
SEQ ID NO:122: RSP3184—PRT;
SEQ ID NO:123: RSP3218—NT;
SEQ ID NO:124: RSP3218—PRT;
SEQ ID NO:125: RSP3440—NT;
SEQ ID NO:126: RSP3440—PRT;
SEQ ID NO:127: RSP3468—NT;
SEQ ID NO:128: RSP3468—PRT;
SEQ ID NO:129: RSP3535—NT;
SEQ ID NO:130: RSP3535—PRT;
SEQ ID NO:131: RSP3538—NT;
SEQ ID NO:132: RSP3538—PRT;
SEQ ID NO:133: RSP3539—NT;
SEQ ID NO:134: RSP3539—PRT;
SEQ ID NO:135: RSP3540—NT;
SEQ ID NO:136: RSP3540—PRT;
SEQ ID NO:137: RSP3888—NT;
SEQ ID NO:138: RSP3888—PRT;
SEQ ID NO:139: RSP3970—NT;
SEQ ID NO:140: RSP3970—PRT;
SEQ ID NO:141: RSP6005—NT;
SEQ ID NO:142: RSP6005—PRT;
SEQ ID NO:143: RSP6038—NT;
SEQ ID NO:144: RSP6038—PRT;
SEQ ID NO:145: RSP7370—NT;
SEQ ID NO:146: RSP7370—PRT;
SEQ ID NO:147: RSP7647—NT; and
SEQ ID NO:148: RSP7647—PRT.

In some versions, the recombinant microorganisms comprise one or more modifications that reduce the activity of one or more of RSP2839 or a homolog thereof, RSP2840 or a homolog thereof, RSP3218 or a homolog thereof, RSP1056 or a homolog thereof, RSP1200 or a homolog thereof, RSP1422 or a homolog thereof, RSP0355 or a homolog thereof, RSP2545 or a homolog thereof, RSP2544 or a homolog thereof, RSP2543 or a homolog thereof, RSP2745 or a homolog thereof, and RSP2293 or a homolog thereof, and/or one or more modifications that increase the activity of RSP1056 or homolog thereof, with respect to a corresponding microorganism not comprising the one or more modifications. The recombinant microorganisms may include modifications that reduce the activity of two or more, three or more, four or more, five or more, six or more, or seven or more of the above-referenced molecular elements. The recombinant microorganisms may include modifications that reduce the activity any of the above-referenced molecular elements in any combination. Exemplary combinations include modifications that reduce the activity of RSP2839 and RSP2840 or homologs thereof or of RSP2545, RSP2544 and RSP2543 or homologs thereof.

The RSP2839 and RSP2840 are parts of the NtrXY two-component signaling system, wherein RSP2839 is a sensor histidine kinase referred to as "NtrY" and RSP2840 is the response regulator referred to as "NtrX." The NtrXY system is involved with regulating a set of genes upon activation. An alternative or additional modification to reducing the activity of RSP2839 and/or RSP2840 or any other modification described herein is directly modifying the expression or activity of the NtrXY target genes or products. Accordingly, in some versions of the invention, the recombinant microorganisms comprise one or more modifications that reduce the activity of one or more of RSP2839 or a homolog thereof, RSP0334 or a homolog thereof, RSP0333 or a homolog thereof, RSP0332 or a homolog thereof, RSP0331 or a homolog thereof, RSP0330 or a homolog thereof, RSP0335 or a homolog thereof, RSP3540 or a homolog thereof, RSP3539 or a homolog thereof, RSP3538 or a homolog thereof, RSP2095 or a homolog thereof, RSP6038 or a homolog thereof, RSP2097 or a homolog thereof, RSP2098 or a homolog thereof, RSP2099 or a homolog thereof, RSP2100 or a homolog thereof, RSP2101 or a homolog thereof, RSP2111 or a homolog thereof, RSP2112 or a homolog thereof, RSP2113 or a homolog thereof, and RSP2916 or a homolog thereof; one or more modifications that increase the activity of RSP1860 or a homolog thereof, with respect to a corresponding microorganism not comprising the one or more modifications; and/or one or more modifications that either increase or reduce the activity of one or more of RSP0339 or a homolog thereof, RSP2974 or a homolog thereof, RSP0892 or a homolog thereof, and RSP2915 or a homolog thereof. Two or more, three or more, four or more, or five or more of the above-referenced molecular elements may be modified for ablated, reduced, or increased activity in the recombinant microorganisms. The above-referenced molecular elements may be modified in any combination within the group itself or any other modification described herein.

The recombinant microorganisms in preferred versions of the invention are configured to exhibit enhanced lipid secretion with respect to a corresponding microorganism. The recombinant microorganisms in such versions may include any one or more of the modifications described herein. Modifications that confer a remarkable enhancement in lipid secretion include those that reduce the activity of any one or more of RSP2839 or a homolog thereof, RSP2840 or a homolog thereof, and RSP1200 or a homolog thereof. An exemplary combination of the above-referenced modifications includes modifications that reduce the activity of RSP2839 or a homolog thereof and RSP2840 or a homolog thereof. Other combinations are within the scope of the present invention.

Any of the above-referenced modifications may be combined with modifications that inhibit the β-oxidation of fatty acids. Exemplary modifications that inhibit the β-oxidation of fatty acids include modifications that reduce the activity of any one or more of an acyl-CoA dehydrogenase, an enoyl-CoA hydratase, a 3-hydroxyacyl-CoA dehydrogenase, and a 3-ketoacyl-CoA thiolase. Acyl-CoA dehydrogenases, enoyl-CoA hydratases, 3-hydroxyacyl-CoA dehydrogenases, and 3-ketoacyl-CoA thiolases are well known in the art and are readily identified in any given microorganism. Exemplary acyl-CoA dehydrogenases, enoyl-CoA hydratases, 3-hydroxyacyl-CoA dehydrogenases, and 3-ketoacyl-CoA thiolases (acetyl-CoA C-acyltransferases) include RSP7647, RSP3018, RSP3535, RSP3970, RSP2196, RSP1687, RSP2197, RSP1354, and RSP3184.

Any of the above-referenced modifications may also or alternatively be combined with modifications that promote lipid synthesis. Exemplary modifications that promote lipid synthesis include modifications that increase expression or activity of any one or more of an acetyl-CoA synthetase, an acetyl-CoA carboxylase, an acetyl CoA:ACP transacylase, a malonyl CoA:ACP transacylase, a 3-ketoacyl-ACP synthase, a 3-ketoacyl-ACP reductase, a 3-hydroxyacyl-ACP dehydrase, an enoyl-ACP reductase, a glycerol-3-phosphate acyltransferase, and a 1-acylglycerol-3-phosphate acyltransferase. Acyl-CoA synthetases, acetyl-CoA carboxylases, acetyl CoA:ACP transacylases, malonyl CoA:ACP transacylases, 3-ketoacyl-ACP synthases, 3-ketoacyl-ACP reductases, 3-hydroxyacyl-ACP dehydrases, enoyl-ACP reductases, glycerol-3-phosphate acyltransferases, and 1-acylglycerol-3-phosphate acyltransferases are well known in the art and are readily identified in any given microorganism. Exemplary acetyl-CoA synthetases, acetyl-CoA carboxylases, acetyl CoA:ACP transacylases, malonyl CoA:ACP transacylases, 3-ketoacyl-ACP synthases (3-oxoacyl-ACP synthases), 3-ketoacyl-ACP reductases (3-oxoacyl-ACP reductases), (3-hydroxyacyl-ACP dehydrases, enoyl-ACP reductases, glycerol-3-phosphate acyltransferases, and 1-acylglycerol-3-phosphate acyltransferases include RSP0579, RSP1772, RSP0190, RSP0191, RSP1293, RSP2464, RSP2612, RSP3177, RSP3468, RSP6005, RSP2371, RSP2461, RSP2538, RSP0747, RSP3062, RSP3440, RSP3888, RSP2712, RSP7370, RSP3178, RSP1256, RSP2344, RSP1004, and RSP0735. Additional modifications may include those that increase expression or activity of homologues of FabG that have been engineered to improve the supply of reduced pyridine nucleotides needed for fatty acid synthesis (RSP2461) (Javidpour et al. 2014) or homologues of FabF (RSP2464) that have been engineered to produce fatty acids of shorter chain lengths (Torella et al. 2013).

Any of the above-referenced modifications may also or alternatively be combined with modifications that reduce the production of polyhydroxybutyrate. An exemplary modification that reduces the production of polyhydroxybutyrate is a modification that reduces the activity of RSP0382 or a homolog thereof.

The recombinant microorganisms of the invention may be configured for the novel production or enhanced production of specific lipids. Examples of such lipids include certain straight-chain fatty acids or non-straight-chain fatty acids. Examples of straight-chain fatty acids include omega-3 fatty acids such as docosahexaenoic acid and omega-6 fatty acids such as arachidonic acid. Examples of non-straight-chain fatty acids include branched-chain fatty acids, furan-containing fatty acids, and cyclic fatty acids. To make certain non-straight-chain fatty acids, the microorganisms may comprise any one or more of the modifications described in US 2015/0376659 to Lemke et al., which is incorporated herein by reference. Accordingly, the recombinant microorganism may comprise one or more modifications that increase the activity of one or more of RSP2144 or a homolog thereof, RSP1091 or a homolog thereof, and RSP1090 or a homolog thereof, with respect to the corresponding microorganism. Such microorganisms may comprise one or more recombinant genes configured to express or overexpress one or more of the RSP2144 or homolog thereof, the RSP1091 or homolog thereof, and the RSP1090 or homolog thereof; a modification that disrupts binding between ChrR and σ^E or homologs thereof; a modification that increases expression of σ^E or a homolog thereof; and/or a modification that eliminates from the microorganism a native ChrR or homolog thereof.

The recombinant microorganisms of the invention may be configured for the novel production or enhanced production of lipid-associated bioproducts. "Lipid-associated bioproducts" refer to products produced by microorganisms that integrate in or associate with cellular lipids, such as membranes. Examples of lipid-associates bioproducts include certain proteins, organic compounds (such as quinones, isoprenoids, etc.), non-organic compounds, or other products. The lipid-associated bioproducts may be lipid-soluble or have lipid-soluble moieties. Lipid-associated bioproducts that are proteins are referred to herein as "lipid-associated proteins." Examples of lipid-associated proteins include various membrane proteins, such as integral membrane proteins and peripheral membrane proteins, as well as soluble proteins contained inside lipid-vesicles. Accordingly, some microorganisms of the invention comprise one or more recombinant genes configured to express lipid-associated proteins. Other microorganisms of the invention comprise one or more recombinant genes configured to express enzymes responsible for producing lipid-associated bioproducts.

Modifications that reduce the activity of a gene or gene product includes any modification to a microorganism that ablates, reduces, inhibits, or otherwise disrupts production of a gene product, renders a produced gene product non-functional, or otherwise reduces or ablates a produced gene product's activity. Accordingly, in some instances, production of a gene product may be completely shut down. "Gene product" refers to products such as an mRNA or a polypeptide encoded and produced by a particular gene. "Gene" refers to a nucleic acid sequence capable of producing a gene product and may include such genetic elements as a coding sequence together with any other genetic elements required for transcription and/or translation of the coding sequence. Such genetic elements may include a promoter, an enhancer, and/or a ribosome binding site (RBS), among others.

There are many well-known ways to reduce the activity of a gene or gene product. This can be accomplished, for example, by introducing one or more genetic modifications. As used herein, "genetic modifications" refer to any differences in the nucleic acid composition of a cell, whether in the cell's native chromosome or in endogenous or exogenous non-chromosomal plasmids harbored within the cell. Examples of genetic modifications that reduce the activity of a gene or gene product include but are not limited to substitutions, partial or complete deletions, insertions, or other variations to a coding sequence or a sequence controlling the transcription or translation of a coding sequence, such as placing a coding sequence under the control of a less active promoter, etc. In some versions, a gene or coding sequence can be replaced with a selection marker or screenable marker. In some versions, the genetic modifications can include the introduction of constructs that express ribozymes or antisense sequences that target the mRNA of the gene of interest. Various other genetic modifications that reduce the activity of a gene or gene product are described elsewhere herein. Various methods for introducing genetic modifications are well known in the art and include homologous recombination, among other mechanisms. See, e.g., Green et al., *Molecular Cloning: A laboratory manual,* 4th ed., Cold Spring Harbor Laboratory Press (2012) and Sambrook et al., *Molecular Cloning: A Laboratory Manual,* 3rd ed., Cold Spring Harbor Laboratory Press (2001). In some instances, reducing the activity of a gene or gene product can be accomplished by chemically inhibiting the activity of a gene product with a small-molecule inhibitor, by expressing a protein that interferes with the activity of the gene product, or by other means.

"Increasing expression" or grammatical variants thereof may refer to expressing a gene product not made by the corresponding microorganism or expressing more of a gene product already made by the corresponding microorganism. Modifying the recombinant microorganisms to increase expression of the gene products described herein can be performed using any methods currently known in the art or discovered in the future. Examples include genetically modifying the microorganism and culturing the microorganism in the presence of factors that increase expression of the gene product. Suitable methods for genetic modification include but are not limited to placing the coding sequence under the control of a more active promoter, increasing the copy number of genes comprising the coding sequence, introducing a translational enhancer on a gene comprising the coding sequence (see, e.g., Olins et al. 1989), and/or modifying factors (e.g., transcription factors or genes therefor) that control expression of a gene comprising the coding sequence. Increasing the copy number of genes comprising a coding sequence can be performed by introducing one or more additional copies of the native gene to the microorganism, introducing one or more a heterologous homologs to the microorganism, introducing one or more copies of recombinant versions of the native gene or heterologous homolog to the microorganism, etc. Genes expressing a given coding sequence may be incorporated into the microbial genome or included on an extrachromosomal genetic construct such as a plasmid. "Exogenous" used in reference to a genetic element means the genetic element is a non-native genetic element. "Heterologous" used in reference to a genetic element means that the genetic element is derived from a different species. A genetic element, such as a promoter, that controls or affects the activity of another genetic element, such as a coding sequence, is herein described as being "operationally connected" thereto.

Some of the microorganisms of the invention may include at least one recombinant nucleic acid configured to express or overexpress a particular product. "Recombinant" as used herein with reference to a nucleic acid molecule or polypeptide is one that has a sequence that is not naturally occurring, has a sequence that is made by an artificial combination of two otherwise separated segments of sequence, or both. This artificial combination can be achieved, for example, by chemical synthesis or by the artificial manipulation of isolated segments of nucleic acid molecules or polypeptides using genetic engineering techniques. A recombinant cell or microorganism is one that contains a recombinant nucleic acid molecule or polypeptide. "Overexpress" as used herein means that a particular gene product is produced at a higher level in one cell, such as a recombinant cell, than in a corresponding cell. For example, a microorganism that includes a recombinant nucleic acid configured to overexpress a gene product produces the gene product at a greater amount than a microorganism of the same species that does not include the recombinant nucleic acid.

In general, proteins and/or protein sequences are "homologous" when they are derived, naturally or artificially, from a common ancestral protein or protein sequence. Similarly, nucleic acids and/or nucleic acid sequences are homologous when they are derived, naturally or artificially, from a common ancestral nucleic acid or nucleic acid sequence. Homology is generally inferred from sequence similarity between two or more nucleic acids or proteins (or sequences thereof). The precise percentage of similarity between sequences that is useful in establishing homology varies with the nucleic acid and protein at issue, but as little as 25% sequence similarity (e.g., identity) over 50, 100, 150 or more residues (nucleotides or amino acids) is routinely used to establish homology (e.g., over the full length of the two sequences to be compared). Higher levels of sequence similarity (e.g., identity), e.g., 30%, 35% 40%, 45% 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% or more, can also be used to establish homology. Accordingly, homologous sequences of the sequences described herein include coding sequences, genes, or gene products (e.g., proteins), respectively, having at least about 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity to the sequences described herein. Methods for determining sequence similarity percentages (e.g., BLASTP and BLASTN using default parameters) are described herein and are generally available. The homologous proteins should demonstrate comparable activities and, if an enzyme, participate in the same or analogous pathways. "Orthologs" are genes or coding sequences thereof in different species that evolved from a common ancestral gene by speciation. Normally, orthologs retain the same or similar function in the course of evolution. As used herein "orthologs" are included in the term "homologs." Homologs also include sequences at least 90%, 95%, or 97% or more identical to the orthologs.

For sequence comparison and homology determination, one sequence typically acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence based on the designated program parameters. A typical reference sequence of the invention is any nucleic acid or amino acid sequence described herein.

Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson & Lipman, Proc. Nat'l. Acad. Sci. USA 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis.), or by visual inspection (see Current Protocols in Molecular Biology, F. M. Ausubel et al., eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (supplemented through 2008)).

One example of an algorithm that is suitable for determining percent sequence identity and sequence similarity for purposes of defining homologs is the BLAST algorithm, which is described in Altschul 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 W in 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 (Altschul et al., supra). 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. Natl. Acad. Sci. USA 90:5873-5787 (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. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001. The above-described techniques are useful in identifying homologous sequences for use in the methods described herein.

The terms "identical" or "percent identity", in the context of two or more nucleic acid or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same, when compared and aligned for maximum correspondence, as measured using one of the sequence comparison algorithms described above (or other algorithms available to persons of skill) or by visual inspection.

The phrase "substantially identical", in the context of two nucleic acids or polypeptides refers to two or more sequences or subsequences that have at least about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90, about 95%, about 98%, or about 99% or more nucleotide or amino acid residue identity, when compared and aligned for maximum correspondence, as measured using a sequence comparison algorithm or by visual inspection. Such "substantially identical" sequences are typically considered to be "homologous" without reference to actual ancestry. Preferably, the "substantial identity" exists over a region of the sequences that is at least about 50 residues in length, more preferably over a region of at least about 100 residues, and most preferably, the sequences are substantially identical over at least about 150 residues, at least about 250 residues, or over the full length of the two sequences to be compared.

Exogenous, heterologous nucleic acids encoding products to be expressed in the microorganism are preferably codon-optimized for the particular microorganism in which they are introduced. Codon optimization can be performed for any nucleic acid by a number of programs, including "GENEGPS"-brand expression optimization algorithm by DNA 2.0 (Menlo Park, Calif.), "GENEOPTIMIZER"-brand gene optimization software by Life Technologies (Grand Island, N.Y.), and "OPTIMUMGENE"-brand gene design system by GenScript (Piscataway, N.J.). Other codon optimization programs or services are well known and commercially available.

Notwithstanding the above discussion, homologs of RSP2839 may also or alternatively include genes identified by the designation "ntrY" or corresponding designations and proteins identified by the designation "NtrY" or corresponding designations. Homologs of RSP2840 include genes identified by the designation "ntrX" or corresponding designations and proteins identified by the designation "NtrX" or corresponding designations. See Atack et al. 2013.

The recombinant microorganisms of the invention may comprise any type of microorganism. The microorganism may be prokaryotic or eukaryotic. Suitable prokaryotes include bacteria and archaea. Suitable types of bacteria include α- and γ-proteobacteria, gram-positive bacteria, gram-negative bacteria, ungrouped bacteria, phototrophs, lithotrophs, and organotrophs. Suitable eukaryotes include yeast and other fungi. Exemplary microorganisms include those from the genus *Rhodobacter*, such as *Rhodobacter sphaeroides*, and those from the genus *Rhodopseudomonas*, such as *Rhodopseudomonas palustris*. In some versions of the invention, the corresponding organism to the recombinant microorganisms of the invention is a non-oleaginous microorganism.

The recombinant microorganisms of the invention preferably exhibit enhanced lipid production with respect to the corresponding microorganism when the recombinant microorganism and the corresponding organism are grown under aerobic conditions. The lipid production may be enhanced by a factor of at least about 1.1, at least about 1.5, at least about 2, at least about 2.5, at least about 3, at least about 3.5, at least about 4, at least about 4.5, at least about 5, at least about 5.5, at least about 6, or at least about 6.5 and/or up to about 6.5, up to about 7, or more. Such increases may reflect an increase by mass.

The recombinant microorganisms of the invention may be configured to be capable of producing lipid in culture in an amount of at least about 0.5 g/L, at least about 0.75 g/L, at least about 1 g/L, or at least about 1.5 g/L and/or up to about 1.7 g/L, up to about 2 g/L, up to about 2.5 g/L or more. Such amounts may reflect the total lipid produced in culture (both intracellular and secreted).

The recombinant microorganisms of the invention may be configured to be capable of secreting lipid in culture in an amount of at least about 0.4 g/L, at least about 0.6 g/L, at least about 0.8 g/L, at least about 1 g/L, at least about 1.2 g/L, or at least about 1.4 g/L, and/or up to about 1.6 g/L or more.

The recombinant microorganisms of the invention may be configured to be capable of secreting an amount of at least about 10% (w/w), at least about 20% (w/w), at least about 30% (w/w), at least about 40% (w/w), at least about 50%

(w/w), at least about 60% (w/w), and/or up to about 60% (w/w), up to about 70% (w/w) or more of total produced lipids.

The recombinant microorganisms of the invention may be configured to be capable of producing lipid in culture in an amount of at least about 15% (w/w) dry cell weight, at least about 20% (w/w) dry cell weight, at least about 25% (w/w) dry cell weight, at least about 30% (w/w) dry cell weight, and/or up to about 30% (w/w) dry cell weight, up to about 35% (w/w) dry cell weight, or more. Such amounts may reflect the total lipid produced in culture (both intracellular and secreted).

The recombinant microorganisms of the invention can be used in methods for producing bioproducts. The bioproducts may include any bioproduct, including those described elsewhere herein such as lipids, proteins, and/or organic compounds. The methods may include culturing the recombinant microorganism as described herein in a medium comprising for a time sufficient to consume nutrients present in the medium and produce the bioproduct.

As shown in the examples, high production of the bioproducts can be obtained through fed-batch culturing, wherein nutrients are freshly added periodically throughout the culturing. In preferred versions, the fed-batch culturing comprises culturing the microorganism at a first level of dissolved oxygen in the medium and adding nutrients to the medium upon detecting an increase in the dissolved oxygen from the first level to a second level of the dissolved oxygen. The nutrients are added in an amount sufficient to reduce the dissolved oxygen from the second level to a third level of dissolved oxygen. The third level may or may not be equivalent to the first level. Such a process may be repeated with 1-500 or more additional iterations, such as 1-200, 110-150, 20-100, or about 60 additional iterations, with the first, second, and third levels in each additional iteration being the same or different as the respective levels in the first iteration.

The medium may comprise a defined set of chemicals or comprise a more complex set of chemicals such as a biomass hydrolysate. The biomass hydrolysate may be included in an amount of at least about 5%, at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, or more.

Biomass is biological material derived from living or once-living organisms. Biomass can be from plant, animal, or other organic material. Biomass is carbon based and is composed of a mixture of organic molecules containing hydrogen atoms, usually including atoms of oxygen, often nitrogen and also small quantities of other atoms, including alkali, alkaline earth and heavy metals.

The biomass hydrolysate for use in the present invention can be produced from any biomass feedstock. Exemplary types of biomass feedstocks include sucrose-rich feedstocks such as sugar cane; starchy materials, such as corn grain; and lignocellulosic biomass, such as costal Bermuda grass, corn cobs, corn stover, cotton seed hairs, grasses, hardwood stems, leaves, newspaper, nut shells, paper, primary wastewater solids, softwood stems, solid cattle manure, sorted refuse, swine waste, switchgrass, waste papers from chemical pulps, wheat straw, wood, and woody residues.

Prior to hydrolysis, the biomass feedstock may be pretreated or non-pretreated. Pretreatment of biomass feedstock removes a large proportion of the lignin and other materials and enhances the porosity of the biomass prior to hydrolysis. The biomass feedstock may be pretreated by any method. Exemplary methods to pretreat or dissolve biomass can include chipping, grinding, milling, steam pretreatment, ammonia fiber expansion (AFEX, also referred to as ammonia fiber explosion), ammonia recycle percolation (ARP), CO_2 explosion, steam explosion, ozonolysis, wet oxidation, acid hydrolysis, dilute-acid hydrolysis, alkaline hydrolysis, organosolv, ionic liquids, gamma-valerolactone, and pulsed electrical field treatment, among others. See, e.g., Kumar et al. 2009.

The pretreated or non-pretreated biomass may be hydrolyzed by any suitable method. Hydrolysis converts biomass polymers to fermentable sugars, such as glucose and xylose, and other monomeric or oligomeric components. Exemplary hydrolysis methods include enzymatic hydrolysis (e.g., with cellulases or other enzymes) and acid hydrolysis (e.g., with sulfurous, sulfuric, hydrochloric, hydrofluoric, phosphoric, nitric, and/or formic acids), among other methods.

The biomass hydrolysate included in the medium may comprise residual organic solutions (often referred to as conversion residue) from distillation of fermentation products or other downstream products of biomass processing. Exemplary instances include the use of conversion residue from microbial biomass ethanol fermentations or others.

The recombinant microorganisms may be cultured for a time of at least about 20 hours, at least about 40 hours, at least about 60 hours, at least about 80 hours, at least about 100 hours, at least about 120 hours, at least about 140 hours, and/or up to about 120 hours, up to about 140 hours, up to about 160 hours or more.

The nutrients included in the medium and consumed by the recombinant microorganism may include any of a number of carbon sources such as organic acids, sugars, or others. Exemplary nutrients include sugars (such as glucose, xylose), organic acids (such as succinate, lactate, and acetate) amino acids or other organic materials present that are used as nutrients for the lipid-producing microorganism.

The culturing may be conducted until recombinant microorganism produces lipid in an amount of at least about 0.5 g/L, at least about 0.75 g/L, at least about 1 g/L, or at least about 1.5 g/L and/or up to about 1.7 g/L, up to about 2 g/L, up to about 2.5 g/L or more. Such amounts may reflect the total lipid produced in culture (both intracellular and secreted). The culturing may be conducted until recombinant microorganism secretes lipid in an amount of at least about 0.4 g/L, at least about 0.6 g/L, at least about 0.8 g/L, at least about 1 g/L, at least about 1.2 g/L, or at least about 1.4 g/L, and/or up to about 1.6 g/L or more.

The culturing may be conducted until recombinant microorganism produces lipid in an amount of at least about 15% (w/w) dry cell weight, at least about 20% (w/w) dry cell weight, at least about 25% (w/w) dry cell weight, at least about 30% (w/w) dry cell weight, and/or up to about 30% (w/w) dry cell weight, up to about 35% (w/w) dry cell weight, or more. Such amounts may reflect the total lipid produced in culture (both intracellular and secreted).

The culturing may be conducted under aerobic or anaerobic conditions.

The methods may further comprise harvesting a bioproduct secreted from the microorganism into the media. The harvesting may comprise centrifuging the microorganism and medium to obtain a supernatant and separating the supernatant from the microorganism.

The elements and method steps described herein can be used in any combination whether explicitly described or not.

All combinations of method steps as used herein can be performed in any order, unless otherwise specified or clearly implied to the contrary by the context in which the referenced combination is made.

As used herein, the singular forms "a," "an," and "the" include plural referents unless the content clearly dictates otherwise.

Numerical ranges as used herein are intended to include every number and subset of numbers contained within that range, whether specifically disclosed or not. Further, these numerical ranges should be construed as providing support for a claim directed to any number or subset of numbers in that range. For example, a disclosure of from 1 to 10 should be construed as supporting a range of from 2 to 8, from 3 to 7, from 5 to 6, from 1 to 9, from 3.6 to 4.6, from 3.5 to 9.9, and so forth.

All patents, patent publications, and peer-reviewed publications (i.e., "references") cited herein are expressly incorporated by reference to the same extent as if each individual reference were specifically and individually indicated as being incorporated by reference. In case of conflict between the present disclosure and the incorporated references, the present disclosure controls.

It is understood that the invention is not confined to the particular construction and arrangement of parts herein illustrated and described, but embraces such modified forms thereof as come within the scope of the claims.

EXAMPLES

Background

Lipids from microbes offer a promising source of renewable alternatives to petroleum-derived compounds. In particular, oleaginous microbes are of interest because they accumulate a large fraction of their biomass as lipids. We investigated whether it is possible to exploit the native metabolic and regulatory pathways of non-oleaginous bacteria, as an example of a prokaryotic microbe, to increase lipid production to oleaginous levels.

We evaluated the possibility of increasing lipid production by rewiring the native metabolic and regulatory pathways of *Rhodobacter sphaeroides*, a non-oleaginous facultative purple non-sulfur bacterium. Unlike many well-studied facultative bacteria, changes in O_2 tension cause significant morphological changes in the cell envelope of this Gram-negative bacterium (Chory et al. 1984, Tavano et al. 2006, Kiley et al. 1988). In response to low O_2 tension, *R. sphaeroides* increases its intracellular membrane surface area, developing specialized intracytoplasmic membrane (ICM) invaginations that protrude into the cytoplasm (Chory et al. 1984, Tavano et al. 2006, Kiley et al. 1988). This remodeling of the cell envelope under low O_2 conditions increases the cellular phospholipid content ~3-fold (Lemmer et al. 2015).

Since *R. sphaeroides* contains regulatory mechanisms to increase lipid production at low O_2, we hypothesized that it could be possible to generate mutants with increased lipid production at high O_2.

We screened a *Rhodobacter sphaeroides* Tn5-mutant library for insertions that increased fatty acid content and identified ten high-lipid mutants for further characterization. These high-lipid mutants exhibited increased sensitivity to drugs that target the bacterial cell envelope, exhibited changes in shape, and, in some cases, secreted lipids. Two high-lipid mutants accumulated ~60% of their total lipids extracellularly. We used one of the highest lipid secreting strains to grow high-density cultures in a fed-batch bioreactor. The strain produced 1.3 g/L fatty acids, corresponding to 33% of dry cell weight (DCW). This lipid content is comparable to that of oleaginous microbes.

Thus, by genetically altering cell surface or envelope functions with single genetic alterations, we have converted *R. sphaeroides* into an oleaginous bacterium. Unlike in native oleaginous microbes, however, the majority of the lipids produced by some of the high-lipid mutants are advantageously excreted. Based on the properties of these high-lipid mutants, we conclude that genetically altering the cell envelope can be used as a previously unreported approach to increase microbial lipid production and secretion, and we propose that this approach can be used to increase production of lipids and additional bioproducts in other microbes.

Materials and Methods

Bacterial Strains and Growth Conditions

Bacterial strains used in the present examples are described in Table 1. *R. sphaeroides* strains were grown in Sistrom's minimal medium (SIS) (Sistrom 1960), with 4 g/L succinate as a carbon source, unless otherwise noted when 4 g/L glucose, xylose, lactate, or acetate was used as the carbon source. For batch culture growth in the presence of O_2, 10-20 ml cultures were grown in 125 ml flasks with shaking at 200 rpm, at 30° C. in the dark. For low O_2 growth, cells were grown by anaerobic photosynthesis; Screw-cap tubes of liquid culture were incubated at room temperature in front of an incandescent light box with a light intensity of 10 W/m^2 measured through a red glass filter. Cultures were grown to a density of 0.5-1.5 OD_{600} for analysis. *Escherichia coli* strains were grown at 37° C. in LB broth-Miller (Atlas et al. 1993). When necessary, media were supplemented with 50 μg/ml kanamycin.

TABLE 1

Strains and plasmids.

Strain	Relevant properties	Source or Reference
E. coli		
DH5α	Host for cloning and plasmid amplification	Bethesda Research Laboratories
DH5α/λpir	Host for cloning Tn5 insertion sites; Φ80dlacZΔM15 Δ(lacZYA-argF) U169 recAl hsdR17 deoR thi-1 supE44 gyrA96 relA1/λpir	Miller et al. 1988
S17-1	Donor for conjugation; C600::RP-4 2-(Tc::Mu) (Kn::Tn7) thi pro hsdR recA Tra$^+$	Simon et al. 1983
BW20767	Donor for conjugation; RP-2-Tc::Mu-1 kan::Tn7 integrant leu-63::I20 recA1 zbf-5 creB510 hsdR17 endAl thi uidA (ΔMluI)::pir+	Metcalf et al. 1996

TABLE 1-continued

Strains and plasmids.

Strain	Relevant properties	Source or Reference
R. sphaeroides		
2.4.1	Wild-type strain	van Niel 1944
Δ0382 (parent strain)	ΔR5P0382 in 2.4.1	Yilmaz et al. 2010
HLM01	Δ0382 with Tn5 insertion at Chr1: 1,471,645; Km^{R}	Present examples
HLM02	Δ0382 with Tn5 insertion at Chr1: 1,469,665; Km^{R}	Present examples
HLM03	Δ0382 with Tn5 insertion at Chr2: 274,987; Km^{R}	Present examples
HLM04	Δ0382 with Tn5 insertion at Chr1: 2,814,885; Km^{R}	Present examples
HLM05	A0382 with Tn5 insertion at Chrl: 2,970,757; Km^{R}	Present examples
HLM06	A0382 with Tn5 insertion at Chr2: 938,456; Km^{R}	Present examples
HLM07	A0382 with Tn5 insertion at Chr1: 2,086,261; Km^{R}	Present examples
HLM08	A0382 with Tn5 insertion at Chr1: 1,189,239; Km^{R}	Present examples
HLM08b	Same as HLM08, isolated independently from screen	Present examples
HLM09	Δ0382 with Tn5 insertion at Chr1: 1,395,725; Km^{R}	Present examples
HLM10	Δ0382 with Tn5 insertion at Chr1: 916,649; Km^{R}	Present examples
ΔNrtXYΔ0382	ΔRSP2839, ΔRSP2840, ΔRSP0382 in 2.4.1	Present examples
ΔChrRANrtXY Δ0382	ΔchrR-1::dfr, ΔRSP2839, ΔRSP2840, ΔRSP0382 in 2.4.1.	Present examples
Δ1200Δ0382	ΔRSP1200, ΔRSP0382 in 2.4.1	Present examples
KL116	HLM02 carrying plasmid pKCL22 to express Myc-tagged NtrX	Present examples
Plasmids		
pRL27	Tn5-RL27 delivery vector (Km^{R}-oriR6 K)	Larsen et al. 2002
pK18mobsacb	Broad host range mobilizable vector; Km^{R} oriV oriT mob sacB	Schafer et al. 1994
pKCL20	5,939-bp *R. sphaeroides* genomic region containing RSP2839 and RSP2840 cloned into the XbaI and HindIII sites of pK18mobsacB; Km^{R}	Present examples
pKCL21	pKCL20 with RSP2839 and RSP2840 deleted; Km^{R}	Present examples
pJDN27	pSUP202-derived suicide plasmid that creates an insertion of Tp^{R} gene into a deletion of chrR gene	Newman et al. 1999
pIND5-myc	Expression vector with IPTG-inducible promoter, includes 3X myc tag; Km^{R}	Imam et al. 2014
pKCL22	N-terminally 3X myc tagged ntrX (RSP 2840) cloned into BamHI and HindIII sites of pIND5-myc	Present examples

Transposon Mutagenesis and Nile Red Screening

The transposon delivery plasmid pRL27 (Larsen et al. 2002) was conjugated into *R. sphaeroides* Δ0382 using *E. coli* donor strain BW20767. Individual exconjugant colonies were inoculated into 200 μl SIS plus kanamycin in 96-well plates, grown in a humidified incubator with shaking at 30° C. to saturation (3 days), and then subcultured into fresh SIS containing 5 mg/ml Nile Red in Nunc™ 96-well black optical-bottom plates (Thermo Scientific). After ~14 hours of incubation, fluorescence (excitation 530 nm/emission 580 nm) and absorbance (650 nm and 850 nm) were measured in an Infinite® M1000 plate reader (Tecan). For candidate strains with fluorescence/OD_{650} that was 60% or more higher than the plate average, Nile Red staining was repeated with replicates before cellular fatty acid analysis. Transposon insertion sites were identified by cloning transposon-containing fragments, from BamHI-digested genomic DNA, as pir-dependent plasmids as previously described (Larsen et al. 2002). Sequencing was performed on the Tn5-containing plasmids with primers tpnRL13-2 and tpnRL17-1 (Table 2).

TABLE 2

Oligonucleotides.

ID Number	Sequence	Purpose
tpnRL13-2	CAGCAACACCTTCTTCACGA (SEQ ID NO: 149)	Sequence out from Tn5 insertion site
tpnRL17-1	AACAAGCCAGGGATGTAACG (SEQ ID NO: 150)	Sequence out from Tn5 insertion site
KCL58	GCATTCTAGACGAGGCCTACG ATTATCTGC (SEQ ID NO: 151)	Amplify R5P2839 and R5P2840 from *R. sphaeroides* DNA (R)
KCL59	CGATAAGCTTGTCGGGTCGTT TACCAGAAC (SEQ ID NO: 152)	Amplify R5P2839 and R5P2840 from *R. sphaeroides* DNA (R)
KCL60	CGGACCGTTCTGCGAAGCA (SEQ ID NO: 153)	Delete R5P2839 and R5P2840 from pKCL20 to make pKCL21 (F)
KCL63	TTCAGGCGCCGACCGGGACT (SEQ ID NO: 154)	Delete RSP2839 and RSP2840 from pKCL20 to make pKCL21 (R)
KCL72	TATCTCTTCGATTTCGAGCAG CCC (SEQ ID NO: 155)	Sequencing primer (F)
KCL84	ATGTTGACCTCGTCGGAATG (SEQ ID NO: 156)	Sequencing primer (R)
KCL85	GCAAGAAGATCACCGACCTC (SEQ ID NO: 157)	Sequencing primer (F)
KCL86	TCCTTGAGCCAGATGTCGAGG AT (SEQ ID NO: 158)	Sequencing primer (R)
KCL87	AGGCCTTGACCAACCTGATGA AGA (SEQ ID NO: 159)	Sequencing primer (F)
KCL88	TTCCAGCTGATGATAGAGCAC CAC (SEQ ID NO: 160)	Sequencing primer (R)
KCL89	TCACCTTCGGCGCTATTTCGAT CT (SEQ ID NO: 161)	Sequencing primer (F)
KCL116	GCCTTTGTCGGGATGGAAC (SEQ ID NO: 162)	Sequencing primer (F)
ChrR-UP1	GCGCCAGCATATGAGTTGAGT GAG (SEQ ID NO: 163)	Sequencing primer (F)
ChrR-DS1	CGTGAATGACAGGGGTCGCC (SEQ ID NO: 164)	Sequencing primer (F)

Chemical Sensitivity Analysis

Selected compounds (Tables 4A and 4B) were tested for their effects on growth of the parent strain to determine the highest doses that cause <30% growth reduction. Parent and high-lipid mutant strains were grown in the presence of the chemicals, or DMSO as a control, in 96-well plates at 30° C. with shaking for 48 hours. Final ODs were read at 595 nm on an Infinite® F500 microplate reader (Tecan). For each strain, final ODs for each drug treatment were first divided by the OD of the DMSO control for that strain to determine relative cell growth, and then the growth value for each treated culture was normalized by the parent strain growth under the same condition. Two-way clustering was performed with Cluster 3.0 and visualized with Java TreeView software (Saldanha 2004).

Fed-Batch Bioreactor Cultures

High-density fed-batch cultures were grown in an Applikon biofermenter (3 L Autoclavable Microbial BioBundle, Applikon Biotechnology). An adapted SIS medium (ASIS) was used as a feeding medium. ASIS used 20-fold higher concentrations of the carbon source, 25-fold higher ammonium sulfate, 2-fold higher dipotassium phosphate, and 5-fold higher of all other SIS components. For inoculation of each experiment, 1 L SIS was mixed with 50-ml of succinate grown culture. During operation, pH, dissolved oxygen, and temperature were monitored and controlled by external programmable logic controllers (ez-Control, Applikon Biotechnology). The pH was maintained between 6.95 and 7.05 with additions of 1 M H_2SO_4 or 10 M KOH; compressed air was used to provide aeration; temperature was maintained at 30° C. and ASIS medium was used to replenish consumed nutrients. Dissolved oxygen was maintained below 5% of saturated air by fixed aeration rate and feeding of ASIS medium.

Analytical Procedures

Analysis was performed on whole culture, or when noted, the culture was separated into cell and media fractions by centrifugation at 10,000×g for 15 min at 4° C. For analysis of samples from the fed-batch reactor, the samples were diluted with deionized water before lipid extraction. Lipid extraction with chloroform-methanol, esterification, gas chromatography-mass spectrometry (GC-MS) analysis and quantification were performed as previously described (Lennon et al. 2014) using 2.5 ml samples. For lipid phosphorus measurements, dried lipid extracts from 2.5 ml samples were digested with perchloric acid and assayed for phosphorus content (Rouser et al. 1970). Organic acids and sugars were analyzed by high performance liquid chromatography (HPLC) as described previously (Austin et al. 2015, Schwalbach et al. 2012). Samples were prepared by filtering aliquots of the culture with 0.22 μm filter before injection into the HPLC. Dry cell weight (DCW) was calculated by measuring chemical oxygen demand (COD) per liter and using the conversion factor of 1.47 gCOD/gDCW, which was determined from the composition of *R. sphaeroides* 2.4.1 biomass (Imam et al. 2011), adjusted for the lack of polyhydroxybutyrate in the parent and high-lipid mutant strains, $C_5H_{9.49}O_{2.23}N_{0.76}S_{0.01}P_{0.24}$. COD was analyzed using High Range COD Test Kits (HACH) according to the manufacturer's protocols. Media fractions were stained with 5 μg/ml Nile Red and fluorescence measured as described above. Lipopolysaccharide was measured using Pierce® LAL Chromogenic Endotoxin Quantitation Kit (Thermo Scientific) according to the manufacturer's protocol. To estimate lipopolysaccharide-associated fatty acid levels, the following conversion factors were used: 1 EU lipopolysaccharide=100 pg, 1 mol lipopolysaccharide=10,000 g, and *R. sphaeroides* lipopolysaccharide contains 5 acyl chains per molecule (Kaltashov et al. 1997). P-values for statistical significance were calculated by unpaired t test using Graph Pad QuickCalcs. For Coenzyme Q10 measurements, 500 μL of supernatant was mixed with either 500 μL ethanol or 500 μL 2 μM Coenzyme Q10 (Sigma Aldrich) and analyzed by LC-MS. The resulting LC-MS data were processed using TraceFinder 4.0 (Thermo Fisher Scientific).

Microscopy

For transmission electron microscopy whole mounts, 5 μL of cell suspension was applied to a transmission electron microscopy grid, post-stained with a negative stain (NanoW, Nanoprobes), blotted after 30 s, and let air dry. Transmission electron microscopy samples were examined using a Tecnai T-12 transmission electron microscope (FEI) operating at 120 kV with a LaB6 filament. Images were collected digitally with a 2x2K Ultrascan 1000 CCD (Gatan).

For structured illumination microscopy, cell culture was fixed by adding to an equal volume 4% paraformaldehyde, incubating for 45 min., and then washing two times with PBS. For staining, 2.5 μl cell suspension, 42.5 μl PBS buffer, and 5 μl Nile Red stock solution (1 mg/ml in ethanol) were mixed, incubated for 10 min, centrifuged, and resuspended in PBS. Samples were dropped onto polylysine coated glass coverslip. Super resolution fluorescence images were collected with a Zeiss Elyra 2 structured illumination microscope. The 63X oil immersion objective, 488 nm wavelength laser fluorescence excitation source, and emission 495-550 nm band pass filter were used. 75 or more cells per sample were measured by custom MATLAB scripts.

Strain Construction

Deletion of the ntrX and ntrY genes (RSP2839 and RSP2840) was carried out to create strain ΔNtrXYΔ0382 using the nonreplicable integration vector pK18mobsacB (Schafer et al. 1994). Both ORFs plus ~1 kb of flanking DNA sequences on either side were amplified from *R. sphaeroides* genomic DNA with primers containing XbaI and HindIII restriction sites. This PCR product was inserted into pK18mobsacB to create plasmid pKCL20. The entire coding regions of RSP2839 and RSP2840 were deleted from the plasmid by performing PCR with primers facing outward from the upstream end of RSP2839 and the downstream end of RSP2840 and ligation of the resulting fragment with T4 DNA ligase (Promega) to create pKCL21. *E. coli* S17-1 was used for conjugation of pKCL21 into *R. sphaeroides* Δ0382 (Yilmaz et al. 2010). Single crossovers were selected by kanamycin resistance, and double crossovers by loss of sucrose sensitivity. Strain ΔChrRΔNtrXYΔ0382 was created by deleting chrR using plasmid pJDN27, as described previously (Newman et al. 1999). Oligonucleotides used in these procedures are listed in Table 2. Deletion of RSP1200 to create strain 4120040382 was performed as described for strain ΔNtrXYΔ0382.

RNA Extraction, qRT-PCR, and Microarray Analyses

RNA extraction and microarray analysis were conducted as previously described (Dangel et al. 2009, Tavano et al. 2005). Briefly, RNA was isolated from exponential-phase *R. sphaeroides* cultures of Δ0382 and ΔNtrXYΔ0382. RNA isolation, cDNA synthesis, labeling, and hybridization to *R. sphaeroides* GeneChip microarrays (Affymetrix) were performed as previously described (Tavano et al. 2005). Microarray datasets were normalized by robust multichip average (RMA) to the $\log_2$ scale with background adjustment and quantile normalization (Bolstad et al. 2003). Statistical analysis of normalized data to identify differentially expressed genes was done using the Limma package (Smyth 2004). Correction for multiple testing was done using Benjamini-Hochberg correction (Benjamini et al. 1995). All analyses were conducted in the R statistical programming environment (http://www.R-project.org).

Chromatin Immunoprecipitation Analysis

Chromatin immunoprecipitation was conducted as previously described (Imam et al. 2014). Briefly, *R. sphaeroides* cells (KL116) were grown aerobically in 500-ml cultures with bubbling, as described above. Cells were treated with 3 μM IPTG at inoculation and harvested at an OD_{600} of ~0.35. Chromatin immunoprecipitation was conducted (Dufour et al. 2008) using polyclonal antibodies against the Myc epitope tag (ab9132; Abcam PLC). Immunoprecipitated DNA samples were PCR amplified, gel purified (size selection of ~200 bp), and sequenced at the UW Biotechnology Center sequencing facility, using the HiSeq 2500 sequencing system (I lumina, Inc.). The 50-bp sequence tags were mapped to the *R. sphaeroides* 2.4.1 genome (ftp://ftp.ncbi.nih.gov/genomes/Bacteria/*Rhodobacter_sphaeroides*_2_4_1_uid57653/) using SOAP version 2.21 (Li et al. 2009), allowing a maximum of 2 mismatches and no gaps.

Peaks were identified using MOSAiCS (Kuan et al. 2011) at a false discovery rate of 0.05. The MOSAiCS analysis was conducted as a two-sample analysis involving a pairwise comparison between with ChIP-seq data obtained from cells with Myc-tagged NtrX and ChIP-seq data obtained from WT cells (with no Myc-tagged proteins) immunoprecipitated using anti-Myc antibodies (used as the control). Motifs were identified from sequences under the peak regions using MEME (Bailey et al. 2009). Genomic locations with both a significant ChIP-seq peak and shared motifs were considered true binding sites.

Results

Identification of High-Lipid Mutants

R. sphaeroides has a native ability to increase its fatty acid content under low O_2 conditions (Lemmer et al. 2015). We sought to identify mutant strains that contain increased lipid levels at high O_2. We used a parent strain (Δ0382) that is unable to make the hydrophobic polymer polyhydroxybutyrate (Yilmaz et al. 2010) so we could use the fluorescence intensity of Nile Red-stained cells as a proxy of lipid content.

To identify potential high-lipid mutants, we screened a library of ~11,400 strains generated by Tn5-transposon mutagenesis. When fatty acid content of the top 30 Nile Red-staining mutants was quantified by GC-MS, we found ten strains (named HML01-10) that had a ≥1.5 increase in fatty acid content per cell when grown at high O_2 (FIG. **1**). Two mutants (HML01 and HLM02) had a ~6-fold increase in fatty acids compared to the parent strain grown at high O_2 (FIG. **1**); an increase twice that observed when the parent strain was grown at low O_2 (FIG. **1**).

Genes and Processes Disrupted in High-Lipid Mutants

The transposon insertion sites identified in these ten high-lipid mutants (Table 3) did not reveal disruption of genes typically targeted for increasing lipid accumulation, such as central carbon metabolism or fatty acid biosynthesis and degradation (Janssen et al. 2014, Lennen et al. 2012). Instead, the genes inactivated in the high-lipid mutants encoded a diverse group of proteins, including a transcription factor, a chaperone, proteases, and putative secreted and cell envelope proteins.

TABLE 3

Transposon-insertion sites in high-lipid mutants.

Strain	FA inc.	Insertion site	ORF(s) disrupted with annotation		Sig. pep.	TM helix
HLM01	6.7	Chr1: 1,471,645	RSP2839	NtrY sensor signal transduction histidine kinase	no	5
			RSP2840	NtrX response regulator	no	none
HLM02	6.1	Chr1: 1,469,665	RSP2840	NtrX response regulator	no	none
HLM03	2.7	Chr2: 274,987	RSP3218	Cob(II)yrinic acid a,c-diamide reductase/ 5,6-dimethylbenzimidazole synthase	no	none
HLM04	2.7	Chr1: 2,814,885	RSP1056	Signal transduction histidine kinase	no	2
HLM05	2.6	Chr1: 2,970,757	RSP1200	Uncharacterized conserved protein YkwD	yes	none
HLM06	1.8	Chr1 938,456	RSP1422	Chromosome partitioning protein, ParB family	no	none
HLM07	1.7	Chr1: 2,086,261	RSP0355	Periplasmic serine protease DegP	no	1
HLM08	1.7	Chr1: 1,189,239	RSP2545	Stationary phase survival protein SurE	no	none
			RSP2544	Protein-L-isoaspartate O-methyltransferase (pcm)	no	none
			RSP2543	Peptidoglycan DD-endopeptidase	yes	none
HLM09	1.5	Chr1: 1,395,725	RSP2745	Stealth protein	no	none
HLM10	1.5	Chr1: 916,649	RSP2293	ClpA, ATP-dependent Clp protease ATP-binding subunit	no	none

Strains are sorted from highest to lowest fold increase in total fatty acid (FA inc.) compared to the parent strain. The presence of a signal peptide (Sig. pep.) was predicted by SignalP 4.1 http://www.cbs.dtu.dk/services/SignalP/, and the number of predicted transmembrane helixes (TM helix) was determined by TMHMM Server v. 2.0 http://www.cbs.dtu.dk/services/TMHMM/.

We used chemical sensitivity analysis to characterize what cellular processes were affected in the high-lipid strains. To do this, we tested the impact on growth of a set of compounds that affect protein synthesis, folic acid biosynthesis, membrane integrity, peptidoglycan biosynthesis, and DNA integrity (Tables 4A and 4B). For some compounds, such as the protein synthesis inhibitor neomycin, we saw no growth difference of the high-lipid mutants compared to the parent strain (FIG. **2**, panel A). For other compounds, including the detergent sodium dodecyl sulfate (SDS), many or all of the high-lipid mutants showed increased sensitivity (FIG. **2**, panel B); while for others, such as the peptidoglycan-active antibiotic amoxicillin, we saw increased sensitivity in one or more high-lipid mutants compared to the parent strain (FIG. **2**, panel C). By analyzing the relative growth of all the high-lipid mutants treated with compounds having common cellular targets, we observed that these strains were most sensitive to compounds active on the cell or outer membranes (62% of the parent cell growth).

TABLE 4A

Compounds used in chemical sensitivity analysis and characteristics thereof.

Drug	Family	Group	General Target
Clotrimazole	azoles	imidizoles	cell envelope
Deoxycholate	detergents	anionic detergent	cell envelope
Monensin	ionophores	polyether	cell envelope
Polymyxin b	peptides	cationic detergent	cell envelope
SDS	detergents	detergents	cell envelope
Triton X-100	detergents	detergents	cell envelope
Valinomycin	ionophores	dodecadepsipeptide	cell envelope
Amoxicillin	beta-lactams	penicillins	cell envelope
Ampicillin	beta-lactams	penicillins	cell envelope
Aztreonam	beta-lactams	monobactams	cell envelope
Bacitracin	peptides	peptides	cell envelope
Ceftriaxone	beta-lactams	cephalosporine	cell envelope
Cephalexin hydrate	beta-lactams	cephalosporine	cell envelope
D-cycloserine	amino acid derivative	amino acid derivative	cell envelope
Meropenem	beta-lactam	carbapenem	cell envelope
Furazolidone	furans	furans	DNA
MMS	alkylating agents	alkylating agents	DNA
Ciprofloxacin	quinilones	quinilones	DNA
Levofloxacin	quinilones	quinilones	DNA
Nalidixic acid	quinilones	quinilones	DNA
Ofloxacin	quinilones	quinilones	DNA
Hydroxyurea	chemotherapeutics	deoxyribonuclotide	DNA
Nitrofurantoin	furans	furans	DNA
Acrylic acid	organics	organics	fatty acid metabolism
Methotrexate	chemotherapeutics	DHFR inhibitor	folic acid biosynthesis
Sulfamethoxazole	chemotherapeutics	sulfonamides	folic acid biosynthesis
Sulfanilamide	chemotherapeutics	sulfonamides	folic acid biosynthesis
Trimethoprim	pyrimidines	DHFR inhibitor	folic acid biosynthesis
Doxicycline	tetracycline antibiotics	tetracyclines	protein synthesis
Neomycin	aminoglycosides	aminoglycosides	protein synthesis
Spectinomycin	aminoglycosides	aminoglycosides	protein synthesis
Tetracycline	tetracycline antibiotics	tetracyclines	protein synthesis
Tigecycline	tetracycline antibiotics	tetracyclines	protein synthesis
Tobramycin	aminoglycosides	aminoglycosides	protein synthesis
Azithromycin	MLS	macrolides	protein synthesis
Chloramphenicol	Peptidyl transferase	amphenicols	protein synthesis
Clarithromycin	MLS	macrolides	protein synthesis
Erythromycin	MLS	macrolides	protein synthesis
Florfenicol	Peptidyl transferase	amphenicols	protein synthesis
Lincomycin	MLS	lincoamides	protein synthesis
Thiamphenicol	Peptidyl transferase	amphenicols	protein synthesis
Fuscidic acid	fusidanes	fusidanes	protein synthesis
Rifampicin	rifamycins	rifamycins	RNAP
Rifaximin	rifamycins	rifamycins	RNAP
NaCl	stress	osmotic stress	stress
Hydrogen peroxide	stress	oxidative stress	stress
Plumbagin	quinones	naphthoquinones	stress
EDTA	stress	stress	stress
Sulbactam	beta-lactams	beta-lactamase inhibitor	

TABLE 4B

Compounds used in chemical sensitivity analysis and characteristics thereof.

Drug	Process Target	Function Target	Gene Target	Conc.
Clotrimazole	cell membrane	membrane permeability/ sterol biosynthesis		4 μg/ml
Deoxycholate	cell membrane	membrane permeability		0.1 mg/ml
Monensin	cell membrane	cation transport		100 μg/ml
Polymyxin b	cell membrane	membrane permeability		0.4 μg/ml

TABLE 4B-continued

Compounds used in chemical sensitivity analysis and characteristics thereof.

Drug	Process Target	Function Target	Gene Target	Conc.
SDS	cell membrane	membrane permeability		25 μg/ml
Triton X-100	cell membrane	membrane permeability		0.1%
Valinomycin	cell membrane	cation transport		10 μg/ml
Amoxicillin	peptidoglycan	PG biosynthesis (transpeptidation)	multiple PBPs	5 μg/ml
Ampicillin	peptidoglycan	PG biosynthesis (transpeptidation)	multiple PBPs	2 μg/ml
Aztreonam	peptidoglycan	PG biosynthesis (transpeptidation)	PBP3 (FtsI)	20 μg/ml
Bacitracin	peptidoglycan	C55 PP pyrophosphatases	BacA, YbjG, PgpB and YeiU	40 μg/ml
Ceftriaxone	peptidoglycan	PG biosynthesis (transpeptidation)	multiple PBPs	2 μg/ml
Cephalexin hydrate	peptidoglycan	PG biosynthesis (transpeptidation)	multiple PBPs	250 μg/ml
D-cycloserine	peptidoglycan	PG biosynthesis (Ala racemase + ligase)	Alr, DadX, DdlA/B	2 μg/ml
Meropenem	peptidoglycan	PG biosynthesis (transpeptidation)	multiple PBPs	0.5 μg/ml
Furazolidone	DNA crosslinking	DNA crosslinking		5 μg/ml
MMS	DNA damage	methylation		0.002%
Ciprofloxacin	DNA supercoiling	DNA gyrase/topoisomerase	GyrA/TopA	0.02 μg/ml
Levofloxacin	DNA supercoiling	DNA gyrase/topoisomerase	GyrA/TopA	0.004 μg/ml
Nalidixic acid	DNA supercoiling	DNA gyrase/topoisomerase	GyrA/TopA	0.4 μg/ml
Ofloxacin	DNA supercoiling	DNA gyrase/topoisomerase	GyrA/TopA	0.02 μg/ml
Hydroxyurea	DNA synthesis	ribonucleotide reductase		5 mM
Nitrofurantoin	mulptiple			10 μg/ml
Acrylic acid	beta-oxidation			200 μg/ml
Methotrexate	folic acid biosynthesis	dihydrofolate reductase	FolA/FolM	2 μg/ml
Sulfamethoxazole	folic acid biosynthesis	dihydropteroate reductase	FolP	100 μg/ml
Sulfanilamide	folic acid biosynthesis	dihydropteroate reductase	FolP	100 μg/ml
Trimethoprim	folic acid biosynthesis	dihydrofolate reductase	FolA/FolM	2 μg/ml
Doxicycline	30S ribosome	tRNA binding		0.01 μg/ml
Neomycin	30S ribosome	translation initiation		10 μg/ml
Spectinomycin	30S ribosome	translation initiation		1 μg/ml
Tetracycline	30S ribosome	tRNA binding		0.02 μg/ml
Tigecycline	30S ribosome	tRNA binding		50 μg/ml
Tobramycin	30S ribosome + 50S ribosome	prevents 70S ribosome formation		0.4 μg/ml
Azithromycin	50S	ribosome transpeptidation		0.02 μg/ml
Chloramphenicol	50S ribosome	peptidyl transferase		0.5 μg/ml
Clarithromycin	50S ribosome	transpeptidation		2 μg/ml
Erythromycin	50S ribosome	transpeptidation		0.5 μg/ml
Florfenicol	50S ribosome	peptidyl transferase		0.5 μg/ml
Lincomycin	50S ribosome	transpeptidation		20 μg/ml
Thiamphenicol	50S ribosome	peptidyl transferase		0.1 μg/ml
Fuscidic acid	G factor	ribosome translocation	FusA	1 μg/ml
Rifampicin	RNAP	RNAP exit channel	RpoB	0.02 μg/ml
Rifaximin	RNAP	RNAP exit channel	RpoB	0.01 μg/ml
NaCl	osmotic stress			50 mM
Hydrogen peroxide	oxidative stress			5 mM
Plumbagin	oxidative stress			0.4 μg/ml
EDTA				0.4 uM
Sulbactam		beta-lactamase		5 μg/ml

Clustering the mutants and the compounds based on relative growth (FIG. **3**) showed that strains HLM01, HLM02 and HLM05 formed a cluster separate from the other strains (labeled A in FIG. **3**). Two of these strains, HLM01 and HLM02, have mutations in genes that are predicted to act in the same pathway (the NtrXY two-component system; Table 3), so it is not surprising that they behave similarly in this analysis. The third strain in this cluster (HLM05) has a mutation in a pathway of no known relation to NtrXY (a conserved uncharacterized membrane protein). These three high-lipid mutants are sensitive to a cluster of compounds (marked * in FIG. **3**) containing membrane-targeting detergents and ionophores, as well as the RNA polymerase inhibitors rifampicin and rifaximin, and the protein synthesis inhibitors erythromycin and clarithromycin. The later 4 compounds do not target the membrane, but it is known that decreased membrane integrity can sensitize cells to these hydrophobic drugs (Vaara 1993). Thus, these three high-lipid mutants share increased sensitivity to compounds that are associated with decreased membrane integrity.

A second cluster of high-lipid mutants (HLM04 and HLM07; labeled B in FIG. **3**) share increased sensitivity to a group of compounds that inhibit peptidoglycan biosynthesis (amoxicillin, aztreonam, bacitracin, and ceftriaxone; marked ** in FIG. **3**). This suggests that the mutations in these two high-lipid strains alter the integrity of the peptidoglycan cell wall.

The appearance of distinct sets of high-lipid mutants with sensitivities to different classes of bioactive compounds suggests that there may be multiple mechanisms causing increased lipid production. While the other high-lipid mutants (HLM03, HLM06 and HLM8-10) showed increased sensitivity to other compounds (e.g., hydrogen peroxide for HLM03), this analysis did not predict specific processes that might be impaired in these strains. In sum, the chemical sensitivity analysis showed that many of the high-lipid mutants had increased sensitivity to compounds that act at the cell envelope, either on the membrane or the cell wall.

Morphological Changes in High-Lipid Mutants

Based on the above finding, we used transmission electron microscopy of whole mount cells to assess morphologic changes in the cell envelope of the high-lipid strains. This analysis revealed that those high-lipid mutants which are sensitive to membrane-active compounds (Cluster A; HLM01, HLM02, HLM05) produced a large amount of extracellular material (FIG. **4**, panels F-H) and irregular shaped particles adjacent to the cells (FIG. **4**, panels B-D), that were not seen in the parent strain (FIG. **4**, panels A and E). Samples of HLM05 had round extracellular structures in the range of 20-50 nm (FIG. **4**, panel H), while samples from HLM01 and HLM02 contained round and irregular structures, as well as stacked structures often observed when liposomes are in aqueous solution (FIG. **4**, panels F and G) (Zhang et al. 2011). The mutations in HLM01 and HLM02 are predicted to inactivate proteins in the same two-component (NtrXY) signal transduction pathway, so it is not surprising to find that they have similar morphological changes. One additional high lipid mutant (HLM08) produced extracellular material, some of which was organized in stacked structures (FIG. **5**, panels A and B). Two other high-lipid mutants (HLM03 and HLM09) did not have a significant amount of extracellular material, but instead had structures that appeared to bulge off of, but remain attached to, the cell surface (FIG. **5**, panels C and D). The membrane protrusions and secretions seen by transmission electron microscopy in HLM01-03, HLM05 and HLM08-09 are consistent with alterations in the cell envelope predicted for some of these strains by chemical sensitivity analysis.

Transmission electron microscopy of the two high-lipid mutants that are sensitive to cell-wall active compounds (Cluster B; HLM04 and HLM07) did not show accumulation of extracellular material, but instead suggested that they had a different shape than the parent strain (FIG. **6**, panels A-C). Measurement of cell dimensions of HLM04 and HLM07 by super-resolution structured illumination microscopy (FIG. **6**, panels D-F, and FIG. **7**) showed that they were shorter than the parent cells but that the cell width was similar (Table 5). Overall, structured illumination microscopy analysis showed that 8 out of the 10 high-lipid mutants had differences in cell length and/or width compared to the parent strain (Table 5), providing additional support for the hypothesis that changes in the cell envelope was a common feature among many of these strains.

TABLE 5

Measurements of cell length and width of Nile Red-stained cells by super resolution fluorescence microscopy.

Strain	Length (μm)	Width (μm)	N	difference
Parent	1.72 ± 0.38	0.72 ± 0.05	75	
HLM01	1.70 ± 0.41	0.76 ± 0.06*	259	wider
HLM02	1.68 ± 0.46	0.73 ± 0.05	205	
HLM03	2.32 ± 0.51*	0.71 ± 0.05	91	longer
HLM04	1.22 ± 0.22*	0.73 ± 0.05	148	shorter
HLM05	2.36 ± 0.49*	0.75 ± 0.06**	111	longer and wider
HLM06	1.79 ± 0.36	0.73 ± 0.06	88	
HLM07	1.41 ± 0.27*	0.73 ± 0.06	86	shorter
HLM08	1.73 ± 0.33	0.67 ± 0.06*	102	narrower
HLM09	1.83 ± 0.46	0.70 ± 0.05**	126	narrower
HLM10	1.60 ± 0.30***	0.74 ± 0.06	104	shorter
Parent low O_2	2.27 ± 0.72*	0.83 ± 0.08*	83	longer and wider

Measurements are expressed as mean ± standard deviation, with N = number of cells measured. Significant differences compared to the parent strain are indicated, $^{*}p < 0.0001$, $^{**}p < 0.002$, $^{***}p < 0.03$.

Lipid Secretion by High-Lipid Mutants

Since we observed materials on the surface or outside of the high-lipid mutants by transmission electron microscopy, we stained the media with Nile Red to test for the presence of hydrophobic compounds. We found that media from all but one of the high-lipid mutants had increased Nile Red staining compared to that of the parent strain (FIG. **8**, panel A). In particular, Cluster A strains (HLM01, HLM02, and HLM05) that had the highest amount of extracellular material by transmission electron microscopy had 13-40-fold increases in fluorescence compared to that of the parent strain (FIG. **8**, panel A).

We tested if the increased Nile Red staining of the high-lipid mutants was due to the presence of extracellular lipid by quantifying fatty acid levels in the cells and culture supernatant. For the parent strain a small level (0.2%) of the fatty acid in the total culture (cells plus supernatant) was present in the media (FIG. **8**, panels B and C), likely representing the background from incomplete separation of cells and media. In contrast, 9 of the 10 high-lipid mutants had a statistically significant increase in fatty acid in the media compared to parent strain. Consistent with the extracellular material observed by transmission electron microscopy, HLM01, HLM02 and HLM05 had the highest percent (≥35%) of the total fatty acid present in the media (FIG. **8**, panels B and C).

To further characterize the secreted material, we analyzed fatty acid and lipid phosphorus levels in the culture supernatants of HLM01, HLM02 and HLM05. For all three of these high-lipid mutants, the fatty acid to lipid phosphorus ratio of the supernatants was 1.5, close to the 2:1 ratio expected for phospholipid (FIG. **9**, panel A). We also quantified lipopolysaccharide in the supernatants and found that lipopolysaccharide-associated fatty acids accounted for a small amount of the secreted fatty acids, less than 1% for HLM01 and HLM02 (FIG. **9**, panel B). Therefore, we conclude that the secreted lipid is composed primarily of phospholipid.

Fatty Acid Productivity of a High-Lipid Secreting Strain

The extracellular accumulation of lipid by some high-lipid mutants could make them attractive for production of biofuels or bioproducts. We chose HLM02, for further characterization since it is one of two high-lipid mutants with the highest level of extracellular lipid.

When we compared the fatty acid productivity (grams fatty acid per liter) of HLM02 cultures to that of the parent strain, they produced similar amounts of intracellular lipid (FIG. **10**, panel A), when grown in batch culture with succinate as a carbon source. However, if one includes cellular and secreted lipids, fatty acid productivity was 2.7-fold higher in the HLM02 culture than the parent strain (FIG. **10**, panel A; $p<0.001$). This increase in culture fatty acid productivity for HLM02 is smaller than the increase observed when measuring fatty acid content per cell (FIG. **1**) because in batch cultures HLM02 does not achieve as high a cell density as the parent strain.

R. sphaeroides can metabolize a wide variety of carbon substrates (Imam et al. 2011), so we also tested fatty acid productivity in batch cultures containing a different organic acid (lactate, which is a common fermentation byproduct (Agler et al. 2011)), as well as sugars (glucose and xylose, which are abundant in cellulosic biomass hydrolysates (Lau et al. 2009)). Fatty acid productivity was increased in HLM02 compared to the parent strain when using each of these carbon sources (FIG. **10**, panel A), with ~50-55% of the total fatty acid found in the culture supernatant. For each of the carbon sources tested, the cellular fatty acids represented 5-6% of the dry cell weight (DCW) in the parent and HLM02 strain. However, when the secreted lipid was included, the total fatty acid content of HLM02 increased to 15-20% of the DCW (FIG. **10**, panel B).

Another common metric is product yield per amount of carbon substrate consumed. For the parent strain, the total fatty acid yield from each of the carbon sources tested was 1.0-1.4% (w/w) (FIG. **10**, panel C). For the HLM02 mutant, the fatty acid yield increased 2.9-3.7-fold ($p\leq0.01$ for all substrates) to 3.5-5.0% (w/w) (FIG. **10**, panel C). There was no significant difference in fatty acid yield of HLM02 between the different carbon sources tested. The maximum theoretical yield, if all of the carbon substrate were converted into fatty acids by HLM02, is ~35% for glucose, xylose, and succinate, and ~28% percent for lactate. Thus, the fatty acid yields measured for HLM02 in batch culture represent 11-14% of the maximum theoretical yield on these carbon sources.

In addition to the four carbon sources described above, acetate was also tested for the production of fatty acid. After 48 hours cultivation, 0.03 g/L fatty acid was produced by the HLM02 mutant and 55% of the produced fatty acid was in the supernatant. Using acetate as carbon source yielded a slower growth rate and thus a lower amount of fatty acid at the time of harvesting, but the cells excreted a comparable proportion of the fatty acids into media.

Extracellular Production of Novel Fatty Acids

The utility of a lipid-secreting mutant would be increased if one could produce increased levels of novel fatty acids extracellularly. *R. sphaeroides* has recently been reported to make a furan-containing fatty acid, 10,13-epoxy-11-methyl-octadecadienoic acid (19Fu-FA) that is potentially valuable due to its antioxidant activity (Lemke et al. 2014). Elevated levels of 19Fu-FA are found in a mutant that lacks the ChrR anti-sigma factor (Lemke et al. 2014). In order to test if *R. sphaeroides* could secrete 19Fu-FA, we constructed a strain that lacked the genes disrupted in HLM01 and HLM02 (ΔNtrXYΔ0382) and chrR (ΔChrRΔNtrXYΔ0382). We found that the ΔChrRΔNtrXYΔ0382 strain made 19Fu-FA as ~3-4% of the total fatty acids in both the cellular and supernatant fractions (Table 6). From this, we conclude that the high-lipid mutants can be used to secrete novel fatty acids as well as those normally present in wild-type cells.

TABLE 6

Relative fatty acid content of *R. sphaeroides* ΔChrRΔNtrXYΔ0382.

	Strain					
	C16:1	C16:0	C18:1	C18:0	19M-UFA	19Fu-FA
Cells	3.2 (0.8)	11.3 (0.8)	69.2 (2.2)	12.5 (0.7)	0.8 (0.6)	2.9 (0.5)
Supernatant	0.9 (0.8)	13.2 (2.1)	64.5 (6.6)	15.9 (3.0)	1.3 (0.3)	4.2 (1.8)

Percentage composition of the individual fatty acid species. 11-methyl-octadecanoate (19M-UFA), 10,13-epoxy-11-methyl-octadecadienoic acid (19Fu-FA). Standard deviation in parentheses. N = 7.

Extracellular Production of Non-Lipid Bioproducts

The ability of the lipid-secreting high-lipid mutants to secrete bioproducts other than lipids was assessed. Supernatant levels of Coenzyme Q10 (CoQ10, also known as ubiquinone, ubidecarenone, coenzyme Q), a compound commonly found in lipid membranes, were tested in the parent strain (Δ0382), the strain lacking the genes disrupted in HLM01 and HLM02 (ΔNtrXYΔ0382), and a strain lacking the genes disrupted in HLM05 (Δ1200Δ0382). Increased levels of CoQ10 were found in the supernatants of both the ΔNtrXYΔ0382 and Δ1200Δ0382 strains compared to the parent strain (FIG. **11** and Table 7). This shows that extracellular production of membrane-bound or -associated bioproducts, such as small molecules, proteins, etc., is increased in the high-lipid mutants.

TABLE 7

Extracellular production of Coenzyme Q10 in parent and high-lipid mutants.

Strain	Replicate	Spike Concentration (μM)	CoQ10 Peak Area	Concentration (μM)	Average	STD Dev
Δ1200	1	0.00	1.57E+06	0.020	0.024	0.004
		1.00	7.97E+07			
	2	0.00	2.13E+06	0.028		
		1.00	7.85E+07			
	3	0.00	1.74E+06	0.023		
		1.00	7.59E+07			
Δ0382	1	0.00	1.94E+05	0.003	0.002	0.000
		1.00	7.51E+07			
	2	0.00	1.93E+05	0.003		
		1.00	7.22E+07			
	3	0.00	1.32E+05	0.002		
		1.00	6.41E+07			
Δntrxy	1	0.00	6.07E+06	0.082	0.085	0.006
		1.00	8.03E+07			
	2	0.00	5.32E+06	0.080		
		1.00	7.15E+07			
	3	0.00	6.75E+06	0.092		
		1.00	8.02E+07			

Δ0382 = parent strain (Δ0382).
Δntrxy = strain lacking the genes disrupted in HLM01 and HLM02 (ΔNtrXYΔ0382).
Δ1200a = strain lacking the genes disrupted in HLM05 (Δ1200Δ0382).

Reactor Engineering to Increase Fatty Acid Yield of a High-Lipid Mutant

Given the properties of high-lipid mutants like HLM02, we reasoned that high-density cultures could be used as a source of extracellular lipid. We opted to use a fed-batch bioreactor (Shiloach et al. 2005, Yen et al. 2010, Zeiger et al. 2010) to obtain high-density cultures since they can bypass the negative impacts of high (toxicity) or low (limitation) nutrient availability in the feedstocks. We reasoned that, if product (fatty acid) formation is tied to cell number, then increasing culture density should increase the reactor productivity.

In our fed-batch reactors, a low level of O_2 was provided by bubbling with saturated air. We used real-time measurement of reactor dissolved oxygen as an indicator of substrate limitation (Seo et al. 1992), since decreased cellular respiration should cause an increase in dissolved oxygen. This is illustrated for a *R. sphaeroides* xylose-fed culture in FIG. **12**: when the dissolved oxygen increases, nutrients are provided to the reactor causing the dissolved oxygen to decrease again, presumably when cellular respiration increases. This feeding cycle is repeated iteratively throughout the reactor run in order to obtain high density cultures.

Using this method, we analyzed fatty acid production when cells were grown using xylose as a carbon source. Control experiments indicated that under the feeding regimen described above, cell density increases for ~120 hours and then plateaus. Under these conditions, the parent strain reached a maximal density of 7.9 gDCW/L (FIG. **13**, panel A). Fatty acid content of the parent strain was stable in this fed-batch reactor at ~7% of DCW (FIG. **13**, panel B), compared to ~5% observed in a xylose fed-batch culture (FIG. **10**, panel B). This small increase in fatty acid content of the parent strain likely reflects the low oxygen tension present in the fed-batch reactor. Use of the fed-batch reactor increased total fatty acid productivity 10-fold, from 0.05 g/L in batch culture (FIG. **10**, panel A) to 0.50 g/L (FIG. **13**, panel C). In addition, the fatty acid yield from xylose increased from 1.4 (w/w) % in batch (FIG. **10**. panel C) to a maximum of 3.6% in the high-density cultures (FIG. **13**, panel D).

Under identical reactor conditions, the HLM02 mutant grew at a slower rate and to lower final cell density than the parent (4.7 gDCW/L) (FIG. **13**, panel A). Despite this, HLM02 produced more than twice the amount of total fatty acids as the parent strain (~1.3 g/L at 120 hours; FIG. **13**, panel C). This is 9 times the amount of fatty acid produced by HLM02 in batch culture, demonstrating that growth in a fed-batch bioreactor increased fatty acid productivity. The fatty acid content of the HLM02 mutant increased over time, up to 33% of DCW at 100 hours (FIG. **13**, panel B), a ~5-fold increase compared to the parent strain under the same conditions, and an 85% increase compared to the fatty acid content of HLM02 grown on xylose in a batch culture. In addition, a higher percentage of the fatty acids produced by HLM02 were secreted in the high-density culture compared to the batch culture (up to 69% of the total fatty acids) (FIG. **13**, panel C). When these cells were examined by transmission electron microscopy, we saw extracellular droplets tightly packed around and away from the cells (FIG. **14**), much more so than the same strain grown in batch (FIG. **4**, panels C and F).

Finally, fatty acid yield per xylose consumed (% w/w) in the fed-batch bioreactor was more than doubled in HLM02 compared to the parent strain at all time points tested (FIG. **13**, panel D). The maximum fatty acid yield observed for HLM02 in the fed batch reactor (8.4%) represents ~24% of the maximum theoretical yield from cells using xylose as a carbon source (35%, see above).

NtrXY Target Genes

The target genes of the NtrXY two-component signaling system were determined by chromatin immunoprecipitation (ChIP), and changes in mRNA expression of the targets were compared between the parental strain and a ΔNtrXY mutant. The results are shown in Table 8.

TABLE 8

NtrX targets as determined by ChIP and changes of expression of the targets.

ID*	Annotation	CHR	Peak Start	Peak Stop	ChIP Fold Enrichment (Rep1/Rep2)***	Gene Expression Fold Change**
RSP1860	Cell wall hydrolase CwlJ, involved in spore germination	chr1	458400	458999	9.5/7.4	−1.5
RSP2839#	Nitrogen regulation protein NtrY Signal transduction histidine kinase	chr1	1472000	1472399	4.5/3.8	1.64
RSP0334# | RSP0335	hypothetical protein | diguanylate cyclase/ phosphodiesterase	chr1	2064600	2065100	2.5/2.5	1.8 | 1.24
RSP3540#	Hemolysin-type calcium-binding region, RTX	chr2	630300	630600	2.5/NA	1.8
RSP0339	Methyltransferase domain-containing protein	chr1	2069800	2070200	2.4/NA	1
RSP2974	Murein DD-endopeptidase MepM and murein hydrolase activator NlpD, contain LysM domain	chr1	1661000	1661399	2.4/2.7	1
RSP0892	ABC transporter, ATP-binding cassette	chr1	2642200	2642600	2.2/NA	1
RSP2095#	hypothetical protein	chr1	694110	695200	2/2.2	1.4
RSP2111#	D-alanine--D-alanine ligase	chr1	711380	712030	2/3.5	2.2

TABLE 8-continued

NtrX targets as determined by ChIP and changes of expression of the targets.

ID*	Annotation	CHR	Peak Start	Peak Stop	ChIP Fold Enrichment (Rep1/Rep2)***	Gene Expression Fold Change**
RSP2916 | RSP2915	hypothetical protein | phosphate regulon sensor histidine kinase PhoR	chr1	1594600	1595000	1.5/NA	1.7 | 1

*The | indicates that the peak was located in an intergenomic region shared by 2 genes (A | B).

**Gene expression is in parental strain relative to the NtrXY mutant, so up genes are upregulated by NtrX.

***NA indicates genes where a ChIP peak was not observed in replicate 2.

#The gene listed is followed by additional genes in the same operon, and thus predicted also to be regulated by NtrX in the same direction (increased expression) as the listed gene. The genes in the same operon as RSP2839 include RSP2840. The genes in the same operon as RSP0334 include RSP0333, RSP0332, RSP0331, RSP0330. The genes in the same operon as RSP3540 include RSP3539, RSP3538. The genes in the same operon as RSP2095 include RSP6038, RSP2097, RSP2098, RSP2099, RSP2100, RSP2101. The genes in the same operon as RSP 2111 include RSP2112 and RSP2113.

Discussion

Using Native Pathways to Engineer Lipid Accumulation

Microbial lipids are energy dense molecules that have many advantages for use as petroleum replacements (d'Espaux et al. 2015). In order to achieve high enough yields to be cost competitive alternatives, a combination of metabolic engineering and process optimization, tailored to the specific organism and lipid product, is necessary. We took a unique approach to produce high levels of microbial lipids. We sought to use a well-studied non-oleaginous bacterium, *R. sphaeroides*, that has a native ability to increase its lipid content, to increase synthesis of these molecules. We showed that by combing genetic and reactor engineering, *R. sphaeroides* can produce and secrete lipids at levels found in oleaginous microbes. Using only a single genetic lesion (disruption of the NtrXY signal transduction pathway), we were able to achieve cells that contain 33% of the DCW as fatty acid, and produce fatty acids at 24% of maximum theoretical yield.

Unique Properties of High-Lipid Mutants

The ten high-lipid mutants that we identified had between a 1.5 to 6.7-fold increase in fatty acid per cell (Table 3), and had increased sensitivity to cell wall and membrane-targeting drugs, changes in cell shape, outer membrane protrusions, and often secreted lipids. These phenotypes suggest that the mutants have cell envelope alterations leading to release of cellular lipids. It is noteworthy that increased lipid production by wild-type *R. sphaeroides* (at low O_2) involves changes in the cell envelope. Specifically, cells increase their inner membrane surface area by creating intracytoplasmic membrane vesicles that protrude into the cytoplasm (Tavano et al. 2006). We are not aware of other reports of changes in the structure of the outer membrane or cell wall leading to increased cellular lipid content. It is also unknown whether any genes disrupted in the high-lipid mutants play a role in increasing lipid content or remodeling the cell envelope that normally occurs at low O_2 tensions in this bacterium.

Genetic Links of High-Lipid Mutants to the Cell Envelope

While none of the genes disrupted in the high-lipid mutants had been studied in *R. sphaeroides*, many of them had predicted functions associated with the cell envelope. The gene product inactivated in HLM05 (RSP1200) encodes an uncharacterized conserved protein that contains a CAP domain. Members of this superfamily are typically secreted, acting extracellularly in signal transduction or protein modification (Gibbs et al. 2008); some family members have been shown to bind lipids (Choudhary et al. 2012, Van Galen et al. 2010). RSP0355 (inactivated in HLM07) encodes one of several periplasmic serine protease (DegP) homologues in this bacterium, a protein that in other bacteria functions in protein quality control, degrading misfolded periplasmic proteins (Lyu et al. 2015). RSP2543 (inactivated in HLM08) encodes a cell wall hydrolase. It contains a signal peptide (Table 3) presumably to target it to the periplasm, a LysM peptidoglycan binding motif (Bateman et al. 2000), and Gly-Gly endopeptidase domain. Thus, RSP2543 could play a previously unreported role in peptidoglycan cell wall remodeling. RSP2745 (inactivated in HLM09) was identified as a Stealth family protein (Sperisen et al. 2005), which in bacteria appear to function in the synthesis of exopolysaccharides (Sperisen et al. 2005). Finally, the gene inactivated in HLM10 (RSP2293) encodes the ClpA subunit of the Clp protease that performs protein quality control in the cell and functions in other regulatory processes. ClpA mutants in some *Pseudomonas* species have cell envelope-related phenotypes (Song et al. 2015, Goff et al. 2009).

Another group of high-lipid mutants contain disruptions in two-component signaling systems. NtrXY (inactivated in HLM01 and HLM02) encode a sensor histidine kinase and its cognate response regulator that acts as a transcription factor in other bacteria. The NtrXY pathway has been implicated in controlling exopolysaccharide production (Wang et al. 2013), as well as regulating anaerobically induced processes (Ishida et al. 2002, Pawlowski et al. 1991, Carrica et al. 2012, Carrica et al. 2013, Gregor et al. 2007). Future studies to further characterize the transcriptional targets of *R. sphaeroides* NtrX and determine how they impinge on the cell envelope, lipid accumulation, and secretion has the potential to improve the production of fatty acids and other membrane-associated compounds. RSP1056 (inactivated in HLM04) is an "orphan" histidine kinase whose response regulator is not genetically linked and has not been identified. We suspect that the Tn5 insertion in this mutant causes a gain of function mutation rather than loss of function.

Finally, some high-lipid mutants have insertions in genes whose product does not seem to directly relate to the cell envelope. RSP3218 (inactivated in HLM03) encodes a nitroreductase that is predicted to function in vitamin B_{12} biosynthesis; and RSP1422 (inactivated in HLM06) encodes a chromosome partitioning protein. In these cases, additional experiments are needed to understand how these mutations lead to the high-lipid phenotype of these strains.

Lipid Secretion by High-Lipid Mutants

When *R. sphaeroides* naturally increases its lipid content it makes additional intracellular membranes, so it was unexpected to find that several of the high-lipid mutants secreted lipids. From analysis of other systems, bacterial lipid secretion often occurs by export of free fatty acids or outer membrane vesicle (OMV) formation (Kulp et al. 2010, Lennen et al. 2010, Ledesma-Amaro et al. 2016). For the high-lipid mutants with the highest levels of secreted lipid (HLM01, HLM02, and HLM05), lipid phosphorus assays indicated the presence of extracellular phospholipid (FIG. **9**). The structures observed in the media of HLM01 and HLM02, (FIG. **4**, panels B, C, F, and G) do not resemble bacterial outer membrane vesicles, which typically appear as 20-250 nm spherical vesicles (Schwechheimer et al. 2015). However, the media of HLM05 does contain spherical vesicles in the 20-50 nm range (FIG. **4**, panel H). Further investigation is needed to determine the cellular source of these lipid secretions (outer membrane, inner membrane, or both), their chemical composition, and the mechanism leading to their production.

R. sphaeroides as an Oleaginous Bacterium

The ability of *R. sphaeroides* to increase production of hydrophobic compounds at low O_2 has led to its use as a source of isoprenoids, quinones and other chemicals (Yen et al. 2010, Kien et al. 2010, Sangkharak et al. 2007). The industrial utility of bacteria as microbial sources of valuable products is often enhanced by the ability to grow cells to high cell density.

By growing HLM02 in a fed-batch bioreactor, total fatty acid productivity increased ~8-fold over what is observed in batch culture. Additionally, in the fed-batch bioreactor, total fatty acid content of HLM02 was ~33% of DCW, classifying this strain as an oleaginous bacterium. We are not aware of any previous examples of microbes accumulating over 20% of its biomass as phospholipid, typically oleaginous organisms accumulate triacylglycerols or wax esters (Waltermann et al. 2005, Liang et al. 2013). Fatty acid yield for HLM02 in the fed-batch bioreactor was 24% of maximum theoretical yield. Considering that, compared to the parent strain, HLM02 had only one genetic lesion, this is a substantial improvement. Further increases in lipid productivity is possible with additional metabolic engineering, e.g., by using other gene disruptions identified herein (Table 3) and/or employing strategies that have been successful in other organisms to either increase flux through fatty acid biosynthesis or decrease β-oxidation (Janssen et al. 2014, Lennen et al. 2012).

Several observations from our studies may be beneficial for increasing the economic feasibility of producing lipid or other bioproducts, either in this or other bacteria that can be engineered to contain similar cell envelope changes. Bioproduct secretion by a microbe has several advantages. First, bioproduct secretion can increase production beyond the amount that can fit within the cell. Second, bioproduct secretion could simplify the ability to harvest, separate and process the product (Caspeta et al. 2013, Arora 2012), as well as minimize intracellular toxicity of this compound. In addition, HLM02 retained its high-lipid phenotype when grown on several different carbon sources, suggesting that the catabolic versatility of *R. sphaeroides* may be advantageous when cells are grown on more complex media. Finally, we found the HLM02 mutant could over-produce and secrete a novel-furan containing fatty acid that has potential value in biofuel, biochemical, and pharmaceutical industries due to its antioxidant activity.

CONCLUSIONS

By combining genetic and bioreactor engineering, we have created an oleaginous strain of *R. sphaeroides*, HLM02, that produced fatty acid at ~24% of the maximum theoretical yield. During this process we also isolated and characterized ten different high-lipid strains. We propose that in many of these mutants, alterations in the cell envelope lead to increased lipid content. The novel properties of these high-lipid mutants also suggests that similar changes in cell envelope structure could be used to increase production of lipids or lipid-associated bioproducts in other microbes.

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Ser Phe Asn Gln Asp Ala Leu Glu Ile Asn Gly His Ala Ile Glu Val
                325                 330                 335

Arg Ile Asn Ala Glu Lys Leu Pro Asn Phe Ser Pro Cys Pro Gly Lys
            340                 345                 350

Val Arg Val Phe His Ala Pro Gly Gly Leu Gly Val Arg Met Asp Ser
        355                 360                 365

Ala Leu Tyr Gly Gly Tyr Ser Ile Pro Pro Tyr Tyr Asp Ser Leu Ile
    370                 375                 380

Gly Lys Leu Ile Val His Gly Arg Asp Arg Pro Glu Ala Leu Ala Arg
385                 390                 395                 400

Leu His Arg Ala Leu Gly Glu Leu Ile Val Asp Gly Ile Asp Thr Thr
                405                 410                 415

Val Pro Leu Phe His Ala Leu Leu Ala Glu Pro Asp Ile Gln Asn Gly
            420                 425                 430

Asp Tyr Asn Ile His Trp Leu Glu Lys Trp Leu Ala Ala Gln Phe Gly
        435                 440                 445


<210> SEQ ID NO 5
<211> LENGTH: 1335
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 5

ttggcgattg cgccctttcg ggtcgtccgg gggcggcgat cccgcccttc gacgcgcgcc     60

aaccgggcgg cggatgccga gctgcggcgc ctccgcgcgc agtttcccga ctgggacgtg    120
```

```
ccgtccgacc tcacgacgct gggccagcag cggtctcccg ccgccgagat cgaccggatc    180

taccggcaga tcgcggccgg agacctgacc gaggcccggc aggcgatgga cgagacgtcg    240

cgcaacttcc ccggatggac gccgccgccc gagatggagc gtcttctggc cacggccgag    300

gcacaggccg ccttcgatgc ggccgccagt gcgggcaatg cgggcgcggc aatcgagatc    360

gcgcggcgga cgcccgcgat cctgcgctgc gaccgggtga acaacgcctg gcggctggcc    420

gagctgcagg cggcggcggg ccagaaggcg gccgcgctgc agagctatcg cggggtgatc    480

gcctcctgct cgggcctgtc cgaggtgacg gcgacgctcg agaaggcgga ggccgtggcc    540

agcgatgcgg agctggtcga gctcttccgg ctggccaatg cgcagcttcc gggctcggga    600

cctgcgctga aggcgctcga gacacggctg agggcgggac gcggcgacac ggcgcccgag    660

gcatcggcgc cggctgccgc agcaacgggc ggagccaagc gcacgccggg ccgcactgcg    720

gtggccgagg cggatctgcc cgcggcgggg cgcccgcgca ctgcgggcgt ggcgcgcagc    780

ggcggagggg cggggctgtc cgcggtccgc gcggcagcgc aacgcggcga ctggcggacc    840

tgcaccggcc tcaccagcgg cgccaccagc gccgacatgc tctacgagcg ggcctggtgc    900

gtctataatc tcgaccggcc gctcgaggcg ctggcggctt tcgagcctgc cgcctcgggg    960

cgcctcgggg cgcaggtcgc gcgggacgcg cgcttcggca agacgctcgc gctgctggcg   1020

ctgaagatga cggaagaggc cgcccggctc gccgccgcga ccgacctgac catccagcag   1080

cggcgcgagg tcgaggccat catcctggat cagcgcgggg tgcgggccta tcagctgaag   1140

gaatatcgcc gcgccatcgc cttcctcacc gcctatgagg atctgacggg ggggctgcgg   1200

cgcgacctcg cgatcatgcg cggctacgcc tacctcaacc tcggcaagcg gaccgaggcc   1260

aagcgcatct tcacggagct gaacaatcag ctcgcgacgc ccgagacccg ggcgggcctg   1320

aacgcgagcc gctga                                                    1335


<210> SEQ ID NO 6
<211> LENGTH: 444
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 6

Met Ala Ile Ala Pro Phe Arg Val Val Arg Gly Arg Arg Ser Arg Pro
1               5                   10                  15

Ser Thr Arg Ala Asn Arg Ala Ala Asp Ala Glu Leu Arg Arg Leu Arg
            20                  25                  30

Ala Gln Phe Pro Asp Trp Asp Val Pro Ser Asp Leu Thr Thr Leu Gly
        35                  40                  45

Gln Gln Arg Ser Pro Ala Ala Glu Ile Asp Arg Ile Tyr Arg Gln Ile
    50                  55                  60

Ala Ala Gly Asp Leu Thr Glu Ala Arg Gln Ala Met Asp Glu Thr Ser
65                  70                  75                  80

Arg Asn Phe Pro Gly Trp Thr Pro Pro Pro Glu Met Glu Arg Leu Leu
                85                  90                  95

Ala Thr Ala Glu Ala Gln Ala Ala Phe Asp Ala Ala Ala Ser Ala Gly
            100                 105                 110

Asn Ala Gly Ala Ala Ile Glu Ile Ala Arg Arg Thr Pro Ala Ile Leu
        115                 120                 125

Arg Cys Asp Arg Val Asn Asn Ala Trp Arg Leu Ala Glu Leu Gln Ala
    130                 135                 140

Ala Ala Gly Gln Lys Ala Ala Ala Leu Gln Ser Tyr Arg Gly Val Ile
145                 150                 155                 160
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Ala Ser Cys Ser Gly Leu Ser Glu Val Thr Ala Thr Leu Glu Lys Ala
                165                 170                 175

Glu Ala Val Ala Ser Asp Ala Glu Leu Val Glu Leu Phe Arg Leu Ala
            180                 185                 190

Asn Ala Gln Leu Pro Gly Ser Gly Pro Ala Leu Lys Ala Leu Glu Thr
        195                 200                 205

Arg Leu Arg Ala Gly Arg Gly Asp Thr Ala Pro Glu Ala Ser Ala Pro
    210                 215                 220

Ala Ala Ala Ala Thr Gly Gly Ala Lys Arg Thr Pro Gly Arg Thr Ala
225                 230                 235                 240

Val Ala Glu Ala Asp Leu Pro Ala Ala Gly Arg Pro Arg Thr Ala Gly
                245                 250                 255

Val Ala Arg Ser Gly Gly Gly Ala Gly Leu Ser Ala Val Arg Ala Ala
            260                 265                 270

Ala Gln Arg Gly Asp Trp Arg Thr Cys Thr Gly Leu Thr Ser Gly Ala
        275                 280                 285

Thr Ser Ala Asp Met Leu Tyr Glu Arg Ala Trp Cys Val Tyr Asn Leu
    290                 295                 300

Asp Arg Pro Leu Glu Ala Leu Ala Ala Phe Glu Pro Ala Ala Ser Gly
305                 310                 315                 320

Arg Leu Gly Ala Gln Val Ala Arg Asp Ala Arg Phe Gly Lys Thr Leu
                325                 330                 335

Ala Leu Leu Ala Leu Lys Met Thr Glu Glu Ala Ala Arg Leu Ala Ala
            340                 345                 350

Ala Thr Asp Leu Thr Ile Gln Gln Arg Arg Glu Val Glu Ala Ile Ile
        355                 360                 365

Leu Asp Gln Arg Gly Val Arg Ala Tyr Gln Leu Lys Glu Tyr Arg Arg
    370                 375                 380

Ala Ile Ala Phe Leu Thr Ala Tyr Glu Asp Leu Thr Gly Gly Leu Arg
385                 390                 395                 400

Arg Asp Leu Ala Ile Met Arg Gly Tyr Ala Tyr Leu Asn Leu Gly Lys
                405                 410                 415

Arg Thr Glu Ala Lys Arg Ile Phe Thr Glu Leu Asn Asn Gln Leu Ala
            420                 425                 430

Thr Pro Glu Thr Arg Ala Gly Leu Asn Ala Ser Arg
        435                 440
```

<210> SEQ ID NO 7
<211> LENGTH: 996
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 7

```
atgaggagac ggaccatcct gacatcggcc gccgccgcgc tgatgctggc ccctgcagga     60

cgcctcctcg cgcagtcggg cagagaggct ttgcctgcgg accacccgct ccaggcggcc    120

tggcgcagct ggaaggatgc gttcctgctg cccgccggcc gcatcgtcga cgggccgcag    180

cagaatgcga gccattccga agggcagggc tacggagcca cgctcgccgc gatcttcggc    240

gacgaggagg ccctgcggcg catcgtcgac tggaccgagg cgaaccttgc gcggcgcgag    300

gacaagcttc tgagctggcg ctggctgccc ggtgtggcgc tggccgtgcc cgacgagaac    360

aacgccaccg acggcgatct cttctacgcc tggggtctcg ccatggccgc gcagcggttc    420

ggcaaggccg attacgccgg gcgggcgacc gaactggcgc gcgccatcgc gctgcattgc    480
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gtgcgtccgc atccggacgg ctccgagcag ctcgtgctgc tgccgggggc cagcggcttc    540

gagacgccgg acggggtggt gctcaacccc tcctactaca tgccccgcgc cctgaccgag    600

ctcgccgcct tcagcggcca ggaccggctg gcgcgctgtg cccgcgacgg ggcggactgg    660

atcgcgtcgc tcgggcttcc gccggactgg gcgctggtca cgcccttcgg cacacagccg    720

gcgccgggcc tgtcccacaa cagcggctac gatgcgctgc gggtgcccct gttcctgctc    780

tggtccgggc tgaccgccaa tcccgcgctg cgccgcgcgg tggaggcggc cggggacgcc    840

gcagccggcg acacgccggt gaggttcgac cgcgacacgg gggcggtgct ggaacggtcc    900

gccgatccgg gcttccgcgc cgtgctcgcg cttggcgatt gcgccctttc gggtcgtccg    960

ggggcggcga tcccgccctt cgacgcgcgc caaccg                              996


<210> SEQ ID NO 8
<211> LENGTH: 332
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 8

Met Arg Arg Arg Thr Ile Leu Thr Ser Ala Ala Ala Ala Leu Met Leu
1               5                   10                  15

Ala Pro Ala Gly Arg Leu Leu Ala Gln Ser Gly Arg Glu Ala Leu Pro
            20                  25                  30

Ala Asp His Pro Leu Gln Ala Ala Trp Arg Ser Trp Lys Asp Ala Phe
        35                  40                  45

Leu Leu Pro Ala Gly Arg Ile Val Asp Gly Pro Gln Gln Asn Ala Ser
    50                  55                  60

His Ser Glu Gly Gln Gly Tyr Gly Ala Thr Leu Ala Ala Ile Phe Gly
65                  70                  75                  80

Asp Glu Glu Ala Leu Arg Arg Ile Val Asp Trp Thr Glu Ala Asn Leu
                85                  90                  95

Ala Arg Arg Glu Asp Lys Leu Leu Ser Trp Arg Trp Leu Pro Gly Val
            100                 105                 110

Ala Leu Ala Val Pro Asp Glu Asn Asn Ala Thr Asp Gly Asp Leu Phe
        115                 120                 125

Tyr Ala Trp Gly Leu Ala Met Ala Ala Gln Arg Phe Gly Lys Ala Asp
    130                 135                 140

Tyr Ala Gly Arg Ala Thr Glu Leu Ala Arg Ala Ile Ala Leu His Cys
145                 150                 155                 160

Val Arg Pro His Pro Asp Gly Ser Glu Gln Leu Val Leu Leu Pro Gly
                165                 170                 175

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

Tyr Met Pro Arg Ala Leu Thr Glu Leu Ala Ala Phe Ser Gly Gln Asp
        195                 200                 205

Arg Leu Ala Arg Cys Ala Arg Asp Gly Ala Asp Trp Ile Ala Ser Leu
    210                 215                 220

Gly Leu Pro Pro Asp Trp Ala Leu Val Thr Pro Phe Gly Thr Gln Pro
225                 230                 235                 240

Ala Pro Gly Leu Ser His Asn Ser Gly Tyr Asp Ala Leu Arg Val Pro
                245                 250                 255

Leu Phe Leu Leu Trp Ser Gly Leu Thr Ala Asn Pro Ala Leu Arg Arg
            260                 265                 270

Ala Val Glu Ala Ala Gly Asp Ala Ala Ala Gly Asp Thr Pro Val Arg
        275                 280                 285
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Phe Asp Arg Asp Thr Gly Ala Val Leu Glu Arg Ser Ala Asp Pro Gly
    290                 295                 300

Phe Arg Ala Val Leu Ala Leu Gly Asp Cys Ala Leu Ser Gly Arg Pro
305                 310                 315                 320

Gly Ala Ala Ile Pro Pro Phe Asp Ala Arg Gln Pro
                325                 330


<210> SEQ ID NO 9
<211> LENGTH: 2178
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 9

atggacatgc gactgctgcc tttccttttc ctcgggacgc tggcgtcgat ggccgcggcg     60

caggacgcgc cgatgatcgt gatcgagggc ctcacctccg aagagccgca ggcgtccccc    120

gatgcggtcg cggaagcggt gccggcggcg gaggtcgccc cctggatcat tccgctgcgc    180

cctctggccg agaccgcgca ggtcgggccg ctcttccgcc tgcagggtca gcaggcgcgc    240

gcggccttcc gcctcttcct gccgaccgaa gcggtcggcg gcacgctcac gctcgcgcag    300

cgcagcagca tcgacatcct gcccgaaagc tcacagatca tcgtgcggat gaacgatcag    360

gagatcggcc gcttcacccc ccgccagttc ggcgctctgg gggccgtcac catgccgctc    420

ggcgaagccg tgcgggcggg cgacaatctc gtgacgatcg aggcgcagca ccggcaccgc    480

atctactgcg gtgcggatgc ggagttcgat ctctggaccg aggtcgatct gagccagagc    540

ggcgtggcgc ttcccgccgc ggcgatcggc accgaaccta cctcgttcat cgcggccctc    600

actgcacagg cggagtcggg ccggccggtc gagatccgca cacccacccc gcccgacgag    660

gcgacgctgc gcaccctcgc ccaggctctc gggcggccat tgcctgacga ggcgctgccg    720

ctcgcgctga gcaagccgtg gtcggccgag accggcccca cctatgcgcg gatcacgctt    780

cttccgtccg acgccgaccg cgtttccata cgccggggcg gggacggggc cgtggttctg    840

gtcctcgaac atccgcccga aggctcaccc aacgcgtcgc tcgtcgccga tcttctggga    900

gcgaccccga cgctgccgcc tccgacgcta ccgcagatcc cgcccggccg cgtcgtcacg    960

ctggccgaca tgggcgtcga caccattctc accgacaacc gctacttcaa ccgcgatatc   1020

gacttccagc tgccggacga ctggctgctg ctggcgagcc agaaggcgca gatcggcatc   1080

gactacggct ttgccggcgg gctgcccgag ggcgcgctgc tgctcgtgaa ggtcaatggc   1140

acgacggtgc gcatgctgcc gctcgaccgc gacgccgccc ccgtcaagcc ccggctcgac   1200

atccgctttc cggcgcggct cctgcatccc ggcccgaacc ggctgtcgtt cgaatcggtc   1260

atcccgggca atccgcccga ccagccctgt cctgcctccg ccggcgacct gatgcaggtg   1320

ctgagctcga ccgatctcga ggtgccgccg tcgccccgga tgcagatggc ggacatggcg   1380

cgggatctgg cgcaggtgac gccggcatcg gtgcatcctg ccacgccgga cggtctggcg   1440

cggacgctgc ccttcatggc ggccttccgc gaggtgcccg acgcggcacc cgtggatctg   1500

acggtggcgg gtctgcacga catcgccacg gttcccctga acgaggaagg cctgacgccg   1560

cgccttctcg ccctgacgct gctaccctcc accgtctccc ggctggtgga gcgtccggcg   1620

acgcccgcgg gtccgccggc caacgccctc gccccgctgg gcgccgcgcc gggcgagggg   1680

gtgatgccgc cgctggtcga gtcgaactgg tcggaccgcg cccagacctt cgtgcaggcc   1740

acgctgcagc ccgtgatcca gacggtccgg cggatgctgc gaccggggga cggcaacctc   1800

gccgagtggc tcgccacgcg caagggcacg gccatgctgc tcgcgcccga accgggcaag   1860
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ctctgggtca tcctcgggcc cgaggccgag ccggcccggg ttgcggaagc cctcgccatg   1920

gcgccgcgct cgcccggcgg gccccgcggt caggtggccg ttctcggctc tgacggacgc   1980

tggtcgagct ggtcgaagcc cggcctcctg ccggagttgc gcgaacccgt gagccttgac   2040

aatgtgcgca gcgtggtggg caacgtcgcg tcggcgcggc cgcccctgct gctcggcggg   2100

atgctgggcc tcgcctggat cagcgctgca atcgccgtgg gcttcgtgct ccgcacccgg   2160

aggaagggcc tgaaatga                                                 2178


<210> SEQ ID NO 10
<211> LENGTH: 725
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 10

Met Asp Met Arg Leu Leu Pro Phe Leu Phe Leu Gly Thr Leu Ala Ser
1               5                   10                  15

Met Ala Ala Ala Gln Asp Ala Pro Met Ile Val Ile Glu Gly Leu Thr
            20                  25                  30

Ser Glu Glu Pro Gln Ala Ser Pro Asp Ala Val Ala Glu Ala Val Pro
        35                  40                  45

Ala Ala Glu Val Ala Pro Trp Ile Ile Pro Leu Arg Pro Leu Ala Glu
    50                  55                  60

Thr Ala Gln Val Gly Pro Leu Phe Arg Leu Gln Gly Gln Gln Ala Arg
65                  70                  75                  80

Ala Ala Phe Arg Leu Phe Leu Pro Thr Glu Ala Val Gly Gly Thr Leu
                85                  90                  95

Thr Leu Ala Gln Arg Ser Ser Ile Asp Ile Leu Pro Glu Ser Ser Gln
            100                 105                 110

Ile Ile Val Arg Met Asn Asp Gln Glu Ile Gly Arg Phe Thr Pro Arg
        115                 120                 125

Gln Phe Gly Ala Leu Gly Ala Val Thr Met Pro Leu Gly Glu Ala Val
    130                 135                 140

Arg Ala Gly Asp Asn Leu Val Thr Ile Glu Ala Gln His Arg His Arg
145                 150                 155                 160

Ile Tyr Cys Gly Ala Asp Ala Glu Phe Asp Leu Trp Thr Glu Val Asp
                165                 170                 175

Leu Ser Gln Ser Gly Val Ala Leu Pro Ala Ala Ala Ile Gly Thr Glu
            180                 185                 190

Pro Thr Ser Phe Ile Ala Ala Leu Thr Ala Gln Ala Glu Ser Gly Arg
        195                 200                 205

Pro Val Glu Ile Arg Thr Pro Thr Pro Pro Asp Glu Ala Thr Leu Arg
    210                 215                 220

Thr Leu Ala Gln Ala Leu Gly Arg Pro Leu Pro Asp Glu Ala Leu Pro
225                 230                 235                 240

Leu Ala Leu Ser Lys Pro Trp Ser Ala Glu Thr Gly Pro Thr Tyr Ala
                245                 250                 255

Arg Ile Thr Leu Leu Pro Ser Asp Ala Asp Arg Val Ser Ile Arg Arg
            260                 265                 270

Gly Gly Asp Gly Ala Val Val Leu Val Leu Glu His Pro Pro Glu Gly
        275                 280                 285

Ser Pro Asn Ala Ser Leu Val Ala Asp Leu Leu Gly Ala Thr Pro Thr
    290                 295                 300

Leu Pro Pro Pro Thr Leu Pro Gln Ile Pro Pro Gly Arg Val Val Thr
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305                 310                 315                 320

Leu Ala Asp Met Gly Val Asp Thr Ile Leu Thr Asp Asn Arg Tyr Phe
                325                 330                 335

Asn Arg Asp Ile Asp Phe Gln Leu Pro Asp Asp Trp Leu Leu Leu Ala
            340                 345                 350

Ser Gln Lys Ala Gln Ile Gly Ile Asp Tyr Gly Phe Ala Gly Gly Leu
        355                 360                 365

Pro Glu Gly Ala Leu Leu Leu Val Lys Val Asn Gly Thr Thr Val Arg
    370                 375                 380

Met Leu Pro Leu Asp Arg Asp Ala Ala Pro Val Lys Pro Arg Leu Asp
385                 390                 395                 400

Ile Arg Phe Pro Ala Arg Leu Leu His Pro Gly Pro Asn Arg Leu Ser
                405                 410                 415

Phe Glu Ser Val Ile Pro Gly Asn Pro Pro Asp Gln Pro Cys Pro Ala
            420                 425                 430

Ser Ala Gly Asp Leu Met Gln Val Leu Ser Ser Thr Asp Leu Glu Val
        435                 440                 445

Pro Pro Ser Pro Arg Met Gln Met Ala Asp Met Ala Arg Asp Leu Ala
    450                 455                 460

Gln Val Thr Pro Ala Ser Val His Pro Ala Thr Pro Asp Gly Leu Ala
465                 470                 475                 480

Arg Thr Leu Pro Phe Met Ala Ala Phe Arg Glu Val Pro Asp Ala Ala
                485                 490                 495

Pro Val Asp Leu Thr Val Ala Gly Leu His Asp Ile Ala Thr Val Pro
            500                 505                 510

Leu Asn Glu Glu Gly Leu Thr Pro Arg Leu Leu Ala Leu Thr Leu Leu
        515                 520                 525

Pro Ser Thr Val Ser Arg Leu Val Glu Arg Pro Ala Thr Pro Ala Gly
    530                 535                 540

Pro Pro Ala Asn Ala Leu Ala Pro Leu Gly Ala Ala Pro Gly Glu Gly
545                 550                 555                 560

Val Met Pro Pro Leu Val Glu Ser Asn Trp Ser Asp Arg Ala Gln Thr
                565                 570                 575

Phe Val Gln Ala Thr Leu Gln Pro Val Ile Gln Thr Val Arg Arg Met
            580                 585                 590

Leu Arg Pro Gly Asp Gly Asn Leu Ala Glu Trp Leu Ala Thr Arg Lys
        595                 600                 605

Gly Thr Ala Met Leu Leu Ala Pro Glu Pro Gly Lys Leu Trp Val Ile
    610                 615                 620

Leu Gly Pro Glu Ala Glu Pro Ala Arg Val Ala Glu Ala Leu Ala Met
625                 630                 635                 640

Ala Pro Arg Ser Pro Gly Gly Pro Arg Gly Gln Val Ala Val Leu Gly
                645                 650                 655

Ser Asp Gly Arg Trp Ser Ser Trp Ser Lys Pro Gly Leu Leu Pro Glu
            660                 665                 670

Leu Arg Glu Pro Val Ser Leu Asp Asn Val Arg Ser Val Val Gly Asn
        675                 680                 685

Val Ala Ser Ala Arg Pro Pro Leu Leu Leu Gly Gly Met Leu Gly Leu
    690                 695                 700

Ala Trp Ile Ser Ala Ala Ile Ala Val Gly Phe Val Leu Arg Thr Arg
705                 710                 715                 720

Arg Lys Gly Leu Lys
                725
```

<210> SEQ ID NO 11
<211> LENGTH: 2367
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 11

atgaccgttc gagccaaggc ccgctccccg ctaagggtcg ttcccgtcct gctgttcctg 60

ctgtgggtgg ctctcctcgt gccgttcggg ctgctggccg ccgcgccggt cgcgccctcg 120

gcgcagggcc tcatcgcttt gtcggcggtg gtgctggtgg cgctgctcaa gcccttcgcc 180

gacaagatgg tgccgcgctt cctgcttctg tccgcggcct cgatgctggt gatgcgctac 240

tggttctggc gcctgttcga aacgctgccg ccgcccgcgc tcgacgcctc gttcctcttc 300

gctctgctgc tcttcgcggt cgagaccttc tcgatctcca tcttcttcct caacggcttt 360

ctcagcgccg acccgaccga ccggcccttc ccgcggccgc tgcagcccga ggagctgccg 420

acggtcgaca ttctcgtgcc ctcctacaac gagcccgccg acatgctgag cgtgacgctc 480

gcggcggcca agaacatgat ctatccggcg cggctgcgca cggtggtgct ctgcgacgac 540

gggggcaccg accagcgctg catgtcgccc gaccccgagc ttgcgcagaa ggcgcaggag 600

cggcggcgcg agttgcagca gctctgccgc gagctgggcg tggtctattc gacgcgcgag 660

cggaacgaac atgccaaggc gggcaacatg tcggccgcgc tcgagcggct gaagggcgag 720

ctcgtggtgg tgttcgatgc cgaccacgtc ccgagccgcg acttccttgc ccggacggtg 780

ggctatttcg tcgaggatcc tgacctcttc ctcgtccaga cgccgcactt cttcatcaac 840

cccgacccga tccagcgcaa cctcgcgctc ggcgaccgct gcccgcccga gaacgagatg 900

ttctacggca agatccaccg cggcctcgac cgctggggcg gggccttctt ctgcggatcg 960

gccgcggtcc tgcgccgccg cgccctcgac gaggcgggcg gctttgccgg cgagaccatc 1020

accgaggatg ccgagaccgc gctcgagatc cattcccgcg gctggaagag cctctatatc 1080

gaccgcgcca tgatcgcggg gctccagccc gagaccttcg cctccttcat ccagcagcgc 1140

ggccgctggg ccaccggcat gatgcagatg ctgctgctga agaacccgct cttccgccgc 1200

ggtctcggga tcgcgcagcg cctgtgctac ctcaactcga tgagcttctg gttcttcccg 1260

ctggtgcgga tgatgttcct cgtggcgccg ctcatctatc tgttcttcgg catcgagatc 1320

ttcgtcgcca ccttcgagga ggtgctggcc tacatgccgg gctatctggc ggtgagcttc 1380

ctcgtgcaga acgcgctgtt tgcgcggcag cgatggccgc tcgtctccga agtctacgag 1440

gtggcacagg cgccctatct ggcgcgcgcc atcgtgacca cgctgctgcg gccgcgcagt 1500

gcccgcttcg cggtgaccgc gaaggacgag acgctgagcg agaactacat ttcgcccatc 1560

taccgtccgc tcctcttcac cttcctgctc tgcctgtccg ggtgctcgc cacgctggtg 1620

cgctgggtgg ccttccccgg cgaccggtcg gtcctcctcg tcgtgggcgg ctgggcggtg 1680

ctcaacgtgc ttctcgtggg cttcgctttg cgggcggtgg ccgagaagca gcagcggcgc 1740

gcggcccccc gtgtgcagat ggaggtgccg gccgaggcgc agatccctgc cttcggcaac 1800

cgctcgctga ccgcgaccgt gctcgacgcc tcgaccagcg gcgtgcgcct tctggtccgg 1860

ctgcccggcg tgggcgatcc gcacccggcg ctcgaggcgg gagggctcat ccagttccag 1920

ccgaagttcc ccgacgcgcc gcagctcgag cgcatggtgc gcggccgcat ccgctcggcg 1980

cgccgcgagg gcggaacggt gatggtgggc gtgatcttcg aggcgggcca accgatcgcg 2040

gtgcgcgaga cggtggccta tctcatcttc ggcgagagcg cgcactggcg cacgatgcgc 2100

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gaggccacga tgcggcccat cgggctcctg cacgggatgg cgcgaatcct gtggatggcg   2160

gccgccagcc tgcccaagac cgcgcgcgac ttcatggacg aaccggcccg ccgccggcgc   2220

cgccacgagg aaccgaagga gaagcaggcg catcttctgg ccttcggcac cgacttcagc   2280

accgaacccg actgggcggg cgagctgctc gatccgacgg cgcaggtctc cgcgcgtccc   2340

aacacggtcg cctgggggtc gaactga                                       2367


<210> SEQ ID NO 12
<211> LENGTH: 788
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 12

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

Leu Leu Phe Leu Leu Trp Val Ala Leu Leu Val Pro Phe Gly Leu Leu
            20                  25                  30

Ala Ala Ala Pro Val Ala Pro Ser Ala Gln Gly Leu Ile Ala Leu Ser
        35                  40                  45

Ala Val Val Leu Val Ala Leu Leu Lys Pro Phe Ala Asp Lys Met Val
    50                  55                  60

Pro Arg Phe Leu Leu Leu Ser Ala Ala Ser Met Leu Val Met Arg Tyr
65                  70                  75                  80

Trp Phe Trp Arg Leu Phe Glu Thr Leu Pro Pro Pro Ala Leu Asp Ala
                85                  90                  95

Ser Phe Leu Phe Ala Leu Leu Leu Phe Ala Val Glu Thr Phe Ser Ile
            100                 105                 110

Ser Ile Phe Phe Leu Asn Gly Phe Leu Ser Ala Asp Pro Thr Asp Arg
        115                 120                 125

Pro Phe Pro Arg Pro Leu Gln Pro Glu Glu Leu Pro Thr Val Asp Ile
    130                 135                 140

Leu Val Pro Ser Tyr Asn Glu Pro Ala Asp Met Leu Ser Val Thr Leu
145                 150                 155                 160

Ala Ala Ala Lys Asn Met Ile Tyr Pro Ala Arg Leu Arg Thr Val Val
                165                 170                 175

Leu Cys Asp Asp Gly Gly Thr Asp Gln Arg Cys Met Ser Pro Asp Pro
            180                 185                 190

Glu Leu Ala Gln Lys Ala Gln Glu Arg Arg Arg Glu Leu Gln Gln Leu
        195                 200                 205

Cys Arg Glu Leu Gly Val Val Tyr Ser Thr Arg Glu Arg Asn Glu His
    210                 215                 220

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

Leu Val Val Val Phe Asp Ala Asp His Val Pro Ser Arg Asp Phe Leu
                245                 250                 255

Ala Arg Thr Val Gly Tyr Phe Val Glu Asp Pro Asp Leu Phe Leu Val
            260                 265                 270

Gln Thr Pro His Phe Phe Ile Asn Pro Asp Pro Ile Gln Arg Asn Leu
        275                 280                 285

Ala Leu Gly Asp Arg Cys Pro Pro Glu Asn Glu Met Phe Tyr Gly Lys
    290                 295                 300

Ile His Arg Gly Leu Asp Arg Trp Gly Gly Ala Phe Phe Cys Gly Ser
305                 310                 315                 320

Ala Ala Val Leu Arg Arg Arg Ala Leu Asp Glu Ala Gly Gly Phe Ala
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                325                 330                 335

Gly Glu Thr Ile Thr Glu Asp Ala Glu Thr Ala Leu Glu Ile His Ser
            340                 345                 350

Arg Gly Trp Lys Ser Leu Tyr Ile Asp Arg Ala Met Ile Ala Gly Leu
        355                 360                 365

Gln Pro Glu Thr Phe Ala Ser Phe Ile Gln Gln Arg Gly Arg Trp Ala
    370                 375                 380

Thr Gly Met Met Gln Met Leu Leu Leu Lys Asn Pro Leu Phe Arg Arg
385                 390                 395                 400

Gly Leu Gly Ile Ala Gln Arg Leu Cys Tyr Leu Asn Ser Met Ser Phe
                405                 410                 415

Trp Phe Phe Pro Leu Val Arg Met Met Phe Leu Val Ala Pro Leu Ile
            420                 425                 430

Tyr Leu Phe Phe Gly Ile Glu Ile Phe Val Ala Thr Phe Glu Glu Val
        435                 440                 445

Leu Ala Tyr Met Pro Gly Tyr Leu Ala Val Ser Phe Leu Val Gln Asn
    450                 455                 460

Ala Leu Phe Ala Arg Gln Arg Trp Pro Leu Val Ser Glu Val Tyr Glu
465                 470                 475                 480

Val Ala Gln Ala Pro Tyr Leu Ala Arg Ala Ile Val Thr Thr Leu Leu
                485                 490                 495

Arg Pro Arg Ser Ala Arg Phe Ala Val Thr Ala Lys Asp Glu Thr Leu
            500                 505                 510

Ser Glu Asn Tyr Ile Ser Pro Ile Tyr Arg Pro Leu Leu Phe Thr Phe
        515                 520                 525

Leu Leu Cys Leu Ser Gly Val Leu Ala Thr Leu Val Arg Trp Val Ala
    530                 535                 540

Phe Pro Gly Asp Arg Ser Val Leu Leu Val Val Gly Gly Trp Ala Val
545                 550                 555                 560

Leu Asn Val Leu Leu Val Gly Phe Ala Leu Arg Ala Val Ala Glu Lys
                565                 570                 575

Gln Gln Arg Arg Ala Ala Pro Arg Val Gln Met Glu Val Pro Ala Glu
            580                 585                 590

Ala Gln Ile Pro Ala Phe Gly Asn Arg Ser Leu Thr Ala Thr Val Leu
        595                 600                 605

Asp Ala Ser Thr Ser Gly Val Arg Leu Leu Val Arg Leu Pro Gly Val
    610                 615                 620

Gly Asp Pro His Pro Ala Leu Glu Ala Gly Gly Leu Ile Gln Phe Gln
625                 630                 635                 640

Pro Lys Phe Pro Asp Ala Pro Gln Leu Glu Arg Met Val Arg Gly Arg
                645                 650                 655

Ile Arg Ser Ala Arg Arg Glu Gly Gly Thr Val Met Val Gly Val Ile
            660                 665                 670

Phe Glu Ala Gly Gln Pro Ile Ala Val Arg Glu Thr Val Ala Tyr Leu
        675                 680                 685

Ile Phe Gly Glu Ser Ala His Trp Arg Thr Met Arg Glu Ala Thr Met
    690                 695                 700

Arg Pro Ile Gly Leu Leu His Gly Met Ala Arg Ile Leu Trp Met Ala
705                 710                 715                 720

Ala Ala Ser Leu Pro Lys Thr Ala Arg Asp Phe Met Asp Glu Pro Ala
                725                 730                 735

Arg Arg Arg Arg Arg His Glu Glu Pro Lys Glu Lys Gln Ala His Leu
            740                 745                 750
```

Leu Ala Phe Gly Thr Asp Phe Ser Thr Glu Pro Asp Trp Ala Gly Glu
        755   760   765

Leu Leu Asp Pro Thr Ala Gln Val Ser Ala Arg Pro Asn Thr Val Ala
    770   775   780

Trp Gly Ser Asn
785

<210> SEQ ID NO 13
<211> LENGTH: 672
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 13

atgacacagg catcgaaatg gtacgcccgg ctaaggcccg gccttccgct ggcggcgctt 60

ctgctgcttc tggcctgcga gtcgacctcc attcccggca ggcccgcgct ctcgatccgc 120

gaggagacgg cgcagttccg caccgtcccc gccagccggg cctgggtcgc cgtgcccggg 180

gcgctcctcg tgcaggagcg ggatctgggc ggcgacctcg agcagcggat cgcgctgccg 240

aacgccacga cgctcgaagg cgacaatatg atcatcttgc gaggccgggc gccgggcgga 300

ccgattctcg agcggctcca gctgcagagc ttcgccgatg ccgatggcgc gctgcccaag 360

cccttcggcc gggtgagcga cagcgctctc agcacgcgcg aggatgtgct cggcaccgtg 420

gtctttgccg aggagcggct tggcgtggac acggtctgcg ttctggccat gcgccggatg 480

ccgcccacgg cccggccggt tccggcgcgg atcgaggcgc tggacgtgat gctgcgcaac 540

tgcacgcgca acggcacgga ggaggcgctg cggcccatcg gcgcggccag cctcggcttc 600

gccccgcccg aagcggtggc cggtacgggg gcagggcgca ccctctcgcc cctcgccgcc 660

ccgatgccct ga 672

<210> SEQ ID NO 14
<211> LENGTH: 223
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 14

Met Thr Gln Ala Ser Lys Trp Tyr Ala Arg Leu Arg Pro Gly Leu Pro
1   5   10   15

Leu Ala Ala Leu Leu Leu Leu Leu Ala Cys Glu Ser Thr Ser Ile Pro
            20   25   30

Gly Arg Pro Ala Leu Ser Ile Arg Glu Glu Thr Ala Gln Phe Arg Thr
        35   40   45

Val Pro Ala Ser Arg Ala Trp Val Ala Val Pro Gly Ala Leu Leu Val
    50   55   60

Gln Glu Arg Asp Leu Gly Gly Asp Leu Glu Gln Arg Ile Ala Leu Pro
65   70   75   80

Asn Ala Thr Thr Leu Glu Gly Asp Asn Met Ile Ile Leu Arg Gly Arg
                85   90   95

Ala Pro Gly Gly Pro Ile Leu Glu Arg Leu Gln Leu Gln Ser Phe Ala
            100   105   110

Asp Ala Asp Gly Ala Leu Pro Lys Pro Phe Gly Arg Val Ser Asp Ser
        115   120   125

Ala Leu Ser Thr Arg Glu Asp Val Leu Gly Thr Val Val Phe Ala Glu
    130   135   140

Glu Arg Leu Gly Val Asp Thr Val Cys Val Leu Ala Met Arg Arg Met
145   150   155   160

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Pro Pro Thr Ala Arg Pro Val Pro Ala Arg Ile Glu Ala Leu Asp Val
                165                 170                 175

Met Leu Arg Asn Cys Thr Arg Asn Gly Thr Glu Glu Ala Leu Arg Pro
            180                 185                 190

Ile Gly Ala Ala Ser Leu Gly Phe Ala Pro Pro Glu Ala Val Ala Gly
        195                 200                 205

Thr Gly Ala Gly Arg Thr Leu Ser Pro Leu Ala Ala Pro Met Pro
    210                 215                 220


<210> SEQ ID NO 15
<211> LENGTH: 2370
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 15

atgacgggca agggacaggg tggatcttgg gtgccggggg tcgtttccgc gaccgaccgc     60

ggcaatttcc atgcaagccc caccaccgcc acggtgcttg acatcatcgg ccgcatcctg    120

cgcgccccgc tctctgccac cgacaccgag atcgagaccg ccctcgcgca ggtggcggac    180

gcctgcagcg cggatgtcgc gcaggtctgc cgtgcgggga ccacgggccc tctcgagccg    240

atccacagct gggtgcgtga cggccatatc gtcttgaaca tccaagactt gtgcaaattc    300

tgcccggggt cggaccagac cgggcccgtc atgctgcgcg acctgaagga ccttcccgag    360

gggccggccc gcgatcggct cgcggggatg gagttgcggt cgctcgtcgc ggtgccgatg    420

ctacggcacg ggtgctggc gggccgggtg cttctgggct ggcagacggc gagcagcgac    480

ctgcgccccg aggatctcgc cgcgctgcag tccctcgccg aggccatgca tgcggccgcg    540

gagcgacgcg aaagcgagcg gctcacgacg gaggcggcag cggcgctgca ggaggaccgg    600

cttcttctcg aatcgatcct gcggaccagc acctcggcca tcctcgcctt cgatgccgat    660

gcccgcatcg tcttcgccaa cgatgaggcg gcggccctcc tcggaacgga cgcgaaccgt    720

ctgccgggat gcaccctcga gggcgtgggc tgccgccttc tgtcgcgcga gggcgagccc    780

ctcccgcccg aggccctgcc ggtcgcgcgc gccattgctg aggggcagac gctccgcgac    840

ctgcaccatg tgctgatggc cgccgacggc cgacagagga tcctgtcgat caacgcggcc    900

cccgtggcgg ccggcgcggc gacagcggtg cgcgtcgtcg ccaccatcga cgacgtgacc    960

ggtcaggtct cggccgacag cgcgctgcgc acggcgctcg ccgaagcgca tcagctcgcc   1020

ttcttcgacc ctctgacggg gctttacaac cgccggggca tcgtcgaggt gctgcgcgac   1080

tgcctccaga cctgcgcccg cgagaaggcc ttcctctcgc ttctctatat cgatctggac   1140

gggatgcggc aggtgaacgg cacccgcggg cactggctgg gcgaccgggt cctgcaggcg   1200

ctgggcgcgc ggctggacaa cctgcggcag gacggcggcg acctcggccg gatctcggcc   1260

gacgaattcg tgctgacctg cggcgagacc catcccgacg ccgccggcgc ggtcgccgcc   1320

gccgaggccg aggcccagcg catcctcgag tcgctgcggg agccgttcgt ggtggatggc   1380

ctcacgctcg aggtcaccgc ctcgatcggc cttgccgcca tttcggccga ggattcggtc   1440

gaggggctgc tgaagggcgt cgatctggcc gtcatggccg ccaaggccgc gggcggcgac   1500

agggcctgtg cctaccgggc cgacatggag caggacatgg tgggtcgcgt ggccctcgcg   1560

caggagttgc gcgaggcgat ccgccgcgac gagttccgca tctacttcga accgatggtc   1620

agcctcggcg agaccgggct cgagatcgtg ggtcaggagg cgctgatccg ctgggagcat   1680

ccgcagcgcg ggcttctggc gcccatcgcc ttcatcccct tcgccgagga gaccggcttc   1740
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atccgcgaca tcgaccgctg ggtgctgcgc gcggcggcac aggagctcgc ccgctgggcc   1800

gaggatcccg cgcgccgcca tctcggggtc tcgatcaaca tcagctcggc gcagttcctg   1860

tccgaggagt tcggccagat ggtgcgcgag gtgctggacg agaccggcgt cgatcccacc   1920

cggatcgagc tggaggtcac cgagggcacg ctcctgtcca atctcggcct cgcgcggacc   1980

acgatgatgg acctgcgctc gctcggcatc tccatcgcgc tggacgattt cggcaccggc   2040

ttctcctcgc tcagctatct gcgggacctg cccgtggacg tgttgaagat cgaccgcagc   2100

ttcttgggcg gcctgtcgga ctcgaaggcg aaccggacca tcctcgaagg gatcatcgga   2160

cttgcctcgg ggctcggcgt ggcgctggtg gccgaggggg tggagacgcc ggcgcagttc   2220

gcctggctgc gggccaaggg atgccggacc ttccagggct acctcttcgg ccgcccggtc   2280

gatgaggcgc agacgcagct cgcgcccgag gtgtccgcgc tcggcggcca cggaggcgac   2340

cgtgcggttt cgggccagat caagggctga                                     2370


<210> SEQ ID NO 16
<211> LENGTH: 789
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 16

Met Thr Gly Lys Gly Gln Gly Gly Ser Trp Val Pro Gly Val Val Ser
1               5                   10                  15

Ala Thr Asp Arg Gly Asn Phe His Ala Ser Pro Thr Thr Ala Thr Val
            20                  25                  30

Leu Asp Ile Ile Gly Arg Ile Leu Arg Ala Pro Leu Ser Ala Thr Asp
        35                  40                  45

Thr Glu Ile Glu Thr Ala Leu Ala Gln Val Ala Asp Ala Cys Ser Ala
    50                  55                  60

Asp Val Ala Gln Val Cys Arg Ala Gly Thr Thr Gly Pro Leu Glu Pro
65                  70                  75                  80

Ile His Ser Trp Val Arg Asp Gly His Ile Val Leu Asn Ile Gln Asp
                85                  90                  95

Leu Cys Lys Phe Cys Pro Gly Ser Asp Gln Thr Gly Pro Val Met Leu
            100                 105                 110

Arg Asp Leu Lys Asp Leu Pro Glu Gly Pro Ala Arg Asp Arg Leu Ala
        115                 120                 125

Gly Met Glu Leu Arg Ser Leu Val Ala Val Pro Met Leu Arg His Gly
    130                 135                 140

Val Leu Ala Gly Arg Val Leu Leu Gly Trp Gln Thr Ala Ser Ser Asp
145                 150                 155                 160

Leu Arg Pro Glu Asp Leu Ala Ala Leu Gln Ser Leu Ala Glu Ala Met
                165                 170                 175

His Ala Ala Ala Glu Arg Arg Glu Ser Glu Arg Leu Thr Thr Glu Ala
            180                 185                 190

Ala Ala Ala Leu Gln Glu Asp Arg Leu Leu Leu Glu Ser Ile Leu Arg
        195                 200                 205

Thr Ser Thr Ser Ala Ile Leu Ala Phe Asp Ala Asp Ala Arg Ile Val
    210                 215                 220

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

Leu Pro Gly Cys Thr Leu Glu Gly Val Gly Cys Arg Leu Leu Ser Arg
                245                 250                 255

Glu Gly Glu Pro Leu Pro Pro Glu Ala Leu Pro Val Ala Arg Ala Ile
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            260                 265                 270

Ala Glu Gly Gln Thr Leu Arg Asp Leu His His Val Leu Met Ala Ala
        275                 280                 285

Asp Gly Arg Gln Arg Ile Leu Ser Ile Asn Ala Ala Pro Val Ala Ala
    290                 295                 300

Gly Ala Ala Thr Ala Val Arg Val Val Ala Thr Ile Asp Asp Val Thr
305                 310                 315                 320

Gly Gln Val Ser Ala Asp Ser Ala Leu Arg Thr Ala Leu Ala Glu Ala
                325                 330                 335

His Gln Leu Ala Phe Phe Asp Pro Leu Thr Gly Leu Tyr Asn Arg Arg
            340                 345                 350

Gly Ile Val Glu Val Leu Arg Asp Cys Leu Gln Thr Cys Ala Arg Glu
        355                 360                 365

Lys Ala Phe Leu Ser Leu Leu Tyr Ile Asp Leu Asp Gly Met Arg Gln
    370                 375                 380

Val Asn Gly Thr Arg Gly His Trp Leu Gly Asp Arg Val Leu Gln Ala
385                 390                 395                 400

Leu Gly Ala Arg Leu Asp Asn Leu Arg Gln Asp Gly Gly Asp Leu Gly
                405                 410                 415

Arg Ile Ser Ala Asp Glu Phe Val Leu Thr Cys Gly Glu Thr His Pro
            420                 425                 430

Asp Ala Ala Gly Ala Val Ala Ala Ala Glu Ala Glu Ala Gln Arg Ile
        435                 440                 445

Leu Glu Ser Leu Arg Glu Pro Phe Val Val Asp Gly Leu Thr Leu Glu
    450                 455                 460

Val Thr Ala Ser Ile Gly Leu Ala Ala Ile Ser Ala Glu Asp Ser Val
465                 470                 475                 480

Glu Gly Leu Leu Lys Gly Val Asp Leu Ala Val Met Ala Ala Lys Ala
                485                 490                 495

Ala Gly Gly Asp Arg Ala Cys Ala Tyr Arg Ala Asp Met Glu Gln Asp
            500                 505                 510

Met Val Gly Arg Val Ala Leu Ala Gln Glu Leu Arg Glu Ala Ile Arg
        515                 520                 525

Arg Asp Glu Phe Arg Ile Tyr Phe Glu Pro Met Val Ser Leu Gly Glu
    530                 535                 540

Thr Gly Leu Glu Ile Val Gly Gln Glu Ala Leu Ile Arg Trp Glu His
545                 550                 555                 560

Pro Gln Arg Gly Leu Leu Ala Pro Ile Ala Phe Ile Pro Phe Ala Glu
                565                 570                 575

Glu Thr Gly Phe Ile Arg Asp Ile Asp Arg Trp Val Leu Arg Ala Ala
            580                 585                 590

Ala Gln Glu Leu Ala Arg Trp Ala Glu Asp Pro Ala Arg Arg His Leu
        595                 600                 605

Gly Val Ser Ile Asn Ile Ser Ser Ala Gln Phe Leu Ser Glu Glu Phe
    610                 615                 620

Gly Gln Met Val Arg Glu Val Leu Asp Glu Thr Gly Val Asp Pro Thr
625                 630                 635                 640

Arg Ile Glu Leu Glu Val Thr Glu Gly Thr Leu Leu Ser Asn Leu Gly
                645                 650                 655

Leu Ala Arg Thr Thr Met Met Asp Leu Arg Ser Leu Gly Ile Ser Ile
            660                 665                 670

Ala Leu Asp Asp Phe Gly Thr Gly Phe Ser Ser Leu Ser Tyr Leu Arg
        675                 680                 685
```

```
Asp Leu Pro Val Asp Val Leu Lys Ile Asp Arg Ser Phe Leu Gly Gly
    690                 695                 700

Leu Ser Asp Ser Lys Ala Asn Arg Thr Ile Leu Glu Gly Ile Ile Gly
705                 710                 715                 720

Leu Ala Ser Gly Leu Gly Val Ala Leu Val Ala Glu Gly Val Glu Thr
                725                 730                 735

Pro Ala Gln Phe Ala Trp Leu Arg Ala Lys Gly Cys Arg Thr Phe Gln
            740                 745                 750

Gly Tyr Leu Phe Gly Arg Pro Val Asp Glu Ala Gln Thr Gln Leu Ala
        755                 760                 765

Pro Glu Val Ser Ala Leu Gly Gly His Gly Gly Asp Arg Ala Val Ser
    770                 775                 780

Gly Gln Ile Lys Gly
785


<210> SEQ ID NO 17
<211> LENGTH: 570
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 17

atgacgctca ccttggccca gaccctggac cgctgcctcg atatcgcagg aaatccgacc      60

gcggcgatca gtttcccgca acggcggatg ctgggtcagg cgctggcgtt cctgccgcgt     120

cagcactacc ggcgtgtgct ggagctcggg tgcgggtcgg gggcgctggc gcgcggtctt     180

tcggcacgct gcgaccatta tgtcggcctc gatgcggacg ccgatgctct ggatgaggcg     240

tccctcatgc cctcgcccta tgcgcagacc gaattccgcc agggccgggt gcccgaggac     300

atccccgagg gtccgttcga tctcgtggtg ctgaacgggg tgctgcagga tctgccggcc     360

gaggcgatcg agcggcttgc ggtgcggttg cgccaggtgg cgccttcggc cgacatcctc     420

tgcctccgca gccttctgtt cgagggtccc gacgaggcgt tccgcccgca ggccgccctg     480

gccgcggccc tcggtcggcc gctcaccgcc tgcaacttcg accggctgtt ccgcatcgac     540

gtgttcgagc cggaacgcgc cgccgcctga                                      570


<210> SEQ ID NO 18
<211> LENGTH: 189
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 18

Met Thr Leu Thr Leu Ala Gln Thr Leu Asp Arg Cys Leu Asp Ile Ala
1               5                   10                  15

Gly Asn Pro Thr Ala Ala Ile Ser Phe Pro Gln Arg Arg Met Leu Gly
            20                  25                  30

Gln Ala Leu Ala Phe Leu Pro Arg Gln His Tyr Arg Arg Val Leu Glu
        35                  40                  45

Leu Gly Cys Gly Ser Gly Ala Leu Ala Arg Gly Leu Ser Ala Arg Cys
    50                  55                  60

Asp His Tyr Val Gly Leu Asp Ala Asp Ala Asp Ala Leu Asp Glu Ala
65                  70                  75                  80

Ser Leu Met Pro Ser Pro Tyr Ala Gln Thr Glu Phe Arg Gln Gly Arg
                85                  90                  95

Val Pro Glu Asp Ile Pro Glu Gly Pro Phe Asp Leu Val Val Leu Asn
            100                 105                 110
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Gly Val Leu Gln Asp Leu Pro Ala Glu Ala Ile Glu Arg Leu Ala Val
        115                 120                 125

Arg Leu Arg Gln Val Ala Pro Ser Ala Asp Ile Leu Cys Leu Arg Ser
    130                 135                 140

Leu Leu Phe Glu Gly Pro Asp Glu Ala Phe Arg Pro Gln Ala Ala Leu
145                 150                 155                 160

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

Phe Arg Ile Asp Val Phe Glu Pro Glu Arg Ala Ala Ala
            180                 185


<210> SEQ ID NO 19
<211> LENGTH: 1638
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 19

gtgacacgat gcctgtcggc ggggccctgc cggcaggctt cacatgagct tgacgggcca      60

agacgccgtt tgcattgcgg cgcatcttgc ccgactgtca cttcggggcg gtgcagcttg     120

cagttggccg ctcagctatc tcgaaaggag tcgggtgtgc agtctcacgc cattaccatc     180

gcccgccgca tccacccggt gcccgcgtcg gtctcgcgtc tcttcctcgc gctgatgctc     240

gggctcgccc tggcgctggc gcaggccgtg gcggtcaagg cgcagaacgc tcccgcaagt     300

ttcgcaggcc tcgccgagaa gatcagcccg gccgtcgtga acatcacgac ctcgaccgtc     360

gtggcggcac ccacgcagaa ttcgcccctc gtgcccgaag gctcgccctt cgaggatttc     420

ttccgtgact tcatggaccc gcagaaccgc ggcgagggcc cgcgccgctc cgaggcgctg     480

ggttcgggct tcgtgatctc ggaagacggc tacatcgtca ccaacaatca tgtcatcgaa     540

ggggccgacg acatccagat cgagttcttc tcgggcaaga agctcgaggc gaagctcgtc     600

ggcaccgatc cgaagaccga catcgcgctg ctgaaggtcg atgggaacca gccgctgccc     660

ttcgtgagct tcggcaactc cgacctcgcc cgcgttggcg actgggtcgt ggcgatgggc     720

aacccgctgg ggcagggctt ctcggtctcg gccggcatcg tgtcggcgcg caaccgggcc     780

ctctccggca cctacgacga ttacatccag accgacgccg ccatcaaccg cggcaattcg     840

ggcggtccgc tgttcaacat ggacgggcag gtgatcggcg tgaacacggc gatcctgtcg     900

ccgaacggcg gctcgatcgg catcggcttc tcgatggcct cgaacgtggt ggtgaaggtc     960

gtgcagcagc tgcgcgagtt cggcgagacc cgccgcggct ggctcggcgt gcggatccag    1020

gacgtgaccc ccgacgtggc cgaggcgatg ggcctcaccg aggccaaagg cgccctcgtg    1080

accgacgtgc cggaaggccc cgcgaaagag gccggcatgc agtctggcga cgtgatcgtg    1140

accttcgata gcgcgcccgt ggcggacacc cgcgatctgg tgcgccgggt ggccgatgcg    1200

cccattggcg aggcggtgcg tgtcatcgtg atgcgcgaag gcaagacccg gaccctgtcg    1260

gtgacgctcg ggcgtcgcga ggaagccgag aacgaaggcc ccgaggcacc cggcgcgacc    1320

gagccgacgg aaccgtcgac ggccgatctt ctgggcctga ccgtggcgcc gctcacggcc    1380

gagcaggccg gagagctggg cctgcccggc ggcaccgagg ggcttgccgt gacggatgtc    1440

gatccggcct ccgaggccta ttccaagggc ttgcgcgagg gagacgtgat caccgaggcc    1500

ggccagcaga aagtggtctc gatcaaggat ctgcaggacc gtgtgaccga ggcgcgggag    1560

gcggggcgga aatcgctgct cctgctgatc cgccgcggcg gcgatccgcg tttcgtggcc    1620

ctgacggtca gcgagtag                                                  1638
```

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<210> SEQ ID NO 20
<211> LENGTH: 545
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 20

Met Thr Arg Cys Leu Ser Ala Gly Pro Cys Arg Gln Ala Ser His Glu
1               5                   10                  15

Leu Asp Gly Pro Arg Arg Arg Leu His Cys Gly Ala Ser Cys Pro Thr
            20                  25                  30

Val Thr Ser Gly Arg Cys Ser Leu Gln Leu Ala Ala Gln Leu Ser Arg
        35                  40                  45

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

His Pro Val Pro Ala Ser Val Ser Arg Leu Phe Leu Ala Leu Met Leu
65                  70                  75                  80

Gly Leu Ala Leu Ala Leu Ala Gln Ala Val Ala Val Lys Ala Gln Asn
                85                  90                  95

Ala Pro Ala Ser Phe Ala Gly Leu Ala Glu Lys Ile Ser Pro Ala Val
            100                 105                 110

Val Asn Ile Thr Thr Ser Thr Val Val Ala Ala Pro Thr Gln Asn Ser
        115                 120                 125

Pro Leu Val Pro Glu Gly Ser Pro Phe Glu Asp Phe Phe Arg Asp Phe
    130                 135                 140

Met Asp Pro Gln Asn Arg Gly Glu Gly Pro Arg Arg Ser Glu Ala Leu
145                 150                 155                 160

Gly Ser Gly Phe Val Ile Ser Glu Asp Gly Tyr Ile Val Thr Asn Asn
                165                 170                 175

His Val Ile Glu Gly Ala Asp Asp Ile Gln Ile Glu Phe Phe Ser Gly
            180                 185                 190

Lys Lys Leu Glu Ala Lys Leu Val Gly Thr Asp Pro Lys Thr Asp Ile
        195                 200                 205

Ala Leu Leu Lys Val Asp Gly Asn Gln Pro Leu Pro Phe Val Ser Phe
    210                 215                 220

Gly Asn Ser Asp Leu Ala Arg Val Gly Asp Trp Val Val Ala Met Gly
225                 230                 235                 240

Asn Pro Leu Gly Gln Gly Phe Ser Val Ser Ala Gly Ile Val Ser Ala
                245                 250                 255

Arg Asn Arg Ala Leu Ser Gly Thr Tyr Asp Asp Tyr Ile Gln Thr Asp
            260                 265                 270

Ala Ala Ile Asn Arg Gly Asn Ser Gly Gly Pro Leu Phe Asn Met Asp
        275                 280                 285

Gly Gln Val Ile Gly Val Asn Thr Ala Ile Leu Ser Pro Asn Gly Gly
    290                 295                 300

Ser Ile Gly Ile Gly Phe Ser Met Ala Ser Asn Val Val Val Lys Val
305                 310                 315                 320

Val Gln Gln Leu Arg Glu Phe Gly Glu Thr Arg Arg Gly Trp Leu Gly
                325                 330                 335

Val Arg Ile Gln Asp Val Thr Pro Asp Val Ala Glu Ala Met Gly Leu
            340                 345                 350

Thr Glu Ala Lys Gly Ala Leu Val Thr Asp Val Pro Glu Gly Pro Ala
        355                 360                 365

Lys Glu Ala Gly Met Gln Ser Gly Asp Val Ile Val Thr Phe Asp Ser
    370                 375                 380
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Ala Pro Val Ala Asp Thr Arg Asp Leu Val Arg Arg Val Ala Asp Ala
385                 390                 395                 400

Pro Ile Gly Glu Ala Val Arg Val Ile Val Met Arg Glu Gly Lys Thr
                405                 410                 415

Arg Thr Leu Ser Val Thr Leu Gly Arg Arg Glu Glu Ala Glu Asn Glu
            420                 425                 430

Gly Pro Glu Ala Pro Gly Ala Thr Glu Pro Thr Glu Pro Ser Thr Ala
        435                 440                 445

Asp Leu Leu Gly Leu Thr Val Ala Pro Leu Thr Ala Glu Gln Ala Gly
    450                 455                 460

Glu Leu Gly Leu Pro Gly Gly Thr Glu Gly Leu Ala Val Thr Asp Val
465                 470                 475                 480

Asp Pro Ala Ser Glu Ala Tyr Ser Lys Gly Leu Arg Glu Gly Asp Val
                485                 490                 495

Ile Thr Glu Ala Gly Gln Gln Lys Val Val Ser Ile Lys Asp Leu Gln
            500                 505                 510

Asp Arg Val Thr Glu Ala Arg Glu Ala Gly Arg Lys Ser Leu Leu Leu
        515                 520                 525

Leu Ile Arg Arg Gly Gly Asp Pro Arg Phe Val Ala Leu Thr Val Ser
    530                 535                 540

Glu
545


<210> SEQ ID NO 21
<211> LENGTH: 1806
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 21

atggcaaccg aagagcagtc tccgggttcc ggccgtgacg ctcagttcga gcgtctgaac      60

gcgaatctca cccgcatcga cgagctgtcg aaacggctga cggccgctct cacgaagcgc     120

aaactgtcgg accccgcgct gcacgggccc tcgggcgacg tcttcctgaa ggcgatgacg     180

gcctacatgg ccgagatgat gcagaacccg gccaagatcc tcgagcatca gatcagtttc     240

tggggcaaga gcctgaaaca ttacgtcgag gctcagcacc agctggtgaa gggcgagctg     300

aagccgccgc cggacgtgac gccgaaggac cgccgcttct cgaacccgct ctggcagacg     360

catcccttct tcaactatct caagcagcag tatctgatga acgccgaggc ggtgaatcag     420

gccgtcgagg cgctggagca tatcgagccg tccgacaaga agcgggtcga atatttctcg     480

cgccagatcg tcgatctttt ctcgcccacg aacttcttcg gcaccaatcc cgacgcgctc     540

gaacgcgcca tcgccaccga cggcgagagc ctggtgcagg ggctggagaa tctcgtgcgc     600

gacatcgagg ccaacaacgg cgatctgctc gtcacgctgg ccgaccccga ggcctttcag     660

gtggggcaga acctcgccac caccgaaggg tcggtcgtct accgcaaccg catgttcgag     720

ctgatccagt acaagcccac gaccgagacg gtccacgaga cgccgctgct gatctttccg     780

ccctggatca acaagttcta catcctcgac ctcaagccgc agaattccct gctgaagtgg     840

ctggtggatc agggcttcac ggtcttcgtc gtctcgtggg tgaaccccga caagagctat     900

gccggcatcg gcatggacga ctacatccgc gaaggctaca tgcgcgccat ggccgaggtg     960

cgctcgatca cccggcagaa gcagatcaac gcggtaggct attgcatcgc gggcaccacg    1020

ctcacgctga cgctggcgca cctgcagaag gcgggcgatc cgtccgtacg ctcggccacc    1080

ttcttcacca cgctcaccga cttttcggac ccgggtgagg tgggggtgtt cctcaacgac    1140
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gatttcgtcg acgggatcga gcggcaggtg gcggtggacg ggatcctcga caagaccttc   1200

atgtcgcgca ccttcagcta tctgcggtcg aacgacctga tctatcagcc ggcgatcaag   1260

agctacatga tgggcgaggc gccgccggcc ttcgacctgc tctactggaa cggagacggc   1320

accaacctgc cggcgcagat ggcggtcgaa tacctgcgtg gcctgtgcca gcaggaccgg   1380

ctggcgggcg gcaccttccc ggtgctgggc tcgcccgtgg ggctgaagga tgtgacgctt   1440

cccgtctgcg ccatcgcctg cgagaccgac catatcgcgc cgtggaaaag cagcttcaac   1500

ggcttccgtc agttcggctc gaccgacaag accttcattc tctctcaatc gggccatgtg   1560

gcgggcatcg tgaacccgcc cagccgcaac aaatacggcc attacaccaa cgagggcccg   1620

gccggcacgc cggagtcgtt ccgggagggg gccgagttcc acgcgggctc ctggtggccg   1680

cgctggggcg cctggctcgc cgagcgatcg ggcaagcagg tcccggcgcg ccagccgggc   1740

gattcgaaac atcccgagct cgcgccggcg cccggatcct atgtggcggc ggtgggcggg   1800

gcttga                                                              1806


<210> SEQ ID NO 22
<211> LENGTH: 601
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 22

Met Ala Thr Glu Glu Gln Ser Pro Gly Ser Gly Arg Asp Ala Gln Phe
1               5                   10                  15

Glu Arg Leu Asn Ala Asn Leu Thr Arg Ile Asp Glu Leu Ser Lys Arg
            20                  25                  30

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

Gly Pro Ser Gly Asp Val Phe Leu Lys Ala Met Thr Ala Tyr Met Ala
    50                  55                  60

Glu Met Met Gln Asn Pro Ala Lys Ile Leu Glu His Gln Ile Ser Phe
65                  70                  75                  80

Trp Gly Lys Ser Leu Lys His Tyr Val Glu Ala Gln His Gln Leu Val
                85                  90                  95

Lys Gly Glu Leu Lys Pro Pro Pro Asp Val Thr Pro Lys Asp Arg Arg
            100                 105                 110

Phe Ser Asn Pro Leu Trp Gln Thr His Pro Phe Phe Asn Tyr Leu Lys
        115                 120                 125

Gln Gln Tyr Leu Met Asn Ala Glu Ala Val Asn Gln Ala Val Glu Ala
    130                 135                 140

Leu Glu His Ile Glu Pro Ser Asp Lys Lys Arg Val Glu Tyr Phe Ser
145                 150                 155                 160

Arg Gln Ile Val Asp Leu Phe Ser Pro Thr Asn Phe Phe Gly Thr Asn
                165                 170                 175

Pro Asp Ala Leu Glu Arg Ala Ile Ala Thr Asp Gly Glu Ser Leu Val
            180                 185                 190

Gln Gly Leu Glu Asn Leu Val Arg Asp Ile Glu Ala Asn Asn Gly Asp
        195                 200                 205

Leu Leu Val Thr Leu Ala Asp Pro Glu Ala Phe Gln Val Gly Gln Asn
    210                 215                 220

Leu Ala Thr Thr Glu Gly Ser Val Val Tyr Arg Asn Arg Met Phe Glu
225                 230                 235                 240

Leu Ile Gln Tyr Lys Pro Thr Thr Glu Thr Val His Glu Thr Pro Leu
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                245                 250                 255

Leu Ile Phe Pro Pro Trp Ile Asn Lys Phe Tyr Ile Leu Asp Leu Lys
            260                 265                 270

Pro Gln Asn Ser Leu Leu Lys Trp Leu Val Asp Gln Gly Phe Thr Val
        275                 280                 285

Phe Val Val Ser Trp Val Asn Pro Asp Lys Ser Tyr Ala Gly Ile Gly
    290                 295                 300

Met Asp Asp Tyr Ile Arg Glu Gly Tyr Met Arg Ala Met Ala Glu Val
305                 310                 315                 320

Arg Ser Ile Thr Arg Gln Lys Gln Ile Asn Ala Val Gly Tyr Cys Ile
                325                 330                 335

Ala Gly Thr Thr Leu Thr Leu Thr Leu Ala His Leu Gln Lys Ala Gly
            340                 345                 350

Asp Pro Ser Val Arg Ser Ala Thr Phe Phe Thr Thr Leu Thr Asp Phe
        355                 360                 365

Ser Asp Pro Gly Glu Val Gly Val Phe Leu Asn Asp Asp Phe Val Asp
    370                 375                 380

Gly Ile Glu Arg Gln Val Ala Val Asp Gly Ile Leu Asp Lys Thr Phe
385                 390                 395                 400

Met Ser Arg Thr Phe Ser Tyr Leu Arg Ser Asn Asp Leu Ile Tyr Gln
                405                 410                 415

Pro Ala Ile Lys Ser Tyr Met Met Gly Glu Ala Pro Pro Ala Phe Asp
            420                 425                 430

Leu Leu Tyr Trp Asn Gly Asp Gly Thr Asn Leu Pro Ala Gln Met Ala
        435                 440                 445

Val Glu Tyr Leu Arg Gly Leu Cys Gln Gln Asp Arg Leu Ala Gly Gly
    450                 455                 460

Thr Phe Pro Val Leu Gly Ser Pro Val Gly Leu Lys Asp Val Thr Leu
465                 470                 475                 480

Pro Val Cys Ala Ile Ala Cys Glu Thr Asp His Ile Ala Pro Trp Lys
                485                 490                 495

Ser Ser Phe Asn Gly Phe Arg Gln Phe Gly Ser Thr Asp Lys Thr Phe
            500                 505                 510

Ile Leu Ser Gln Ser Gly His Val Ala Gly Ile Val Asn Pro Pro Ser
        515                 520                 525

Arg Asn Lys Tyr Gly His Tyr Thr Asn Glu Gly Pro Ala Gly Thr Pro
    530                 535                 540

Glu Ser Phe Arg Glu Gly Ala Glu Phe His Ala Gly Ser Trp Trp Pro
545                 550                 555                 560

Arg Trp Gly Ala Trp Leu Ala Glu Arg Ser Gly Lys Gln Val Pro Ala
                565                 570                 575

Arg Gln Pro Gly Asp Ser Lys His Pro Glu Leu Ala Pro Ala Pro Gly
            580                 585                 590

Ser Tyr Val Ala Ala Val Gly Gly Ala
        595                 600


<210> SEQ ID NO 23
<211> LENGTH: 1962
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 23

atggatcacg ctcaggcgaa tgcggtctat accgcgtcgg cagatttcat tgcgcaagcc      60

catgtcgacg cggccggcta cgagcggatg tatgctgcat ccgtggccga cccggaggcg     120
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ttctggggcg aacagggcaa gcggctcgac tggatcaagc cctacaccaa ggtcaagaac 180

acgaacttcc ggccgggcga ggtctcgatc aagtggttcg aggacggcac gctgaacatc 240

gcctggaact gcatcgaccg gcatctggcg acgcgggcca agcagaccgc gatcatctgg 300

gagccggacg atccgaacgt gccggcccag cacatcagct atcaggagct gcacgacaac 360

gtctgccgca tggccaacgt gctggtgagc cagggcgtgc gcaagggcga ccgggtggtg 420

atgtatctgc cgatgatccc cgaggccgcc tatgcgatgc tggcgtgcgc ccggatcggc 480

gccatccatt ccgtcgtctt cgcgggcttc tcgcccgacg cgctggcgaa ccggatcaac 540

gactgtcagg ccaaggtggt catcaccgcc gacacggctc cgcgtggcgg ccggcgcacg 600

cccttgaagt cgaacaccga cgcagccctt ctccattgct cggaccgggt gcgctgcctc 660

gtcgtcaagc acacgggcga ccagatccac tggatggacg gccgcgacgt ggacgtgaag 720

gagctgatgc gccacgcctc gcccgactgc ccgatcgagg aggtgaatgc cgaggatccg 780

ctcttcatcc tctatacctc gggctcgacc ggcaagccga agggggtcgt gcacacctcg 840

ggcggctatc tgacctatgc cgccatgacc catcagatga ccttcgacta ccatgacggc 900

gacgtcttct ggtgcaccgc ggacgtgggc tgggtcacgg gccacagcta catcgtctac 960

ggcccgctgg cgaacggcgc gaccacgctc atgttcgagg gcgtgccgac ctatcccgat 1020

gcgggccgct tctgggccgt ctgcgagaag cacaaggtga accagttcta caccgcgccc 1080

acggcgatcc gctcgctgat gggcctcggg ccggaatggg tcgacaagta cgacctgtcg 1140

tcgctgaagc tcttgggctc ggtgggcgag ccgatcaacc ccgaggcctg gagctggtac 1200

aacacccatg tcggcaaggg ccgctgcccg atcgtcgaca ccttctggca gaccgagacc 1260

ggcggccaca tgatcacgcc gctgccgggc gcgatcccgg tgaagccggg cgcggcctcg 1320

aagcccttct tcggggtgaa gccggtgatc ctcgacccga ccgacgggca cgagctgcac 1380

gaaaccgcga ccgagggggt gctctgcatc gccgacagct ggccggggca gatgcgcacg 1440

ctctggggcg accacgagcg gttcgaagag gcctatttct cgcaatacaa gggctattac 1500

ttcaccggcg acggctgccg ccgcgatgcg gacggctatt actgggtcac gggccgggtc 1560

gatgacgtca tcaacgtctc gggccaccgg atgggcaccg ccgaggtgga atccgcgctc 1620

gtcgcccatg cgcaggtcgc cgaagccgcg gtggtgggct atccgcacga catcaagggg 1680

cagggcatct atgcctatgt cacgctgatg aacggggtcc agccgaccga ggagctgcgc 1740

aaggatctgg tgaaatgggt ccgcaccgag atcggcccca tcgcctcgcc ggacgtgatc 1800

cagtgggcgc cgggcctgcc caagacccgc tcgggcaaga tcatgcgccg catcctgcgc 1860

aagatcgccg agaacgactt cggctcgctc ggcgacacca cgacgctggc cgatccgtcg 1920

gtggtcgacg acctgatcgc caaccgcaag aaccggggct ga 1962

<210> SEQ ID NO 24
<211> LENGTH: 653
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 24

```
Met Asp His Ala Gln Ala Asn Ala Val Tyr Thr Ala Ser Ala Asp Phe
1               5                   10                  15

Ile Ala Gln Ala His Val Asp Ala Ala Gly Tyr Glu Arg Met Tyr Ala
            20                  25                  30

Ala Ser Val Ala Asp Pro Glu Ala Phe Trp Gly Glu Gln Gly Lys Arg
        35                  40                  45
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Leu Asp Trp Ile Lys Pro Tyr Thr Lys Val Lys Asn Thr Asn Phe Arg
    50                  55                  60

Pro Gly Glu Val Ser Ile Lys Trp Phe Glu Asp Gly Thr Leu Asn Ile
65                  70                  75                  80

Ala Trp Asn Cys Ile Asp Arg His Leu Ala Thr Arg Ala Lys Gln Thr
                85                  90                  95

Ala Ile Ile Trp Glu Pro Asp Asp Pro Asn Val Pro Ala Gln His Ile
            100                 105                 110

Ser Tyr Gln Glu Leu His Asp Asn Val Cys Arg Met Ala Asn Val Leu
        115                 120                 125

Val Ser Gln Gly Val Arg Lys Gly Asp Arg Val Val Met Tyr Leu Pro
    130                 135                 140

Met Ile Pro Glu Ala Ala Tyr Ala Met Leu Ala Cys Ala Arg Ile Gly
145                 150                 155                 160

Ala Ile His Ser Val Val Phe Ala Gly Phe Ser Pro Asp Ala Leu Ala
                165                 170                 175

Asn Arg Ile Asn Asp Cys Gln Ala Lys Val Val Ile Thr Ala Asp Thr
            180                 185                 190

Ala Pro Arg Gly Gly Arg Arg Thr Pro Leu Lys Ser Asn Thr Asp Ala
        195                 200                 205

Ala Leu Leu His Cys Ser Asp Arg Val Arg Cys Leu Val Val Lys His
    210                 215                 220

Thr Gly Asp Gln Ile His Trp Met Asp Gly Arg Asp Val Asp Val Lys
225                 230                 235                 240

Glu Leu Met Arg His Ala Ser Pro Asp Cys Pro Ile Glu Glu Val Asn
                245                 250                 255

Ala Glu Asp Pro Leu Phe Ile Leu Tyr Thr Ser Gly Ser Thr Gly Lys
            260                 265                 270

Pro Lys Gly Val Val His Thr Ser Gly Gly Tyr Leu Thr Tyr Ala Ala
        275                 280                 285

Met Thr His Gln Met Thr Phe Asp Tyr His Asp Gly Asp Val Phe Trp
    290                 295                 300

Cys Thr Ala Asp Val Gly Trp Val Thr Gly His Ser Tyr Ile Val Tyr
305                 310                 315                 320

Gly Pro Leu Ala Asn Gly Ala Thr Thr Leu Met Phe Glu Gly Val Pro
                325                 330                 335

Thr Tyr Pro Asp Ala Gly Arg Phe Trp Ala Val Cys Glu Lys His Lys
            340                 345                 350

Val Asn Gln Phe Tyr Thr Ala Pro Thr Ala Ile Arg Ser Leu Met Gly
        355                 360                 365

Leu Gly Pro Glu Trp Val Asp Lys Tyr Asp Leu Ser Ser Leu Lys Leu
    370                 375                 380

Leu Gly Ser Val Gly Glu Pro Ile Asn Pro Glu Ala Trp Ser Trp Tyr
385                 390                 395                 400

Asn Thr His Val Gly Lys Gly Arg Cys Pro Ile Val Asp Thr Phe Trp
                405                 410                 415

Gln Thr Glu Thr Gly Gly His Met Ile Thr Pro Leu Pro Gly Ala Ile
            420                 425                 430

Pro Val Lys Pro Gly Ala Ala Ser Lys Pro Phe Phe Gly Val Lys Pro
        435                 440                 445

Val Ile Leu Asp Pro Thr Asp Gly His Glu Leu His Glu Thr Ala Thr
    450                 455                 460
```

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Glu Gly Val Leu Cys Ile Ala Asp Ser Trp Pro Gly Gln Met Arg Thr
465                 470                 475                 480

Leu Trp Gly Asp His Glu Arg Phe Glu Glu Ala Tyr Phe Ser Gln Tyr
                485                 490                 495

Lys Gly Tyr Tyr Phe Thr Gly Asp Gly Cys Arg Arg Asp Ala Asp Gly
            500                 505                 510

Tyr Tyr Trp Val Thr Gly Arg Val Asp Asp Val Ile Asn Val Ser Gly
        515                 520                 525

His Arg Met Gly Thr Ala Glu Val Glu Ser Ala Leu Val Ala His Ala
    530                 535                 540

Gln Val Ala Glu Ala Ala Val Val Gly Tyr Pro His Asp Ile Lys Gly
545                 550                 555                 560

Gln Gly Ile Tyr Ala Tyr Val Thr Leu Met Asn Gly Val Gln Pro Thr
                565                 570                 575

Glu Glu Leu Arg Lys Asp Leu Val Lys Trp Val Arg Thr Glu Ile Gly
            580                 585                 590

Pro Ile Ala Ser Pro Asp Val Ile Gln Trp Ala Pro Gly Leu Pro Lys
        595                 600                 605

Thr Arg Ser Gly Lys Ile Met Arg Arg Ile Leu Arg Lys Ile Ala Glu
    610                 615                 620

Asn Asp Phe Gly Ser Leu Gly Asp Thr Thr Thr Leu Ala Asp Pro Ser
625                 630                 635                 640

Val Val Asp Asp Leu Ile Ala Asn Arg Lys Asn Arg Gly
                645                 650


<210> SEQ ID NO 25
<211> LENGTH: 726
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 25

atgcgcaccg cgctgcaatg gatccggtcc atcctcttca acatcgtgat gtatgtctcg      60

atgatcgcca tcgcgctggc cttcacgccg ctcgtgctgg tcgaccgcaa gtgggcgccg     120

gtctggatgc ggatcttcgc gcgctggacg cgcttcacgc tgcgctggat cgcggggctc     180

cggaccgagg tgcggggcga gatccccacg accggcgcgc tcatcgcctc gaagcaccag     240

agcttcctcg attccatcct gctcttctcg gtgctgcccg cgccgcgctt catcatgaag     300

aagcagctgg cctggatccc gctgatgggc tggatggcgc ttcaggcggg cttcattccg     360

gtggaccgcg gcaagcgggg cgcggccatc aagaagatga tggccgatgt cgagaagggc     420

cgcgcgacgc cgggccagct catcatctat ccgcagggca cccgcgtggc tccgggcgcg     480

catctgccct acaagatggg caccgccgcc ctctacggcc agctcgatca gccctgctat     540

ccggtggcgg ccaatgtggg cgtcttctgg ccgcggcacg ggatctatcg ccggcccggc     600

accgccgtgg tggagttcct gccgccgatc cagcccggcc aaacggccgc ggccttcatg     660

gtcgagctgg agaccgcgat cgaggacgcc tcgaaccggc tgatcgccga ggcccggcag     720

ggctga                                                                726


<210> SEQ ID NO 26
<211> LENGTH: 241
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 26

Met Arg Thr Ala Leu Gln Trp Ile Arg Ser Ile Leu Phe Asn Ile Val
```

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1               5                   10                  15

Met Tyr Val Ser Met Ile Ala Ile Ala Leu Ala Phe Thr Pro Leu Val
            20                  25                  30

Leu Val Asp Arg Lys Trp Ala Pro Val Trp Met Arg Ile Phe Ala Arg
        35                  40                  45

Trp Thr Arg Phe Thr Leu Arg Trp Ile Ala Gly Leu Arg Thr Glu Val
    50                  55                  60

Arg Gly Glu Ile Pro Thr Thr Gly Ala Leu Ile Ala Ser Lys His Gln
65                  70                  75                  80

Ser Phe Leu Asp Ser Ile Leu Leu Phe Ser Val Leu Pro Ala Pro Arg
                85                  90                  95

Phe Ile Met Lys Lys Gln Leu Ala Trp Ile Pro Leu Met Gly Trp Met
            100                 105                 110

Ala Leu Gln Ala Gly Phe Ile Pro Val Asp Arg Gly Lys Arg Gly Ala
        115                 120                 125

Ala Ile Lys Lys Met Met Ala Asp Val Glu Lys Gly Arg Ala Thr Pro
    130                 135                 140

Gly Gln Leu Ile Ile Tyr Pro Gln Gly Thr Arg Val Ala Pro Gly Ala
145                 150                 155                 160

His Leu Pro Tyr Lys Met Gly Thr Ala Ala Leu Tyr Gly Gln Leu Asp
                165                 170                 175

Gln Pro Cys Tyr Pro Val Ala Ala Asn Val Gly Val Phe Trp Pro Arg
            180                 185                 190

His Gly Ile Tyr Arg Arg Pro Gly Thr Ala Val Val Glu Phe Leu Pro
        195                 200                 205

Pro Ile Gln Pro Gly Gln Thr Ala Ala Ala Phe Met Val Glu Leu Glu
    210                 215                 220

Thr Ala Ile Glu Asp Ala Ser Asn Arg Leu Ile Ala Glu Ala Arg Gln
225                 230                 235                 240

Gly


<210> SEQ ID NO 27
<211> LENGTH: 723
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 27

atgtccaagg ttgctctggt gacgggcggt tcgcggggca tcggcgccgc catctcggtg      60

gcgctgaaga acgcgggcta cacggtcgcc gcgaactatg cgggcaatga cgaggcggcg     120

cggaagttca ccgaagagac cggcatcaag acctacaaat ggtccgtcgc ggattacgat     180

gcctgcgctg cgggcatcgc gcaggtcgag gccgagctcg ggccggtggc tgtgctggtg     240

aacaacgccg gcatcacgcg ggattcgatg ttccacaaga tgacgcgcga ccagtggaaa     300

gaggtgatcg acaccaacct gtcgggcctc ttcaacatga cccacccggt ctggtccggg     360

atgcgggacc gcaagttcgg ccggatcatc aacatctctt cgatcaacgg ccagaagggc     420

caggccgggc aggcgaacta ttccgcggcc aaggcgggcg acctcggctt caccaaggcg     480

ctggcgcagg agggcgcgcg ggcgggcatc accgtcaatg cgatctgccc cggctatatc     540

gcgaccgaga tggtgatggc cgtgccggaa aaggtgcgcg agtcgatcat cgcccagatc     600

ccgaccggcc gcctcggcga gccggaggag attgcccgct gcgtggtctt cctcgcctcc     660

gacgatgcgg gcttcgtcac cggatcgacc atcacggcga acggcggcca gtatttcgtc     720

tga                                                                  723
```

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<210> SEQ ID NO 28
<211> LENGTH: 240
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 28

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

Ala Ile Ser Val Ala Leu Lys Asn Ala Gly Tyr Thr Val Ala Ala Asn
            20                  25                  30

Tyr Ala Gly Asn Asp Glu Ala Ala Arg Lys Phe Thr Glu Glu Thr Gly
        35                  40                  45

Ile Lys Thr Tyr Lys Trp Ser Val Ala Asp Tyr Asp Ala Cys Ala Ala
    50                  55                  60

Gly Ile Ala Gln Val Glu Ala Glu Leu Gly Pro Val Ala Val Leu Val
65                  70                  75                  80

Asn Asn Ala Gly Ile Thr Arg Asp Ser Met Phe His Lys Met Thr Arg
                85                  90                  95

Asp Gln Trp Lys Glu Val Ile Asp Thr Asn Leu Ser Gly Leu Phe Asn
            100                 105                 110

Met Thr His Pro Val Trp Ser Gly Met Arg Asp Arg Lys Phe Gly Arg
        115                 120                 125

Ile Ile Asn Ile Ser Ser Ile Asn Gly Gln Lys Gly Gln Ala Gly Gln
    130                 135                 140

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

Leu Ala Gln Glu Gly Ala Arg Ala Gly Ile Thr Val Asn Ala Ile Cys
                165                 170                 175

Pro Gly Tyr Ile Ala Thr Glu Met Val Met Ala Val Pro Glu Lys Val
            180                 185                 190

Arg Glu Ser Ile Ile Ala Gln Ile Pro Thr Gly Arg Leu Gly Glu Pro
        195                 200                 205

Glu Glu Ile Ala Arg Cys Val Val Phe Leu Ala Ser Asp Asp Ala Gly
    210                 215                 220

Phe Val Thr Gly Ser Thr Ile Thr Ala Asn Gly Gly Gln Tyr Phe Val
225                 230                 235                 240


<210> SEQ ID NO 29
<211> LENGTH: 1737
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 29

atgacgcgaa gcgacaatcg caagggactg gaggagctgc gcgccgtccg ccgcagcacc      60

atgggcgcgc tgacgtccgt gttcctcttc agcatcttcg tcaatctgct gatgctgacg     120

ggcccgctct acatgctgca ggtctacgac cgggtgctcg gctcgcgctc cgaggagacg     180

ctgctcgcgc tgtccctgct cgtgaccttc ctgttcgtcg ccatgggcgt gctcgaccat     240

gcgcgggcgc gcgtcatggc gcgcgtgggc gcaggctttc aggagaagct cgaccgccgc     300

gtcttcgagg ccgcggtgcg gcggctctcg ctcgcgcccg gcgatccgtc ggccgtggca     360

gcgcagcgcg atctcgaatc ggtgcagcgg ctctgggcct cgccggtgct gatcgcgctc     420

ttcgacattc cctggacccc gttcttcctc gcggccatct tcgtcttcca cccctacatg     480

ggctggctcg ccatcggggg cggcgtcgtc ctcgtgatcg tgacgatcct gaaccagcgc     540
```

```
ctgtccgagg ggccgatgca gaaggccaac atcgtggcgc tgcaggccga ccggtttgcc    600

gagaacctca agtcggaatc cgaggtggtg caggcgctcg gcatggcggg caacggcttc    660

gaccgctggc acaaggcgcg tgccgccgcg ctcgacgcga acatggcggc ggccgacctg    720

acgggcgcct tcggcacgct gaccaagacg ctgcgcctct tcctgcagtc ggcgatgctg    780

gggctcggcg cgtggctcgt cctgcagcag gaactgagcg cgggcgccat gatcgcgggc    840

tcgatcctga tgggccgggc gctcgccccg atcgagagcg ccatcggcca gtgggcgctg    900

gtgcagcgcg cctccgaagg ctggcgacgg ctgggagagc tgctgacccg ccagccggtc    960

gagccgccgc gcatcgccct gccccgcccg cgggcgctga tcgaggcgca gaacctctcc   1020

gtggtgccgc cgggcgaggc ggtcgcggtg ctgcgcggcg tgagcttccg gctggatccg   1080

ggtcaggcgc tcggggtcat cggcccctcc gggtcgggca agtccacgct ggcgcgggcc   1140

ctgatcgggg tctggcgtcc ggccgcgggc aaggtccggc tcgatggcgc cgccctcgac   1200

cagtatgacc cggacgtgct cggcggctat atcggttacc tgccccagcg cgtgacgctg   1260

ttcgagggca ccatcgccga gaatatcgcg cgcctccggg gcgcgcccga tggtgacgcc   1320

gtggtggccg ccgcgcgcaa ggccgccgcg cacgacatga tcgtggcact tccctcgggc   1380

tacgacaccc gcgtctcggc cctgggtggc cggctgtccg gcgggcagat ccagcgcatc   1440

gggctcgcgc gcgccatgta cggcaacccc gtgttcctcg tcctcgacga gccgaactcg   1500

aacctcgaca atgagggctc gcttgcgctg aacgcggcga tccgctcgat gaagcaggcg   1560

ggagggtcgg tgttcatcat ggcccaccgc cccgccgcaa ttcaggagtg cgacctcctc   1620

atggtgatgg agaacggaat gcgcgccgcc ttcggccagc gcgacgccgt gctgcgcgac   1680

atggtgaaga accataccga gatcgtgcga aacgcaggcc ccggaggcgt gacatga      1737
```

<210> SEQ ID NO 30
<211> LENGTH: 578
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 30

```
Met Thr Arg Ser Asp Asn Arg Lys Gly Leu Glu Glu Leu Arg Ala Val
1               5                   10                  15

Arg Arg Ser Thr Met Gly Ala Leu Thr Ser Val Phe Leu Phe Ser Ile
            20                  25                  30

Phe Val Asn Leu Leu Met Leu Thr Gly Pro Leu Tyr Met Leu Gln Val
        35                  40                  45

Tyr Asp Arg Val Leu Gly Ser Arg Ser Glu Glu Thr Leu Leu Ala Leu
    50                  55                  60

Ser Leu Leu Val Thr Phe Leu Phe Val Ala Met Gly Val Leu Asp His
65                  70                  75                  80

Ala Arg Ala Arg Val Met Ala Arg Val Gly Ala Gly Phe Gln Glu Lys
                85                  90                  95

Leu Asp Arg Arg Val Phe Glu Ala Ala Val Arg Arg Leu Ser Leu Ala
            100                 105                 110

Pro Gly Asp Pro Ser Ala Val Ala Ala Gln Arg Asp Leu Glu Ser Val
        115                 120                 125

Gln Arg Leu Trp Ala Ser Pro Val Leu Ile Ala Leu Phe Asp Ile Pro
    130                 135                 140

Trp Thr Pro Phe Phe Leu Ala Ala Ile Phe Val Phe His Pro Tyr Met
145                 150                 155                 160
```

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```
Gly Trp Leu Ala Ile Gly Gly Gly Val Val Leu Val Ile Val Thr Ile
                165                 170                 175

Leu Asn Gln Arg Leu Ser Glu Gly Pro Met Gln Lys Ala Asn Ile Val
            180                 185                 190

Ala Leu Gln Ala Asp Arg Phe Ala Glu Asn Leu Lys Ser Glu Ser Glu
        195                 200                 205

Val Val Gln Ala Leu Gly Met Ala Gly Asn Gly Phe Asp Arg Trp His
    210                 215                 220

Lys Ala Arg Ala Ala Ala Leu Asp Ala Asn Met Ala Ala Ala Asp Leu
225                 230                 235                 240

Thr Gly Ala Phe Gly Thr Leu Thr Lys Thr Leu Arg Leu Phe Leu Gln
                245                 250                 255

Ser Ala Met Leu Gly Leu Gly Ala Trp Leu Val Leu Gln Gln Glu Leu
            260                 265                 270

Ser Ala Gly Ala Met Ile Ala Gly Ser Ile Leu Met Gly Arg Ala Leu
        275                 280                 285

Ala Pro Ile Glu Ser Ala Ile Gly Gln Trp Ala Leu Val Gln Arg Ala
    290                 295                 300

Ser Glu Gly Trp Arg Arg Leu Gly Glu Leu Leu Thr Arg Gln Pro Val
305                 310                 315                 320

Glu Pro Pro Arg Ile Ala Leu Pro Arg Pro Arg Ala Leu Ile Glu Ala
                325                 330                 335

Gln Asn Leu Ser Val Val Pro Pro Gly Glu Ala Val Ala Val Leu Arg
            340                 345                 350

Gly Val Ser Phe Arg Leu Asp Pro Gly Gln Ala Leu Gly Val Ile Gly
        355                 360                 365

Pro Ser Gly Ser Gly Lys Ser Thr Leu Ala Arg Ala Leu Ile Gly Val
    370                 375                 380

Trp Arg Pro Ala Ala Gly Lys Val Arg Leu Asp Gly Ala Ala Leu Asp
385                 390                 395                 400

Gln Tyr Asp Pro Asp Val Leu Gly Gly Tyr Ile Gly Tyr Leu Pro Gln
                405                 410                 415

Arg Val Thr Leu Phe Glu Gly Thr Ile Ala Glu Asn Ile Ala Arg Leu
            420                 425                 430

Arg Gly Ala Pro Asp Gly Asp Ala Val Val Ala Ala Ala Arg Lys Ala
        435                 440                 445

Ala Ala His Asp Met Ile Val Ala Leu Pro Ser Gly Tyr Asp Thr Arg
    450                 455                 460

Val Ser Ala Leu Gly Gly Arg Leu Ser Gly Gly Gln Ile Gln Arg Ile
465                 470                 475                 480

Gly Leu Ala Arg Ala Met Tyr Gly Asn Pro Val Phe Leu Val Leu Asp
                485                 490                 495

Glu Pro Asn Ser Asn Leu Asp Asn Glu Gly Ser Leu Ala Leu Asn Ala
            500                 505                 510

Ala Ile Arg Ser Met Lys Gln Ala Gly Gly Ser Val Phe Ile Met Ala
        515                 520                 525

His Arg Pro Ala Ala Ile Gln Glu Cys Asp Leu Leu Met Val Met Glu
    530                 535                 540

Asn Gly Met Arg Ala Ala Phe Gly Gln Arg Asp Ala Val Leu Arg Asp
545                 550                 555                 560

Met Val Lys Asn His Thr Glu Ile Val Arg Asn Ala Gly Pro Gly Gly
                565                 570                 575

Val Thr
```

<210> SEQ ID NO 31
<211> LENGTH: 606
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 31

```
atgccggcca tcgaaagcgg cctttgggcg ctgatcctga cgggagtgct gggctatctg     60

ctcggctcga tcccgttcgg catcgtcatc acccgcgcgc tggggctggg cgacctgcgc    120

aagatcggct cgggcaatat cggcgcgacc aacgtgctcc ggacgggcaa caagcccgcg    180

gcgctggcca cgctgctcct cgattcgggc aagggcgcca tcgccgtgct gatcgcgcgc    240

gcggccgtgg gcgaggatgc ggcgcagctt gcggccttca cctcgtttct ggggcacctt    300

ttcccggtct ggctcggctt ccgcggcggc aagggggtcg cgaccttcct cggcacgctg    360

ctggcactcg catggcccgt ggggctcgcc tgctgcctca cctggctcgc gaccgcggcc    420

ctgggccgga tctcctcgct ctcggccctc gtggctgcgg cgagcggtgt cctctggatg    480

atccttctgg gctacggcca gatggcggcg ctgggggcgg tgctcgcggt gctgatcttc    540

atccgccacc atgcgaacat ccgccggatc ctcgccggca ccgagccgcg gatcgggaag    600

aagtaa                                                               606
```

<210> SEQ ID NO 32
<211> LENGTH: 201
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 32

```
Met Pro Ala Ile Glu Ser Gly Leu Trp Ala Leu Ile Leu Thr Gly Val
1               5                   10                  15

Leu Gly Tyr Leu Leu Gly Ser Ile Pro Phe Gly Ile Val Ile Thr Arg
            20                  25                  30

Ala Leu Gly Leu Gly Asp Leu Arg Lys Ile Gly Ser Gly Asn Ile Gly
        35                  40                  45

Ala Thr Asn Val Leu Arg Thr Gly Asn Lys Pro Ala Ala Leu Ala Thr
    50                  55                  60

Leu Leu Leu Asp Ser Gly Lys Gly Ala Ile Ala Val Leu Ile Ala Arg
65                  70                  75                  80

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

Leu Gly His Leu Phe Pro Val Trp Leu Gly Phe Arg Gly Gly Lys Gly
            100                 105                 110

Val Ala Thr Phe Leu Gly Thr Leu Leu Ala Leu Ala Trp Pro Val Gly
        115                 120                 125

Leu Ala Cys Cys Leu Thr Trp Leu Ala Thr Ala Ala Leu Gly Arg Ile
    130                 135                 140

Ser Ser Leu Ser Ala Leu Val Ala Ala Ala Ser Gly Val Leu Trp Met
145                 150                 155                 160

Ile Leu Leu Gly Tyr Gly Gln Met Ala Ala Leu Gly Ala Val Leu Ala
                165                 170                 175

Val Leu Ile Phe Ile Arg His His Ala Asn Ile Arg Arg Ile Leu Ala
            180                 185                 190

Gly Thr Glu Pro Arg Ile Gly Lys Lys
        195                 200
```

```
<210> SEQ ID NO 33
<211> LENGTH: 1401
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 33

ttgcggcggt tcctgaacac gctctccggg cggttcctga tgctgaccgc cgccttcgtc      60

atgctggcgg aggtgctgat cctcgtgccc tcggtggcgc gcttccgcga ggattacctc     120

ctcctccggc tggagaaggc gcagatcgcg tcgctggccc tgctggcggc ggacgacatg     180

atcgcgcccg acctcgaggc ggagcttctg gccaatgcgg gcgtctacaa cgtggtgctg     240

cgccgcgacg aggtgcgcca gcttgtgctg tcctcgccca ttcccgtgcc ggtggagcag     300

acctacgacc tgcgcttcgc gggccccctc gggctgatcc gcgacacctt catggatgtg     360

ctcgacaagc agggcgtgat tcgggtgatc ggcgaaccgg tggagagcgg cggccagcag     420

atcgaggtcg cgctcgaacg gggccccatg cgcaaggcca tgctcgagca tggggcgcgg     480

gtgctcgtct tctcggcgct gatctcgatg gtgacggcgc ttctgctgtt ccttgcggtg     540

cggcggcttc tggtggtgcc gatccggcgg gtcgtcaccc acatgaccgc ctatgccgaa     600

gcgcccgagg atgcgcgccg cgtgatcgcg cccaccgcgg gcatccgcga gctgcgcgag     660

gccgaggagg cgctgcagat gatgcagacc cagctcatcg gcgcgctgcg ccagaaggag     720

cggctggccc agctcggcgg ggcggtggcc aagatcagcc acgacctgcg caacatcctg     780

acgacggcgc agctgtttgc cgaccggctg tcggcctccg acgatccggc ggtggcccgg     840

gcggcgccga agctggtggg atcgatccgg cgcgcggtct cgctttgcga atcgacgctg     900

accttcgggc gcgccgagga gccgccgccc cagatcgcgc gcgtgccgct gcgccggctg     960

atggaggagg tggccgaggc cgaatcgctg gtggcggatg ccagcgtggg ctgcctgatc    1020

gatgtggcgc cgaacatggt gatccgtgcc gacggcgagc agctctaccg cgtgctgggc    1080

aacctcgtgc gcaatgcgcg gcaggcgctg gagacggcgg gccggcccgg caccatcgag    1140

ctctcggcgg gcgagggcga ggaagagtgg tggatcaagg tgggcgacac cgggccgggc    1200

ctgccgccca aggcgcgcga acatctcttc accgccttcc agggcggggc gcgcaagggg    1260

ggctcgggcc tcgggctcgc catctcggcc gagctggtgc gtggtcacgg cggacggctc    1320

gacctgttgc ggagcgacag cgacgggacg gagttcatca tccgcctgcc caaggggccc    1380

ggtctcagcg ccctcgtctg a                                              1401


<210> SEQ ID NO 34
<211> LENGTH: 466
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 34

Met Arg Arg Phe Leu Asn Thr Leu Ser Gly Arg Phe Leu Met Leu Thr
1               5                   10                  15

Ala Ala Phe Val Met Leu Ala Glu Val Leu Ile Leu Val Pro Ser Val
            20                  25                  30

Ala Arg Phe Arg Glu Asp Tyr Leu Leu Leu Arg Leu Glu Lys Ala Gln
        35                  40                  45

Ile Ala Ser Leu Ala Leu Leu Ala Ala Asp Asp Met Ile Ala Pro Asp
    50                  55                  60

Leu Glu Ala Glu Leu Leu Ala Asn Ala Gly Val Tyr Asn Val Val Leu
65                  70                  75                  80

Arg Arg Asp Glu Val Arg Gln Leu Val Leu Ser Ser Pro Ile Pro Val
```

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                 85                  90                  95

Pro Val Glu Gln Thr Tyr Asp Leu Arg Phe Ala Gly Pro Leu Gly Leu
            100                 105                 110

Ile Arg Asp Thr Phe Met Asp Val Leu Asp Lys Gln Gly Val Ile Arg
        115                 120                 125

Val Ile Gly Glu Pro Val Glu Ser Gly Gly Gln Gln Ile Glu Val Ala
    130                 135                 140

Leu Glu Arg Gly Pro Met Arg Lys Ala Met Leu Glu His Gly Ala Arg
145                 150                 155                 160

Val Leu Val Phe Ser Ala Leu Ile Ser Met Val Thr Ala Leu Leu Leu
                165                 170                 175

Phe Leu Ala Val Arg Arg Leu Leu Val Val Pro Ile Arg Arg Val Val
            180                 185                 190

Thr His Met Thr Ala Tyr Ala Glu Ala Pro Glu Asp Ala Arg Arg Val
        195                 200                 205

Ile Ala Pro Thr Ala Gly Ile Arg Glu Leu Arg Glu Ala Glu Glu Ala
    210                 215                 220

Leu Gln Met Met Gln Thr Gln Leu Ile Gly Ala Leu Arg Gln Lys Glu
225                 230                 235                 240

Arg Leu Ala Gln Leu Gly Gly Ala Val Ala Lys Ile Ser His Asp Leu
                245                 250                 255

Arg Asn Ile Leu Thr Thr Ala Gln Leu Phe Ala Asp Arg Leu Ser Ala
            260                 265                 270

Ser Asp Asp Pro Ala Val Ala Arg Ala Ala Pro Lys Leu Val Gly Ser
        275                 280                 285

Ile Arg Arg Ala Val Ser Leu Cys Glu Ser Thr Leu Thr Phe Gly Arg
    290                 295                 300

Ala Glu Glu Pro Pro Pro Gln Ile Ala Arg Val Pro Leu Arg Arg Leu
305                 310                 315                 320

Met Glu Glu Val Ala Glu Ala Glu Ser Leu Val Ala Asp Ala Ser Val
                325                 330                 335

Gly Cys Leu Ile Asp Val Ala Pro Asn Met Val Ile Arg Ala Asp Gly
            340                 345                 350

Glu Gln Leu Tyr Arg Val Leu Gly Asn Leu Val Arg Asn Ala Arg Gln
        355                 360                 365

Ala Leu Glu Thr Ala Gly Arg Pro Gly Thr Ile Glu Leu Ser Ala Gly
    370                 375                 380

Glu Gly Glu Glu Glu Trp Trp Ile Lys Val Gly Asp Thr Gly Pro Gly
385                 390                 395                 400

Leu Pro Pro Lys Ala Arg Glu His Leu Phe Thr Ala Phe Gln Gly Gly
                405                 410                 415

Ala Arg Lys Gly Gly Ser Gly Leu Gly Leu Ala Ile Ser Ala Glu Leu
            420                 425                 430

Val Arg Gly His Gly Gly Arg Leu Asp Leu Leu Arg Ser Asp Ser Asp
        435                 440                 445

Gly Thr Glu Phe Ile Ile Arg Leu Pro Lys Gly Ala Gly Leu Ser Ala
    450                 455                 460

Leu Val
465
```

<210> SEQ ID NO 35
<211> LENGTH: 750
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

```
<400> SEQUENCE: 35

atgtgggtcg atcatgtgca gggcgagacc ttccacgggc gcaagggggc gctcggcaac      60

agctttcgct acggggtgga ttatctgctg atcgatcccg aggcggtgga ggggccggcg     120

ctcttctcgc gcaaccgggc caacctcatc tcgctccacg atcgcgacta cggcggtgcg     180

ccgggcgagg gacggggcgc agcgtgggtg cgcgaggtgc tggcggcgca ggggctgccg     240

cccgccgcgc gcatcctgct gctgacccag ccgcgggtgc tgggccatgt gttcaacccg     300

gtcagcttct ggctctgcga ggatgccgcg ggcgcgctcc gctgcgtggt ggccgaggtc     360

agcaacacct tcggcgaccg gcactggtat ctctgcgcca agcccgacgg ctccgtcatc     420

gagcggacgg acacgctcga ggcggccaag atcatgcatg tctcgccctt ccagccgatc     480

gagggcggct atcgcttccg cttcgacatc cgcgaggatc gggtgggcgt ctggatcgac     540

tacagctccg ccgagggcgg gctctatgcc acgcttacgg gccggcgagc gcggctgtcg     600

aaccggggga tcctgcgcgc ctgcctccgg cggcccttcg ggtcgcgccg cgtgctggcg     660

ctgatccact ggcaggcgct taagctggcg ctgaaggggg cgcgctaccg cagccgcccc     720

gcgccgccgc tgcaagacgt cacgcggtga                                      750


<210> SEQ ID NO 36
<211> LENGTH: 249
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 36

Met Trp Val Asp His Val Gln Gly Glu Thr Phe His Gly Arg Lys Gly
1               5                   10                  15

Ala Leu Gly Asn Ser Phe Arg Tyr Gly Val Asp Tyr Leu Leu Ile Asp
            20                  25                  30

Pro Glu Ala Val Glu Gly Pro Ala Leu Phe Ser Arg Asn Arg Ala Asn
    35                      40                  45

Leu Ile Ser Leu His Asp Arg Asp Tyr Gly Gly Ala Pro Gly Glu Gly
    50                  55                  60

Arg Gly Ala Ala Trp Val Arg Glu Val Leu Ala Ala Gln Gly Leu Pro
65                  70                  75                  80

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

Val Phe Asn Pro Val Ser Phe Trp Leu Cys Glu Asp Ala Ala Gly Ala
            100                 105                 110

Leu Arg Cys Val Val Ala Glu Val Ser Asn Thr Phe Gly Asp Arg His
        115                 120                 125

Trp Tyr Leu Cys Ala Lys Pro Asp Gly Ser Val Ile Glu Arg Thr Asp
    130                 135                 140

Thr Leu Glu Ala Ala Lys Ile Met His Val Ser Pro Phe Gln Pro Ile
145                 150                 155                 160

Glu Gly Gly Tyr Arg Phe Arg Phe Asp Ile Arg Glu Asp Arg Val Gly
                165                 170                 175

Val Trp Ile Asp Tyr Ser Ser Ala Glu Gly Gly Leu Tyr Ala Thr Leu
            180                 185                 190

Thr Gly Arg Arg Ala Arg Leu Ser Asn Arg Gly Ile Leu Arg Ala Cys
        195                 200                 205

Leu Arg Arg Pro Phe Gly Ser Arg Arg Val Leu Ala Leu Ile His Trp
    210                 215                 220
```

```
Gln Ala Leu Lys Leu Ala Leu Lys Gly Ala Arg Tyr Arg Ser Arg Pro
225                 230                 235                 240

Ala Pro Pro Leu Gln Asp Val Thr Arg
                245


<210> SEQ ID NO 37
<211> LENGTH: 1293
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 37

atgccattcg agacgtctga gttcgcgcgg cggcgcgttg cggtgatcgg tgggggcatc      60

tcggggatgg ctgcggcgca tcttctggcc tccgaccatg cggtcgtgct gttcgaggcc     120

gagaagcggc tcgggggca cgcccgcacg gtcctcgcgg gcaagcgcgg cgaccagcct     180

gtcgacacgg gcttcatcgt gttcaacaag gtgaattatc cgcacctcac gcggctcttc     240

gacgagctcg gcgtgccggt ggcgaagagt gacatgagct tcggcgcctc ggttcgcggc     300

gggcggctgg aatacggcct caagaacctg aaatccgtct tcgcgcagaa gcgcaacatg     360

gcggatccgc gcttcctcaa catgatgatg gatgtgctgc gcttcaacgc ccatgcgctc     420

gaccatgcgg acgatccggc catgacgatc cgcgagctgc tcgcgcggct cgacctcggc     480

gactggttcc gggactatta cctcctgccg atctcggggg cgatctggtc cacgccctcg     540

cgcgggatcc tcgacttccc ggcgcaggca ctgctgcgct tcttccagaa ccatgcgctc     600

ctgtcccata cggggcagca ccagtggttc acggtcgagg gcggctcgat cgaatatgtc     660

acccggctgc aggccgcgat ggcggcgcgc ggggtggacc tgcgcaccgg ggcgcaggtg     720

gccggcgtgc gccgcgcgga cggcggggtg cgggtgcggg ccgagggcgg cgagtgggag     780

gccttcgacg aggtgatctt cgccacccat tccgacgata cgctgcggct tctgtccgat     840

gcgacggagg ccgagacgag cgcgctcggg gccgtgcgct accagccgaa ccgggcggtg     900

ctgcattccg atccgtcggt catgccgaag cgcaaggccg cctgggcctc ctgggtctat     960

gtcgagcctg acgatccgga ggcgcccatc gacatcacct actggatgaa ctcgctgcag    1020

cccatcccgc aggacgatcc gctgttcgtg acgctgaacg gcacccgccc ggtgcgcgag    1080

gaactggtgc atgatgtggc gaccttccgc cacccggtct acgacctcgc ggcgcagctg    1140

ggcgtggcgg cgctgcggat gatgaacggc cagcgtcaga cctggttcgc gggcgcctgg    1200

atgcgcaacg gcttccacga ggatggcttt gccagcgctg tggatgttgt cgaggcgatg    1260

cgccggcgca ttcccgcctc ggccgcggcc tga                                 1293


<210> SEQ ID NO 38
<211> LENGTH: 430
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 38

Met Pro Phe Glu Thr Ser Glu Phe Ala Arg Arg Arg Val Ala Val Ile
1               5                   10                  15

Gly Gly Gly Ile Ser Gly Met Ala Ala Ala His Leu Leu Ala Ser Asp
            20                  25                  30

His Ala Val Val Leu Phe Glu Ala Glu Lys Arg Leu Gly Gly His Ala
        35                  40                  45

Arg Thr Val Leu Ala Gly Lys Arg Gly Asp Gln Pro Val Asp Thr Gly
    50                  55                  60

Phe Ile Val Phe Asn Lys Val Asn Tyr Pro His Leu Thr Arg Leu Phe
```

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```
65                  70                  75                  80

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

Ser Val Arg Gly Gly Arg Leu Glu Tyr Gly Leu Lys Asn Leu Lys Ser
            100                 105                 110

Val Phe Ala Gln Lys Arg Asn Met Ala Asp Pro Arg Phe Leu Asn Met
        115                 120                 125

Met Met Asp Val Leu Arg Phe Asn Ala His Ala Leu Asp His Ala Asp
    130                 135                 140

Asp Pro Ala Met Thr Ile Arg Glu Leu Leu Ala Arg Leu Asp Leu Gly
145                 150                 155                 160

Asp Trp Phe Arg Asp Tyr Tyr Leu Leu Pro Ile Ser Gly Ala Ile Trp
                165                 170                 175

Ser Thr Pro Ser Arg Gly Ile Leu Asp Phe Pro Ala Gln Ala Leu Leu
            180                 185                 190

Arg Phe Phe Gln Asn His Ala Leu Leu Ser His Thr Gly Gln His Gln
        195                 200                 205

Trp Phe Thr Val Glu Gly Gly Ser Ile Glu Tyr Val Thr Arg Leu Gln
    210                 215                 220

Ala Ala Met Ala Ala Arg Gly Val Asp Leu Arg Thr Gly Ala Gln Val
225                 230                 235                 240

Ala Gly Val Arg Arg Ala Asp Gly Gly Val Arg Val Arg Ala Glu Gly
                245                 250                 255

Gly Glu Trp Glu Ala Phe Asp Glu Val Ile Phe Ala Thr His Ser Asp
            260                 265                 270

Asp Thr Leu Arg Leu Leu Ser Asp Ala Thr Glu Ala Glu Thr Ser Ala
        275                 280                 285

Leu Gly Ala Val Arg Tyr Gln Pro Asn Arg Ala Val Leu His Ser Asp
    290                 295                 300

Pro Ser Val Met Pro Lys Arg Lys Ala Ala Trp Ala Ser Trp Val Tyr
305                 310                 315                 320

Val Glu Pro Asp Asp Pro Glu Ala Pro Ile Asp Ile Thr Tyr Trp Met
                325                 330                 335

Asn Ser Leu Gln Pro Ile Pro Gln Asp Asp Pro Leu Phe Val Thr Leu
            340                 345                 350

Asn Gly Thr Arg Pro Val Arg Glu Glu Leu Val His Asp Val Ala Thr
        355                 360                 365

Phe Arg His Pro Val Tyr Asp Leu Ala Ala Gln Leu Gly Val Ala Ala
    370                 375                 380

Leu Arg Met Met Asn Gly Gln Arg Gln Thr Trp Phe Ala Gly Ala Trp
385                 390                 395                 400

Met Arg Asn Gly Phe His Glu Asp Gly Phe Ala Ser Ala Val Asp Val
                405                 410                 415

Val Glu Ala Met Arg Arg Arg Ile Pro Ala Ser Ala Ala Ala
            420                 425                 430


<210> SEQ ID NO 39
<211> LENGTH: 540
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 39

atgaagacta tctccgcgtt cgccctctgt ggcgccctgg tcctttcggc ctgcgcctcg      60

acgacgccga tggcgctggg gcccgacgga aagccgctgc cgcaggtcta caagatcacg     120
```

```
tccgctcagg agggtgaagt cacctaccgg ctgctggatt cggtcaatgc gctgcgccag    180

gcgaaggggg cggctccgct ccagctcaac tcgcagctca ccgccgccgc ggccacccac    240

tcgcgcgaca tgtcggtgca gaaccgcccc tggcacttcg ggtcggacgg ctcctcgcct    300

cttctgcggg tgcagcgcgc gggctatcag ggcaagctga agggtgagct gatctcggaa    360

acctaccaga ccgagctcga gacgctggcc gtctggatgg agcagaagga cacgcgcgag    420

atcgtgctgg atccgaccgc gaccgacctc ggcttcgcct ggtatcagga gccgcagggc    480

aagatctggt ggaccgtcgt gacgggcagt tccgcgccca tggcggtggc gggtctctga    540
```

```
<210> SEQ ID NO 40
<211> LENGTH: 179
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 40

Met Lys Thr Ile Ser Ala Phe Ala Leu Cys Gly Ala Leu Val Leu Ser
1               5                   10                  15

Ala Cys Ala Ser Thr Thr Pro Met Ala Leu Gly Pro Asp Gly Lys Pro
            20                  25                  30

Leu Pro Gln Val Tyr Lys Ile Thr Ser Ala Gln Glu Gly Glu Val Thr
        35                  40                  45

Tyr Arg Leu Leu Asp Ser Val Asn Ala Leu Arg Gln Ala Lys Gly Ala
    50                  55                  60

Ala Pro Leu Gln Leu Asn Ser Gln Leu Thr Ala Ala Ala Ala Thr His
65                  70                  75                  80

Ser Arg Asp Met Ser Val Gln Asn Arg Pro Trp His Phe Gly Ser Asp
                85                  90                  95

Gly Ser Ser Pro Leu Leu Arg Val Gln Arg Ala Gly Tyr Gln Gly Lys
            100                 105                 110

Leu Lys Gly Glu Leu Ile Ser Glu Thr Tyr Gln Thr Glu Leu Glu Thr
        115                 120                 125

Leu Ala Val Trp Met Glu Gln Lys Asp Thr Arg Glu Ile Val Leu Asp
    130                 135                 140

Pro Thr Ala Thr Asp Leu Gly Phe Ala Trp Tyr Gln Glu Pro Gln Gly
145                 150                 155                 160

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

Ala Gly Leu
```

```
<210> SEQ ID NO 41
<211> LENGTH: 759
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 41

atgctgaagg gaaaatatgg gctggtggtg ggtgtcgcca acggccagtc gatcgccgcc     60

ggatgcgccc gcgccttcgc gggcgccggg gccgagcttg cgctgaccta tctgaacgag    120

cgcgccctgc cccatgtcca gccggtggcc gaggaggtgg acgccgcggc gctgctgccg    180

ctcgacctgt cgcaggaaga tgcgctggaa gcggtcttcg agagcgtcag gcaacgctgg    240

gggcgtctcg acttcctgct ccattcggtg gccttctgcc cgaaggagga tctgcacggc    300

cgcgtcaccg actgttcggc ccggggcttc gcacaggcca tggacatctc ctgccactcg    360

ttcctgcgga tggcgaagct ggccgaaccg ctgatgagcg cgggcggcag cctgatgacg    420
```

```
gtcagctact acggcgccga gaaggtggtg gaccattaca acatcatggg tccggtgaag    480

gccgcgctcg aagcctgcac ccgccatgtg gcggccgagc tcgggccgca ggggatccgg    540

gccaacgtgc tctcgcccgg cccgatcgcg acccgcgcag cgagcggcat cgaccatttc    600

gacgcgctga tcgaggatgc caagacccgc tcgcccgagc ggcgtctcgt gaccatcgac    660

gaggtgggtg ccgtggccgc cttcctcgcc tccgatgccg cctcgggcgt caccggaacc    720

gtgacccaca tcgacggagg ccgacatgtt cggatgtga                           759
```

<210> SEQ ID NO 42
<211> LENGTH: 252
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 42

```
Met Leu Lys Gly Lys Tyr Gly Leu Val Val Gly Val Ala Asn Gly Gln
1               5                   10                  15

Ser Ile Ala Ala Gly Cys Ala Arg Ala Phe Ala Gly Ala Gly Ala Glu
            20                  25                  30

Leu Ala Leu Thr Tyr Leu Asn Glu Arg Ala Leu Pro His Val Gln Pro
        35                  40                  45

Val Ala Glu Glu Val Asp Ala Ala Ala Leu Leu Pro Leu Asp Leu Ser
    50                  55                  60

Gln Glu Asp Ala Leu Glu Ala Val Phe Glu Ser Val Arg Gln Arg Trp
65                  70                  75                  80

Gly Arg Leu Asp Phe Leu Leu His Ser Val Ala Phe Cys Pro Lys Glu
                85                  90                  95

Asp Leu His Gly Arg Val Thr Asp Cys Ser Ala Arg Gly Phe Ala Gln
            100                 105                 110

Ala Met Asp Ile Ser Cys His Ser Phe Leu Arg Met Ala Lys Leu Ala
        115                 120                 125

Glu Pro Leu Met Ser Ala Gly Gly Ser Leu Met Thr Val Ser Tyr Tyr
    130                 135                 140

Gly Ala Glu Lys Val Val Asp His Tyr Asn Ile Met Gly Pro Val Lys
145                 150                 155                 160

Ala Ala Leu Glu Ala Cys Thr Arg His Val Ala Ala Glu Leu Gly Pro
                165                 170                 175

Gln Gly Ile Arg Ala Asn Val Leu Ser Pro Gly Pro Ile Ala Thr Arg
            180                 185                 190

Ala Ala Ser Gly Ile Asp His Phe Asp Ala Leu Ile Glu Asp Ala Lys
        195                 200                 205

Thr Arg Ser Pro Glu Arg Arg Leu Val Thr Ile Asp Glu Val Gly Ala
    210                 215                 220

Val Ala Ala Phe Leu Ala Ser Asp Ala Ala Ser Gly Val Thr Gly Thr
225                 230                 235                 240

Val Thr His Ile Asp Gly Gly Arg His Val Arg Met
                245                 250
```

<210> SEQ ID NO 43
<211> LENGTH: 1035
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 43

```
atgagggtcg tcgtcgtctg tcccggccgc ggcacctaca ccaaggcaga actgggctct     60
```

-continued

```
ctcggccggc tccatcccga caaggccgcg ctgttcgccc ggttcgatgc ccagcgccgg    120

gtggcggggc aggagacgct ggccgatctc gacggcgaag cgagctattc cgtggcgcgc    180

cacacgcggg gcgacaatgc ctcggcgctg atctatgccg cgggctacgc cgatttcctg    240

tcgctcacgg gcgtcgaggt ggtggccgtc accggcaatt cgatgggctg gtatacggcg    300

ctggcctgcg gcggcgccct ttcggccgaa gacggcttcc gggtcgtcaa cacgatgggc    360

acgctgatgc aggaggcgct gatcggcggc cagatcgtcc atccggtcat gggcgaggac    420

tggcggcccg accttgcccg ccgcgcgcaa ctgctggatc aggtggccgg gatcgacgcc    480

cgcccggggc gcatcctcgg cctctccatc gcgctcggcg ggatgctcgt gctggcgggc    540

aatgccgaag gtctggccga tttcgaggcc gaagtgccgc ccgaacaggg ccgcttcccg    600

atgcgccttg ccaatcacgc ggccttccac accgcccttc aggcgccggt cgccgcgcgc    660

ggacaggcgg cgctgcccga ggcgctgttc ggtcagccgc ggctgccgct catcgacggg    720

cgcggcgccg tctggtggcc gaaagccacc gacgcggcgg cgctccgggc ctatacgctc    780

ggccatcagg tcacggagcc ctacgatttc acccgcgcca tcgcggtcgc cgcgcgggaa    840

ttcgcgcccg acgccttcgt cgtactcggc cccggcacca cgctgggcgg ggccgtggcg    900

cagagcttga tcctcgccgg ctggcgcggg atgaaggacc gcaaggattt ccagacccgt    960

caggccgaga gccccctgct gatcgcactg ggcgagaggg accagcgcgg gcacgtcaca   1020

ggaggaccca gatga                                                    1035
```

<210> SEQ ID NO 44
<211> LENGTH: 344
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 44

```
Met Arg Val Val Val Val Cys Pro Gly Arg Gly Thr Tyr Thr Lys Ala
1               5                   10                  15

Glu Leu Gly Ser Leu Gly Arg Leu His Pro Asp Lys Ala Ala Leu Phe
            20                  25                  30

Ala Arg Phe Asp Ala Gln Arg Arg Val Ala Gly Gln Glu Thr Leu Ala
        35                  40                  45

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

Asp Asn Ala Ser Ala Leu Ile Tyr Ala Ala Gly Tyr Ala Asp Phe Leu
65                  70                  75                  80

Ser Leu Thr Gly Val Glu Val Val Ala Val Thr Gly Asn Ser Met Gly
                85                  90                  95

Trp Tyr Thr Ala Leu Ala Cys Gly Gly Ala Leu Ser Ala Glu Asp Gly
            100                 105                 110

Phe Arg Val Val Asn Thr Met Gly Thr Leu Met Gln Glu Ala Leu Ile
        115                 120                 125

Gly Gly Gln Ile Val His Pro Val Met Gly Glu Asp Trp Arg Pro Asp
    130                 135                 140

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

Arg Pro Gly Arg Ile Leu Gly Leu Ser Ile Ala Leu Gly Gly Met Leu
                165                 170                 175

Val Leu Ala Gly Asn Ala Glu Gly Leu Ala Asp Phe Glu Ala Glu Val
            180                 185                 190

Pro Pro Glu Gln Gly Arg Phe Pro Met Arg Leu Ala Asn His Ala Ala
```

```
        195                 200                 205

Phe His Thr Ala Leu Gln Ala Pro Val Ala Ala Arg Gly Gln Ala Ala
    210                 215                 220

Leu Pro Glu Ala Leu Phe Gly Gln Pro Arg Leu Pro Leu Ile Asp Gly
225                 230                 235                 240

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

Ala Tyr Thr Leu Gly His Gln Val Thr Glu Pro Tyr Asp Phe Thr Arg
            260                 265                 270

Ala Ile Ala Val Ala Ala Arg Glu Phe Ala Pro Asp Ala Phe Val Val
        275                 280                 285

Leu Gly Pro Gly Thr Thr Leu Gly Gly Ala Val Ala Gln Ser Leu Ile
    290                 295                 300

Leu Ala Gly Trp Arg Gly Met Lys Asp Arg Lys Asp Phe Gln Thr Arg
305                 310                 315                 320

Gln Ala Glu Ser Pro Leu Leu Ile Ala Leu Gly Arg Glu Asp Gln Arg
                325                 330                 335

Gly His Val Thr Gly Gly Pro Arg
            340


<210> SEQ ID NO 45
<211> LENGTH: 1170
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 45

atgtccgaca tcctcgtcct ctccgccgtc cgcaccgcca tcggcggctt cggcggcgcg      60

ctcgccgcgg tcccgccggg cgatctcgcc accaccgtca cccgtgccgc gctggagcgc     120

gcaggcgtgg agcccggccg cgtggggcat gtggtcttcg gccatgtcat caacaccgaa     180

ccgcgcgaca tgtatctctc gcgcgtggcg gcgatgcagg cgggtatccc gtcggaggtg     240

ccggcgatga acgtgaaccg gctctgcggc tcgggcgtgc aggccgtcgt ctcggccatg     300

caggcgctga tgctgggcga tgccgaggtg gcgctggcgg gcggcgcgga atcgatgagc     360

cgcgcgccct atgcgctgac gacggcgcgg tggggccaga agatgggcga cacgcgcgcg     420

ctcgacatga tgacgggggc gctcaactgc cccttcggca ccggccacat gggcatcacc     480

gccgagatcg tggccgagcg ccacggcatc agccgcgagg atcaggacgc gttcgcgctg     540

gaaagccaga cccgcaccgc ccgcgcgcag gaggagggcc gcttcgacgg ccagatcgtt     600

ccggtcgaga tcgcctcgcg gaaggggccg gtctccttct cccgcgacga acatcccaag     660

gccaccaccc tcgaggcgct cgcggggctg cgtcccgcct tccagaaagg cggcacggtg     720

accgcaggca atgcgagcgg gatcaacgac ggggccgggg cgctgatcct cgcgcgcgag     780

gggggccgtgc ccgacgcgcg tccgctcggc cggctgatcg gctatgccca tgcgggcgtc    840

gatcccgagg tgatggggct ggggccgatc ccggcggtaa aggcgctctg cgcgcgcacc     900

ggcctctcgg tcgcggattt cgacgtgatc gagtcgaacg aggccttcgc ggcacaggcg     960

ctggccgtgg cgcgcgcgct cgatttcgat ccggccaggg tgaacccgaa cggcggcgcc    1020

atcgcgctcg gccatccggt cggcgccacc ggggcgatca tcacggtgaa ggcgctccac    1080

gagctgcacc ggacgggcgg gcgccgggcc ctcgtcacca tgtgcatcgg cggcgggcag    1140

gggatcgcgc tggcgctcga gcgggtctga                                     1170


<210> SEQ ID NO 46
```

```
<211> LENGTH: 389
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 46

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

Phe Gly Gly Ala Leu Ala Ala Val Pro Pro Gly Asp Leu Ala Thr Thr
            20                  25                  30

Val Thr Arg Ala Ala Leu Glu Arg Ala Gly Val Glu Pro Gly Arg Val
        35                  40                  45

Gly His Val Val Phe Gly His Val Ile Asn Thr Glu Pro Arg Asp Met
    50                  55                  60

Tyr Leu Ser Arg Val Ala Ala Met Gln Ala Gly Ile Pro Ser Glu Val
65                  70                  75                  80

Pro Ala Met Asn Val Asn Arg Leu Cys Gly Ser Gly Val Gln Ala Val
                85                  90                  95

Val Ser Ala Met Gln Ala Leu Met Leu Gly Asp Ala Glu Val Ala Leu
            100                 105                 110

Ala Gly Gly Ala Glu Ser Met Ser Arg Ala Pro Tyr Ala Leu Thr Thr
        115                 120                 125

Ala Arg Trp Gly Gln Lys Met Gly Asp Thr Arg Ala Leu Asp Met Met
    130                 135                 140

Thr Gly Ala Leu Asn Cys Pro Phe Gly Thr Gly His Met Gly Ile Thr
145                 150                 155                 160

Ala Glu Ile Val Ala Glu Arg His Gly Ile Ser Arg Glu Asp Gln Asp
                165                 170                 175

Ala Phe Ala Leu Glu Ser Gln Thr Arg Thr Ala Arg Ala Gln Glu Glu
            180                 185                 190

Gly Arg Phe Asp Gly Gln Ile Val Pro Val Glu Ile Ala Ser Arg Lys
        195                 200                 205

Gly Pro Val Ser Phe Ser Arg Asp Glu His Pro Lys Ala Thr Thr Leu
    210                 215                 220

Glu Ala Leu Ala Gly Leu Arg Pro Ala Phe Gln Lys Gly Gly Thr Val
225                 230                 235                 240

Thr Ala Gly Asn Ala Ser Gly Ile Asn Asp Gly Ala Gly Ala Leu Ile
                245                 250                 255

Leu Ala Arg Glu Gly Ala Val Pro Asp Ala Arg Pro Leu Gly Arg Leu
            260                 265                 270

Ile Gly Tyr Ala His Ala Gly Val Asp Pro Glu Val Met Gly Leu Gly
        275                 280                 285

Pro Ile Pro Ala Val Lys Ala Leu Cys Ala Arg Thr Gly Leu Ser Val
    290                 295                 300

Ala Asp Phe Asp Val Ile Glu Ser Asn Glu Ala Phe Ala Ala Gln Ala
305                 310                 315                 320

Leu Ala Val Ala Arg Ala Leu Asp Phe Asp Pro Ala Arg Val Asn Pro
                325                 330                 335

Asn Gly Gly Ala Ile Ala Leu Gly His Pro Val Gly Ala Thr Gly Ala
            340                 345                 350

Ile Ile Thr Val Lys Ala Leu His Glu Leu His Arg Thr Gly Gly Arg
        355                 360                 365

Arg Ala Leu Val Thr Met Cys Ile Gly Gly Gly Gln Gly Ile Ala Leu
    370                 375                 380

Ala Leu Glu Arg Val
```

```
385


<210> SEQ ID NO 47
<211> LENGTH: 1086
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 47

atggcgaagc gcagacggct tgaggctccc tcggcggaag aactcgagga gctggagacc     60

ggtttcgccc gcgaaacctc caccagcacg cggccgccca tcgcacaggt ggcggcggat    120

gcggcctcgc tggccatgcc gatgcccacg gccgaacgtg ccgcggccgc gaaggacagc    180

gccgatgcca cacggctgag gcaggccgag gccgaagggt tgcttctgct cgagatcccg    240

ctggccgaga tccgcgccga tgatctgacg cgcgaccggc tgaagatcga cggcgaggaa    300

atggacgagc tgcgcgcctc gatccgagcg catgggctgc ggttgccggt cgaggtgttc    360

gagcggccgg aggggcaggg agagcgctac ggtctgatct ccggctggcg gcgtctgtgg    420

gcgctgcgct cgctccatgc cgagacgggc gacgggcgct tcgcccgggt gcgtgcgctg    480

gtgcggcggc cgaccgacgt ctcggcagcc tatgtcgcga tggtcgagga aaacgagatc    540

cgctctgacc tctcgcctta cgagcgcggc aggatcgcgg ccctcgctgc ggggcagggg    600

gcgttcgggt cggtcgagga agcggtcgac gtgctgttcg gcgcggcctc gaaggcgaag    660

cggtcgaaga tccgcagctt cgcgcttatc catgaagagc tgggcgatct tctgggtttc    720

gccacgacgc tgggcgagcg gcccggcctg cgtctggccc acgccctgcg gctgggctac    780

gccggagcac tgcgcgaggc gctggcggcg gggcagggcg gcgatgccga ggcggagtgg    840

ctgctgatgg agcccttggt gaaggccgcc gaagggacgg tggcggaccc gtcgcgcggc    900

ggccgcccgc cccgtaaaca ggttcctgtg gcagcaacgg tccagatcga gcggtcgggc    960

gacggtccgg gctacctgtt gcggttggag ggtgacgacg tcgacgaagc gctggcgcag   1020

cgtgtcgcgc aggagttgcg aaagctgctg gcgtcgggga gggtttcgcc ggcgaaaccc   1080

ggttga                                                              1086


<210> SEQ ID NO 48
<211> LENGTH: 361
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 48

Met Ala Lys Arg Arg Arg Leu Glu Ala Pro Ser Ala Glu Glu Leu Glu
1               5                   10                  15

Glu Leu Glu Thr Gly Phe Ala Arg Glu Thr Ser Thr Ser Thr Arg Pro
            20                  25                  30

Pro Ile Ala Gln Val Ala Ala Asp Ala Ala Ser Leu Ala Met Pro Met
        35                  40                  45

Pro Thr Ala Glu Arg Ala Ala Ala Ala Lys Asp Ser Ala Asp Ala Thr
    50                  55                  60

Arg Leu Arg Gln Ala Glu Ala Glu Gly Leu Leu Leu Leu Glu Ile Pro
65                  70                  75                  80

Leu Ala Glu Ile Arg Ala Asp Asp Leu Thr Arg Asp Arg Leu Lys Ile
                85                  90                  95

Asp Gly Glu Glu Met Asp Glu Leu Arg Ala Ser Ile Arg Ala His Gly
            100                 105                 110

Leu Arg Leu Pro Val Glu Val Phe Glu Arg Pro Glu Gly Gln Gly Glu
        115                 120                 125
```

```
Arg Tyr Gly Leu Ile Ser Gly Trp Arg Arg Leu Trp Ala Leu Arg Ser
    130                 135                 140

Leu His Ala Glu Thr Gly Asp Gly Arg Phe Ala Arg Val Arg Ala Leu
145                 150                 155                 160

Val Arg Arg Pro Thr Asp Val Ser Ala Ala Tyr Val Ala Met Val Glu
                165                 170                 175

Glu Asn Glu Ile Arg Ser Asp Leu Ser Pro Tyr Glu Arg Gly Arg Ile
            180                 185                 190

Ala Ala Leu Ala Ala Gly Gln Gly Ala Phe Gly Ser Val Glu Glu Ala
        195                 200                 205

Val Asp Val Leu Phe Gly Ala Ala Ser Lys Ala Lys Arg Ser Lys Ile
    210                 215                 220

Arg Ser Phe Ala Leu Ile His Glu Glu Leu Gly Asp Leu Leu Gly Phe
225                 230                 235                 240

Ala Thr Thr Leu Gly Glu Arg Pro Gly Leu Arg Leu Ala His Ala Leu
                245                 250                 255

Arg Leu Gly Tyr Ala Gly Ala Leu Arg Glu Ala Leu Ala Ala Gly Gln
            260                 265                 270

Gly Gly Asp Ala Glu Ala Glu Trp Leu Leu Met Glu Pro Leu Val Lys
        275                 280                 285

Ala Ala Glu Gly Thr Val Ala Asp Pro Ser Arg Gly Gly Arg Pro Pro
    290                 295                 300

Arg Lys Gln Val Pro Val Ala Ala Thr Val Gln Ile Glu Arg Ser Gly
305                 310                 315                 320

Asp Gly Pro Gly Tyr Leu Leu Arg Leu Glu Gly Asp Asp Val Asp Glu
                325                 330                 335

Ala Leu Ala Gln Arg Val Ala Gln Glu Leu Arg Lys Leu Leu Ala Ser
            340                 345                 350

Gly Arg Val Ser Pro Ala Lys Pro Gly
        355                 360
```

<210> SEQ ID NO 49
<211> LENGTH: 876
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 49

```
atggagatcc gcaaggtcgg cgtcgtgggc gcgggacaga tgggcagcgg tatcgcgcat      60

gtcttctcgc tcgcgggcta cgaggtgctg ctgaacgaca tcagcgccga agggctgaac     120

aaggcgctct cgaccatcga gcgcaacatg gagcggcagg tctcgcgcgg gaaggtctcg     180

gccgaggaca aggccgcggc gctcgggcgg atccgcacca cccagaccct caccgacatc     240

gccaggagcg acctcgtgat cgaggccgcc accgagcgcg agacggtgaa acaggcgatc     300

ttcgaggatc tggtgccgca tcttctgccg cacacgatcc tgacctcgaa cacctcctcg     360

atctcgatca cacggcttgc ctcgcgcacg gaccggcccg agaaattcat gggctttcac     420

ttcatgaacc cggtgccggt gatgcagctc gtcgagctga tccgcggcat cgcgaccgac     480

gacccgacct atcaggcgct gctcaaggtg gtgcagagcc tcggcaagac cgcggccagc     540

gccgaggatt tcccggcctt catcgtcaac cgcatcctcg tgccgatgat caacgaagcg     600

gtctacacgc tctatgaagg cgtgggctcg gtgcgctcga tcgacgagtc gatgaagctc     660

ggggcgaatc atccgatggg gccgctggag ctcgcggatt tcatcgggct cgacacctgc     720

cttgcgatca tgaacgtgct gcacgacggg ctggccgata cgaaataccg gccctgcccg     780
```

```
cttctggtga aatatgtcga ggcaggatgg ctcggccgga agaccgcccg cggcttctac    840

gattatcgcg gcgagacgcc ggtgccgaca cggtag                               876


<210> SEQ ID NO 50
<211> LENGTH: 291
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 50

Met Glu Ile Arg Lys Val Gly Val Val Gly Ala Gly Gln Met Gly Ser
1               5                   10                  15

Gly Ile Ala His Val Phe Ser Leu Ala Gly Tyr Glu Val Leu Leu Asn
            20                  25                  30

Asp Ile Ser Ala Glu Gly Leu Asn Lys Ala Leu Ser Thr Ile Glu Arg
        35                  40                  45

Asn Met Glu Arg Gln Val Ser Arg Gly Lys Val Ser Ala Glu Asp Lys
    50                  55                  60

Ala Ala Ala Leu Gly Arg Ile Arg Thr Thr Gln Thr Leu Thr Asp Ile
65                  70                  75                  80

Ala Arg Ser Asp Leu Val Ile Glu Ala Ala Thr Glu Arg Glu Thr Val
                85                  90                  95

Lys Gln Ala Ile Phe Glu Asp Leu Val Pro His Leu Leu Pro His Thr
            100                 105                 110

Ile Leu Thr Ser Asn Thr Ser Ser Ile Ser Ile Thr Arg Leu Ala Ser
        115                 120                 125

Arg Thr Asp Arg Pro Glu Lys Phe Met Gly Phe His Phe Met Asn Pro
    130                 135                 140

Val Pro Val Met Gln Leu Val Glu Leu Ile Arg Gly Ile Ala Thr Asp
145                 150                 155                 160

Asp Pro Thr Tyr Gln Ala Leu Leu Lys Val Val Gln Ser Leu Gly Lys
                165                 170                 175

Thr Ala Ala Ser Ala Glu Asp Phe Pro Ala Phe Ile Val Asn Arg Ile
            180                 185                 190

Leu Val Pro Met Ile Asn Glu Ala Val Tyr Thr Leu Tyr Glu Gly Val
        195                 200                 205

Gly Ser Val Arg Ser Ile Asp Glu Ser Met Lys Leu Gly Ala Asn His
    210                 215                 220

Pro Met Gly Pro Leu Glu Leu Ala Asp Phe Ile Gly Leu Asp Thr Cys
225                 230                 235                 240

Leu Ala Ile Met Asn Val Leu His Asp Gly Leu Ala Asp Thr Lys Tyr
                245                 250                 255

Arg Pro Cys Pro Leu Leu Val Lys Tyr Val Glu Ala Gly Trp Leu Gly
            260                 265                 270

Arg Lys Thr Ala Arg Gly Phe Tyr Asp Tyr Arg Gly Glu Thr Pro Val
        275                 280                 285

Pro Thr Arg
    290


<210> SEQ ID NO 51
<211> LENGTH: 960
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 51

atgaactatc tcgaattcga aaagccgctg tccgagatcg agggcaaggc cgaggagttg     60
```

cgcgcgctcg cgcggggcaa cagggagatg gacgtcgaga aggaagcgtc ggcgctcgac   120

aagaaggccg agacgctgct gaaggatctc tacaaggacc tgaccccctg gcggaagtgc   180

caggtggcgc gccatcccga ccgcccgcac tgcaaggact atatcgaggg cctcttcacc   240

gaatatacgc cgctcgcggg cgaccggaac ttcgccgacg accatgcgat catgggcggg   300

ctcgcgcggt tcaacgacaa tccggtggtg gtgatcggtc aggagaaggg ccacgacacc   360

aagacccgga tcgagcgcaa cttcggcatg gcccgccccg agggctatcg caaagccatc   420

cggctgatgg agatggcgca ccgcttccgg ctgccggtca tcacgctcgt ggatacgccc   480

ggcgcctatc ccggcaaggg tgcggaagag cgcggccagg ccgaggccat tgcgcgggcc   540

acgcagaaat gcctcgagat cggcgtgccg ctggtggcgg tggtgatcgg cgagggcggc   600

tcgggcgggg cggtggcgct ggccacggcg aaccggatcg ccatgctcga acattcggtc   660

tattcggtga tctcgcccga gggctgcgcc tcgatcctgt ggaaggatgc cgagaagatg   720

cgcgaagccg ccgaagccct gcggctgacc gcgcaggatc tccacaagct cggcgtgatc   780

gaccggatca tcaaggagcc gctcggcggg gcgcagcgcg gacgccgcga gacggtcgac   840

gccgtgggca aggccatcga gatgatgctg aaggagctgg tgggccgcaa gcccgagtgg   900

ctcgtgaagg atcggcgcaa caagttcctc gacatggggt cgaagggcct cgcggcgtga   960

<210> SEQ ID NO 52
<211> LENGTH: 319
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 52

Met Asn Tyr Leu Glu Phe Glu Lys Pro Leu Ser Glu Ile Glu Gly Lys
1   5   10   15

Ala Glu Glu Leu Arg Ala Leu Ala Arg Gly Asn Arg Glu Met Asp Val
            20   25   30

Glu Lys Glu Ala Ser Ala Leu Asp Lys Lys Ala Glu Thr Leu Leu Lys
        35   40   45

Asp Leu Tyr Lys Asp Leu Thr Pro Trp Arg Lys Cys Gln Val Ala Arg
    50   55   60

His Pro Asp Arg Pro His Cys Lys Asp Tyr Ile Glu Gly Leu Phe Thr
65   70   75   80

Glu Tyr Thr Pro Leu Ala Gly Asp Arg Asn Phe Ala Asp Asp His Ala
                85   90   95

Ile Met Gly Gly Leu Ala Arg Phe Asn Asp Asn Pro Val Val Val Ile
            100   105   110

Gly Gln Glu Lys Gly His Asp Thr Lys Thr Arg Ile Glu Arg Asn Phe
        115   120   125

Gly Met Ala Arg Pro Glu Gly Tyr Arg Lys Ala Ile Arg Leu Met Glu
    130   135   140

Met Ala His Arg Phe Arg Leu Pro Val Ile Thr Leu Val Asp Thr Pro
145   150   155   160

Gly Ala Tyr Pro Gly Lys Gly Ala Glu Glu Arg Gly Gln Ala Glu Ala
                165   170   175

Ile Ala Arg Ala Thr Gln Lys Cys Leu Glu Ile Gly Val Pro Leu Val
            180   185   190

Ala Val Val Ile Gly Glu Gly Gly Ser Gly Gly Ala Val Ala Leu Ala
        195   200   205

Thr Ala Asn Arg Ile Ala Met Leu Glu His Ser Val Tyr Ser Val Ile

```
    210                 215                 220

Ser Pro Glu Gly Cys Ala Ser Ile Leu Trp Lys Asp Ala Glu Lys Met
225                 230                 235                 240

Arg Glu Ala Ala Glu Ala Leu Arg Leu Thr Ala Gln Asp Leu His Lys
                245                 250                 255

Leu Gly Val Ile Asp Arg Ile Ile Lys Glu Pro Leu Gly Gly Ala Gln
            260                 265                 270

Arg Gly Arg Arg Glu Thr Val Asp Ala Val Gly Lys Ala Ile Glu Met
        275                 280                 285

Met Leu Lys Glu Leu Val Gly Arg Lys Pro Glu Trp Leu Val Lys Asp
    290                 295                 300

Arg Arg Asn Lys Phe Leu Asp Met Gly Ser Lys Gly Leu Ala Ala
305                 310                 315
```

<210> SEQ ID NO 53
<211> LENGTH: 723
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 53

```
atgcgcttgc ttgatatctg gatgcgcagt gccgcggcac tgatgctcct gagcggagcg      60

gccttcgccg atgtgacggt gagccagtcc aacgatccgt ccgtcagtct gggcgggcag     120

ctttcggccc ttctgggcgc cgagcggagc gccctcggga ccctgccggc ccagcggctc     180

gagcaggtgg cggccgccgt ggcccgcccc gaggcgaagc ccgaggcgcc ggtcaaggcg     240

gtggcgacca agggcaaccg cggcgccaag gccgcggacg acgctccggc gccgcgctac     300

gacgaggcct ggctcgcctc gcagccggcg accgcgaagg actcggacga gtggaagtgt     360

ctggccacgg cgctctattt cgaggcgcgc ggcgagtcga tccagggcca gttcgcggtg     420

gccgaggtca tcatgaaccg cgtcgaccgc cccggctatc ccgggtccat ctgcggcgtg     480

gtccggcagg gcgggcagtt ctccttcatg ttcgacggca agcccgaaac gatccgcgag     540

aaggcggcct tccagcgtgc gggcaagatc gcggcgctga tgctggcggg cgctccgcgc     600

cagctcacgc agggcgccac ccacttccac acccgcgccg tccgccccgg ttgggcgcac     660

cgcttcccgc gcacggcggc catcggcgcg catctgttct accgccagcc cggcggctcc     720

tga                                                                   723
```

<210> SEQ ID NO 54
<211> LENGTH: 240
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 54

```
Met Arg Leu Leu Asp Ile Trp Met Arg Ser Ala Ala Ala Leu Met Leu
1               5                   10                  15

Leu Ser Gly Ala Ala Phe Ala Asp Val Thr Val Ser Gln Ser Asn Asp
            20                  25                  30

Pro Ser Val Ser Leu Gly Gly Gln Leu Ser Ala Leu Leu Gly Ala Glu
        35                  40                  45

Arg Ser Ala Leu Gly Thr Leu Pro Ala Gln Arg Leu Glu Gln Val Ala
    50                  55                  60

Ala Ala Val Ala Arg Pro Glu Ala Lys Pro Glu Ala Pro Val Lys Ala
65                  70                  75                  80

Val Ala Thr Lys Gly Asn Arg Gly Ala Lys Ala Ala Asp Asp Ala Pro
                85                  90                  95
```

```
Ala Pro Arg Tyr Asp Glu Ala Trp Leu Ala Ser Gln Pro Ala Thr Ala
            100                 105                 110

Lys Asp Ser Asp Glu Trp Lys Cys Leu Ala Thr Ala Leu Tyr Phe Glu
        115                 120                 125

Ala Arg Gly Glu Ser Ile Gln Gly Gln Phe Ala Val Ala Glu Val Ile
    130                 135                 140

Met Asn Arg Val Asp Arg Pro Gly Tyr Pro Gly Ser Ile Cys Gly Val
145                 150                 155                 160

Val Arg Gln Gly Gly Gln Phe Ser Phe Met Phe Asp Gly Lys Pro Glu
                165                 170                 175

Thr Ile Arg Glu Lys Ala Ala Phe Gln Arg Ala Gly Lys Ile Ala Ala
            180                 185                 190

Leu Met Leu Ala Gly Ala Pro Arg Gln Leu Thr Gln Gly Ala Thr His
        195                 200                 205

Phe His Thr Arg Ala Val Arg Pro Gly Trp Ala His Arg Phe Pro Arg
    210                 215                 220

Thr Ala Ala Ile Gly Ala His Leu Phe Tyr Arg Gln Pro Gly Gly Ser
225                 230                 235                 240
```

<210> SEQ ID NO 55
<211> LENGTH: 507
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 55

```
gtggcggagg cgttcagagg cgaatacaac cagaaggttg acgccaaggc gcgggtgtcg      60

atcccggccc ccttccgtcg tgtcatcgaa gcgggcgatc ccaaattctc cggcggccgg     120

tcgagcttcg tgctcgtcta tggcggcgac cgctcctacg tcgaatgcta caccatttcc     180

gagatggagc ggatcgagga acggatccgc agcctgccca tgggcacgcc caagcggcgc     240

tatctcgaac gcaacatgat caccctcgcg cttaacatgg agctcgacga ggacggccgg     300

atcgtgctgc cgcccaaggg ccgcgagaag ctgggcatct cgcccgacga gctgaagggc     360

ggcaccgaag ccacctttgc gggcacgctc aacaagttcc agatctggaa ggccgacacc     420

tacgcagccg agctcgccgc cgaagaggag gtgctcctgc ctccgggcgc cgacatgctc     480

tcgctgctcg aagagacggg gctctga                                         507
```

<210> SEQ ID NO 56
<211> LENGTH: 168
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 56

```
Met Ala Glu Ala Phe Arg Gly Glu Tyr Asn Gln Lys Val Asp Ala Lys
1               5                   10                  15

Ala Arg Val Ser Ile Pro Ala Pro Phe Arg Arg Val Ile Glu Ala Gly
            20                  25                  30

Asp Pro Lys Phe Ser Gly Gly Arg Ser Ser Phe Val Leu Val Tyr Gly
        35                  40                  45

Gly Asp Arg Ser Tyr Val Glu Cys Tyr Thr Ile Ser Glu Met Glu Arg
    50                  55                  60

Ile Glu Glu Arg Ile Arg Ser Leu Pro Met Gly Thr Pro Lys Arg Arg
65                  70                  75                  80

Tyr Leu Glu Arg Asn Met Ile Thr Leu Ala Leu Asn Met Glu Leu Asp
                85                  90                  95
```

```
Glu Asp Gly Arg Ile Val Leu Pro Pro Lys Gly Arg Glu Lys Leu Gly
            100                 105                 110

Ile Ser Pro Asp Glu Leu Lys Gly Gly Thr Glu Ala Thr Phe Ala Gly
        115                 120                 125

Thr Leu Asn Lys Phe Gln Ile Trp Lys Ala Asp Thr Tyr Ala Ala Glu
    130                 135                 140

Leu Ala Ala Glu Glu Glu Val Leu Leu Pro Pro Gly Ala Asp Met Leu
145                 150                 155                 160

Ser Leu Leu Glu Glu Thr Gly Leu
                165


<210> SEQ ID NO 57
<211> LENGTH: 360
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 57

atgcgccccg tgctctatgt cctcaccttc ctcgccgtga tggggctggc cttctgggcc      60

taccgtgaga actatgccac gcagcaggcg ctcaaggatg tctcggcgct caaccgcgag     120

atcgcgaccc tgcgcgagtc gctctcggtg cagcgcgcgg aatgggccta tctgaaccgt     180

cccgaccggc tgcgcgagct ggcggcgctg aacttcgacc gtctgggcct gctgccgctc     240

gaggccgtgc aattcggctc ggccgcgcag gtctcctacc cgccggatcc gcttcaggtg     300

gtcacgccgc aggatctgcg gccgggcgac atctcgggcg aagtgggaga gccgctgtga     360


<210> SEQ ID NO 58
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 58

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

Ala Phe Trp Ala Tyr Arg Glu Asn Tyr Ala Thr Gln Gln Ala Leu Lys
            20                  25                  30

Asp Val Ser Ala Leu Asn Arg Glu Ile Ala Thr Leu Arg Glu Ser Leu
        35                  40                  45

Ser Val Gln Arg Ala Glu Trp Ala Tyr Leu Asn Arg Pro Asp Arg Leu
    50                  55                  60

Arg Glu Leu Ala Ala Leu Asn Phe Asp Arg Leu Gly Leu Leu Pro Leu
65                  70                  75                  80

Glu Ala Val Gln Phe Gly Ser Ala Ala Gln Val Ser Tyr Pro Pro Asp
                85                  90                  95

Pro Leu Gln Val Val Thr Pro Gln Asp Leu Arg Pro Gly Asp Ile Ser
            100                 105                 110

Gly Glu Val Gly Glu Pro Leu
        115


<210> SEQ ID NO 59
<211> LENGTH: 1794
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 59

gtgatccgca cgccgctgcg tcccctcgcc cggatcctcg acgcccgcgc caagggcgag      60

aatcccgatt ccatcgagcg cgagaaccgc cgcatccgcc acgaggcgat gcgcgacaag     120
```

```
gcgcgcaacc gcgccgaggg ccggctcctg ctgctcggcc tcagcttctt cctcgccttc    180

tccgtcattg gggcgcgcat ggggcttctg gcctcgaccc agcccatgga gccgcgcgcg    240

gcggcgagcg gggccgagat cctgaaccag cgggccgaca ttaccgaccg ctcgggccgg    300

atcctcgcca cgaacctgct gacccattcg ctctacgccc atccgcagga catggtggat    360

cccctccggg tcgcccgcga gctggcggcg atcttccccg aactgaagga agaggatctc    420

gccaagcgct tcaccgacgg ccgccgcttc ctctggatcc gcaagaagct ctcgcccgag    480

cagatgcagc aggtgcatga catcggcgac ccgggcctgc tcttcggccc gcgcgagatg    540

cgcctctatc ccaacggccg gctggcggcc catgtgctcg gcggcaccag cttcggcgcc    600

gagggcgtcc attcggcgga agtgatcggc acggccggca tcgagaaggc gctcgacacg    660

cggctgcgcg atccggcggc ggccggagag ccgctgcagc tctccatcga cctgaccgtg    720

caggcggcca tcaccgaggt tctcggcgcc ggcatgaaga tgatgaacgc caagggcgcg    780

acggcgatcc tgatggaggc gcacagcggc gagatcctcg cgctcgcctc gctgcccgac    840

ttcgatccga acgaccgtcc ggcgcccctc gtcgatcgca acgccgatcc cggcgacagc    900

ccgctcttca accgcgcggt gcagggcgtc tacgaactcg gctcgacctt caagatcttc    960

accgtggctc aggcgatgga gctgggcctc gtgaatgcgc agaccatcgt cgatgccaat   1020

gcgccgatgc gctggggccg gttcctcatc aaggaattca agaaccacaa ttacggcccg   1080

ctcctctcgg tcaccgacgt catcgtgaaa agctcgaacg tgggtgtggc gcggctcgcg   1140

ctccagatcg gggggctgcg ccagcaggcc ttcctgaaat cgctgggctt cttcgatccg   1200

accccggtcg agctggtcga ggcaccctat gcccgcccgc tcgtccccgc gaaatgggcc   1260

gagatcacca cgatcaccac ctcctacggc cacgggctcg ccgcgagccc gctgcatctg   1320

gccgcggcct acggcacgat cgcgaacggc ggcatcaccg tgaaacccac gctccttcat   1380

gggaacgacc gtccgcaggg cgcgcgcgcc atgcgggccg aggtcgcgca cgattcgctc   1440

gcgatgctgc ggcaggtggt gacgcgcggc acggcctcct acggcgacgt cgagggttac   1500

gaggtggcgg gcaagaccgg caccgccgac aagcccaacc cgcgcggcgg ctattatcac   1560

gacaaggtgg tgaacacctt cgcctccatc ttccccgcct cggacccgcg ctatgtgctg   1620

atcgtcacgc tcgacgagcc ggtcgagacc tcgggtcccc agccgcgccg gacggccggc   1680

tacaccgccg tccccgtggc cgccgagatc atccgtcgca cggcgccgct cctcggcctg   1740

cgccccaagg ttgaagcccc acccgtggat cggataacag cggtgcgcaa ctga         1794
```

```
<210> SEQ ID NO 60
<211> LENGTH: 597
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 60

Met Ile Arg Thr Pro Leu Arg Pro Leu Ala Arg Ile Leu Asp Ala Arg
1               5                   10                  15

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

Arg His Glu Ala Met Arg Asp Lys Ala Arg Asn Arg Ala Glu Gly Arg
        35                  40                  45

Leu Leu Leu Leu Gly Leu Ser Phe Phe Leu Ala Phe Ser Val Ile Gly
    50                  55                  60

Ala Arg Met Gly Leu Leu Ala Ser Thr Gln Pro Met Glu Pro Arg Ala
65                  70                  75                  80
```

-continued

```
Ala Ala Ser Gly Ala Glu Ile Leu Asn Gln Arg Ala Asp Ile Thr Asp
                85                  90                  95

Arg Ser Gly Arg Ile Leu Ala Thr Asn Leu Leu Thr His Ser Leu Tyr
            100                 105                 110

Ala His Pro Gln Asp Met Val Asp Pro Leu Arg Val Ala Arg Glu Leu
        115                 120                 125

Ala Ala Ile Phe Pro Glu Leu Lys Glu Glu Asp Leu Ala Lys Arg Phe
    130                 135                 140

Thr Asp Gly Arg Arg Phe Leu Trp Ile Arg Lys Lys Leu Ser Pro Glu
145                 150                 155                 160

Gln Met Gln Gln Val His Asp Ile Gly Asp Pro Gly Leu Leu Phe Gly
                165                 170                 175

Pro Arg Glu Met Arg Leu Tyr Pro Asn Gly Arg Leu Ala Ala His Val
            180                 185                 190

Leu Gly Gly Thr Ser Phe Gly Ala Glu Gly Val His Ser Ala Glu Val
        195                 200                 205

Ile Gly Thr Ala Gly Ile Glu Lys Ala Leu Asp Thr Arg Leu Arg Asp
    210                 215                 220

Pro Ala Ala Ala Gly Glu Pro Leu Gln Leu Ser Ile Asp Leu Thr Val
225                 230                 235                 240

Gln Ala Ala Ile Thr Glu Val Leu Gly Ala Gly Met Lys Met Met Asn
                245                 250                 255

Ala Lys Gly Ala Thr Ala Ile Leu Met Glu Ala His Ser Gly Glu Ile
            260                 265                 270

Leu Ala Leu Ala Ser Leu Pro Asp Phe Asp Pro Asn Asp Arg Pro Ala
        275                 280                 285

Pro Leu Val Asp Arg Asn Ala Asp Pro Gly Asp Ser Pro Leu Phe Asn
    290                 295                 300

Arg Ala Val Gln Gly Val Tyr Glu Leu Gly Ser Thr Phe Lys Ile Phe
305                 310                 315                 320

Thr Val Ala Gln Ala Met Glu Leu Gly Leu Val Asn Ala Gln Thr Ile
                325                 330                 335

Val Asp Ala Asn Ala Pro Met Arg Trp Gly Arg Phe Leu Ile Lys Glu
            340                 345                 350

Phe Lys Asn His Asn Tyr Gly Pro Leu Leu Ser Val Thr Asp Val Ile
        355                 360                 365

Val Lys Ser Ser Asn Val Gly Val Ala Arg Leu Ala Leu Gln Ile Gly
    370                 375                 380

Gly Leu Arg Gln Gln Ala Phe Leu Lys Ser Leu Gly Phe Phe Asp Pro
385                 390                 395                 400

Thr Pro Val Glu Leu Val Glu Ala Pro Tyr Ala Arg Pro Leu Val Pro
                405                 410                 415

Ala Lys Trp Ala Glu Ile Thr Thr Ile Thr Thr Ser Tyr Gly His Gly
            420                 425                 430

Leu Ala Ala Ser Pro Leu His Leu Ala Ala Ala Tyr Gly Thr Ile Ala
        435                 440                 445

Asn Gly Gly Ile Thr Val Lys Pro Thr Leu Leu His Gly Asn Asp Arg
    450                 455                 460

Pro Gln Gly Ala Arg Ala Met Arg Ala Glu Val Ala His Asp Ser Leu
465                 470                 475                 480

Ala Met Leu Arg Gln Val Val Thr Arg Gly Thr Ala Ser Tyr Gly Asp
                485                 490                 495
```

-continued

```
Val Glu Gly Tyr Glu Val Ala Gly Lys Thr Gly Thr Ala Asp Lys Pro
            500                 505                 510

Asn Pro Arg Gly Gly Tyr Tyr His Asp Lys Val Val Asn Thr Phe Ala
        515                 520                 525

Ser Ile Phe Pro Ala Ser Asp Pro Arg Tyr Val Leu Ile Val Thr Leu
    530                 535                 540

Asp Glu Pro Val Glu Thr Ser Gly Pro Gln Pro Arg Arg Thr Ala Gly
545                 550                 555                 560

Tyr Thr Ala Val Pro Val Ala Ala Glu Ile Ile Arg Arg Thr Ala Pro
                565                 570                 575

Leu Leu Gly Leu Arg Pro Lys Val Glu Ala Pro Pro Val Asp Arg Ile
            580                 585                 590

Thr Ala Val Arg Asn
        595


<210> SEQ ID NO 61
<211> LENGTH: 1488
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 61

atggcggatc gcgcagcaac actctcggcg ctcgggctca cgcccgcagg cggccgcgga     60

ggcgacatcg ccgtgaccgg cctcgcggtt gacagccggc aagtgcgccc cggcaccctc    120

ttcgcggcgc tgcccggctc ccgcagccac ggcgcgagct tcgtgccggc ggcgctcgcc    180

gcaggcgcca ccgcgatcct caccgatgcc gccggcgcgg cgctcgcgcg cgaggcgctc    240

gcgggctcgg gcgcggccct cgtcctggcc gaggatcccc gccagaccct cgccggcgcg    300

gccgccctct ggttcggccg ccagcccgcg accgtggtcg ccgtaacggg caccaacggc    360

aagacctcgg tcgcgacctt cacccgccag atctgggcgg ccctcggcca tgccgcgatc    420

aacatcggca cgaccggcgt cgagggcgcc ttcgcagccc cctccgccca taccacgccc    480

gagcccatca ccctccaccg gctcctcgcc gaggcggccg aggcgggcgt cacccatgcc    540

gccatggagg cctcctccca cgggctcgag cagcgccgcc tcgacggcgt gcatctcgcg    600

gccgcgggct tcaccaactt cacccaggac catctcgact atcacgagac cttcgaggcc    660

tatttcgccg ccaaggccgg gctcttcacc cgggtcttgc ccgacgaggg cacggcggtc    720

gtcaatctcg acgatccccg cggccccgag atcgcggccc tcgcgcgggc gcgcgcgcaa    780

cgggtgatcg gcacgggctt tcacgccgat gcggacctgc gccttctctc gcagcgcttc    840

gacgcgaccg ggcaggacct ccgcttctcc tggcagggcg aggtgcatct cgcgcgtctg    900

ccgctgatcg gcggcttcca ggcctggaac gtcgcggtcg cggccagcct cgccatcggc    960

gcgggcgacg cccccgagcg ggtcttcgcc accttctccc ggcttcaggg cgtgcgcggg   1020

cggatgcagc tcgccgccac ccgcaagaac ggtgcctcgg tcttcgtcga ttatgcccat   1080

acgcccgacg ccctcgccac cgccctcaag gcgctgcgcc cgcatgtgat ggggcgcatc   1140

gtcgtcgtct tcggtgccgg cggcgaccgc gaccgcggca agcgcccgct gatgggccgc   1200

gccgcggcag accatgccga cgtgctctat gtcaccgacg acaatccccg caccgaggat   1260

cccgccgcca tccgccgcgc catcctcgag gcctgccccg aggcgcatga ggtgggcgac   1320

cgggccgagg ccatcctgcg cggcgtcgat gcgctcacgc cgggcgacgc gctcctcatc   1380

gcgggcaagg gccacgaatc gggccaggtg gtgggcaccg acatcttccc cttcgacgat   1440

gccgaacagg cgagcatcgc caccgccgcg ctggacgggc tgatatga                1488
```

```
<210> SEQ ID NO 62
<211> LENGTH: 495
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 62

Met Ala Asp Arg Ala Ala Thr Leu Ser Ala Leu Gly Leu Thr Pro Ala
1               5                   10                  15

Gly Gly Arg Gly Gly Asp Ile Ala Val Thr Gly Leu Ala Val Asp Ser
            20                  25                  30

Arg Gln Val Arg Pro Gly Thr Leu Phe Ala Ala Leu Pro Gly Ser Arg
        35                  40                  45

Ser His Gly Ala Ser Phe Val Pro Ala Ala Leu Ala Ala Gly Ala Thr
    50                  55                  60

Ala Ile Leu Thr Asp Ala Ala Gly Ala Ala Leu Ala Arg Glu Ala Leu
65                  70                  75                  80

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

Leu Ala Gly Ala Ala Ala Leu Trp Phe Gly Arg Gln Pro Ala Thr Val
            100                 105                 110

Val Ala Val Thr Gly Thr Asn Gly Lys Thr Ser Val Ala Thr Phe Thr
        115                 120                 125

Arg Gln Ile Trp Ala Ala Leu Gly His Ala Ala Ile Asn Ile Gly Thr
    130                 135                 140

Thr Gly Val Glu Gly Ala Phe Ala Ala Pro Ser Ala His Thr Thr Pro
145                 150                 155                 160

Glu Pro Ile Thr Leu His Arg Leu Leu Ala Glu Ala Ala Glu Ala Gly
                165                 170                 175

Val Thr His Ala Ala Met Glu Ala Ser Ser His Gly Leu Glu Gln Arg
            180                 185                 190

Arg Leu Asp Gly Val His Leu Ala Ala Ala Gly Phe Thr Asn Phe Thr
        195                 200                 205

Gln Asp His Leu Asp Tyr His Glu Thr Phe Glu Ala Tyr Phe Ala Ala
    210                 215                 220

Lys Ala Gly Leu Phe Thr Arg Val Leu Pro Asp Glu Gly Thr Ala Val
225                 230                 235                 240

Val Asn Leu Asp Asp Pro Arg Gly Pro Glu Ile Ala Ala Leu Ala Arg
                245                 250                 255

Ala Arg Ala Gln Arg Val Ile Gly Thr Gly Phe His Ala Asp Ala Asp
            260                 265                 270

Leu Arg Leu Leu Ser Gln Arg Phe Asp Ala Thr Gly Gln Asp Leu Arg
        275                 280                 285

Phe Ser Trp Gln Gly Glu Val His Leu Ala Arg Leu Pro Leu Ile Gly
    290                 295                 300

Gly Phe Gln Ala Trp Asn Val Ala Val Ala Ala Ser Leu Ala Ile Gly
305                 310                 315                 320

Ala Gly Asp Ala Pro Glu Arg Val Phe Ala Thr Phe Ser Arg Leu Gln
                325                 330                 335

Gly Val Arg Gly Arg Met Gln Leu Ala Ala Thr Arg Lys Asn Gly Ala
            340                 345                 350

Ser Val Phe Val Asp Tyr Ala His Thr Pro Asp Ala Leu Ala Thr Ala
        355                 360                 365

Leu Lys Ala Leu Arg Pro His Val Met Gly Arg Ile Val Val Val Phe
    370                 375                 380
```

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```
Gly Ala Gly Gly Asp Arg Asp Arg Gly Lys Arg Pro Leu Met Gly Arg
385                 390                 395                 400

Ala Ala Ala Asp His Ala Asp Val Leu Tyr Val Thr Asp Asp Asn Pro
                405                 410                 415

Arg Thr Glu Asp Pro Ala Ala Ile Arg Arg Ala Ile Leu Glu Ala Cys
            420                 425                 430

Pro Glu Ala His Glu Val Gly Asp Arg Ala Glu Ala Ile Leu Arg Gly
        435                 440                 445

Val Asp Ala Leu Thr Pro Gly Asp Ala Leu Leu Ile Ala Gly Lys Gly
    450                 455                 460

His Glu Ser Gly Gln Val Val Gly Thr Asp Ile Phe Pro Phe Asp Asp
465                 470                 475                 480

Ala Glu Gln Ala Ser Ile Ala Thr Ala Ala Leu Asp Gly Leu Ile
                485                 490                 495


<210> SEQ ID NO 63
<211> LENGTH: 1434
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 63

atgacccccc tctggacctc cgacgaggcc gccgccacga cgggcggccg cgccacccgc      60

gccttcgccg ccacaggcgt ctcgatcgac acccgcagcc tcgggccggg cgacctcttc     120

gtggcgctca ccgaccagcg cgacggccac gccttcgtgg ccgaggcgct ggcccgtggc     180

gccgccgcgg cgctggtctc gcgccgcccg gaaggcctcc ccgaggatgc gccgctcctt     240

ctcgtgcccg atgtgctgga agggctccgc gcgctcggcc gcgcggcccg cgcccggacc     300

cgcgcccgcg tcgtgggcgt gacgggctcg gtcggcaaga cctcgaccaa ggagatgctg     360

cgcgccacgc tcggcgggca gggcaccgtc catgccgccg aggcctccta caacaaccac     420

tggggcgtgc cgctcacgct ggcgcggatg cccgccgacg tggatttcgc cgtcgtcgag     480

atcggcatga accatccggg cgagatcgcc ccgctgtcgc gcctcgcccg gccgcatctg     540

gccctcatca ccaccgtggc cgcggcccat ctcgaggcct tcgacagcct ctccgccatc     600

gccgaggaga aggccgcgat cctcgagggg ctcgagccgg ccgggcgcgc gatcttgccc     660

gccgggctcg aggtgtcgcc ggtgctcgca gcccgcgccg cggcgctggg cgtgccggcc     720

gtgaccttcg gccagacggc cgacgccgac tggcgcctcg ccgacatcca gatcaccccc     780

gaggccaccg tcgcgcgggc gagccatgcc ggcggaacct tcctcttcaa ggtgctgacg     840

ccgggccggc atttcgcctc gaacgcgctc gccactctgg ccgcggccga ggcgctcggg     900

ctcgatctca ccatcgccgc ctgcgacttg ggtctctgga cgccgccctc gggccgcggc     960

acgcgcgagc gcatcgcgct cgacccggtg gacgaggcag gcttcgacct gatcgacgat    1020

gccttcaacg ccaatcccgc ctcgatggcg gcgagcctcg agcttctggc cgcgatggcg    1080

cccaccgacg gggtcgggcg gatcgccgcc ggccgccgga tcgccatcct cggcgacatg    1140

ctcgaactcg ggcccaccga ggcagagctg catcgtgcgg tggccgacca tcccgccctg    1200

gccgagatcg ccctcgttca ctgcgtgggc cccggatgc gggcgctcca cgaggcgctg    1260

ccgcgccgcc agcgcggcga atgggtcgag accgcggccg agctcgtgcc gcgggcccgt    1320

ctgctcgtcg atgcgggcga catcgtgctg gtgaagggct cgaaagggat caaggtcagc    1380

ctggtggttg acgcgctccg caaactgggc cagtcgagcc catccaggac ctga          1434
```

```
<210> SEQ ID NO 64
<211> LENGTH: 477
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 64

Met Thr Pro Leu Trp Thr Ser Asp Glu Ala Ala Ala Thr Thr Gly Gly
1               5                   10                  15

Arg Ala Thr Arg Ala Phe Ala Ala Thr Gly Val Ser Ile Asp Thr Arg
            20                  25                  30

Ser Leu Gly Pro Gly Asp Leu Phe Val Ala Leu Thr Asp Gln Arg Asp
        35                  40                  45

Gly His Ala Phe Val Ala Glu Ala Leu Ala Arg Gly Ala Ala Ala Ala
    50                  55                  60

Leu Val Ser Arg Arg Pro Glu Gly Leu Pro Glu Asp Ala Pro Leu Leu
65                  70                  75                  80

Leu Val Pro Asp Val Leu Glu Gly Leu Arg Ala Leu Gly Arg Ala Ala
                85                  90                  95

Arg Ala Arg Thr Arg Ala Arg Val Val Gly Val Thr Gly Ser Val Gly
            100                 105                 110

Lys Thr Ser Thr Lys Glu Met Leu Arg Ala Thr Leu Gly Gly Gln Gly
        115                 120                 125

Thr Val His Ala Ala Glu Ala Ser Tyr Asn Asn His Trp Gly Val Pro
    130                 135                 140

Leu Thr Leu Ala Arg Met Pro Ala Asp Val Asp Phe Ala Val Val Glu
145                 150                 155                 160

Ile Gly Met Asn His Pro Gly Glu Ile Ala Pro Leu Ser Arg Leu Ala
                165                 170                 175

Arg Pro His Leu Ala Leu Ile Thr Thr Val Ala Ala Ala His Leu Glu
            180                 185                 190

Ala Phe Asp Ser Leu Ser Ala Ile Ala Glu Glu Lys Ala Ala Ile Leu
        195                 200                 205

Glu Gly Leu Glu Pro Ala Gly Arg Ala Ile Leu Pro Ala Gly Leu Glu
    210                 215                 220

Val Ser Pro Val Leu Ala Ala Arg Ala Ala Ala Leu Gly Val Pro Ala
225                 230                 235                 240

Val Thr Phe Gly Gln Thr Ala Asp Ala Asp Trp Arg Leu Ala Asp Ile
                245                 250                 255

Gln Ile Thr Pro Glu Ala Thr Val Ala Arg Ala Ser His Ala Gly Gly
            260                 265                 270

Thr Phe Leu Phe Lys Val Leu Thr Pro Gly Arg His Phe Ala Ser Asn
        275                 280                 285

Ala Leu Ala Thr Leu Ala Ala Ala Glu Ala Leu Gly Leu Asp Leu Thr
    290                 295                 300

Ile Ala Ala Cys Asp Leu Gly Leu Trp Thr Pro Pro Ser Gly Arg Gly
305                 310                 315                 320

Thr Arg Glu Arg Ile Ala Leu Asp Pro Val Asp Glu Ala Gly Phe Asp
                325                 330                 335

Leu Ile Asp Asp Ala Phe Asn Ala Asn Pro Ala Ser Met Ala Ala Ser
            340                 345                 350

Leu Glu Leu Leu Ala Ala Met Ala Pro Thr Asp Gly Val Gly Arg Ile
        355                 360                 365

Ala Ala Gly Arg Arg Ile Ala Ile Leu Gly Asp Met Leu Glu Leu Gly
    370                 375                 380
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Pro Thr Glu Ala Glu Leu His Arg Ala Val Ala Asp His Pro Ala Leu
385                 390                 395                 400

Ala Glu Ile Ala Leu Val His Cys Val Gly Pro Arg Met Arg Ala Leu
                405                 410                 415

His Glu Ala Leu Pro Arg Arg Gln Arg Gly Glu Trp Val Glu Thr Ala
            420                 425                 430

Ala Glu Leu Val Pro Arg Ala Arg Leu Leu Val Asp Ala Gly Asp Ile
        435                 440                 445

Val Leu Val Lys Gly Ser Lys Gly Ile Lys Val Ser Leu Val Val Asp
    450                 455                 460

Ala Leu Arg Lys Leu Gly Gln Ser Ser Pro Ser Arg Thr
465                 470                 475


<210> SEQ ID NO 65
<211> LENGTH: 1083
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 65

atgctgtatc tcctgaccgc cttctccgac ggcggcgaca ttttcaacct cttccgctac      60

ctgaccttcc gggccggagc cgccttcttc accgcgctga tcttcggctt cctcttcggc     120

cgcccgctga tcgacttcct gcgccgcaag cagggcaagg gccagccgat ccgggacgac     180

gggccgacca cccacttcgc caaggcgggc acccccacca tgggcggcct tctgatcctc     240

tcggcacttg tggtctcgac cctcctctgg gcgcggctcg acaatcctta cgtctggatc     300

gtcctcctcg tgaccgtggc cttcggcctg atcggcttcg ccgacgacta tgccaaggtg     360

aagaagcaga acaccaaggg cgtgccgggc cgggtgcgtt tcctgatcgg gctcctgatc     420

gccgcgctcg cggccatcgc ggccgcctgg tcgcatccgc cggatctgac gctccagctc     480

gccatgccct tcttcaagga tgcgctcatc aatctcggct ggttcttcgt gcccttcgcc     540

atggtggtga tcgtgggcgc ggccaatgcg gtgaacctca ccgacgggct cgacgggctg     600

gccatcatgc cggtgatgat cgcgggcacc accctcggcg tgatcgccta tgtcgtcggc     660

aacttcaatc tgaccgacta tctgggcgtc catttcgtcc ccggcacggg cgagcttctg     720

atcttcagct ccgcgctcgt gggggcgggg ctgggctttc tgtggtacaa cgcgcccccg     780

gccgcggtct tcatgggcga cacgggctcg ctcgccctgg gcggcgcgct cggcgccatc     840

gcggtctgca ccaagcacga gatcgtgctc gcgatcgtgg gcggcctctt cgtcaccgag     900

gcgctctcgg tcatcatcca ggttctctat ttcaagcgca ccgggcggcg ggtgttcctg     960

atggcgccga tccaccacca tttcgagaag aagggctggg ccgagccgca gatcgtgatc    1020

cgcttctgga tcatctcgct gatcctcgcc ctgatcggcc tctcgaccct caagctgcgc    1080

tga                                                                  1083


<210> SEQ ID NO 66
<211> LENGTH: 360
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 66

Met Leu Tyr Leu Leu Thr Ala Phe Ser Asp Gly Gly Asp Ile Phe Asn
1               5                   10                  15

Leu Phe Arg Tyr Leu Thr Phe Arg Ala Gly Ala Ala Phe Phe Thr Ala
            20                  25                  30

Leu Ile Phe Gly Phe Leu Phe Gly Arg Pro Leu Ile Asp Phe Leu Arg
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        35                  40                  45

Arg Lys Gln Gly Lys Gly Gln Pro Ile Arg Asp Asp Gly Pro Thr Thr
    50                  55                  60

His Phe Ala Lys Ala Gly Thr Pro Thr Met Gly Gly Leu Leu Ile Leu
65                  70                  75                  80

Ser Ala Leu Val Val Ser Thr Leu Leu Trp Ala Arg Leu Asp Asn Pro
                85                  90                  95

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

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

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

Ala Ile Ala Ala Ala Trp Ser His Pro Pro Asp Leu Thr Leu Gln Leu
145                 150                 155                 160

Ala Met Pro Phe Phe Lys Asp Ala Leu Ile Asn Leu Gly Trp Phe Phe
                165                 170                 175

Val Pro Phe Ala Met Val Val Ile Val Gly Ala Ala Asn Ala Val Asn
            180                 185                 190

Leu Thr Asp Gly Leu Asp Gly Leu Ala Ile Met Pro Val Met Ile Ala
        195                 200                 205

Gly Thr Thr Leu Gly Val Ile Ala Tyr Val Val Gly Asn Phe Asn Leu
    210                 215                 220

Thr Asp Tyr Leu Gly Val His Phe Val Pro Gly Thr Gly Glu Leu Leu
225                 230                 235                 240

Ile Phe Ser Ser Ala Leu Val Gly Gly Gly Leu Gly Phe Leu Trp Tyr
                245                 250                 255

Asn Ala Pro Pro Ala Ala Val Phe Met Gly Asp Thr Gly Ser Leu Ala
            260                 265                 270

Leu Gly Gly Ala Leu Gly Ala Ile Ala Val Cys Thr Lys His Glu Ile
        275                 280                 285

Val Leu Ala Ile Val Gly Gly Leu Phe Val Thr Glu Ala Leu Ser Val
    290                 295                 300

Ile Ile Gln Val Leu Tyr Phe Lys Arg Thr Gly Arg Arg Val Phe Leu
305                 310                 315                 320

Met Ala Pro Ile His His His Phe Glu Lys Lys Gly Trp Ala Glu Pro
                325                 330                 335

Gln Ile Val Ile Arg Phe Trp Ile Ile Ser Leu Ile Leu Ala Leu Ile
            340                 345                 350

Gly Leu Ser Thr Leu Lys Leu Arg
        355                 360


<210> SEQ ID NO 67
<211> LENGTH: 924
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 67

atggcgggac agtccggcag gacgttcccc agggttgctg tgctgatggg cggggcctcg      60

accgagcgcg aggtgtcgct gtcgtcgggc cattcgtgca gcgcagccct gcgggacgca     120

ggctatgagg tgacggaggt cgatgccggc cccgacctcg cccgcgtgct ggcggagctt     180

tctcccgatg cggtcttcaa cgcgctccac ggccgctggg gcgaggatgg ctgcgtgcag     240

ggcctgctcg agtggctgcg cattccctac acccattccg ggtgctggc ctcggcgctg     300
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gccatggaca aggcccgcgc gaaggaggtc ttcgccgcgg ccgggctgcc cgtgacccag    360

agcgtgctcg ccacgcccga ggaggtacgg gcgcgccaca tcctgccgcc gccctatgtg    420

gtcaagccca atgccgaggg ctcttcggta ggcgtctata tcgtgcacga ggatgccaac    480

ggtccgccgc agctcgcggc cgacatgccg caagacctga tggtcgagac ctatgtcccc    540

ggccgcgaac tcaccgtcac cgtgatgggc gaccgggtgc tcgcggtcac cgatatcctg    600

tccgacggct ggtacgatta cgacgccaaa taccgtcccg gcggctcgcg tcatatcgtg    660

cctgcggacc tgccggccga gatcaccgag gcctgccacg acatcgcact ccgtgcccac    720

cgcgcgctcg gttgccgcgg catctcgcgc tcggacctgc gctgggacga agcgcgcggg    780

ttggcggggc tgatcctcct tgagaccaac actcagccgg gcatgacccc cacctcgctc    840

tcgcccgagc aggcggcgca ttgcggctat tccttccccg agttctgcgc ctggttggtg    900

gaggacgcct catgcagtcg ctga                                            924


<210> SEQ ID NO 68
<211> LENGTH: 307
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 68

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

Gly Gly Ala Ser Thr Glu Arg Glu Val Ser Leu Ser Ser Gly His Ser
            20                  25                  30

Cys Ser Ala Ala Leu Arg Asp Ala Gly Tyr Glu Val Thr Glu Val Asp
        35                  40                  45

Ala Gly Pro Asp Leu Ala Arg Val Leu Ala Glu Leu Ser Pro Asp Ala
    50                  55                  60

Val Phe Asn Ala Leu His Gly Arg Trp Gly Glu Asp Gly Cys Val Gln
65                  70                  75                  80

Gly Leu Leu Glu Trp Leu Arg Ile Pro Tyr Thr His Ser Gly Val Leu
                85                  90                  95

Ala Ser Ala Leu Ala Met Asp Lys Ala Arg Ala Lys Glu Val Phe Ala
            100                 105                 110

Ala Ala Gly Leu Pro Val Thr Gln Ser Val Leu Ala Thr Pro Glu Glu
        115                 120                 125

Val Arg Ala Arg His Ile Leu Pro Pro Pro Tyr Val Val Lys Pro Asn
    130                 135                 140

Ala Glu Gly Ser Ser Val Gly Val Tyr Ile Val His Glu Asp Ala Asn
145                 150                 155                 160

Gly Pro Pro Gln Leu Ala Ala Asp Met Pro Gln Asp Leu Met Val Glu
                165                 170                 175

Thr Tyr Val Pro Gly Arg Glu Leu Thr Val Thr Val Met Gly Asp Arg
            180                 185                 190

Val Leu Ala Val Thr Asp Ile Leu Ser Asp Gly Trp Tyr Asp Tyr Asp
        195                 200                 205

Ala Lys Tyr Arg Pro Gly Gly Ser Arg His Ile Val Pro Ala Asp Leu
    210                 215                 220

Pro Ala Glu Ile Thr Glu Ala Cys His Asp Ile Ala Leu Arg Ala His
225                 230                 235                 240

Arg Ala Leu Gly Cys Arg Gly Ile Ser Arg Ser Asp Leu Arg Trp Asp
                245                 250                 255
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Glu Ala Arg Gly Leu Ala Gly Leu Ile Leu Leu Glu Thr Asn Thr Gln
            260                 265                 270

Pro Gly Met Thr Pro Thr Ser Leu Ser Pro Glu Gln Ala Ala His Cys
        275                 280                 285

Gly Tyr Ser Phe Pro Glu Phe Cys Ala Trp Leu Val Glu Asp Ala Ser
    290                 295                 300

Cys Ser Arg
305


<210> SEQ ID NO 69
<211> LENGTH: 927
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 69

atgcagtcgc tgagcttccc gccgaaccgc cgcacccccc ggctcgcgcc gccgcgccgc     60

gagaccggcc gccgcgaccc tgcgccctcg cgctgggcct atcgcgcgca gcggctctgg    120

ctcacgccca tgttccgcac ggcgctccgc gtggggctgc cgatcgtggg cgtgctgctg    180

gtggtggcgc tgatcttcgc cagcgccgac cggcgcgccg ccatggcggg cgccttcacc    240

ggcctcgtcg acagcttcca gcaacgcccc gaattcatgg taacgctgct ttcggtcgat    300

ggcgcctcgc cggaactctc agaccggatc cgggccacgc tggcgctgaa gctgccgctc    360

agctcgttcg acatcgacct gaccgccgcc cgcgcccgca tcgagagcat cgacgcggtg    420

gcgcaggccg aggtgcgggt gcgctcgggc ggactgctcg aggtgcgcgt gaccgagcgc    480

gaacccgcga tcatctggcg ccgggccgcg aacctcgtgc ttctcgacgg gaccggccgc    540

cgcgtggacg atctcgcctt ccgcagcgag cggggcgatc tggcggtgat cgcgggcgag    600

ggcgccgagc gcgccgtgcc cgaggcgctc gagattctcg ccgccgcccg ccccatcctc    660

gagcggatcc gcgggctcgt gcggatgggc gagcggcgct gggacatcgt gctcgaccgc    720

gggcagcgca ttcagctgcc cgtcgaggaa cccgtggctg ccgtcgagcg gatgatcgcg    780

ctcgacgagg ccgaggacct tctggaccgc gacgtgattt ccgtcgacct gcgcatcaag    840

gaccgtccgg tgctgaggct cgcgccctac gccctgaacg ccgtccgccg cgcgcggggc    900

attgatacaa gtggaagcga cctatga                                        927


<210> SEQ ID NO 70
<211> LENGTH: 308
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 70

Met Gln Ser Leu Ser Phe Pro Pro Asn Arg Arg Thr Pro Arg Leu Ala
1               5                   10                  15

Pro Pro Arg Arg Glu Thr Gly Arg Arg Asp Pro Ala Pro Ser Arg Trp
            20                  25                  30

Ala Tyr Arg Ala Gln Arg Leu Trp Leu Thr Pro Met Phe Arg Thr Ala
        35                  40                  45

Leu Arg Val Gly Leu Pro Ile Val Gly Val Leu Leu Val Val Ala Leu
    50                  55                  60

Ile Phe Ala Ser Ala Asp Arg Arg Ala Ala Met Ala Gly Ala Phe Thr
65                  70                  75                  80

Gly Leu Val Asp Ser Phe Gln Gln Arg Pro Glu Phe Met Val Thr Leu
                85                  90                  95

Leu Ser Val Asp Gly Ala Ser Pro Glu Leu Ser Asp Arg Ile Arg Ala
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            100                 105                 110

Thr Leu Ala Leu Lys Leu Pro Leu Ser Ser Phe Asp Ile Asp Leu Thr
        115                 120                 125

Ala Ala Arg Ala Arg Ile Glu Ser Ile Asp Ala Val Ala Gln Ala Glu
    130                 135                 140

Val Arg Val Arg Ser Gly Gly Leu Leu Glu Val Arg Val Thr Glu Arg
145                 150                 155                 160

Glu Pro Ala Ile Ile Trp Arg Arg Ala Ala Asn Leu Val Leu Leu Asp
                165                 170                 175

Gly Thr Gly Arg Arg Val Asp Asp Leu Ala Phe Arg Ser Glu Arg Gly
            180                 185                 190

Asp Leu Ala Val Ile Ala Gly Glu Gly Ala Glu Arg Ala Val Pro Glu
        195                 200                 205

Ala Leu Glu Ile Leu Ala Ala Arg Pro Ile Leu Glu Arg Ile Arg
    210                 215                 220

Gly Leu Val Arg Met Gly Glu Arg Arg Trp Asp Ile Val Leu Asp Arg
225                 230                 235                 240

Gly Gln Arg Ile Gln Leu Pro Val Glu Glu Pro Val Ala Ala Val Glu
                245                 250                 255

Arg Met Ile Ala Leu Asp Glu Ala Glu Asp Leu Leu Asp Arg Asp Val
            260                 265                 270

Ile Ser Val Asp Leu Arg Ile Lys Asp Arg Pro Val Leu Arg Leu Ala
        275                 280                 285

Pro Tyr Ala Leu Asn Ala Val Arg Arg Ala Arg Gly Ile Asp Thr Ser
    290                 295                 300

Gly Ser Asp Leu
305


<210> SEQ ID NO 71
<211> LENGTH: 1335
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 71

atgaccgacc tctatcagtc ccagcgcgcc atgcggaaca tgcgccgcgc cgccatgcag      60

cggggcgtga tcgcgatcct cgacgtgggc tcttccaaga tcacctgcct gatcctgcgc     120

ttcgacgggc cggaccggct gcgcgagcat gacggggtgg ggccgatggc cgggcagtcc     180

tcgttccggg tcatcggggc cgccaccacc cggtcgcgcg gggtgcattt cggcgagatc     240

tcggtgatga acgagaccga gcgcgcgatc cgcaccgcgg tgcaggcggc gcagaagatg     300

gccaacgtcc gggtggacca tgtgatcgcc tgtttcgccg gcgccgatcc gcgcagctac     360

ggcctcgcgg gcgagtggga gctgcaggat tcggtcgtga ccgagcagga tgtggcccgc     420

gtgatggccg cctgcgacgt gcccgacttc ggtcagggcc gcgaggtgct gcacgcccag     480

ccggtgaact tcgccctcga ccaccgcacc gggctcggcg atccgcgggg ccagatcggc     540

aaccggctgg cggtggacat gcacctgctc accgtcgagg cggacgcgat ccagaacctg     600

ctctactgca tcaagcgctg cgacctcgaa ctcgcgggga tcgcctcctc ggcctatgtc     660

tcgggcgtct cgtcgctcgt cgaggacgag caggagctgg gggccgcctg catcgacatg     720

ggcggcggtg ccacgggcct gtcgatcttc atcaagaagc acatgatctt cgcggattcg     780

gtgcggatgg gcggcgacca tgtgacctcg gacatttcca agggcctgca ggtgccgctt     840

gccaccgccg agaagatcaa gacgcggcac ggcggcgtcg tggccaccgg catggacgac     900
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cgcgagatga tcgacatcgg cgcggacacc ggcgactggg acaaggaccg ccgcaccgtc    960

agccgggccg agctgatcgg catcatgcgt ccgcgcgtcg aggagatcct cgaagaggcg   1020

cgcgcgcgtc tcgatgcggc cggtttcgag catctgccga gccagcagat cgtcatcacc   1080

gggggcggca gccagatccc gggtctcgac ggtctcgcgg cccggatcct cggccagcgg   1140

gtccgtctgg ggcgcccgct gcgcgttcag ggcctgccgc agcaggtctc cgggccgggc   1200

ttctcctcgg ccgtggggct ctgcctcttt gcggcccatc cgcaggacga atggtgggat   1260

ttcgacattc cggcagagcg ctatcccgcc cggtccctgc ggagggccat caaatggttc   1320

aaggacaact ggtaa                                                     1335


<210> SEQ ID NO 72
<211> LENGTH: 444
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 72

Met Thr Asp Leu Tyr Gln Ser Gln Arg Ala Met Arg Asn Met Arg Arg
1               5                   10                  15

Ala Ala Met Gln Arg Gly Val Ile Ala Ile Leu Asp Val Gly Ser Ser
            20                  25                  30

Lys Ile Thr Cys Leu Ile Leu Arg Phe Asp Gly Pro Asp Arg Leu Arg
        35                  40                  45

Glu His Asp Gly Val Gly Pro Met Ala Gly Gln Ser Ser Phe Arg Val
    50                  55                  60

Ile Gly Ala Ala Thr Thr Arg Ser Arg Gly Val His Phe Gly Glu Ile
65                  70                  75                  80

Ser Val Met Asn Glu Thr Glu Arg Ala Ile Arg Thr Ala Val Gln Ala
                85                  90                  95

Ala Gln Lys Met Ala Asn Val Arg Val Asp His Val Ile Ala Cys Phe
            100                 105                 110

Ala Gly Ala Asp Pro Arg Ser Tyr Gly Leu Ala Gly Glu Trp Glu Leu
        115                 120                 125

Gln Asp Ser Val Val Thr Glu Gln Asp Val Ala Arg Val Met Ala Ala
    130                 135                 140

Cys Asp Val Pro Asp Phe Gly Gln Gly Arg Glu Val Leu His Ala Gln
145                 150                 155                 160

Pro Val Asn Phe Ala Leu Asp His Arg Thr Gly Leu Gly Asp Pro Arg
                165                 170                 175

Gly Gln Ile Gly Asn Arg Leu Ala Val Asp Met His Leu Leu Thr Val
            180                 185                 190

Glu Ala Asp Ala Ile Gln Asn Leu Leu Tyr Cys Ile Lys Arg Cys Asp
        195                 200                 205

Leu Glu Leu Ala Gly Ile Ala Ser Ser Ala Tyr Val Ser Gly Val Ser
    210                 215                 220

Ser Leu Val Glu Asp Glu Gln Glu Leu Gly Ala Ala Cys Ile Asp Met
225                 230                 235                 240

Gly Gly Gly Ala Thr Gly Leu Ser Ile Phe Ile Lys Lys His Met Ile
                245                 250                 255

Phe Ala Asp Ser Val Arg Met Gly Gly Asp His Val Thr Ser Asp Ile
            260                 265                 270

Ser Lys Gly Leu Gln Val Pro Leu Ala Thr Ala Glu Lys Ile Lys Thr
        275                 280                 285

Arg His Gly Gly Val Val Ala Thr Gly Met Asp Asp Arg Glu Met Ile
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    290                 295                 300

Asp Ile Gly Ala Asp Thr Gly Asp Trp Asp Lys Asp Arg Arg Thr Val
305                 310                 315                 320

Ser Arg Ala Glu Leu Ile Gly Ile Met Arg Pro Arg Val Glu Glu Ile
                325                 330                 335

Leu Glu Glu Ala Arg Ala Arg Leu Asp Ala Ala Gly Phe Glu His Leu
            340                 345                 350

Pro Ser Gln Gln Ile Val Ile Thr Gly Gly Gly Ser Gln Ile Pro Gly
        355                 360                 365

Leu Asp Gly Leu Ala Ala Arg Ile Leu Gly Gln Arg Val Arg Leu Gly
    370                 375                 380

Arg Pro Leu Arg Val Gln Gly Leu Pro Gln Gln Val Ser Gly Pro Gly
385                 390                 395                 400

Phe Ser Ser Ala Val Gly Leu Cys Leu Phe Ala Ala His Pro Gln Asp
                405                 410                 415

Glu Trp Trp Asp Phe Asp Ile Pro Ala Glu Arg Tyr Pro Ala Arg Ser
            420                 425                 430

Leu Arg Arg Ala Ile Lys Trp Phe Lys Asp Asn Trp
        435                 440


<210> SEQ ID NO 73
<211> LENGTH: 1212
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 73

atgacggctc tgaccagcac gcgcggccag caggatctgc cgcgctattt ctcgcaggtg      60

ttcgacgtga tgcagggact gcgccacggt cggctcgact tcgtgctcga cgacgggcgg     120

cgcttccggg tcgaggggca ggggccgggg ccggtcgccg aactcgacat tcatgatgcg     180

gatctcttcg cccgtctgat ccgcgagggc gacctcggct tctgcgaggc ctatctcgac     240

ggcggctggt cgacgccgga cctgcaggcc ttcatggatc tgatccatgc cgacaatgac     300

gatgtctatg acggctttcc cggtcagggg ctgctgcgcg cctacgagaa cctgcgccac     360

tggctgcgcg gcaactcgaa gcggcaggcc cgccgcaaca tcgcggccca ttacgacctc     420

ggcaacgact tctacgccct ctggctcgac gagagcatga cctattcctc ggcgctcttc     480

cggaccgggc aggagagcct cgaggaggcg cagcgggcga aatatgccag catggtcgac     540

cggatcggcg cgcagcccgg cgagcatgtg ctggagatcg gctgcggttg gggcggcttc     600

gccgaatatg cggcgcgcga gcgggggctg cgggtgacgg gcctcaccat cagccaggcg     660

cagcacgatt atgcggtcga gcggatcgcg cgggcgggcc tgtcggaccg ggtcgagatc     720

cggcttcagg actaccgcga cgagcggggc agcttcgacg gcatcgcctc gatcgagatg     780

ttcgaggcgg tgggcgagaa atactggccg gtctatttcc agaccctgcg cgagcggctg     840

aagcccgggc gcaatgccac gctgcagatc atcaccgtgc aggacaagag gtgggaggtc     900

taccggcggg gggtggattt cattcagaag tacatcttcc ccggcgggat gctgccctcg     960

cccaccgcgc tccgggtcga ggtggcgaag gcggggctgc atgtaacgga ctcggtcgag    1020

ttcggcgaga gctattccat gacgctgcgc cgctggcacg agaccttcaa cgaccgctgg    1080

gaccgggtgg cggcgctggg cttcgacgag aggttccgcc gcatgtggaa cttctatctc    1140

acctcttgcg caggctcatt cgacggcgga aactgcgacg tgacgcagat caccgtaacg    1200

cgggccgcgt aa                                                        1212
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<210> SEQ ID NO 74
<211> LENGTH: 403
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 74

Met Thr Ala Leu Thr Ser Thr Arg Gly Gln Gln Asp Leu Pro Arg Tyr
1               5                   10                  15

Phe Ser Gln Val Phe Asp Val Met Gln Gly Leu Arg His Gly Arg Leu
            20                  25                  30

Asp Phe Val Leu Asp Asp Gly Arg Arg Phe Arg Val Glu Gly Gln Gly
        35                  40                  45

Pro Gly Pro Val Ala Glu Leu Asp Ile His Asp Ala Asp Leu Phe Ala
    50                  55                  60

Arg Leu Ile Arg Glu Gly Asp Leu Gly Phe Cys Glu Ala Tyr Leu Asp
65                  70                  75                  80

Gly Gly Trp Ser Thr Pro Asp Leu Gln Ala Phe Met Asp Leu Ile His
                85                  90                  95

Ala Asp Asn Asp Asp Val Tyr Asp Gly Phe Pro Gly Gln Gly Leu Leu
            100                 105                 110

Arg Ala Tyr Glu Asn Leu Arg His Trp Leu Arg Gly Asn Ser Lys Arg
        115                 120                 125

Gln Ala Arg Arg Asn Ile Ala Ala His Tyr Asp Leu Gly Asn Asp Phe
    130                 135                 140

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

Arg Thr Gly Gln Glu Ser Leu Glu Glu Ala Gln Arg Ala Lys Tyr Ala
                165                 170                 175

Ser Met Val Asp Arg Ile Gly Ala Gln Pro Gly Glu His Val Leu Glu
            180                 185                 190

Ile Gly Cys Gly Trp Gly Gly Phe Ala Glu Tyr Ala Ala Arg Glu Arg
        195                 200                 205

Gly Leu Arg Val Thr Gly Leu Thr Ile Ser Gln Ala Gln His Asp Tyr
    210                 215                 220

Ala Val Glu Arg Ile Ala Arg Ala Gly Leu Ser Asp Arg Val Glu Ile
225                 230                 235                 240

Arg Leu Gln Asp Tyr Arg Asp Glu Arg Gly Ser Phe Asp Gly Ile Ala
                245                 250                 255

Ser Ile Glu Met Phe Glu Ala Val Gly Glu Lys Tyr Trp Pro Val Tyr
            260                 265                 270

Phe Gln Thr Leu Arg Glu Arg Leu Lys Pro Gly Arg Asn Ala Thr Leu
        275                 280                 285

Gln Ile Ile Thr Val Gln Asp Lys Arg Trp Glu Val Tyr Arg Arg Gly
    290                 295                 300

Val Asp Phe Ile Gln Lys Tyr Ile Phe Pro Gly Gly Met Leu Pro Ser
305                 310                 315                 320

Pro Thr Ala Leu Arg Val Glu Val Ala Lys Ala Gly Leu His Val Thr
                325                 330                 335

Asp Ser Val Glu Phe Gly Glu Ser Tyr Ser Met Thr Leu Arg Arg Trp
            340                 345                 350

His Glu Thr Phe Asn Asp Arg Trp Asp Arg Val Ala Ala Leu Gly Phe
        355                 360                 365

Asp Glu Arg Phe Arg Arg Met Trp Asn Phe Tyr Leu Thr Ser Cys Ala
    370                 375                 380
```

Gly Ser Phe Asp Gly Gly Asn Cys Asp Val Thr Gln Ile Thr Val Thr
385 390 395 400

Arg Ala Ala

<210> SEQ ID NO 75
<211> LENGTH: 2202
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 75

atgaccgatt tcaccagccg gaccgacgcg gacggggtct gcaccatcac ctgggacgtg 60

ccgggcaagt cgatgaacgt catgtcgatg gcgggatttg ccgagctcga cgggctgatc 120

gccgcggcgc tcggcgatcc gtctgtcaag ggcgtgatcc tcacctcggg caagaaggac 180

tttgccgcgg ggatggatct caatgtcatc gcccgcatga aggaggaagg cggcgacgat 240

ccggcccggg ccgtgttcga gggcgtgatg gagatgcatg ccgtcctgcg ccggatcgag 300

cgcgcgggca tggatccgaa gacgctgaag gggggcaagc ccatcgtggc ggccctgccc 360

ggcaccgccc tgggcctggg gctcgagctg ccgctggcct gccaccgcat catcgcggcc 420

gacaatccca aggccaagat cggcctgccc gagatcatgg tggggatctt ccccggcggc 480

ggcggcacga cgcggctcgt ccgcaggctc ggcgccatga tggcggctcc cctcctcctc 540

gagggcaagc tgaacgatcc caagggcgcc aaggccatgg gtgtcgtcga cgaggtggtg 600

ccggccgatc agctgctccc gcgggcgaag gaatgggtgc tcggcgcgaa ggacgcggat 660

ctggtgaagc cgtgggacgc caagggctac aagatgcctg gcggcgcgcc ctaccatccg 720

gcgggcttca tgaccttcgt cggcgcctcg gccatggtga cgggcaagac gatgggcgtc 780

tatccggcgg ccaagggcct gctcgccgcg gtctacgagg gcgcgctcgt gcccttcgac 840

accgcgctga agatcgaggc gcgctggttc acccatgtgc tgatgaatcc ctcctcgtcg 900

gcgatgatcc ggtcgctctt catcaacaag gaggcgctgg agaagggcgc cgtccgccct 960

gccctgcccg accagtcggt ccggaagctg ggcgtgatcg ggcgggcat gatgggcgcg 1020

ggcatcgccc atgtcgcggc caatgcgggc atcgaggtcg tgctgatcga cgcgacgcag 1080

gaggcggccg accgcggcaa gtcccattcg gaaggtctcc tcgacaaggg gatgaagcgg 1140

ggcaaggtct cggccgagaa gaaggccgag gtgctgggcc ggatcgccgc caccaccgac 1200

tatgcggccc tctcgggctg cgatctgatc gtcgaggcgg tgttcgagga tcccgcggtg 1260

aaggccgagg tcactcagaa ggtcgaggcc gcggtcgggc ccgactgtat cttcgcaacc 1320

aacacctcga ccctgccgat ctcggggttg gccaaggcga gccgcgatcc ggcgcagttc 1380

atcggcatcc atttcttctc gcccgtggac aagatgatgc tggtcgagat catccgcggc 1440

aaggccaccg gcgaccgcgc cgtggccaag gcgctcgatt tcgtgcgcca gatccgcaag 1500

acgcccatcg tcgtccacga tgcgcgcttc ttctacgcca accgctgcat catcccctac 1560

ctcaacgagg ggatccgcat ggtggccgaa ggcgtggcgc ccgcgctgat cgagaatgcg 1620

gcgaagctgg tggggatgcc gctcggcccc cttcagctgg tggacgaaac ctcgatcgac 1680

ctcggggtga agatcgccaa ggccacgaag gccgccctgg gcgaggccta tccggacgcg 1740

gcggtggatg cggtgatctt cccgctggcg gacgaggggc ggctcggccg caaggcgggc 1800

gcgggcttct atgcctacga cgccgccggc aagcgcgaag gtctctggcc gggcctcgcc 1860

gaccgctggc cgcaggccga ggcgcagccc gagcttgccg aggtgcagca ccggcttctc 1920

ttcgcgcagg tgctcgaggc ggtgcgcgcg ctcgaggagg gcgtgctgac cgacatccgc 1980

```
gagggcgacg tgggcgccat tctcggctgg ggcttcgcgc cctggtcggg cggcccgttc   2040

agctggctcg acatgatcgg cgcgccgcgc gcggtggaga tctgcgaggg gctggccgag   2100

cgtcacggca gccgcttcgc gccgccgaag ctgctggtcg agatggccgg caagggcgag   2160

agcttctacg cccgcttcgc accgcaggcc cgcgcggcct ga                       2202


<210> SEQ ID NO 76
<211> LENGTH: 733
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 76

Met Thr Asp Phe Thr Ser Arg Thr Asp Ala Asp Gly Val Cys Thr Ile
1               5                   10                  15

Thr Trp Asp Val Pro Gly Lys Ser Met Asn Val Met Ser Met Ala Gly
            20                  25                  30

Phe Ala Glu Leu Asp Gly Leu Ile Ala Ala Ala Leu Gly Asp Pro Ser
        35                  40                  45

Val Lys Gly Val Ile Leu Thr Ser Gly Lys Lys Asp Phe Ala Ala Gly
    50                  55                  60

Met Asp Leu Asn Val Ile Ala Arg Met Lys Glu Glu Gly Gly Asp Asp
65                  70                  75                  80

Pro Ala Arg Ala Val Phe Glu Gly Val Met Glu Met His Ala Val Leu
                85                  90                  95

Arg Arg Ile Glu Arg Ala Gly Met Asp Pro Lys Thr Leu Lys Gly Gly
            100                 105                 110

Lys Pro Ile Val Ala Ala Leu Pro Gly Thr Ala Leu Gly Leu Gly Leu
        115                 120                 125

Glu Leu Pro Leu Ala Cys His Arg Ile Ile Ala Ala Asp Asn Pro Lys
    130                 135                 140

Ala Lys Ile Gly Leu Pro Glu Ile Met Val Gly Ile Phe Pro Gly Gly
145                 150                 155                 160

Gly Gly Thr Thr Arg Leu Val Arg Arg Leu Gly Ala Met Met Ala Ala
                165                 170                 175

Pro Leu Leu Leu Glu Gly Lys Leu Asn Asp Pro Lys Gly Ala Lys Ala
            180                 185                 190

Met Gly Val Val Asp Glu Val Val Pro Ala Asp Gln Leu Leu Pro Arg
        195                 200                 205

Ala Lys Glu Trp Val Leu Gly Ala Lys Asp Ala Asp Leu Val Lys Pro
    210                 215                 220

Trp Asp Ala Lys Gly Tyr Lys Met Pro Gly Gly Ala Pro Tyr His Pro
225                 230                 235                 240

Ala Gly Phe Met Thr Phe Val Gly Ala Ser Ala Met Val Thr Gly Lys
                245                 250                 255

Thr Met Gly Val Tyr Pro Ala Ala Lys Gly Leu Leu Ala Ala Val Tyr
            260                 265                 270

Glu Gly Ala Leu Val Pro Phe Asp Thr Ala Leu Lys Ile Glu Ala Arg
        275                 280                 285

Trp Phe Thr His Val Leu Met Asn Pro Ser Ser Ser Ala Met Ile Arg
    290                 295                 300

Ser Leu Phe Ile Asn Lys Glu Ala Leu Glu Lys Gly Ala Val Arg Pro
305                 310                 315                 320

Ala Leu Pro Asp Gln Ser Val Arg Lys Leu Gly Val Ile Gly Ala Gly
                325                 330                 335
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Met Met Gly Ala Gly Ile Ala His Val Ala Ala Asn Ala Gly Ile Glu
            340                 345                 350

Val Val Leu Ile Asp Ala Thr Gln Glu Ala Ala Asp Arg Gly Lys Ser
        355                 360                 365

His Ser Glu Gly Leu Leu Asp Lys Gly Met Lys Arg Gly Lys Val Ser
    370                 375                 380

Ala Glu Lys Lys Ala Glu Val Leu Gly Arg Ile Ala Ala Thr Thr Asp
385                 390                 395                 400

Tyr Ala Ala Leu Ser Gly Cys Asp Leu Ile Val Glu Ala Val Phe Glu
                405                 410                 415

Asp Pro Ala Val Lys Ala Glu Val Thr Gln Lys Val Glu Ala Ala Val
            420                 425                 430

Gly Pro Asp Cys Ile Phe Ala Thr Asn Thr Ser Thr Leu Pro Ile Ser
        435                 440                 445

Gly Leu Ala Lys Ala Ser Arg Asp Pro Ala Gln Phe Ile Gly Ile His
    450                 455                 460

Phe Phe Ser Pro Val Asp Lys Met Met Leu Val Glu Ile Ile Arg Gly
465                 470                 475                 480

Lys Ala Thr Gly Asp Arg Ala Val Ala Lys Ala Leu Asp Phe Val Arg
                485                 490                 495

Gln Ile Arg Lys Thr Pro Ile Val Val His Asp Ala Arg Phe Phe Tyr
            500                 505                 510

Ala Asn Arg Cys Ile Ile Pro Tyr Leu Asn Glu Gly Ile Arg Met Val
        515                 520                 525

Ala Glu Gly Val Ala Pro Ala Leu Ile Glu Asn Ala Ala Lys Leu Val
    530                 535                 540

Gly Met Pro Leu Gly Pro Leu Gln Leu Val Asp Glu Thr Ser Ile Asp
545                 550                 555                 560

Leu Gly Val Lys Ile Ala Lys Ala Thr Lys Ala Ala Leu Gly Glu Ala
                565                 570                 575

Tyr Pro Asp Ala Ala Val Asp Ala Val Ile Phe Pro Leu Ala Asp Glu
            580                 585                 590

Gly Arg Leu Gly Arg Lys Ala Gly Ala Gly Phe Tyr Ala Tyr Asp Ala
        595                 600                 605

Ala Gly Lys Arg Glu Gly Leu Trp Pro Gly Leu Ala Asp Arg Trp Pro
    610                 615                 620

Gln Ala Glu Ala Gln Pro Glu Leu Ala Glu Val Gln His Arg Leu Leu
625                 630                 635                 640

Phe Ala Gln Val Leu Glu Ala Val Arg Ala Leu Glu Glu Gly Val Leu
                645                 650                 655

Thr Asp Ile Arg Glu Gly Asp Val Gly Ala Ile Leu Gly Trp Gly Phe
            660                 665                 670

Ala Pro Trp Ser Gly Gly Pro Phe Ser Trp Leu Asp Met Ile Gly Ala
        675                 680                 685

Pro Arg Ala Val Glu Ile Cys Glu Gly Leu Ala Glu Arg His Gly Ser
    690                 695                 700

Arg Phe Ala Pro Pro Lys Leu Leu Val Glu Met Ala Gly Lys Gly Glu
705                 710                 715                 720

Ser Phe Tyr Ala Arg Phe Ala Pro Gln Ala Arg Ala Ala
                725                 730


<210> SEQ ID NO 77
<211> LENGTH: 1212
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<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 77

atgacggaag cctatatcta cgacgccctg cgcaccccgc gcggcaaggg ccggcccgac     60

ggcgcgctgc atgaggtgac ctcggtcgcg ctgtcggcga aggtgctgaa cgcggtcaag    120

gagcgcaacc atctcgacgg cgccgcggtc gaggatgtga tctggggcaa tgccacgcag    180

gtgggcgaac agggcggctg cctcgcgcgc tcggcggtgc tgctctcgga tctcgacgag    240

tcgatccccg gcctctcgat caaccgcttc tgtgcaagcg ggatggaggc ggtgaacctc    300

gccgcgaacc aagtgcgcgc cggggcgggc gaggcctata tcgcgggcgg cgtcgagatg    360

atgagccgcg tcgccatggg ctcggacggg gcggcggtgg cggcggaccc ttctctcgcc    420

atgaagacct atttcgtgcc gcagggcatc tcggccgaca tcatcgcgac ccgctacggc    480

ttcagccgcg acgaggccga tgcgctggcg gtggaaagcc agaagcgcgc cgccgcggcc    540

tgggccgagg gccgcttcgc ccggtcggtc gtgccggtgc gcgaccagaa cggcgtgacg    600

atcctcgagc gcgacgaata tctgcggccc aacaccgaca tgcagtcgct gggcgcgctg    660

aagcccgcct tcaaggagat gggcgaacag atgccgggct tcgacaagct cgcgctgatg    720

aaatatcccg agctggagcg ggtcgagcat atccaccacg ccggcaattc ctcgggcatc    780

gtggacgggg cggcggccgt gctgatcggc agccgtgcct tcggcgaggc ccatggcctg    840

cgcccgcgcg cgcgcatccg cgccaccgcg aagatcggca ccgaccctac gatcatgctg    900

acgggtccgg tgccggtgac ccagaagatc ctgcgcgagg ccgggatgca gatctcggac    960

atcgatctct tcgaggtgaa cgaggccttc gcggcggtcg tgctgcgctt ccagcaggcc   1020

ttcggcgtgg atcccgcgcg cgtgaacccg aacggcggcg ccatcgccat gggccacccg   1080

ctgggcgcga ccggcgccat catcatcggc acgctcctcg acgaactcga gcgcaccgac   1140

cgctcggtgg gcctcgccac gctctgcgtg gcctcgggca tggcgccgc caccatcatc   1200

gaacgcgtct ga                                                       1212


<210> SEQ ID NO 78
<211> LENGTH: 403
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 78

Met Thr Glu Ala Tyr Ile Tyr Asp Ala Leu Arg Thr Pro Arg Gly Lys
1               5                   10                  15

Gly Arg Pro Asp Gly Ala Leu His Glu Val Thr Ser Val Ala Leu Ser
            20                  25                  30

Ala Lys Val Leu Asn Ala Val Lys Glu Arg Asn His Leu Asp Gly Ala
        35                  40                  45

Ala Val Glu Asp Val Ile Trp Gly Asn Ala Thr Gln Val Gly Glu Gln
    50                  55                  60

Gly Gly Cys Leu Ala Arg Ser Ala Val Leu Leu Ser Asp Leu Asp Glu
65                  70                  75                  80

Ser Ile Pro Gly Leu Ser Ile Asn Arg Phe Cys Ala Ser Gly Met Glu
                85                  90                  95

Ala Val Asn Leu Ala Ala Asn Gln Val Arg Ala Gly Ala Gly Glu Ala
            100                 105                 110

Tyr Ile Ala Gly Gly Val Glu Met Met Ser Arg Val Ala Met Gly Ser
        115                 120                 125
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Asp Gly Ala Ala Val Ala Ala Asp Pro Ser Leu Ala Met Lys Thr Tyr
    130                 135                 140

Phe Val Pro Gln Gly Ile Ser Ala Asp Ile Ile Ala Thr Arg Tyr Gly
145                 150                 155                 160

Phe Ser Arg Asp Glu Ala Asp Ala Leu Ala Val Glu Ser Gln Lys Arg
                165                 170                 175

Ala Ala Ala Ala Trp Ala Glu Gly Arg Phe Ala Arg Ser Val Val Pro
            180                 185                 190

Val Arg Asp Gln Asn Gly Val Thr Ile Leu Glu Arg Asp Glu Tyr Leu
        195                 200                 205

Arg Pro Asn Thr Asp Met Gln Ser Leu Gly Ala Leu Lys Pro Ala Phe
    210                 215                 220

Lys Glu Met Gly Glu Gln Met Pro Gly Phe Asp Lys Leu Ala Leu Met
225                 230                 235                 240

Lys Tyr Pro Glu Leu Glu Arg Val Glu His Ile His His Ala Gly Asn
                245                 250                 255

Ser Ser Gly Ile Val Asp Gly Ala Ala Ala Val Leu Ile Gly Ser Arg
            260                 265                 270

Ala Phe Gly Glu Ala His Gly Leu Arg Pro Arg Ala Arg Ile Arg Ala
        275                 280                 285

Thr Ala Lys Ile Gly Thr Asp Pro Thr Ile Met Leu Thr Gly Pro Val
    290                 295                 300

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

Ile Asp Leu Phe Glu Val Asn Glu Ala Phe Ala Ala Val Val Leu Arg
                325                 330                 335

Phe Gln Gln Ala Phe Gly Val Asp Pro Ala Arg Val Asn Pro Asn Gly
            340                 345                 350

Gly Ala Ile Ala Met Gly His Pro Leu Gly Ala Thr Gly Ala Ile Ile
        355                 360                 365

Ile Gly Thr Leu Leu Asp Glu Leu Glu Arg Thr Asp Arg Ser Val Gly
    370                 375                 380

Leu Ala Thr Leu Cys Val Ala Ser Gly Met Gly Ala Ala Thr Ile Ile
385                 390                 395                 400

Glu Arg Val


<210> SEQ ID NO 79
<211> LENGTH: 2316
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 79

gtgccatctt tttcgaccac tctcgagcaa gccatccacg gcgctctggc gcttgcgaat     60

gcccgccgtc atgaactcgc cacgctcgag cacctgttgc ttgcgctgat cgacgagccc    120

gacgcctcgc gcgtcatgaa ggcctgctcg gtcgacctcg acgagttgcg caagacgctc    180

gtcgacttca tcgacgatga tctgtccacc ctcgtgacct ctgtcgaggg ctccgaggcc    240

gtgccgacgg ccgccttcca gcgcgtgatc cagcgcgccg ccatccatgt gcaatcctcc    300

ggccggaccg aggtcacggg cgccaacgtg ctcgtcgcca tcttcgccga acgggagtcg    360

aatgccgcct atttcctgca ggagcaggac atgacccgct acgacgcggt caacttcatc    420

gcgcatggcg tggcgaagga cccgtcctat ggcgagccgc gcccggtcac cggcgcggaa    480

gagcatcatg agaccccgaa ggctgaagct ggtgaggcga aggagtctgc gttgtcgaaa    540
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tattgcgttg acctgaacgt caaggcccgc aagggcgacg tcgacccgct catcggccgc    600

gagcacgagg tcgaacgctg cattcaggtt ctctgccgcc ggcggaagaa caacccgctc    660

ctggtgggcg acccgggcgt gggcaagacg gccatcgccg aagggctcgc gcgcaagatc    720

gtcaacggcg agacgcccga catcctcgcc cgcgccacga tcttctcgct cgacatgggc    780

gcgctgctcg ccggcacccg ctaccgcggc gatttcgagg agcggctgaa ggccgtggtc    840

aaggagatgg aggatcaccc cgacgcgatc ctcttcatcg acgagatcca caccgtgatc    900

ggcgccggcg ccacctcggg cggcgcgatg gatgcctcga acctgctcaa gcccgcgctg    960

cagggcggca agctgcgctg catgggctcg accacctaca aggaatatcg tcagcatttc   1020

gagaaggacc gcgcgctcag ccgccggttc cagaagatcg acgtgaacga gccctcggtc   1080

gaggatacgg tcaagatcct gatgggcctc aagccctatt tcgaggagca tcacgacctg   1140

cgctacacgc aggacgcgat ccggaccgcg gtggaactgt ccgcgcgcta catccatgac   1200

cgcaagctgc cggacaaggc gatcgacgtg atcgacgagg ccggcgcggc ccagcacctg   1260

ctggccgaca gcaagcggcg caagactatc ggtccgcgtg agatcgaggc ggtggtggcc   1320

aagatcgccc gcatcccccc gaagagcgtc tcgaaggacg atgccgaagt gctgcgcgac   1380

ctcgagaaga ccctcaagcg ggtggtgttc ggtcaggacc gggccatcga ggccctgtcc   1440

tcggccatca agctggcgcg cgccggcctg cgcgagcccg agaagccgat cggcaactat   1500

ctcttcgcgg gcccgaccgg cgtcggcaag accgaggtgg cgaagcagct ggcaagcatc   1560

ctcggcgtgg aactgctgcg cttcgacatg tcggaatata tggagaagca cgccgtctcc   1620

cgactgatcg gcgcgcctcc gggttacgtc ggcttcgatc agggtgggat gctgaccgat   1680

ggcgtggacc agcatccgca ttgcgtgctg ctgctcgacg agatcgagaa ggcccacccg   1740

gatgtctaca acatcctgct gcaggtgatg gaccacggga aactcaccga ccacaacggc   1800

cggtcggtcg atttccgcaa cgtgatcctg atcatgacct cgaacgcagg cgcggccgag   1860

ctggccaagt ccgcgatcgg cttcggacgc gaccggcgcg agggcgagga tacggccgcc   1920

atcgagcgga ccttcacgcc cgagttccgc aaccgtctcg atgcagtcat ctccttcgcg   1980

cccctcggca aggagatcat cctgcaggtg gtcgagaagt tcgtcctcca gctcgaggcc   2040

cagctcatgg accgtggcgt gcatatcgag ctctcgccgg aagcggcggc ctggctcggc   2100

gacaagggct acgacgacaa gatgggagcg cgcccgctgg gccgcgtgat ccaggagaac   2160

atcaagaagc cgctggccga ggaactcctg ttcggccggc tggtgaaggg cggcgtcgtg   2220

aaggtcggcg tgaaggacga tacgatcgac ctgcagatcg aggaaccgaa gccgcgcctc   2280

accgggtcca agccgccgct tctgacggcc gactga                             2316


<210> SEQ ID NO 80
<211> LENGTH: 771
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 80

Met Pro Ser Phe Ser Thr Thr Leu Glu Gln Ala Ile His Gly Ala Leu
1               5                   10                  15

Ala Leu Ala Asn Ala Arg Arg His Glu Leu Ala Thr Leu Glu His Leu
            20                  25                  30

Leu Leu Ala Leu Ile Asp Glu Pro Asp Ala Ser Arg Val Met Lys Ala
        35                  40                  45

Cys Ser Val Asp Leu Asp Glu Leu Arg Lys Thr Leu Val Asp Phe Ile
    50                  55                  60
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Asp Asp Asp Leu Ser Thr Leu Val Thr Ser Val Glu Gly Ser Glu Ala
65                  70                  75                  80

Val Pro Thr Ala Ala Phe Gln Arg Val Ile Gln Arg Ala Ala Ile His
                85                  90                  95

Val Gln Ser Ser Gly Arg Thr Glu Val Thr Gly Ala Asn Val Leu Val
            100                 105                 110

Ala Ile Phe Ala Glu Arg Glu Ser Asn Ala Ala Tyr Phe Leu Gln Glu
        115                 120                 125

Gln Asp Met Thr Arg Tyr Asp Ala Val Asn Phe Ile Ala His Gly Val
    130                 135                 140

Ala Lys Asp Pro Ser Tyr Gly Glu Pro Arg Pro Val Thr Gly Ala Glu
145                 150                 155                 160

Glu His His Glu Thr Pro Lys Ala Glu Ala Gly Glu Ala Lys Glu Ser
                165                 170                 175

Ala Leu Ser Lys Tyr Cys Val Asp Leu Asn Val Lys Ala Arg Lys Gly
            180                 185                 190

Asp Val Asp Pro Leu Ile Gly Arg Glu His Glu Val Glu Arg Cys Ile
        195                 200                 205

Gln Val Leu Cys Arg Arg Arg Lys Asn Asn Pro Leu Leu Val Gly Asp
    210                 215                 220

Pro Gly Val Gly Lys Thr Ala Ile Ala Glu Gly Leu Ala Arg Lys Ile
225                 230                 235                 240

Val Asn Gly Glu Thr Pro Asp Ile Leu Ala Arg Ala Thr Ile Phe Ser
                245                 250                 255

Leu Asp Met Gly Ala Leu Leu Ala Gly Thr Arg Tyr Arg Gly Asp Phe
            260                 265                 270

Glu Glu Arg Leu Lys Ala Val Val Lys Glu Met Glu Asp His Pro Asp
        275                 280                 285

Ala Ile Leu Phe Ile Asp Glu Ile His Thr Val Ile Gly Ala Gly Ala
    290                 295                 300

Thr Ser Gly Gly Ala Met Asp Ala Ser Asn Leu Leu Lys Pro Ala Leu
305                 310                 315                 320

Gln Gly Gly Lys Leu Arg Cys Met Gly Ser Thr Thr Tyr Lys Glu Tyr
                325                 330                 335

Arg Gln His Phe Glu Lys Asp Arg Ala Leu Ser Arg Arg Phe Gln Lys
            340                 345                 350

Ile Asp Val Asn Glu Pro Ser Val Glu Asp Thr Val Lys Ile Leu Met
        355                 360                 365

Gly Leu Lys Pro Tyr Phe Glu Glu His His Asp Leu Arg Tyr Thr Gln
    370                 375                 380

Asp Ala Ile Arg Thr Ala Val Glu Leu Ser Ala Arg Tyr Ile His Asp
385                 390                 395                 400

Arg Lys Leu Pro Asp Lys Ala Ile Asp Val Ile Asp Glu Ala Gly Ala
                405                 410                 415

Ala Gln His Leu Leu Ala Asp Ser Lys Arg Arg Lys Thr Ile Gly Pro
            420                 425                 430

Arg Glu Ile Glu Ala Val Val Ala Lys Ile Ala Arg Ile Pro Pro Lys
        435                 440                 445

Ser Val Ser Lys Asp Asp Ala Glu Val Leu Arg Asp Leu Glu Lys Thr
    450                 455                 460

Leu Lys Arg Val Val Phe Gly Gln Asp Arg Ala Ile Glu Ala Leu Ser
465                 470                 475                 480
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Ser Ala Ile Lys Leu Ala Arg Ala Gly Leu Arg Glu Pro Glu Lys Pro
                485                 490                 495

Ile Gly Asn Tyr Leu Phe Ala Gly Pro Thr Gly Val Gly Lys Thr Glu
            500                 505                 510

Val Ala Lys Gln Leu Ala Ser Ile Leu Gly Val Glu Leu Leu Arg Phe
        515                 520                 525

Asp Met Ser Glu Tyr Met Glu Lys His Ala Val Ser Arg Leu Ile Gly
    530                 535                 540

Ala Pro Pro Gly Tyr Val Gly Phe Asp Gln Gly Gly Met Leu Thr Asp
545                 550                 555                 560

Gly Val Asp Gln His Pro His Cys Val Leu Leu Leu Asp Glu Ile Glu
                565                 570                 575

Lys Ala His Pro Asp Val Tyr Asn Ile Leu Leu Gln Val Met Asp His
            580                 585                 590

Gly Lys Leu Thr Asp His Asn Gly Arg Ser Val Asp Phe Arg Asn Val
        595                 600                 605

Ile Leu Ile Met Thr Ser Asn Ala Gly Ala Ala Glu Leu Ala Lys Ser
    610                 615                 620

Ala Ile Gly Phe Gly Arg Asp Arg Arg Glu Gly Glu Asp Thr Ala Ala
625                 630                 635                 640

Ile Glu Arg Thr Phe Thr Pro Glu Phe Arg Asn Arg Leu Asp Ala Val
                645                 650                 655

Ile Ser Phe Ala Pro Leu Gly Lys Glu Ile Ile Leu Gln Val Val Glu
            660                 665                 670

Lys Phe Val Leu Gln Leu Glu Ala Gln Leu Met Asp Arg Gly Val His
        675                 680                 685

Ile Glu Leu Ser Pro Glu Ala Ala Ala Trp Leu Gly Asp Lys Gly Tyr
    690                 695                 700

Asp Asp Lys Met Gly Ala Arg Pro Leu Gly Arg Val Ile Gln Glu Asn
705                 710                 715                 720

Ile Lys Lys Pro Leu Ala Glu Glu Leu Leu Phe Gly Arg Leu Val Lys
                725                 730                 735

Gly Gly Val Val Lys Val Gly Val Lys Asp Asp Thr Ile Asp Leu Gln
            740                 745                 750

Ile Glu Glu Pro Lys Pro Arg Leu Thr Gly Ser Lys Pro Pro Leu Leu
        755                 760                 765

Thr Ala Asp
    770
```

<210> SEQ ID NO 81
<211> LENGTH: 825
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 81

```
atggcgaacg gactgctggc tggcaagcgt gggctcatca tggggctggc gaacgacaag      60

tccatcgcct ggggcatcgc gaaatgctgc gccgaccagg gagccgagct ggccttctcc     120

tatcagggcg atgcgctgaa gaagcgcgtc gaaccgctgg ccgcctcgat cggggcgacc     180

gagatggtgg aatgcgacgt gtccgacgag gcctcgctcg accggctctt cgcgcatctg     240

aaggaggtct ggggcacgct cgacttcgtc gtccatgcca tcggcttctc ggacaagtcc     300

gagctgcgcg gccgctatgt cgacacgacg cccgcgaact tccgcatgac gatggacatt     360

tcggtctatt ccttcaccgc cgtctgccag cgcgcctgcg ccatgatgcc cgcgggcggc     420
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agccttctca cgctgaccta ctacggcgcc gagaaggtga tgccgcacta caatgtgatg    480

ggaatcgcca aggccgcgct cgagacctcg gtgcagtata tcgccgagga tctgggcaag    540

gacggcatcc gcgtgaatgc gatctcggcc ggcccgatca agacgctggc cgccagcggc    600

atcggcgact tccgctacat catgaagtgg aacgagctga attcgccgct gcgccgcaac    660

gtcacgcagg aagaggtggg caaggccgcg ctctatctgc tgtcggatct gggttcgggc    720

acgacgggcg aggtgctgca tgtggatgcg ggctatcacg tcgtcggcat gaaggccgtg    780

gacgcgcccg acatcgacgc cgtgaccggc cgcaaggacc actga                   825


<210> SEQ ID NO 82
<211> LENGTH: 274
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 82

Met Ala Asn Gly Leu Leu Ala Gly Lys Arg Gly Leu Ile Met Gly Leu
1               5                   10                  15

Ala Asn Asp Lys Ser Ile Ala Trp Gly Ile Ala Lys Cys Cys Ala Asp
            20                  25                  30

Gln Gly Ala Glu Leu Ala Phe Ser Tyr Gln Gly Asp Ala Leu Lys Lys
        35                  40                  45

Arg Val Glu Pro Leu Ala Ala Ser Ile Gly Ala Thr Glu Met Val Glu
    50                  55                  60

Cys Asp Val Ser Asp Glu Ala Ser Leu Asp Arg Leu Phe Ala His Leu
65                  70                  75                  80

Lys Glu Val Trp Gly Thr Leu Asp Phe Val Val His Ala Ile Gly Phe
                85                  90                  95

Ser Asp Lys Ser Glu Leu Arg Gly Arg Tyr Val Asp Thr Thr Pro Ala
            100                 105                 110

Asn Phe Arg Met Thr Met Asp Ile Ser Val Tyr Ser Phe Thr Ala Val
        115                 120                 125

Cys Gln Arg Ala Cys Ala Met Met Pro Ala Gly Gly Ser Leu Leu Thr
    130                 135                 140

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

Gly Ile Ala Lys Ala Ala Leu Glu Thr Ser Val Gln Tyr Ile Ala Glu
                165                 170                 175

Asp Leu Gly Lys Asp Gly Ile Arg Val Asn Ala Ile Ser Ala Gly Pro
            180                 185                 190

Ile Lys Thr Leu Ala Ala Ser Gly Ile Gly Asp Phe Arg Tyr Ile Met
        195                 200                 205

Lys Trp Asn Glu Leu Asn Ser Pro Leu Arg Arg Asn Val Thr Gln Glu
    210                 215                 220

Glu Val Gly Lys Ala Ala Leu Tyr Leu Leu Ser Asp Leu Gly Ser Gly
225                 230                 235                 240

Thr Thr Gly Glu Val Leu His Val Asp Ala Gly Tyr His Val Val Gly
                245                 250                 255

Met Lys Ala Val Asp Ala Pro Asp Ile Asp Ala Val Thr Gly Arg Lys
            260                 265                 270

Asp His


<210> SEQ ID NO 83
<211> LENGTH: 747
<212> TYPE: DNA
```

<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 83

atgacgaaga cggcggttgt gacgggggcg gcgcgcggga tcgggcgcgc gctcgcggtg 60

gggctcgcag aggcgggcta cgatgtggcg gtgacggatc tggccgcgca ggccgacggg 120

ctggccgaga cgcgcgcgct gatcgaggcc gcgggccggc gcgccttcgt cgagacggtg 180

gatgtctcgg accgggccgc ggtcgtcgcc gcgatggcgc ggatcgagga cgccgcgggc 240

gggatcgacg tgctggtgaa caatgcgggc atcctgaagc ccgcgcggct cgaggatctc 300

tcggaggccg actgggacgc gcatatggac gtgaacgtga agggcgtcct ctcctgctgt 360

caggcggtgc tgccgggaat gcgcgcgcgc aaggcggggc ggatcgtcaa catcgcctcc 420

atcgcgggcc gtcagggcgt gccgacccaa ggccattatg cggcgaccaa ggccgccgtc 480

attaccctga cgcgggtgct ggcgcaggag gccggcatgg acgggatcac cgtcaatgcc 540

atctgcccgg gcatcatcct gaccgagatg ggcaagaaca acctcggctc ggacgaggcc 600

atccgccact gggaagaggt ggccgcgctg aagcgtctcg gcgcgcccga agatatcgtg 660

gggccggtcc tgttcttcgc gggcgagcag tcggccttcg tcaccgggca ggcgctgaac 720

gtctgcggcg ggatctactt ccattag 747

<210> SEQ ID NO 84
<211> LENGTH: 248
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 84

Met Thr Lys Thr Ala Val Val Thr Gly Ala Ala Arg Gly Ile Gly Arg
1   5   10   15

Ala Leu Ala Val Gly Leu Ala Glu Ala Gly Tyr Asp Val Ala Val Thr
            20   25   30

Asp Leu Ala Ala Gln Ala Asp Gly Leu Ala Glu Thr Arg Ala Leu Ile
        35   40   45

Glu Ala Ala Gly Arg Arg Ala Phe Val Glu Thr Val Asp Val Ser Asp
    50   55   60

Arg Ala Ala Val Val Ala Ala Met Ala Arg Ile Glu Asp Ala Ala Gly
65   70   75   80

Gly Ile Asp Val Leu Val Asn Asn Ala Gly Ile Leu Lys Pro Ala Arg
                85   90   95

Leu Glu Asp Leu Ser Glu Ala Asp Trp Asp Ala His Met Asp Val Asn
            100   105   110

Val Lys Gly Val Leu Ser Cys Cys Gln Ala Val Leu Pro Gly Met Arg
        115   120   125

Ala Arg Lys Ala Gly Arg Ile Val Asn Ile Ala Ser Ile Ala Gly Arg
    130   135   140

Gln Gly Val Pro Thr Gln Gly His Tyr Ala Ala Thr Lys Ala Ala Val
145   150   155   160

Ile Thr Leu Thr Arg Val Leu Ala Gln Glu Ala Gly Met Asp Gly Ile
                165   170   175

Thr Val Asn Ala Ile Cys Pro Gly Ile Ile Leu Thr Glu Met Gly Lys
            180   185   190

Asn Asn Leu Gly Ser Asp Glu Ala Ile Arg His Trp Glu Glu Val Ala
        195   200   205

Ala Leu Lys Arg Leu Gly Ala Pro Glu Asp Ile Val Gly Pro Val Leu
    210   215   220

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

Val Cys Gly Gly Ile Tyr Phe His
245

<210> SEQ ID NO 85
<211> LENGTH: 738
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 85

atgttcgatc tgacgggaaa atcggcgctc atcaccggcg cttcgggcgg catcggcggc 60

ggcatcgcgc gcgcgctcca tgcggcgggg gcgacggtgg cgctctccgg cacgcggacg 120

ggaccgctcg aagagctggc ggccgagctg gggatcgcg cccatgtgct cgcctgcaac 180

ctctcggatg cggcggccgt cgaggcgctg ccgaagcagg cggccgaggc gatgggcgcg 240

gtcgacatcc tcgtgaacaa tgcgggcatc acccgcgatc agctcgccat gcgcatgtcg 300

gacgaggatt gggagcaggt gatcgaggtg aacctgacct cgaccttccg gctctgccgc 360

ggcgtgctgc gcggcatgat gaaggcgcgc tgggggcgga tcgtcaacat cacctccatc 420

gtgggcgcga cgggcaatcc ggggcaggcc aattatgccg cctcgaaggc gggcgtcgtg 480

gccatgtcga aaagctttgc ggccgaggtg gcgagccgcg gcatcaccgt caatgcggtg 540

gcgccgggct tcatcgcgac cgcgatgacc gacaagctga acgacgagca gaaggcgcgg 600

attctgggtc aggtgccgat gggccggatg ggcgcccccg acgatatcgc ggcggccgtg 660

ctctatctgg ccagtcccgc ggcgggctat gtgacggggg ccacgctcca tgtgaacggc 720

ggcatggcga tgctgtga 738

<210> SEQ ID NO 86
<211> LENGTH: 245
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 86

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

Gly Ile Gly Gly Gly Ile Ala Arg Ala Leu His Ala Ala Gly Ala Thr
20   25   30

Val Ala Leu Ser Gly Thr Arg Thr Gly Pro Leu Glu Glu Leu Ala Ala
35   40   45

Glu Leu Gly Asp Arg Ala His Val Leu Ala Cys Asn Leu Ser Asp Ala
50   55   60

Ala Ala Val Glu Ala Leu Pro Lys Gln Ala Ala Glu Ala Met Gly Ala
65   70   75   80

Val Asp Ile Leu Val Asn Asn Ala Gly Ile Thr Arg Asp Gln Leu Ala
85   90   95

Met Arg Met Ser Asp Glu Asp Trp Glu Gln Val Ile Glu Val Asn Leu
100   105   110

Thr Ser Thr Phe Arg Leu Cys Arg Gly Val Leu Arg Gly Met Met Lys
115   120   125

Ala Arg Trp Gly Arg Ile Val Asn Ile Thr Ser Ile Val Gly Ala Thr
130   135   140

Gly Asn Pro Gly Gln Ala Asn Tyr Ala Ala Ser Lys Ala Gly Val Val
145   150   155   160

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Ala Met Ser Lys Ser Phe Ala Ala Glu Val Ala Ser Arg Gly Ile Thr
                165                 170                 175

Val Asn Ala Val Ala Pro Gly Phe Ile Ala Thr Ala Met Thr Asp Lys
            180                 185                 190

Leu Asn Asp Glu Gln Lys Ala Arg Ile Leu Gly Gln Val Pro Met Gly
        195                 200                 205

Arg Met Gly Ala Pro Asp Asp Ile Ala Ala Ala Val Leu Tyr Leu Ala
    210                 215                 220

Ser Pro Ala Ala Gly Tyr Val Thr Gly Ala Thr Leu His Val Asn Gly
225                 230                 235                 240

Gly Met Ala Met Leu
                245


<210> SEQ ID NO 87
<211> LENGTH: 1263
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 87

atgcgtcgag tggttgtcac ggggctgggc atggtcacgc cgctggcgtg cggcgtcgag      60

gagacctgga agcggctgct ggccgggcag tccggcgcgg gtccgatcca gcggttcgac     120

acgtccaacg tgaccacgca atatgcctgc gagatcccgg tgggcgacgg cagcgacggc     180

accttcaacg ccgacgactg gatggagccc aaggacaggc gcaaggtcga cgatttcatc     240

ctctatgcca tggccgcggc cacgcaggcg gtgaaggatt ccggctggga gccgcaatcc     300

gaggaagacc gctgccgcac gggcgtgatg atcggctcgg gcatcggcgg cctctcggcc     360

atcgccgaca cggccgtgct catcaaggaa aaggggccga agcgcgtctc gcccttcttc     420

atcccctcgg cgctcatcaa cctggcctcg gggcaggtct cgatccgctt cggctacaag     480

ggtccgaacc atgccgtcgt gaccgcctgc tcgaccggcg cccatgcgat cggcgacgcg     540

gcccggctga tccagctcgg cgatgccgac gtgatgctcg cgggcggcgc cgagagcccg     600

atctccgaga tcggcatcgc gggcttcaac gcctgcaagg cgctctcgac caagcggggc     660

aacgagcccg aggccgcctc gcggccctgg gacgccgacc gcgacggatt cgtgatgggc     720

gagggcgcgg gcgtcgtcgt gctcgaggaa tatgaacatg ccagggcgcg cggcgccaag     780

atctatgccg aggtgctggg ctacggtctt tccggcgatg cctaccacat caccgccccc     840

tcggaagacg gggacggcgg cttccgctcg atgaccatgg cgctgaagcg cgcgggcctc     900

gaaccctcgg cggtcgacta tatcaacgcc cacggcacct cgaccatggc cgacgtgatc     960

gaactcggcg cggtcgagcg gcttctgggc gaggcggcgg cggcggccac catgtcctcg    1020

accaagtcga gcatcgggca cctgctgggc gctgcgggcg cggtcgaggc gatcttctgc    1080

gtgctggcca tccgcgatca ggtggcgccg cccacgctga acctcgacaa cccggccgtg    1140

gaggcgagga tcgacctcgc acccaaggcg gcgcgcccgc gcaagatcga cgtggcgcta    1200

tcgaattcct tcggcttcgg cggcacgaac gcgtcgctgg tgctgggacg ggtcacctcg    1260

tga                                                                  1263


<210> SEQ ID NO 88
<211> LENGTH: 420
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 88

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

Cys Gly Val Glu Glu Thr Trp Lys Arg Leu Leu Ala Gly Gln Ser Gly
            20                  25                  30

Ala Gly Pro Ile Gln Arg Phe Asp Thr Ser Asn Val Thr Thr Gln Tyr
        35                  40                  45

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

Asp Asp Trp Met Glu Pro Lys Asp Arg Arg Lys Val Asp Asp Phe Ile
65                  70                  75                  80

Leu Tyr Ala Met Ala Ala Ala Thr Gln Ala Val Lys Asp Ser Gly Trp
                85                  90                  95

Glu Pro Gln Ser Glu Glu Asp Arg Cys Arg Thr Gly Val Met Ile Gly
            100                 105                 110

Ser Gly Ile Gly Gly Leu Ser Ala Ile Ala Asp Thr Ala Val Leu Ile
        115                 120                 125

Lys Glu Lys Gly Pro Lys Arg Val Ser Pro Phe Phe Ile Pro Ser Ala
    130                 135                 140

Leu Ile Asn Leu Ala Ser Gly Gln Val Ser Ile Arg Phe Gly Tyr Lys
145                 150                 155                 160

Gly Pro Asn His Ala Val Val Thr Ala Cys Ser Thr Gly Ala His Ala
                165                 170                 175

Ile Gly Asp Ala Ala Arg Leu Ile Gln Leu Gly Asp Ala Asp Val Met
            180                 185                 190

Leu Ala Gly Gly Ala Glu Ser Pro Ile Ser Glu Ile Gly Ile Ala Gly
        195                 200                 205

Phe Asn Ala Cys Lys Ala Leu Ser Thr Lys Arg Gly Asn Glu Pro Glu
    210                 215                 220

Ala Ala Ser Arg Pro Trp Asp Ala Asp Arg Asp Gly Phe Val Met Gly
225                 230                 235                 240

Glu Gly Ala Gly Val Val Val Leu Glu Glu Tyr Glu His Ala Arg Ala
                245                 250                 255

Arg Gly Ala Lys Ile Tyr Ala Glu Val Leu Gly Tyr Gly Leu Ser Gly
            260                 265                 270

Asp Ala Tyr His Ile Thr Ala Pro Ser Glu Asp Gly Asp Gly Gly Phe
        275                 280                 285

Arg Ser Met Thr Met Ala Leu Lys Arg Ala Gly Leu Glu Pro Ser Ala
    290                 295                 300

Val Asp Tyr Ile Asn Ala His Gly Thr Ser Thr Met Ala Asp Val Ile
305                 310                 315                 320

Glu Leu Gly Ala Val Glu Arg Leu Leu Gly Glu Ala Ala Ala Ala Ala
                325                 330                 335

Thr Met Ser Ser Thr Lys Ser Ser Ile Gly His Leu Leu Gly Ala Ala
            340                 345                 350

Gly Ala Val Glu Ala Ile Phe Cys Val Leu Ala Ile Arg Asp Gln Val
        355                 360                 365

Ala Pro Pro Thr Leu Asn Leu Asp Asn Pro Ala Val Glu Ala Arg Ile
    370                 375                 380

Asp Leu Ala Pro Lys Ala Ala Arg Pro Arg Lys Ile Asp Val Ala Leu
385                 390                 395                 400

Ser Asn Ser Phe Gly Phe Gly Gly Thr Asn Ala Ser Leu Val Leu Gly
                405                 410                 415

Arg Val Thr Ser
            420
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<210> SEQ ID NO 89
<211> LENGTH: 780
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 89

atggatctgg gtattcgcgg tcgccgggca ctggtctgcg cctcgtcgaa ggggctgggc      60

cttggctgtg cggcggctct ggccgaggcc ggtgtcgatc tgatgatgaa cgcgcgcggc     120

gccgaggcgc tcgaggcggc ggccgaggat ctgcggcagc ggttcggcgc gaacgtgacc     180

acggtggcgg cagacatcgt ctcggaagag gggcgggcgc gggtgctcga ggccgcgggc     240

gcggtcgaca tcctcgtgac caacgcgggc ggcccccgc ccggcctctg gtcggactgg     300

acgcgcgacg atttcatccg ggcgctcgat gccaacatgc tgacgcccat cgcgctgatg     360

accgcgctgc tgccggccat gatcgaaagc ggctggggcc gcgtcgtcaa catcacctcg     420

cagtcggtgc gcgccccgat cccggcgctc ggcctgtcga actcggcgcg cacggggctg     480

acgggctatg tggcgggcac ctcgcggcag gtggcgcagc acggtgtctg catcaacaac     540

ctgctgccgg gcatccatga caccgaccgg gccgaggcgc tcgaccgcaa tgcgatgaag     600

gcgcagggca tcacgcgcga agaggcccgc gcgcagcggg cggccagcat ccccacccgc     660

cactacggcc gggccgagga tttcggcgcc gcctgcgcct tcctctgctc cgagcatgcg     720

cgcttcatcg tgggccagaa cctgctggtc gacggcggcg gcaccaacct cacggtctga     780


<210> SEQ ID NO 90
<211> LENGTH: 259
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 90

Met Asp Leu Gly Ile Arg Gly Arg Arg Ala Leu Val Cys Ala Ser Ser
1               5                   10                  15

Lys Gly Leu Gly Leu Gly Cys Ala Ala Ala Leu Ala Glu Ala Gly Val
            20                  25                  30

Asp Leu Met Met Asn Ala Arg Gly Ala Glu Ala Leu Glu Ala Ala Ala
        35                  40                  45

Glu Asp Leu Arg Gln Arg Phe Gly Ala Asn Val Thr Thr Val Ala Ala
    50                  55                  60

Asp Ile Val Ser Glu Glu Gly Arg Ala Arg Val Leu Glu Ala Ala Gly
65                  70                  75                  80

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

Trp Ser Asp Trp Thr Arg Asp Asp Phe Ile Arg Ala Leu Asp Ala Asn
            100                 105                 110

Met Leu Thr Pro Ile Ala Leu Met Thr Ala Leu Leu Pro Ala Met Ile
        115                 120                 125

Glu Ser Gly Trp Gly Arg Val Val Asn Ile Thr Ser Gln Ser Val Arg
    130                 135                 140

Ala Pro Ile Pro Ala Leu Gly Leu Ser Asn Ser Ala Arg Thr Gly Leu
145                 150                 155                 160

Thr Gly Tyr Val Ala Gly Thr Ser Arg Gln Val Ala Gln His Gly Val
                165                 170                 175

Cys Ile Asn Asn Leu Leu Pro Gly Ile His Asp Thr Asp Arg Ala Glu
            180                 185                 190
```

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Ala Leu Asp Arg Asn Ala Met Lys Ala Gln Gly Ile Thr Arg Glu Glu
        195                 200                 205

Ala Arg Ala Gln Arg Ala Ala Ser Ile Pro Thr Arg His Tyr Gly Arg
    210                 215                 220

Ala Glu Asp Phe Gly Ala Ala Cys Ala Phe Leu Cys Ser Glu His Ala
225                 230                 235                 240

Arg Phe Ile Val Gly Gln Asn Leu Leu Val Asp Gly Gly Gly Thr Asn
                245                 250                 255

Leu Thr Val


<210> SEQ ID NO 91
<211> LENGTH: 1200
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 91

atgttccacc gtcccacgcg cgcaggcgcc ctttgcatga cggcgacgct gacgatcctc      60

gccgcctgca gcacttcgga cctagactgg gacctgcgcg gtcgccccgg cgggctcagc     120

acggccgagg ccgcgcgggc ggtcagcgcc ccccgccccc gcgccgacga ccgcgggatc     180

atctcctatc cgacctatca ggtggccgtt gcccggcagg gcgagacggt cgcctcgctc     240

tcgagccgcc tcgggctcga tgccacgcag gtcgcgagct acaatgccct ctcgccgcag     300

aaccctctgc gcgccggaga agtggtcgtg ctgccgcagc gcgtggcggc ggctcccgcc     360

atgaccccgg cgcccgtcat gacggcgccc ggcgcggcga gccccggcgg catcgacgtg     420

accgccatcg ccaccagcgc cctcgaccgg gcgggccctg ccaccgcgcc ggtggccgcc     480

gctcccgctc cggcccccgt gcagtctgcc gcgacagagc ctgcccgcca ccgtgtgtcg     540

cggggagaga ccgcctattc gatcgcgcgc agctacaatg tctcgcccaa ggcgctggcg     600

gactggaacg ggctcgggcc ggatctcgcg atccgcgagg gccagtatct gatgatcccg     660

accgcctctg cgcccccgcc cacggtgccc gccaatgtga ccgcggtcac ggtgcccggg     720

gcaggctcgc cgacgcccac cccgccctcg gcggccaagc cgctgcccgc cgagtcgacc     780

acgcccgcct cgaaacccgc aggccagccg gcctcgcccg acatgggcgc acagcgcacg     840

caggcctccg cctcgcggct gggattcccg gtgcagggca agatcatccg cggctatgtg     900

aagaagaaga acgacggcat cgacatctcg gcggccgtgg gcacgccggt ggcggcggcc     960

gcggacggga cggtggcggc catcacgcag gacaccgatc aggtgccgat cctcgtgatc    1020

cggcaccccg acaacctgct gacggtctat gccaatatcg acggcatcaa ggtcaccaag    1080

ggtgccagcg tgaagcgcgg acagcccatc gccgtggtgc gcgcggccga cccgcccttc    1140

gtccatttcg aggtccgcaa ggggttcgag agcgtcgatc cgatgcccta tcttcagtag    1200


<210> SEQ ID NO 92
<211> LENGTH: 399
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 92

Met Phe His Arg Pro Thr Arg Ala Gly Ala Leu Cys Met Thr Ala Thr
1               5                   10                  15

Leu Thr Ile Leu Ala Ala Cys Ser Thr Ser Asp Leu Asp Trp Asp Leu
            20                  25                  30

Arg Gly Arg Pro Gly Gly Leu Ser Thr Ala Glu Ala Ala Arg Ala Val
        35                  40                  45
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Ser Ala Pro Arg Pro Arg Ala Asp Asp Arg Gly Ile Ile Ser Tyr Pro
    50                  55                  60

Thr Tyr Gln Val Ala Val Ala Arg Gln Gly Glu Thr Val Ala Ser Leu
65                  70                  75                  80

Ser Ser Arg Leu Gly Leu Asp Ala Thr Gln Val Ala Ser Tyr Asn Ala
                85                  90                  95

Leu Ser Pro Gln Asn Pro Leu Arg Ala Gly Glu Val Val Val Leu Pro
            100                 105                 110

Gln Arg Val Ala Ala Ala Pro Ala Met Thr Pro Ala Pro Val Met Thr
        115                 120                 125

Ala Pro Gly Ala Ala Ser Pro Gly Gly Ile Asp Val Thr Ala Ile Ala
    130                 135                 140

Thr Ser Ala Leu Asp Arg Ala Gly Pro Ala Thr Ala Pro Val Ala Ala
145                 150                 155                 160

Ala Pro Ala Pro Ala Pro Val Gln Ser Ala Ala Thr Glu Pro Ala Arg
                165                 170                 175

His Arg Val Ser Arg Gly Glu Thr Ala Tyr Ser Ile Ala Arg Ser Tyr
            180                 185                 190

Asn Val Ser Pro Lys Ala Leu Ala Asp Trp Asn Gly Leu Gly Pro Asp
        195                 200                 205

Leu Ala Ile Arg Glu Gly Gln Tyr Leu Met Ile Pro Thr Ala Ser Ala
    210                 215                 220

Pro Pro Pro Thr Val Pro Ala Asn Val Thr Ala Val Thr Val Pro Gly
225                 230                 235                 240

Ala Gly Ser Pro Thr Pro Thr Pro Pro Ser Ala Ala Lys Pro Leu Pro
                245                 250                 255

Ala Glu Ser Thr Thr Pro Ala Ser Lys Pro Ala Gly Gln Pro Ala Ser
            260                 265                 270

Pro Asp Met Gly Ala Gln Arg Thr Gln Ala Ser Ala Ser Arg Leu Gly
        275                 280                 285

Phe Pro Val Gln Gly Lys Ile Ile Arg Gly Tyr Val Lys Lys Lys Asn
    290                 295                 300

Asp Gly Ile Asp Ile Ser Ala Ala Val Gly Thr Pro Val Ala Ala Ala
305                 310                 315                 320

Ala Asp Gly Thr Val Ala Ala Ile Thr Gln Asp Thr Asp Gln Val Pro
                325                 330                 335

Ile Leu Val Ile Arg His Pro Asp Asn Leu Leu Thr Val Tyr Ala Asn
            340                 345                 350

Ile Asp Gly Ile Lys Val Thr Lys Gly Ala Ser Val Lys Arg Gly Gln
        355                 360                 365

Pro Ile Ala Val Val Arg Ala Ala Asp Pro Pro Phe Val His Phe Glu
    370                 375                 380

Val Arg Lys Gly Phe Glu Ser Val Asp Pro Met Pro Tyr Leu Gln
385                 390                 395


<210> SEQ ID NO 93
<211> LENGTH: 660
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 93

atgacggcag aggcagacgg ggaggatccg gccgaacgca agatgcggtt cctgttcgcc      60

gtccgctcgc ggggcgtcac ggatgcccgc gtgctcgccg ccatggagcg gatcgaccgc     120

ggcgccttcg tccgcggcat cttcgccgac cgtgcctatg aggacatgcc gctgcccatc     180
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gcctgcggcc agaccatcag ccagccctcg gtcgtggggc tgatgagcca ggcgctggcg    240

gtgaacccgc gcgacaaggt gctcgaggtg ggaaccggct cgggctatca ggccgccgtc    300

ctgagccagc tcgcccgccg cgtctacacc gtcgaccgtc atcgccgcct cgtgcgcgag    360

gcgaccgagg tcttccaccg cctgtccctg accaacatca ccgcgctcat tgcggacggc    420

agtttcggcc tgccggaaca ggccccgttc gaccggatcc tcgtcactgc cgcggccgag    480

gacccgcccg gcccccctgtt ggcacaattg aagatcggcg gtatcatggt cgtcccggtc    540

ggccagaccg atgcggtgca gaacctgatc aaggtgaccc ggctcgagca gggttacgat    600

tacgaggaac ttcgtccggt gcgcttcgtg cctctggtcg aaggcatcgg gtcggactga    660


<210> SEQ ID NO 94
<211> LENGTH: 219
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 94

Met Thr Ala Glu Ala Asp Gly Glu Asp Pro Ala Glu Arg Lys Met Arg
1               5                   10                  15

Phe Leu Phe Ala Val Arg Ser Arg Gly Val Thr Asp Ala Arg Val Leu
            20                  25                  30

Ala Ala Met Glu Arg Ile Asp Arg Gly Ala Phe Val Arg Gly Ile Phe
        35                  40                  45

Ala Asp Arg Ala Tyr Glu Asp Met Pro Leu Pro Ile Ala Cys Gly Gln
    50                  55                  60

Thr Ile Ser Gln Pro Ser Val Val Gly Leu Met Ser Gln Ala Leu Ala
65                  70                  75                  80

Val Asn Pro Arg Asp Lys Val Leu Glu Val Gly Thr Gly Ser Gly Tyr
                85                  90                  95

Gln Ala Ala Val Leu Ser Gln Leu Ala Arg Arg Val Tyr Thr Val Asp
            100                 105                 110

Arg His Arg Arg Leu Val Arg Glu Ala Thr Glu Val Phe His Arg Leu
        115                 120                 125

Ser Leu Thr Asn Ile Thr Ala Leu Ile Ala Asp Gly Ser Phe Gly Leu
    130                 135                 140

Pro Glu Gln Ala Pro Phe Asp Arg Ile Leu Val Thr Ala Ala Ala Glu
145                 150                 155                 160

Asp Pro Pro Gly Pro Leu Leu Ala Gln Leu Lys Ile Gly Gly Ile Met
                165                 170                 175

Val Val Pro Val Gly Gln Thr Asp Ala Val Gln Asn Leu Ile Lys Val
            180                 185                 190

Thr Arg Leu Glu Gln Gly Tyr Asp Tyr Glu Glu Leu Arg Pro Val Arg
        195                 200                 205

Phe Val Pro Leu Val Glu Gly Ile Gly Ser Asp
    210                 215


<210> SEQ ID NO 95
<211> LENGTH: 786
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 95

atgcgcatcc tgatcacgaa cgacgacggc atcaacgctc ccggcctcga ggtgctcgag     60

cagatcgccc tcgaactggc cggccccgag ggcgaggtct ggaccgtcgc tcccgccttc    120
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gagcagtccg gcgtctcgca cgcgatcagc tacacgcatc cgatgatgat cgccaagctc    180

ggtccgcgcc gctacgcagc ggagggcagc cccgccgact gcgtgctcgc cgcgctctac    240

gacgtgctgc agggcgcccg ccccgacctc gtgctctcgg gcgtgaaccg gggcaacaac    300

tccgccgaga acgtgctcta ttccggcacg gtgggcggcg cgctcgaggc ggcgctgcag    360

ggcctgcccg ccatcgccct gtcccagttc ctcggccccg aaacggaggg gctggccgat    420

ccgttcgaat gcgcccgcac ccatggcgcg cgcatcgtac gcctcctgct cgagcgcggg    480

ctctgggacg gcgaggacta ccggctgttc tacaacgtga acttcccgcc cgtgccggct    540

gcgaacctgc gcggccaccg cgtggcggcg cagggcttcc ggcgcgacac ctccttcggg    600

gtcgagccgc acatgtcgcc ctcgggtcgc cgcttcctct ggatccgggg cggcgcccag    660

cagagcccga cgctgcccgg caccgatgcg gccgtgaacc tcgaagggtt cgtctcgatc    720

acgccgctgc gcgcggatct gactgcgcat gaccggctgg ccgagctgga ggcgctcatc    780

ggatga                                                               786
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<210> SEQ ID NO 96
<211> LENGTH: 261
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 96

Met Arg Ile Leu Ile Thr Asn Asp Asp Gly Ile Asn Ala Pro Gly Leu
1               5                   10                  15

Glu Val Leu Glu Gln Ile Ala Leu Glu Leu Ala Gly Pro Glu Gly Glu
            20                  25                  30

Val Trp Thr Val Ala Pro Ala Phe Glu Gln Ser Gly Val Ser His Ala
        35                  40                  45

Ile Ser Tyr Thr His Pro Met Met Ile Ala Lys Leu Gly Pro Arg Arg
    50                  55                  60

Tyr Ala Ala Glu Gly Ser Pro Ala Asp Cys Val Leu Ala Ala Leu Tyr
65                  70                  75                  80

Asp Val Leu Gln Gly Ala Arg Pro Asp Leu Val Leu Ser Gly Val Asn
                85                  90                  95

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

Gly Ala Leu Glu Ala Ala Leu Gln Gly Leu Pro Ala Ile Ala Leu Ser
        115                 120                 125

Gln Phe Leu Gly Pro Glu Thr Glu Gly Leu Ala Asp Pro Phe Glu Cys
    130                 135                 140

Ala Arg Thr His Gly Ala Arg Ile Val Arg Leu Leu Leu Glu Arg Gly
145                 150                 155                 160

Leu Trp Asp Gly Glu Asp Tyr Arg Leu Phe Tyr Asn Val Asn Phe Pro
                165                 170                 175

Pro Val Pro Ala Ala Asn Leu Arg Gly His Arg Val Ala Ala Gln Gly
            180                 185                 190

Phe Arg Arg Asp Thr Ser Phe Gly Val Glu Pro His Met Ser Pro Ser
        195                 200                 205

Gly Arg Arg Phe Leu Trp Ile Arg Gly Gly Ala Gln Gln Ser Pro Thr
    210                 215                 220

Leu Pro Gly Thr Asp Ala Ala Val Asn Leu Glu Gly Phe Val Ser Ile
225                 230                 235                 240

Thr Pro Leu Arg Ala Asp Leu Thr Ala His Asp Arg Leu Ala Glu Leu
                245                 250                 255
```

```
Glu Ala Leu Ile Gly
            260


<210> SEQ ID NO 97
<211> LENGTH: 972
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 97

atgacaatac gcgccgtggt gaggggcgtc gggcactatc tgcccgaccg tgtcgtcccg      60

aactccgaac tcgaggcgat cgtcgagacg accgacgaat ggatccgcac ccggtcgggc     120

atcgaacggc ggcatttcgc ggcggaggga cagacgacct ccgacctcgc cgcccgcgcg     180

gcgcgtgcag cgctcgagga cgcggggctt cagccggacg acatcgacac gctgatcgtc     240

gccacctcca cggccgatct caccttcccc tccgccgcca ccatggtgca ggcggccttg     300

ggcatgaccc gcggcttcgc cttcgacgtg caggcggtct gcgcgggctt cgtctatgcg     360

ctggccaatg ccgatgcgct gatccgctcg ggtcaggcgc agcgcgtgct cgtgatcggg     420

gccgagacct tcagccgcct gatggactgg aacgaccggg ccacctgcgt gctcttcggc     480

gatggcgcgg gcgcggtggt gctcgagggc accgagagcg ccggcacctc cgccgaccgc     540

ggcatccttg cgaccgacct gcattcggac ggccgcttca aggacctgct ctatgtcgat     600

ggcggctcct cgaccggcac cacgggccac ctgcggatgc agggacgcga ggttttccgc     660

catgccgttg agaagcttgc agaaacagcg catacggcac tggagaaggc gggcctcggc     720

gccggcgatg tcgactggat cgtgccgcat caggccaacc tgcgcatcat ctcggccacc     780

gcccagcgga tgcaggttcc gatggaccgc gtgatcctga cggtgcagga tcacggcaat     840

acctcggccg cctcgattcc cctggccctc tcggtcggca aggcacgcgg gcagatcaag     900

gaaggcgacc ttctggtcac cgaagcgatc ggcggcgggc tcgcctgggg ctcggtggtc     960

ctccgctggt ag                                                         972


<210> SEQ ID NO 98
<211> LENGTH: 323
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 98

Met Thr Ile Arg Ala Val Val Arg Gly Val Gly His Tyr Leu Pro Asp
1               5                   10                  15

Arg Val Val Pro Asn Ser Glu Leu Glu Ala Ile Val Glu Thr Thr Asp
            20                  25                  30

Glu Trp Ile Arg Thr Arg Ser Gly Ile Glu Arg Arg His Phe Ala Ala
        35                  40                  45

Glu Gly Gln Thr Thr Ser Asp Leu Ala Ala Arg Ala Ala Arg Ala Ala
    50                  55                  60

Leu Glu Asp Ala Gly Leu Gln Pro Asp Asp Ile Asp Thr Leu Ile Val
65                  70                  75                  80

Ala Thr Ser Thr Ala Asp Leu Thr Phe Pro Ser Ala Ala Thr Met Val
                85                  90                  95

Gln Ala Ala Leu Gly Met Thr Arg Gly Phe Ala Phe Asp Val Gln Ala
            100                 105                 110

Val Cys Ala Gly Phe Val Tyr Ala Leu Ala Asn Ala Asp Ala Leu Ile
        115                 120                 125

Arg Ser Gly Gln Ala Gln Arg Val Leu Val Ile Gly Ala Glu Thr Phe
```

130 135 140

Ser Arg Leu Met Asp Trp Asn Asp Arg Ala Thr Cys Val Leu Phe Gly
145 150 155 160

Asp Gly Ala Gly Ala Val Val Leu Glu Gly Thr Glu Ser Ala Gly Thr
165 170 175

Ser Ala Asp Arg Gly Ile Leu Ala Thr Asp Leu His Ser Asp Gly Arg
180 185 190

Phe Lys Asp Leu Leu Tyr Val Asp Gly Gly Ser Ser Thr Gly Thr Thr
195 200 205

Gly His Leu Arg Met Gln Gly Arg Glu Val Phe Arg His Ala Val Glu
210 215 220

Lys Leu Ala Glu Thr Ala His Thr Ala Leu Glu Lys Ala Gly Leu Gly
225 230 235 240

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

Ile Ser Ala Thr Ala Gln Arg Met Gln Val Pro Met Asp Arg Val Ile
260 265 270

Leu Thr Val Gln Asp His Gly Asn Thr Ser Ala Ala Ser Ile Pro Leu
275 280 285

Ala Leu Ser Val Gly Lys Ala Arg Gly Gln Ile Lys Glu Gly Asp Leu
290 295 300

Leu Val Thr Glu Ala Ile Gly Gly Gly Leu Ala Trp Gly Ser Val Val
305 310 315 320

Leu Arg Trp

<210> SEQ ID NO 99
<211> LENGTH: 468
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 99

atgaccgaag ccgcagaagc gacgctctcc gccgatatcc agttgatcca gcggatcatc 60

ccgcaccgtt acccgttcct gctggtggac cgggtgcgcg acatcgtccc gaacaagagc 120

gccgtcggca tcaaatgcgt cacgatgaac gagccgcagt tcacggggca cttccccggc 180

ctgccgatct tcccgggcgt gcagatcatc gaggccatgg cgcagacttc ggccgtgctg 240

gtcggcgtct cgatggatct cgccgacaag ggcgccaagg tctatttcat gggcatcgac 300

ggggccaagt tccggcgcaa ggtcgtgccg ggcgacgtgc tcgagatgac cgtcaccgtg 360

aagcgcggcg gcggcaaggt ctggaagttc gagggccggg cctccgtcga cggggaactg 420

gccgccgagg cggaattctc cgccatgctc gatttgccga aaggataa 468

<210> SEQ ID NO 100
<211> LENGTH: 155
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 100

Met Thr Glu Ala Ala Glu Ala Thr Leu Ser Ala Asp Ile Gln Leu Ile
1 5 10 15

Gln Arg Ile Ile Pro His Arg Tyr Pro Phe Leu Leu Val Asp Arg Val
20 25 30

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

Met Asn Glu Pro Gln Phe Thr Gly His Phe Pro Gly Leu Pro Ile Phe

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    50                  55                  60

Pro Gly Val Gln Ile Ile Glu Ala Met Ala Gln Thr Ser Ala Val Leu
65                  70                  75                  80

Val Gly Val Ser Met Asp Leu Ala Asp Lys Gly Ala Lys Val Tyr Phe
                85                  90                  95

Met Gly Ile Asp Gly Ala Lys Phe Arg Arg Lys Val Val Pro Gly Asp
            100                 105                 110

Val Leu Glu Met Thr Val Thr Val Lys Arg Gly Gly Gly Lys Val Trp
        115                 120                 125

Lys Phe Glu Gly Arg Ala Ser Val Asp Gly Glu Leu Ala Ala Glu Ala
    130                 135                 140

Glu Phe Ser Ala Met Leu Asp Leu Pro Lys Gly
145                 150                 155


<210> SEQ ID NO 101
<211> LENGTH: 933
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 101

atgatcgatg ccgtcgtgac ctgggtggat ggtgccgatc cggcccatca cgccaagcgc      60

ctgcgtcatc agggggaggc gggcgttcat caggcggcaa ccgctccgac ccgcttcgcc     120

cattccggcg agatccgctt ctgcgtcctg tccctcctgc gcttctgccc cttcgtcgag     180

cgcatccaca tcgtcaccga cgaccagcat cccgccgtgc tggacccgat cctcgacgat     240

ccgcactggc gggaccgcat cgcggtcgtg gatcaccgcg ccatctacgg cgagcatgcc     300

gatctgcttc ccgtcttctc ctcgcgctcg atcgagacga tgatccaccg gatcccgggc     360

ctcgcgccgc gcttcatcta cctcaacgac gacatcttcg tcgggcgccc gctggacgag     420

agccatttct tcgacggaga ccgggccgtc ctgcgcggcc ggatgcagcc ctttcccaat     480

ccgctcgtca cccggctgaa acgctggctg aagcgcgagc ggccgggcta caagaccgcg     540

cagcaggcgg ccgcgcggct gacgggccgg acgagcgact atttcctgac cgagcaccag     600

ccgcatccga tgcaccgcga caggcttgcc agcttctatg cgggcgatcc gcaggcgctg     660

cgccggcagg cgggccaccg tttccgctcg gcagatcagg tctcgcccat cggcctcgcg     720

aaccatctcg agatcgaggc ccgcgccgtg atcgcgccgc cgctcgacgt gggctacatc     780

cgccccggcc gcccgaccgg cacggccctc gcccggacga tggagcggct ctgcgccaac     840

ggctatgcct cgttctgcgt ccagagtctc gacgccatgt ccgaggccga ccgccgctgc     900

gtgctggagg ggctggagcg ccattacgcc tga                                  933


<210> SEQ ID NO 102
<211> LENGTH: 310
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 102

Met Ile Asp Ala Val Val Thr Trp Val Asp Gly Ala Asp Pro Ala His
1               5                   10                  15

His Ala Lys Arg Leu Arg His Gln Gly Glu Ala Gly Val His Gln Ala
            20                  25                  30

Ala Thr Ala Pro Thr Arg Phe Ala His Ser Gly Glu Ile Arg Phe Cys
        35                  40                  45

Val Leu Ser Leu Leu Arg Phe Cys Pro Phe Val Glu Arg Ile His Ile
    50                  55                  60
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Val Thr Asp Asp Gln His Pro Ala Val Leu Asp Pro Ile Leu Asp Asp
65                  70                  75                  80

Pro His Trp Arg Asp Arg Ile Ala Val Val Asp His Arg Ala Ile Tyr
                85                  90                  95

Gly Glu His Ala Asp Leu Leu Pro Val Phe Ser Ser Arg Ser Ile Glu
            100                 105                 110

Thr Met Ile His Arg Ile Pro Gly Leu Ala Pro Arg Phe Ile Tyr Leu
        115                 120                 125

Asn Asp Asp Ile Phe Val Gly Arg Pro Leu Asp Glu Ser His Phe Phe
    130                 135                 140

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

Pro Leu Val Thr Arg Leu Lys Arg Trp Leu Lys Arg Glu Arg Pro Gly
                165                 170                 175

Tyr Lys Thr Ala Gln Gln Ala Ala Ala Arg Leu Thr Gly Arg Thr Ser
            180                 185                 190

Asp Tyr Phe Leu Thr Glu His Gln Pro His Pro Met His Arg Asp Arg
        195                 200                 205

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

Gly His Arg Phe Arg Ser Ala Asp Gln Val Ser Pro Ile Gly Leu Ala
225                 230                 235                 240

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

Val Gly Tyr Ile Arg Pro Gly Arg Pro Thr Gly Thr Ala Leu Ala Arg
            260                 265                 270

Thr Met Glu Arg Leu Cys Ala Asn Gly Tyr Ala Ser Phe Cys Val Gln
        275                 280                 285

Ser Leu Asp Ala Met Ser Glu Ala Asp Arg Arg Cys Val Leu Glu Gly
    290                 295                 300

Leu Glu Arg His Tyr Ala
305                 310


<210> SEQ ID NO 103
<211> LENGTH: 2262
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 103

gtgcggactg ctgtgcgcag caacacctgg atcaagctcg cgcgcctgcg caggcagcgg      60

cgattccaga cggcgatggc cttcggcctc gtcctgctgg ggccggtgct ggcgctggcg     120

accttccttg cattggggcc gatgaatcag ggggcgaatt cgccctcgct gcgattcgtg     180

ctgctggccg atctggtcta cgtcctcgcg gtggcggcgc tggtgatcgc gcggatcgcc     240

cgcatggtct cggaccggcg cagccagtcg gcgggctcgc ggctgcatct gcggctggtg     300

ggcaccttcg cggggctcgc gctcgtgccc accatcctcg tcgcggtctt cgcgatgctc     360

acggtgaacg tgggtctgga gggctggttc tctgagcggg tgcggcaggt ggtgggggcc     420

tcgctcgagg cagccgaggc ctatcaggaa gagcaccgcc gcgatctgat cgaggatgcc     480

gaggcgctgg cggcctatct caacgtggcc aagcaatcga ccttcttcct gcgcgacgac     540

cagctgcggc cgcttctcac gcagggacag gagaagatcc agcgcggcct gcgcgaggcc     600

ttcctgatcg atggcagcgg cgtgctccgc acccggggcg aacgcagcta tctcttcgat     660
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ttcgagcagc ccgatgccac cgacatcgag cgggcgcgcg cgggccagac ggtcctgatc    720

caggactggg ccaacaacga attccgcgcc ctcgtccatc tcacggcctt ccccgaccgc    780

ttcctctatg tctcgcgcac ggtggacggc tcgatcctga gcctgctcga cgatacgcgc    840

gagacggtgg tgctctatca tcagctggaa gccgagcgcg ggcggatgct gttcgagttc    900

gggctgctct acctcggctt cgcgctgatc ctgatccttg ccgccgtctg gctggggttc    960

tggttcgccg agcggctgtc gcgccccgtg gggcggctcg caggggctgc gcagcgcgtg   1020

ggtgcgggcg atctcgacgt gcaggtgccc gaggaggagg gcgacgacga gatcgcgatg   1080

ctgggccggc tcttcaacca gatgacccgg cagctgaagg gccagcgcga cgcgctgatg   1140

gacaacaacc gccagaccga gcggcggcgg cggctgttcg actcggtgct ctcctcggtc   1200

acggcggggg tgatcgggct cgacgcggtg gggcaggtcg atttcatcaa ccgcgccgcc   1260

cagcggctgc tcgaactgcc gcaggcgggc aacatgtccc tgtccaccgc cgtgccggag   1320

ttcgcggccc tcttcgcgcg gctgcgcgag acgggggcgg ccgtgcagga ggagatccgc   1380

ctgatccgca agggccggat ggagagcctt ctcgtccgca tgagcccgcg gcgcaacgag   1440

agcggccggc tcgaaggcta tgtggtggcc ttcgacgacg tgaccgacct cgtctcggcg   1500

cagcggatgg ccgcctgggg cgacgtggcg cggcgcatcg cgcatgagat caagaacccg   1560

ctgacgccga tccagctctc ggccgagcgg atcaagcgca agttccgccc gctcgtgggc   1620

gagcaggcgg gcgatctcga ccaatattcc gatgtcatca tccgccagac caacgatctg   1680

cgccgtatcg tggacgaatt ctcgaaattc gcccggatgc ccgagcccga ccggcgcgag   1740

gcggatctcg tgaagctcgt ccgcgacgcg gtggtgctgc aggaggcggg ccagcccgag   1800

gtgcggatcg aggcgcggct gccgtcggat ccctggccca tcgacatcga cacgaccatg   1860

atcgggcagg ccttgaccaa cctgatgaag aacgcgggcg aggcgatcga ggcccgccgc   1920

gaggcggaag gtcaggggtt cgaacccgag atccgcgtct cgcttacggt caacgaggat   1980

caggcgctgc tgcgcatcgc cgacaatggc acggggcttc cgcccgaccg gacgcggctc   2040

ttcgaaccct atgtcaccac gcgtgagaag ggcaccggcc tcggcctgcc catcgtgaag   2100

aagatcatcg aggaacatgg cggcatcctg acgctcagcg atgccgaccc cttcacccat   2160

gacggccacc gcggggccat ggccgagatc cggctgcccc gcatcctgcg cagccgggcg   2220

cgggccgcga agaccggcga ggcgagaccg gaggacacat ga                      2262


<210> SEQ ID NO 104
<211> LENGTH: 753
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 104

Met Arg Thr Ala Val Arg Ser Asn Thr Trp Ile Lys Leu Ala Arg Leu
1               5                   10                  15

Arg Arg Gln Arg Arg Phe Gln Thr Ala Met Ala Phe Gly Leu Val Leu
            20                  25                  30

Leu Gly Pro Val Leu Ala Leu Ala Thr Phe Leu Ala Leu Gly Pro Met
        35                  40                  45

Asn Gln Gly Ala Asn Ser Pro Ser Leu Arg Phe Val Leu Leu Ala Asp
    50                  55                  60

Leu Val Tyr Val Leu Ala Val Ala Ala Leu Val Ile Ala Arg Ile Ala
65                  70                  75                  80

Arg Met Val Ser Asp Arg Arg Ser Gln Ser Ala Gly Ser Arg Leu His
                85                  90                  95
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Leu Arg Leu Val Gly Thr Phe Ala Gly Leu Ala Leu Val Pro Thr Ile
            100                 105                 110

Leu Val Ala Val Phe Ala Met Leu Thr Val Asn Val Gly Leu Glu Gly
        115                 120                 125

Trp Phe Ser Glu Arg Val Arg Gln Val Val Gly Ala Ser Leu Glu Ala
    130                 135                 140

Ala Glu Ala Tyr Gln Glu Glu His Arg Arg Asp Leu Ile Glu Asp Ala
145                 150                 155                 160

Glu Ala Leu Ala Ala Tyr Leu Asn Val Ala Lys Gln Ser Thr Phe Phe
                165                 170                 175

Leu Arg Asp Asp Gln Leu Arg Pro Leu Leu Thr Gln Gly Gln Glu Lys
            180                 185                 190

Ile Gln Arg Gly Leu Arg Glu Ala Phe Leu Ile Asp Gly Ser Gly Val
        195                 200                 205

Leu Arg Thr Arg Gly Glu Arg Ser Tyr Leu Phe Asp Phe Glu Gln Pro
    210                 215                 220

Asp Ala Thr Asp Ile Glu Arg Ala Arg Ala Gly Gln Thr Val Leu Ile
225                 230                 235                 240

Gln Asp Trp Ala Asn Asn Glu Phe Arg Ala Leu Val His Leu Thr Ala
                245                 250                 255

Phe Pro Asp Arg Phe Leu Tyr Val Ser Arg Thr Val Asp Gly Ser Ile
            260                 265                 270

Leu Ser Leu Leu Asp Asp Thr Arg Glu Thr Val Val Leu Tyr His Gln
        275                 280                 285

Leu Glu Ala Glu Arg Gly Arg Met Leu Phe Glu Phe Gly Leu Leu Tyr
    290                 295                 300

Leu Gly Phe Ala Leu Ile Leu Ile Leu Ala Ala Val Trp Leu Gly Phe
305                 310                 315                 320

Trp Phe Ala Glu Arg Leu Ser Arg Pro Val Gly Arg Leu Ala Gly Ala
                325                 330                 335

Ala Gln Arg Val Gly Ala Gly Asp Leu Asp Val Gln Val Pro Glu Glu
            340                 345                 350

Glu Gly Asp Asp Glu Ile Ala Met Leu Gly Arg Leu Phe Asn Gln Met
        355                 360                 365

Thr Arg Gln Leu Lys Gly Gln Arg Asp Ala Leu Met Asp Asn Asn Arg
    370                 375                 380

Gln Thr Glu Arg Arg Arg Arg Leu Phe Asp Ser Val Leu Ser Ser Val
385                 390                 395                 400

Thr Ala Gly Val Ile Gly Leu Asp Ala Val Gly Gln Val Asp Phe Ile
                405                 410                 415

Asn Arg Ala Ala Gln Arg Leu Leu Glu Leu Pro Gln Ala Gly Asn Met
            420                 425                 430

Ser Leu Ser Thr Ala Val Pro Glu Phe Ala Ala Leu Phe Ala Arg Leu
        435                 440                 445

Arg Glu Thr Gly Ala Ala Val Gln Glu Glu Ile Arg Leu Ile Arg Lys
    450                 455                 460

Gly Arg Met Glu Ser Leu Leu Val Arg Met Ser Pro Arg Arg Asn Glu
465                 470                 475                 480

Ser Gly Arg Leu Glu Gly Tyr Val Val Ala Phe Asp Asp Val Thr Asp
                485                 490                 495

Leu Val Ser Ala Gln Arg Met Ala Ala Trp Gly Asp Val Ala Arg Arg
            500                 505                 510
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Ile Ala His Glu Ile Lys Asn Pro Leu Thr Pro Ile Gln Leu Ser Ala
        515                 520                 525

Glu Arg Ile Lys Arg Lys Phe Arg Pro Leu Val Gly Glu Gln Ala Gly
    530                 535                 540

Asp Leu Asp Gln Tyr Ser Asp Val Ile Ile Arg Gln Thr Asn Asp Leu
545                 550                 555                 560

Arg Arg Ile Val Asp Glu Phe Ser Lys Phe Ala Arg Met Pro Glu Pro
                565                 570                 575

Asp Arg Arg Glu Ala Asp Leu Val Lys Leu Val Arg Asp Ala Val Val
            580                 585                 590

Leu Gln Glu Ala Gly Gln Pro Glu Val Arg Ile Glu Ala Arg Leu Pro
        595                 600                 605

Ser Asp Pro Trp Pro Ile Asp Ile Asp Thr Thr Met Ile Gly Gln Ala
    610                 615                 620

Leu Thr Asn Leu Met Lys Asn Ala Gly Glu Ala Ile Glu Ala Arg Arg
625                 630                 635                 640

Glu Ala Glu Gly Gln Gly Phe Glu Pro Glu Ile Arg Val Ser Leu Thr
                645                 650                 655

Val Asn Glu Asp Gln Ala Leu Leu Arg Ile Ala Asp Asn Gly Thr Gly
            660                 665                 670

Leu Pro Pro Asp Arg Thr Arg Leu Phe Glu Pro Tyr Val Thr Thr Arg
        675                 680                 685

Glu Lys Gly Thr Gly Leu Gly Leu Pro Ile Val Lys Lys Ile Ile Glu
    690                 695                 700

Glu His Gly Gly Ile Leu Thr Leu Ser Asp Ala Asp Pro Phe Thr His
705                 710                 715                 720

Asp Gly His Arg Gly Ala Met Ala Glu Ile Arg Leu Pro Arg Ile Leu
                725                 730                 735

Arg Ser Arg Ala Arg Ala Ala Lys Thr Gly Glu Ala Arg Pro Glu Asp
            740                 745                 750

Thr


<210> SEQ ID NO 105
<211> LENGTH: 1431
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 105

atgagcagca ttctgatcgt cgatgacgag cgcgacatcc gcgagctgat cggggacatc      60

ctgcgcgacg agggcttcca gatccgcctc gccgccaatt ccgacgagtg catggcggcg     120

gtgaatgccg agccgccggc gctgatgatc ctcgacatct ggctcaagga cagccggatg     180

gacgggatcg acatcctgaa gcgcaccaag cgcgacaatc ccgacgtgcc ggtggtcatc     240

atctcggggc acggcaacat cgagatcgcg gtggcggcga tcaagcaggg cgcctacgac     300

ttcatcgaga agcccttcaa catcgaccag ctcatggtgg tggtccagcg cgcgatggag     360

acggcgcgtc tgcggcgcga gaacagcgag ctgcgccggc gcgacgtctc ggcggccgag     420

atgctgggcg gctcgaccgc ctaccggctg ctgaagtcgc agctcgagaa ggtcaccaag     480

tcgaacgggc gcgtcatgct ctcagggccc gcgggcgccg ggaaagagct ggccgcgcgc     540

ttcatccacg ccaattcggg ccgggcaggg gcgcccttca tctcggtctc ctcggccacc     600

gtcgagcccg accggatgga ggaggtcctc ttcggccgcg agacggccga gcgcgggatc     660

gagcaggggc tgctcgagca ggcgcacggc ggcatcgtct atttcgacga ggtggcggac     720
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atgccgctcg gcacccagtc gaagatcctg cgcgtgctga ccgaacagca attcacccgg    780

cagggcggca ccgacaaggt gcgggtcgac ctgcgggtga tctcttcgac gacgcgcgac    840

ctgcgcaccg agatcgccgc gggccgcttc cggcaggaac tttacgaccg gctgaacgtg    900

gtgccgatcg aggtgccggc gctgaccgac cggcgcgagg atattccgat gctggcccgg    960

cacttcatcg agatgttcca ccgcagtcag ggcctgccgc tgcgcagcct cacctccgag   1020

gccgaggcaa tgctccagac gatgccgtgg ccgggcaacg tgcgccagct gcgcaacgtg   1080

atcgagcggg tgctgatcct cggcgacgga tcgggcccca tcgaggcgcg cgagctgccg   1140

ggcaacgagg gcccgggcga ggaggggcgg ctgatcctcg gcggggcgct cgccacgctc   1200

ccgcttcgag aggcacgcga gctcttcgag cgcgaatatc ttctcaccca gatcaaccgc   1260

ttcggcggga acatcagccg cacggcggcc tttgtcggga tggaacgctc ggccctgcac   1320

cgcaagctga agtcgctggg cgtggtgacc accgcgaagg gaggcagccg gcttgcccga   1380

atcgaggacg attacgagga cgaggaggag ccgctcgggg cgccggattg a            1431


<210> SEQ ID NO 106
<211> LENGTH: 476
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 106

Met Ser Ser Ile Leu Ile Val Asp Asp Glu Arg Asp Ile Arg Glu Leu
1               5                   10                  15

Ile Gly Asp Ile Leu Arg Asp Glu Gly Phe Gln Ile Arg Leu Ala Ala
            20                  25                  30

Asn Ser Asp Glu Cys Met Ala Ala Val Asn Ala Glu Pro Pro Ala Leu
        35                  40                  45

Met Ile Leu Asp Ile Trp Leu Lys Asp Ser Arg Met Asp Gly Ile Asp
    50                  55                  60

Ile Leu Lys Arg Thr Lys Arg Asp Asn Pro Asp Val Pro Val Val Ile
65                  70                  75                  80

Ile Ser Gly His Gly Asn Ile Glu Ile Ala Val Ala Ala Ile Lys Gln
                85                  90                  95

Gly Ala Tyr Asp Phe Ile Glu Lys Pro Phe Asn Ile Asp Gln Leu Met
            100                 105                 110

Val Val Val Gln Arg Ala Met Glu Thr Ala Arg Leu Arg Arg Glu Asn
        115                 120                 125

Ser Glu Leu Arg Arg Arg Asp Val Ser Ala Ala Glu Met Leu Gly Gly
    130                 135                 140

Ser Thr Ala Tyr Arg Leu Leu Lys Ser Gln Leu Glu Lys Val Thr Lys
145                 150                 155                 160

Ser Asn Gly Arg Val Met Leu Ser Gly Pro Ala Gly Ala Gly Lys Glu
                165                 170                 175

Leu Ala Ala Arg Phe Ile His Ala Asn Ser Gly Arg Ala Gly Ala Pro
            180                 185                 190

Phe Ile Ser Val Ser Ser Ala Thr Val Glu Pro Asp Arg Met Glu Glu
        195                 200                 205

Val Leu Phe Gly Arg Glu Thr Ala Glu Arg Gly Ile Glu Gln Gly Leu
    210                 215                 220

Leu Glu Gln Ala His Gly Gly Ile Val Tyr Phe Asp Glu Val Ala Asp
225                 230                 235                 240

Met Pro Leu Gly Thr Gln Ser Lys Ile Leu Arg Val Leu Thr Glu Gln
                245                 250                 255
```

```
Gln Phe Thr Arg Gln Gly Gly Thr Asp Lys Val Arg Val Asp Leu Arg
            260                 265                 270

Val Ile Ser Ser Thr Thr Arg Asp Leu Arg Thr Glu Ile Ala Ala Gly
        275                 280                 285

Arg Phe Arg Gln Glu Leu Tyr Asp Arg Leu Asn Val Val Pro Ile Glu
    290                 295                 300

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

His Phe Ile Glu Met Phe His Arg Ser Gln Gly Leu Pro Leu Arg Ser
                325                 330                 335

Leu Thr Ser Glu Ala Glu Ala Met Leu Gln Thr Met Pro Trp Pro Gly
            340                 345                 350

Asn Val Arg Gln Leu Arg Asn Val Ile Glu Arg Val Leu Ile Leu Gly
        355                 360                 365

Asp Gly Ser Gly Pro Ile Glu Ala Arg Glu Leu Pro Gly Asn Glu Gly
    370                 375                 380

Pro Gly Glu Glu Gly Arg Leu Ile Leu Gly Gly Ala Leu Ala Thr Leu
385                 390                 395                 400

Pro Leu Arg Glu Ala Arg Glu Leu Phe Glu Arg Glu Tyr Leu Leu Thr
                405                 410                 415

Gln Ile Asn Arg Phe Gly Gly Asn Ile Ser Arg Thr Ala Ala Phe Val
            420                 425                 430

Gly Met Glu Arg Ser Ala Leu His Arg Lys Leu Lys Ser Leu Gly Val
        435                 440                 445

Val Thr Thr Ala Lys Gly Gly Ser Arg Leu Ala Arg Ile Glu Asp Asp
    450                 455                 460

Tyr Glu Asp Glu Glu Glu Pro Leu Gly Ala Pro Asp
465                 470                 475
```

<210> SEQ ID NO 107
<211> LENGTH: 1041
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 107

```
atgcaggcgc aggatgcaac tcagcttctg gagggtgtgc cgctgcccct cgtgctgatc      60

ggcccggatg agcggatccg ggcggccaac gcgccggcgc agcggctgtt cggcgccgcg     120

agcgtggcgc ggcattatgt gatggcgatg cggcagccgg cgctgctcga tgcgatcgag     180

ggcgcgatcc ggctcgatcg gccggggcgc gcgcgctaca tcatcaccgg accctcgcgg     240

gaggtgacct atcgcgcgac ggtgacgccg gtccgcatcc acggcgagag ctgcgcgctc     300

tgcgccttcg aggacatcac cgagcaggag cagatgggcg cgatccggcg cgacttcgtg     360

gcgaacgtga gccacgaact gcgcaccccc ctcacggcgc tcctcggctt catcgagacg     420

ctgcagggcg ctgcgcgcga cgatcccgcg gcacggagcc ggtttctcgg catcatggcg     480

cgggaggcgg gccggatgaa ccggctggtg caggacctcc tgtcgctgag ccgggtggaa     540

tcggaagaga gggtgcggcc gaagaccccg gtggatgtga cggcggtgat cggacaggcc     600

atcgcggcgc tgcgccccat ggccgaggcc gcgggcgtcg agatccagcg tcagggcgag     660

gcggggccga tcctgctgcc gggagacccc gaccagctca cgcaggtctt tcacaacctc     720

atcgagaatg cggtgaaata cggcgcttcg ggcaagcttg tcaccgtcgg gatctcccgc     780

gatgccgagg gcctcgcgcg gctcgggccc gcggtgcgga tcgaggtggt ggatcggggc     840
```

```
gaggggatcg acgccatcca tctgccgcgg ctgaccgagc ggttctaccg cgtggacaac    900

caccgctcgc gcgagaaggg cggcaccggg ctgggcctcg ccatcgtgaa gcatatcgtg    960

aaccggcacc gcggccgctt cctcatcgag agcgagctgg ggcagggcag ccgcttcatc   1020

gtgacgctgc ctctggcctg a                                             1041


<210> SEQ ID NO 108
<211> LENGTH: 346
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 108

Met Gln Ala Gln Asp Ala Thr Gln Leu Leu Glu Gly Val Pro Leu Pro
1               5                   10                  15

Leu Val Leu Ile Gly Pro Asp Glu Arg Ile Arg Ala Ala Asn Ala Pro
            20                  25                  30

Ala Gln Arg Leu Phe Gly Ala Ala Ser Val Ala Arg His Tyr Val Met
        35                  40                  45

Ala Met Arg Gln Pro Ala Leu Leu Asp Ala Ile Glu Gly Ala Ile Arg
    50                  55                  60

Leu Asp Arg Pro Gly Arg Ala Arg Tyr Ile Ile Thr Gly Pro Ser Arg
65                  70                  75                  80

Glu Val Thr Tyr Arg Ala Thr Val Thr Pro Val Arg Ile His Gly Glu
                85                  90                  95

Ser Cys Ala Leu Cys Ala Phe Glu Asp Ile Thr Glu Gln Glu Gln Met
            100                 105                 110

Gly Ala Ile Arg Arg Asp Phe Val Ala Asn Val Ser His Glu Leu Arg
        115                 120                 125

Thr Pro Leu Thr Ala Leu Leu Gly Phe Ile Glu Thr Leu Gln Gly Ala
    130                 135                 140

Ala Arg Asp Asp Pro Ala Ala Arg Ser Arg Phe Leu Gly Ile Met Ala
145                 150                 155                 160

Arg Glu Ala Gly Arg Met Asn Arg Leu Val Gln Asp Leu Leu Ser Leu
                165                 170                 175

Ser Arg Val Glu Ser Glu Glu Arg Val Arg Pro Lys Thr Pro Val Asp
            180                 185                 190

Val Thr Ala Val Ile Gly Gln Ala Ile Ala Ala Leu Arg Pro Met Ala
        195                 200                 205

Glu Ala Ala Gly Val Glu Ile Gln Arg Gln Gly Glu Ala Gly Pro Ile
    210                 215                 220

Leu Leu Pro Gly Asp Pro Asp Gln Leu Thr Gln Val Phe His Asn Leu
225                 230                 235                 240

Ile Glu Asn Ala Val Lys Tyr Gly Ala Ser Gly Lys Leu Val Thr Val
                245                 250                 255

Gly Ile Ser Arg Asp Ala Glu Gly Leu Ala Arg Leu Gly Pro Ala Val
            260                 265                 270

Arg Ile Glu Val Val Asp Arg Gly Glu Gly Ile Asp Ala Ile His Leu
        275                 280                 285

Pro Arg Leu Thr Glu Arg Phe Tyr Arg Val Asp Asn His Arg Ser Arg
    290                 295                 300

Glu Lys Gly Gly Thr Gly Leu Gly Leu Ala Ile Val Lys His Ile Val
305                 310                 315                 320

Asn Arg His Arg Gly Arg Phe Leu Ile Glu Ser Glu Leu Gly Gln Gly
                325                 330                 335
```

Ser Arg Phe Ile Val Thr Leu Pro Leu Ala
340 345

<210> SEQ ID NO 109
<211> LENGTH: 492
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 109

atgcctcttc aaccggaccc gatcgggaac ctgaacattt ctttcgaaac aaatccggcg 60

ggggcaggta tcggggtgag acgacaggac gcgagcaggc acgggcggcc ttggctgaga 120

ctggtctggg acggcgaaaa gcgggtcgca ccgctgcccg atacggcggg tccatcgcgg 180

ctgagggacg gtcccgccgc catccggctg atcgcgaccg agggcggacc tcccgggccg 240

tcctccatgg ccgagaccgg tctctcgggc ctcaccgcgc tgcttctggc cgatcttgca 300

cccgcggctg tctcggtgcc gctgatcgcg gccgattgcg acgccgtgga tcttctccac 360

cggctgcgcg ggctgggcta tgcggggcgc gtgatcgtgc gctgcccgcc gctgcccgcg 420

ccggatctgg tcgagcgcga gctctcccgc catgcggcgg gcctcgccat aaacctcgtg 480

gccggggact ag 492

<210> SEQ ID NO 110
<211> LENGTH: 163
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 110

Met Pro Leu Gln Pro Asp Pro Ile Gly Asn Leu Asn Ile Ser Phe Glu
1 5 10 15

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

Arg His Gly Arg Pro Trp Leu Arg Leu Val Trp Asp Gly Glu Lys Arg
35 40 45

Val Ala Pro Leu Pro Asp Thr Ala Gly Pro Ser Arg Leu Arg Asp Gly
50 55 60

Pro Ala Ala Ile Arg Leu Ile Ala Thr Glu Gly Gly Pro Pro Gly Pro
65 70 75 80

Ser Ser Met Ala Glu Thr Gly Leu Ser Gly Leu Thr Ala Leu Leu Leu
85 90 95

Ala Asp Leu Ala Pro Ala Ala Val Ser Val Pro Leu Ile Ala Ala Asp
100 105 110

Cys Asp Ala Val Asp Leu Leu His Arg Leu Arg Gly Leu Gly Tyr Ala
115 120 125

Gly Arg Val Ile Val Arg Cys Pro Pro Leu Pro Ala Pro Asp Leu Val
130 135 140

Glu Arg Glu Leu Ser Arg His Ala Ala Gly Leu Ala Ile Asn Leu Val
145 150 155 160

Ala Gly Asp

<210> SEQ ID NO 111
<211> LENGTH: 1344
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 111

gtgctgacgc gacttcatta tcggattcac acgagcctcg aacgcatcct tccggagcgt 60 cggctttttc ttaaatccga tagcgacacg cgcttcatcc ggctccgacc cgtgacgcag 120

ctcgccgctc tcgccggcgg cacgctcctc gtaagctgga cgatcctcgc cacctccatc 180

gtgctgatgg actcggtgac cgcgggcggc acccgcgacc agacccagcg ccagcaggcg 240

ctctacgaat cccgcctcaa tgccctctcc gccgaccgcg accgccgcgc cgacgaagcc 300

gtgcgcgcgc aggagcggtt caacctcgcg ctcgccgagg tctcgaagat gcagacggcg 360

ctcctcgcca ccgaggatcg ccgcaaggaa ctcgagaccg gcatcgaggt gctgcaggac 420

acgctgatcc gcaccatcaa ggaacgcgac gacgcccgcg aggagtccga gcgcgtgacg 480

gtcgcgctgg ccgaacagac cggctcggcg cgcaccgacg gctcgcggat ggccgatgcc 540

gaggcgacgc tcgaccagct gtcctccacg ctcgcggcca ccgcccgcca gcgtgacgac 600

atggccaatg ccgtgctctt ggccaaggaa gagaccgagg aggtcctgca ggagaaggcc 660

gagcttcagg cgcgcaacga cctcatcttc ggccggctcg aggaagcggt gaccgtctcg 720

atggaaccgc tcgacaagat gttccgcgcc gcgggcctct cgaccgactc gctgctgaag 780

caggtgcgcc gcggctattc gggtcagggc ggcccactct cgaagctgac ggtctcgaca 840

atgggcggcg gcgatctcac ccccgaggag cgccgcgcca acgagatcct gaacgggctc 900

gaccgcatga acctctaccg gctcgcggcc accaaggcgc ccttctcgat gccggtcaag 960

accgccttcc gctacacctc gggcttcggc gggcgcaacg acccgttcgg gcgcggcaac 1020

cgccgccacg agggcatcga catggccggc gcgagcggca gcccgatcta ttccaccgcc 1080

gacggcgtgg tgatccaggc gggcacggcc agcggctatg gcaaggtcat caagatccgc 1140

cacgagttcg gcatccagac cgtctacggc cacctgtccc gaatccgggt ggagaaggga 1200

caaagggtat cgcgcggcga ccggatcggt gatatgggct caacaggccg gtccaccggc 1260

acccatcttc actatgaggt ccgcgtggac ggctcgcccg tcaacccgat gaccttcatc 1320

aaggcggcga aagatgtttt ctaa 1344

<210> SEQ ID NO 112
<211> LENGTH: 447
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 112

Met Leu Thr Arg Leu His Tyr Arg Ile His Thr Ser Leu Glu Arg Ile
1 5 10 15

Leu Pro Glu Arg Arg Leu Phe Leu Lys Ser Asp Ser Asp Thr Arg Phe
20 25 30

Ile Arg Leu Arg Pro Val Thr Gln Leu Ala Ala Leu Ala Gly Gly Thr
35 40 45

Leu Leu Val Ser Trp Thr Ile Leu Ala Thr Ser Ile Val Leu Met Asp
50 55 60

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

Leu Tyr Glu Ser Arg Leu Asn Ala Leu Ser Ala Asp Arg Asp Arg Arg
85 90 95

Ala Asp Glu Ala Val Arg Ala Gln Glu Arg Phe Asn Leu Ala Leu Ala
100 105 110

Glu Val Ser Lys Met Gln Thr Ala Leu Leu Ala Thr Glu Asp Arg Arg
115 120 125

Lys Glu Leu Glu Thr Gly Ile Glu Val Leu Gln Asp Thr Leu Ile Arg
130 135 140

```
Thr Ile Lys Glu Arg Asp Asp Ala Arg Glu Glu Ser Glu Arg Val Thr
145                 150                 155                 160

Val Ala Leu Ala Glu Gln Thr Gly Ser Ala Arg Thr Asp Gly Ser Arg
                165                 170                 175

Met Ala Asp Ala Glu Ala Thr Leu Asp Gln Leu Ser Ser Thr Leu Ala
            180                 185                 190

Ala Thr Ala Arg Gln Arg Asp Asp Met Ala Asn Ala Val Leu Leu Ala
        195                 200                 205

Lys Glu Glu Thr Glu Glu Val Leu Gln Glu Lys Ala Glu Leu Gln Ala
    210                 215                 220

Arg Asn Asp Leu Ile Phe Gly Arg Leu Glu Glu Ala Val Thr Val Ser
225                 230                 235                 240

Met Glu Pro Leu Asp Lys Met Phe Arg Ala Ala Gly Leu Ser Thr Asp
                245                 250                 255

Ser Leu Leu Lys Gln Val Arg Arg Gly Tyr Ser Gly Gln Gly Gly Pro
            260                 265                 270

Leu Ser Lys Leu Thr Val Ser Thr Met Gly Gly Gly Asp Leu Thr Pro
        275                 280                 285

Glu Glu Arg Arg Ala Asn Glu Ile Leu Asn Gly Leu Asp Arg Met Asn
    290                 295                 300

Leu Tyr Arg Leu Ala Ala Thr Lys Ala Pro Phe Ser Met Pro Val Lys
305                 310                 315                 320

Thr Ala Phe Arg Tyr Thr Ser Gly Phe Gly Gly Arg Asn Asp Pro Phe
                325                 330                 335

Gly Arg Gly Asn Arg Arg His Glu Gly Ile Asp Met Ala Gly Ala Ser
            340                 345                 350

Gly Ser Pro Ile Tyr Ser Thr Ala Asp Gly Val Val Ile Gln Ala Gly
        355                 360                 365

Thr Ala Ser Gly Tyr Gly Lys Val Ile Lys Ile Arg His Glu Phe Gly
    370                 375                 380

Ile Gln Thr Val Tyr Gly His Leu Ser Arg Ile Arg Val Glu Lys Gly
385                 390                 395                 400

Gln Arg Val Ser Arg Gly Asp Arg Ile Gly Asp Met Gly Ser Thr Gly
                405                 410                 415

Arg Ser Thr Gly Thr His Leu His Tyr Glu Val Arg Val Asp Gly Ser
            420                 425                 430

Pro Val Asn Pro Met Thr Phe Ile Lys Ala Ala Lys Asp Val Phe
        435                 440                 445
```

<210> SEQ ID NO 113
<211> LENGTH: 1173
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 113

```
atgttcgacg ataccacccc gatgatcgag cgcgtccgcg cgatccttcc ccggattgcg      60

gcgaatgcct ccagagcgga ggagatgcgc gaggtgccga aggagaacat cgacctgctc     120

aagagcaccg gcctgcaccg cgccttccag ccgaaggcct atggcgggct cgagatgccg     180

ttgccggact tcgagaattg catcgcgctg atcgccaccg cctgcgggtc caccgcctgg     240

gccttctcgc tcctggccga gcacgcgcac cagatcgcgc tctattcgaa gcaattgcag     300

gacgagatct ggcaggacga tcccgacacg gtctgctcct cttcgatcgc cccttacgga     360

aaagcccagg acgtcgaggg cggcgtccgc ttctcgggcg agttcggctg gtcgtcgggc     420
```

```
tgcgatcacg cgcaatgggc gatccttggc ttcctgcgcg acacgcccga aggcggcaag    480

gtctacagct tcgccatcct tccccgcagc gactatgaga tcaaggacac ctggttcacc    540

gccgggatgc ggggcaccgg ctcgaagacc ctcgtggtca gggacgcctt cgtgcccgag    600

caccggatcg agaccgtgcc ggcgctgatg actctgacct cggcgggcgg cggcctctat    660

cccggaagca ccacctatca tgtgcccttc atctacgtct tcgccagctg cttctccgcc    720

gtgtctctgg gcatcgcgga gcggatgatc cagctttaca ccgagcggac acggaaccgc    780

gtccgcgcct acaccggcgc caaggtgagt cagtccattc ccgcctgcat gcgtctggcg    840

gaaagcacgc atcaggtggc cgcgggccgg gccttcctcg agaagacctg ggaggacatg    900

cgcgaccacg ccgagcgccg cgtctttccg gacgagacca ggatggcctt ctggcggacc    960

aatcaggcct atgcggtgaa gatgttcgtc gctgcggtgg accggctgtt cgaagcgtcc   1020

ggcggatcgt cctggttcga cgatgccgaa gggcagcgcc tgttccgcga cgcgcacatg   1080

actgccgccc acgcctacac cgactacgac atctgcgccc agatcctcgg gcgggcgctg   1140

atggggctgg agcgggatcc ctccctgttc tga                                1173
```

```
<210> SEQ ID NO 114
<211> LENGTH: 390
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 114

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

Pro Arg Ile Ala Ala Asn Ala Ser Arg Ala Glu Glu Met Arg Glu Val
            20                  25                  30

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

Phe Gln Pro Lys Ala Tyr Gly Gly Leu Glu Met Pro Leu Pro Asp Phe
    50                  55                  60

Glu Asn Cys Ile Ala Leu Ile Ala Thr Ala Cys Gly Ser Thr Ala Trp
65                  70                  75                  80

Ala Phe Ser Leu Leu Ala Glu His Ala His Gln Ile Ala Leu Tyr Ser
                85                  90                  95

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

Ser Ser Ser Ile Ala Pro Tyr Gly Lys Ala Gln Asp Val Glu Gly Gly
        115                 120                 125

Val Arg Phe Ser Gly Glu Phe Gly Trp Ser Ser Gly Cys Asp His Ala
    130                 135                 140

Gln Trp Ala Ile Leu Gly Phe Leu Arg Asp Thr Pro Glu Gly Gly Lys
145                 150                 155                 160

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

Thr Trp Phe Thr Ala Gly Met Arg Gly Thr Gly Ser Lys Thr Leu Val
            180                 185                 190

Val Arg Asp Ala Phe Val Pro Glu His Arg Ile Glu Thr Val Pro Ala
        195                 200                 205

Leu Met Thr Leu Thr Ser Ala Gly Gly Gly Leu Tyr Pro Gly Ser Thr
    210                 215                 220

Thr Tyr His Val Pro Phe Ile Tyr Val Phe Ala Ser Cys Phe Ser Ala
225                 230                 235                 240
```

```
Val Ser Leu Gly Ile Ala Glu Arg Met Ile Gln Leu Tyr Thr Glu Arg
                245                 250                 255

Thr Arg Asn Arg Val Arg Ala Tyr Thr Gly Ala Lys Val Ser Gln Ser
            260                 265                 270

Ile Pro Ala Cys Met Arg Leu Ala Glu Ser Thr His Gln Val Ala Ala
        275                 280                 285

Gly Arg Ala Phe Leu Glu Lys Thr Trp Glu Asp Met Arg Asp His Ala
    290                 295                 300

Glu Arg Arg Val Phe Pro Asp Glu Thr Arg Met Ala Phe Trp Arg Thr
305                 310                 315                 320

Asn Gln Ala Tyr Ala Val Lys Met Phe Val Ala Ala Val Asp Arg Leu
                325                 330                 335

Phe Glu Ala Ser Gly Gly Ser Ser Trp Phe Asp Asp Ala Glu Gly Gln
            340                 345                 350

Arg Leu Phe Arg Asp Ala His Met Thr Ala Ala His Ala Tyr Thr Asp
        355                 360                 365

Tyr Asp Ile Cys Ala Gln Ile Leu Gly Arg Ala Leu Met Gly Leu Glu
    370                 375                 380

Arg Asp Pro Ser Leu Phe
385                 390


<210> SEQ ID NO 115
<211> LENGTH: 696
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 115

atgagccgcg tcatcgccat caccggcacg cgcaagggca tcggccgcgc gctggccgag      60

acctatctcg cgcgcggctg gaccgtcgtc ggctgctcgc gcgatgcgag cgacctcacg     120

cacccggcct atcgccacta cacgctcgac gtggccgacg agcgggcggt cgcgggcatg     180

atgcaggatg tgcgccggac gcatggacgg ctcgacgcgc ttctgaacaa tgccggcatc     240

gcctcgatga accatgcgct gctgaccccc ggcagcacgg tcgagcgggt gttcgcgacc     300

aatgtcttcg gcaccttcct gttctgccgc gaggccgcca agctgatggg ccgccgccgc     360

accggccgga tcgtgaactt cgccaccgtg gccacgccgc tcaagctcga gggcgaggcg     420

gtctatgccg cctccaaggc cgcggtcgtg tcgctgaccg aggtgctggc gcgcgagctg     480

gcgcccatgg gcatcaccgt caatgccgtg gggccgaccc cggtgcccac cgacctcgtc     540

ggcgccgtgc ccgaggagaa gatgcgcgcg ctgatcgccc ggcaggccat tccgcgctac     600

ggcaagatgg aggatgtgct caacgtctgc gacttcttcc tgcgcgacga atccgatttc     660

gtgaccggcc agacgatcta tctcggaggg gtctga                               696


<210> SEQ ID NO 116
<211> LENGTH: 231
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 116

Met Ser Arg Val Ile Ala Ile Thr Gly Thr Arg Lys Gly Ile Gly Arg
1               5                   10                  15

Ala Leu Ala Glu Thr Tyr Leu Ala Arg Gly Trp Thr Val Val Gly Cys
            20                  25                  30

Ser Arg Asp Ala Ser Asp Leu Thr His Pro Ala Tyr Arg His Tyr Thr
        35                  40                  45
```

Leu Asp Val Ala Asp Glu Arg Ala Val Ala Gly Met Met Gln Asp Val
50 55 60

Arg Arg Thr His Gly Arg Leu Asp Ala Leu Leu Asn Asn Ala Gly Ile
65 70 75 80

Ala Ser Met Asn His Ala Leu Leu Thr Pro Gly Ser Thr Val Glu Arg
85 90 95

Val Phe Ala Thr Asn Val Phe Gly Thr Phe Leu Phe Cys Arg Glu Ala
100 105 110

Ala Lys Leu Met Gly Arg Arg Arg Thr Gly Arg Ile Val Asn Phe Ala
115 120 125

Thr Val Ala Thr Pro Leu Lys Leu Glu Gly Glu Ala Val Tyr Ala Ala
130 135 140

Ser Lys Ala Ala Val Val Ser Leu Thr Glu Val Leu Ala Arg Glu Leu
145 150 155 160

Ala Pro Met Gly Ile Thr Val Asn Ala Val Gly Pro Thr Pro Val Pro
165 170 175

Thr Asp Leu Val Gly Ala Val Pro Glu Glu Lys Met Arg Ala Leu Ile
180 185 190

Ala Arg Gln Ala Ile Pro Arg Tyr Gly Lys Met Glu Asp Val Leu Asn
195 200 205

Val Cys Asp Phe Phe Leu Arg Asp Glu Ser Asp Phe Val Thr Gly Gln
210 215 220

Thr Ile Tyr Leu Gly Gly Val
225 230

<210> SEQ ID NO 117
<211> LENGTH: 1230
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 117

atgcgccgcg tcgtcatcac cgggatcggc atcgtctcgc cgatcgggaa caatgccgcc 60

gaagtggaag cgagcctgcg cgccggccgc tcgggcatct ccttctcgga ggactatgcc 120

caccacggct tccgcagcca gatccacggg atgcccgatc tcgtgctcga ggaccatgtc 180

gacaagcgcg acctgcgctt catgggcgcc ggagccgcct acaacttcat cgcgatggag 240

caggcgatca aggattcggg cctcgaggcc accgaggtct cgaacccgcg caccggtctc 300

gtgatgggct cgggcgggcc gtcgacctcg aacttcttcc aggcccacaa gatcgtcatc 360

gagaagggct cgcccaagcg gatgggtccc ttcatggtga cgcgctgcat gagctcgacc 420

aactcggcct gccttgccac gcccttcaag atcaagggcg tgaactattc gatcacctcg 480

gcctgctcca cctcggccca ttgcatcggc aacggcaccg agctgatcca gatgggcaag 540

caggacatcg tcttcgccgg cggcggggaa gagctcgact ggacgctctc ctgcctcttc 600

gacgcgatgg gggccatgtc gtcgaaatac aacgatgcgc ccgagaccgc ctcgcggccg 660

ttcgacgcca cgcgcgacgg gttcgtgatc gcgggcggcg gcggcgtggt cgtgctggaa 720

gagctcgagc atgcgctggc gcgcggcgcg aagatctatg ccgaagtgac cggctacggg 780

gccacctcgg acggggccga catggtggcg ccgtcgggcg aaggcggcga gcggtcgatg 840

cggctggcgc tcggcacgct gcccgagggg cgccgggtcg attacatcaa cgcacacggc 900

acctcgacgc ccgcgggcga cgtgaccgag gtgcgcgcga tccggcggat cttcggcgag 960

ggcaaggttc cgccgatctc ctccaccaag tcgctcaccg gccattcgct gggggccacc 1020

ggcgtgcacg aggcgatcta ttcgatcctg atgatgcagg gcgacttcat cgcggcctcg 1080

```
gccaacgtga cccagctcga ccccgagatc cagccggacg agatcgccac caccctgcgc   1140

gagggggtcg agatcgactc ggtcctgtcc aacagcttcg gcttcggcgg caccaacgcc   1200

agtctgctcc tgagcaagtt caacaactga                                   1230


<210> SEQ ID NO 118
<211> LENGTH: 409
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 118

Met Arg Arg Val Val Ile Thr Gly Ile Gly Ile Val Ser Pro Ile Gly
1               5                   10                  15

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

Ile Ser Phe Ser Glu Asp Tyr Ala His His Gly Phe Arg Ser Gln Ile
        35                  40                  45

His Gly Met Pro Asp Leu Val Leu Glu Asp His Val Asp Lys Arg Asp
    50                  55                  60

Leu Arg Phe Met Gly Ala Gly Ala Ala Tyr Asn Phe Ile Ala Met Glu
65                  70                  75                  80

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

Arg Thr Gly Leu Val Met Gly Ser Gly Gly Pro Ser Thr Ser Asn Phe
            100                 105                 110

Phe Gln Ala His Lys Ile Val Ile Glu Lys Gly Ser Pro Lys Arg Met
        115                 120                 125

Gly Pro Phe Met Val Thr Arg Cys Met Ser Ser Thr Asn Ser Ala Cys
    130                 135                 140

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

Ala Cys Ser Thr Ser Ala His Cys Ile Gly Asn Gly Thr Glu Leu Ile
                165                 170                 175

Gln Met Gly Lys Gln Asp Ile Val Phe Ala Gly Gly Gly Glu Glu Leu
            180                 185                 190

Asp Trp Thr Leu Ser Cys Leu Phe Asp Ala Met Gly Ala Met Ser Ser
        195                 200                 205

Lys Tyr Asn Asp Ala Pro Glu Thr Ala Ser Arg Pro Phe Asp Ala Thr
    210                 215                 220

Arg Asp Gly Phe Val Ile Ala Gly Gly Gly Gly Val Val Val Leu Glu
225                 230                 235                 240

Glu Leu Glu His Ala Leu Ala Arg Gly Ala Lys Ile Tyr Ala Glu Val
                245                 250                 255

Thr Gly Tyr Gly Ala Thr Ser Asp Gly Ala Asp Met Val Ala Pro Ser
            260                 265                 270

Gly Glu Gly Gly Glu Arg Ser Met Arg Leu Ala Leu Gly Thr Leu Pro
        275                 280                 285

Glu Gly Arg Arg Val Asp Tyr Ile Asn Ala His Gly Thr Ser Thr Pro
    290                 295                 300

Ala Gly Asp Val Thr Glu Val Arg Ala Ile Arg Arg Ile Phe Gly Glu
305                 310                 315                 320

Gly Lys Val Pro Pro Ile Ser Ser Thr Lys Ser Leu Thr Gly His Ser
                325                 330                 335

Leu Gly Ala Thr Gly Val His Glu Ala Ile Tyr Ser Ile Leu Met Met
```

```
            340                 345                 350

Gln Gly Asp Phe Ile Ala Ala Ser Ala Asn Val Thr Gln Leu Asp Pro
        355                 360                 365

Glu Ile Gln Pro Asp Glu Ile Ala Thr Thr Leu Arg Glu Gly Val Glu
    370                 375                 380

Ile Asp Ser Val Leu Ser Asn Ser Phe Gly Phe Gly Gly Thr Asn Ala
385                 390                 395                 400

Ser Leu Leu Leu Ser Lys Phe Asn Asn
                405


<210> SEQ ID NO 119
<211> LENGTH: 510
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 119

atggcggact atccgacgag cttcgacaaa gaggcgctgc tggcttgcgc gcggggcgag      60

ctcttcgggc ctggcaatgc ccagctcccg ttgccgccga tgctgatgat ggaccgcatc     120

accgacattt cggccgatgg cgggctgcat ggcaaggggc atgtcgtggc cgagttcgac     180

atccatcccg acctatggtt cttcgaatgc catttcccgg gcaatccagt catgccgggc     240

tgcctcgggc tcgacgggct ctggcagctc acgggcttca acctcggctg gcgcggctgg     300

cagggccagg gcttcgcgct cggcgtgggc gaggtgaagc tctcgggcat ggtccgcccg     360

gaccgcaagc tcgtcaccta ccacgtcgat ttcacccgcg tgatcgaccg ccgcctcaag     420

atgggcgtgg cggacggccg cgtcttcgcc gatggcgaag agatctacag cgtcaaggac     480

atgaaagtcg gtctggccgc tgcggcctga                                      510


<210> SEQ ID NO 120
<211> LENGTH: 169
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 120

Met Ala Asp Tyr Pro Thr Ser Phe Asp Lys Glu Ala Leu Leu Ala Cys
1               5                   10                  15

Ala Arg Gly Glu Leu Phe Gly Pro Gly Asn Ala Gln Leu Pro Leu Pro
            20                  25                  30

Pro Met Leu Met Met Asp Arg Ile Thr Asp Ile Ser Ala Asp Gly Gly
        35                  40                  45

Leu His Gly Lys Gly His Val Val Ala Glu Phe Asp Ile His Pro Asp
    50                  55                  60

Leu Trp Phe Phe Glu Cys His Phe Pro Gly Asn Pro Val Met Pro Gly
65                  70                  75                  80

Cys Leu Gly Leu Asp Gly Leu Trp Gln Leu Thr Gly Phe Asn Leu Gly
                85                  90                  95

Trp Arg Gly Trp Gln Gly Gln Gly Phe Ala Leu Gly Val Gly Glu Val
            100                 105                 110

Lys Leu Ser Gly Met Val Arg Pro Asp Arg Lys Leu Val Thr Tyr His
        115                 120                 125

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

Asp Gly Arg Val Phe Ala Asp Gly Glu Glu Ile Tyr Ser Val Lys Asp
145                 150                 155                 160

Met Lys Val Gly Leu Ala Ala Ala Ala
```

165

<210> SEQ ID NO 121
<211> LENGTH: 1161
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 121

atggcagcgg aaccgatcgt gatcgcgggg gcggcgcgga cgccgatggg cgcctttcag 60

ggtgcgctca agggccggac gggggtcgag ctcggcgcgg cggcgatctc ggccgcgctc 120

gcgcgggcgg gcctcgcccc cgaggcggtc gaggaggtcg tgatgggctg cgtgctgccc 180

gcgggcctcg ggcaggcgcc ggcgcggcag gcggctctgg gcgcggggct gccgctctcg 240

gtgccctgcg ctacgctgaa caaggtctgc ggctcgggga tgaaggccgc catggccgcg 300

catgacatga tccgggcggg cagcgcgggc atcgtcgtcg cgggcggtat ggagagcatg 360

tcgaacgcgc cctatctgct cgacaaggcg cgcggcggct accggatcgg gcatgggcgc 420

gtgctggacc acatgttcct cgacgggctc gaggatgcct acgaccgcgg ccgcgccatg 480

ggcaccttcg ccgaggattg cgccgaggcc taccagttca cccgcgacgc gcaggatgcc 540

tatgcgctgg cctcgctggc ccgggcgcag gcggccattg ccgaggggcg cttcgcggcc 600

gaggtggtgg cagtggacgg ggtggcggtt gacgaggccc cgggccgcgc ccgcccgag 660

aagatccccc agctcaggcc cgccttccgc gagggcggca cggtgacggc ggccaacagc 720

tcctcgatct cggacggggc ggcggcgctc gtgatcgcct cggccggcgc ggccgaggcg 780

caggggctga ccccgctcgc cacgatccgc ggccatgcaa gccatgcgca ggcgccgaac 840

ctttttacca cggcgccgat cttcgccatc gggaagcttc tcgagcggtt gggctggagc 900

gcggccgagg tcgatctctt cgagatcaac gaggctttcg cagtggtggc catggccgcg 960

atgcgcgacc tagacctgcc ccacgacaag gtcaatgtga acggcggcgc ctgcgcgctc 1020

ggccatccga tcggctgctc gggggcgcgg atcgtggtga ctttgatcga ggcgctgcgg 1080

gcgcggggat tgagacgcgg cgtggcctcg ctctgcatcg gcggcggcga ggcgacggcg 1140

ctggcggtgg aggtgatctg a 1161

<210> SEQ ID NO 122
<211> LENGTH: 386
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 122

Met Ala Ala Glu Pro Ile Val Ile Ala Gly Ala Ala Arg Thr Pro Met
1 5 10 15

Gly Ala Phe Gln Gly Ala Leu Lys Gly Arg Thr Gly Val Glu Leu Gly
20 25 30

Ala Ala Ala Ile Ser Ala Ala Leu Ala Arg Ala Gly Leu Ala Pro Glu
35 40 45

Ala Val Glu Glu Val Val Met Gly Cys Val Leu Pro Ala Gly Leu Gly
50 55 60

Gln Ala Pro Ala Arg Gln Ala Ala Leu Gly Ala Gly Leu Pro Leu Ser
65 70 75 80

Val Pro Cys Ala Thr Leu Asn Lys Val Cys Gly Ser Gly Met Lys Ala
85 90 95

Ala Met Ala Ala His Asp Met Ile Arg Ala Gly Ser Ala Gly Ile Val
100 105 110

```
Val Ala Gly Gly Met Glu Ser Met Ser Asn Ala Pro Tyr Leu Leu Asp
        115                 120                 125

Lys Ala Arg Gly Gly Tyr Arg Ile Gly His Gly Arg Val Leu Asp His
    130                 135                 140

Met Phe Leu Asp Gly Leu Glu Asp Ala Tyr Asp Arg Gly Arg Ala Met
145                 150                 155                 160

Gly Thr Phe Ala Glu Asp Cys Ala Glu Ala Tyr Gln Phe Thr Arg Asp
                165                 170                 175

Ala Gln Asp Ala Tyr Ala Leu Ala Ser Leu Ala Arg Ala Gln Ala Ala
            180                 185                 190

Ile Ala Glu Gly Arg Phe Ala Ala Glu Val Val Ala Val Asp Gly Val
        195                 200                 205

Ala Val Asp Glu Ala Pro Gly Arg Ala Arg Pro Glu Lys Ile Pro Gln
    210                 215                 220

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

Ser Ser Ile Ser Asp Gly Ala Ala Ala Leu Val Ile Ala Ser Ala Gly
                245                 250                 255

Ala Ala Glu Ala Gln Gly Leu Thr Pro Leu Ala Thr Ile Arg Gly His
            260                 265                 270

Ala Ser His Ala Gln Ala Pro Asn Leu Phe Thr Thr Ala Pro Ile Phe
        275                 280                 285

Ala Ile Gly Lys Leu Leu Glu Arg Leu Gly Trp Ser Ala Ala Glu Val
    290                 295                 300

Asp Leu Phe Glu Ile Asn Glu Ala Phe Ala Val Val Ala Met Ala Ala
305                 310                 315                 320

Met Arg Asp Leu Asp Leu Pro His Asp Lys Val Asn Val Asn Gly Gly
                325                 330                 335

Ala Cys Ala Leu Gly His Pro Ile Gly Cys Ser Gly Ala Arg Ile Val
            340                 345                 350

Val Thr Leu Ile Glu Ala Leu Arg Ala Arg Gly Leu Arg Arg Gly Val
        355                 360                 365

Ala Ser Leu Cys Ile Gly Gly Gly Glu Ala Thr Ala Leu Ala Val Glu
    370                 375                 380

Val Ile
385


<210> SEQ ID NO 123
<211> LENGTH: 693
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 123

atgccggatt ttcctcccgt cgagccgcgc ccggcgcgcc gcttcaccga aaccgagcgt      60

caggcgctcc atgacatcat cgccgagagg cgcgacgtgc gcgacgagtt cctgccggat     120

ccggtggatc ccgaggcgct gcgccgggtg ctcgaggccg cgcaccgcgc gccctcggtg     180

ggcttcatgc agccgtggaa cttcctcctg atccgcgatg ccgcgcgcag ggccgaggtc     240

cacaaggcct tccgccgcgc caacgacgag gcggcgctgc tcttccccga ggagaagcgc     300

gacacctacc gcgcgctgaa gctgcagggc atcctgaagg cgccgctcaa catctgcgtc     360

acctgcgacc gcgaccgctg cggcgaggtg gtgctggggc ggacccacaa tcccgagatg     420

gatctctatt cgaccgtctg cgcggtgcag aacctctggc tcgccgcgcg ggccgagggg     480

ctgggcgtgg gctgggtcag catctaccgc gaggaggagc tgcgggcgat cctcggcatc     540
```

```
cccgagcgcg tcaagatcgt ggcctatctc tgcgtgggcc atgtggaccg cttctacagc    600

gcgccggaac tggccttgaa gggttggcgt cagcggctgc cgctcgacga tctgctcatg    660

gaggaaggct ggcaggccga ccgcgctttg tga                                  693
```

<210> SEQ ID NO 124
<211> LENGTH: 230
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 124

```
Met Pro Asp Phe Pro Pro Val Glu Pro Arg Pro Ala Arg Arg Phe Thr
1               5                   10                  15

Glu Thr Glu Arg Gln Ala Leu His Asp Ile Ile Ala Glu Arg Arg Asp
            20                  25                  30

Val Arg Asp Glu Phe Leu Pro Asp Pro Val Asp Pro Glu Ala Leu Arg
        35                  40                  45

Arg Val Leu Glu Ala Ala His Arg Ala Pro Ser Val Gly Phe Met Gln
    50                  55                  60

Pro Trp Asn Phe Leu Leu Ile Arg Asp Ala Ala Arg Arg Ala Glu Val
65                  70                  75                  80

His Lys Ala Phe Arg Arg Ala Asn Asp Glu Ala Ala Leu Leu Phe Pro
                85                  90                  95

Glu Glu Lys Arg Asp Thr Tyr Arg Ala Leu Lys Leu Gln Gly Ile Leu
            100                 105                 110

Lys Ala Pro Leu Asn Ile Cys Val Thr Cys Asp Arg Asp Arg Cys Gly
        115                 120                 125

Glu Val Val Leu Gly Arg Thr His Asn Pro Glu Met Asp Leu Tyr Ser
    130                 135                 140

Thr Val Cys Ala Val Gln Asn Leu Trp Leu Ala Ala Arg Ala Glu Gly
145                 150                 155                 160

Leu Gly Val Gly Trp Val Ser Ile Tyr Arg Glu Glu Glu Leu Arg Ala
                165                 170                 175

Ile Leu Gly Ile Pro Glu Arg Val Lys Ile Val Ala Tyr Leu Cys Val
            180                 185                 190

Gly His Val Asp Arg Phe Tyr Ser Ala Pro Glu Leu Ala Leu Lys Gly
        195                 200                 205

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

Gln Ala Asp Arg Ala Leu
225                 230
```

<210> SEQ ID NO 125
<211> LENGTH: 786
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 125

```
atggatctgg gcatcagagg caagacggcg ctggttctgg gcgcgggcgg gggcctcggc     60

ggcgccatcg cccgctcgct cgcccgcgag ggcgcgcggg tggcgctcgg cgacatcgac    120

ctcgccgcgg ccgaagccac cgccgaggcg atccgggccg agggcggcac ggcgctgccg    180

ctcgcctggg atctggccga cctcggcgcc atcgagacga acgtgagcct gatcgaggcc    240

gagctgggcc cggtcgacat cctcgtgaac aacacgggcg ggccgaagcc ctcgccgatc    300

gccgggcagg aggccgcgct ctggcgcgcg agcttcgagt ccatggtgct ctcggtcatc    360
```

```
tccatcaccg accgcgtgct gccgggcatg aaggcccgca aatggggccg catcatcacc    420

tcgacctcgt cgggcgtggt ggcgccgatc ccgaacctcg gcctgtcgaa cgcgctgcgc    480

atctcgctcg tgggctggtc gaagacgctc gcgcgcgagg tgggccgcga cggcatcacg    540

gccaacgtcg tgctgcccgg ccgcgtcgcc accaagcgca tcaccttcct cgacgagcag    600

aaggccgcgc gcgaaggccg ggccgtggcc gaagtggccg ccgagagcgt ggcctcgatc    660

ccgctcggcc gctatggtca gcccgaggaa tatggcgatg ccgtggcctt cctcgcctcg    720

gcccgcgcct cctacatcac cggcagcacc atccgcatcg acggcggcct gatcgccagc    780

gtctga                                                                786


<210> SEQ ID NO 126
<211> LENGTH: 261
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 126

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

Gly Gly Leu Gly Gly Ala Ile Ala Arg Ser Leu Ala Arg Glu Gly Ala
            20                  25                  30

Arg Val Ala Leu Gly Asp Ile Asp Leu Ala Ala Ala Glu Ala Thr Ala
        35                  40                  45

Glu Ala Ile Arg Ala Glu Gly Gly Thr Ala Leu Pro Leu Ala Trp Asp
    50                  55                  60

Leu Ala Asp Leu Gly Ala Ile Glu Thr Asn Val Ser Leu Ile Glu Ala
65                  70                  75                  80

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

Pro Ser Pro Ile Ala Gly Gln Glu Ala Ala Leu Trp Arg Ala Ser Phe
            100                 105                 110

Glu Ser Met Val Leu Ser Val Ile Ser Ile Thr Asp Arg Val Leu Pro
        115                 120                 125

Gly Met Lys Ala Arg Lys Trp Gly Arg Ile Ile Thr Ser Thr Ser Ser
    130                 135                 140

Gly Val Val Ala Pro Ile Pro Asn Leu Gly Leu Ser Asn Ala Leu Arg
145                 150                 155                 160

Ile Ser Leu Val Gly Trp Ser Lys Thr Leu Ala Arg Glu Val Gly Arg
                165                 170                 175

Asp Gly Ile Thr Ala Asn Val Val Leu Pro Gly Arg Val Ala Thr Lys
            180                 185                 190

Arg Ile Thr Phe Leu Asp Glu Gln Lys Ala Ala Arg Glu Gly Arg Ala
        195                 200                 205

Val Ala Glu Val Ala Ala Glu Ser Val Ala Ser Ile Pro Leu Gly Arg
    210                 215                 220

Tyr Gly Gln Pro Glu Glu Tyr Gly Asp Ala Val Ala Phe Leu Ala Ser
225                 230                 235                 240

Ala Arg Ala Ser Tyr Ile Thr Gly Ser Thr Ile Arg Ile Asp Gly Gly
                245                 250                 255

Leu Ile Ala Ser Val
            260


<210> SEQ ID NO 127
<211> LENGTH: 1092
```

```
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 127

atggctgagc tgcggggcct cgcccccggc ctgtcggtgg tgggctacgg catgtggacg     60

gcgctcgggc cggacggccc cacgacggtc gcgggcctcg acgcccggct gatcgtctcg    120

cagtcgggcg acctgcgcga gcccctgacc ggcgcggccc tcccctgctt ccggctcgcg    180

gcccagcatt ggtgggcggg gccgagcttc ctgtccgaga tgcttctgcc cgtcctcggg    240

gaatgcgccg agcagctggc cgcactgccc gcgccgctcc ggcgaccggc ctcggaggtg    300

ccggtgctga tcgccgtggc cccgtgcggg cgtcccgcac gcccggacga tctcgaggcg    360

cggctgctgg cggagctcga ggcccggctg ggccgctgc ccgaaggcag cgcggtcgtg    420

ggcgccggac gggtgggtct gccgcatctg atcgcgcggg ccgcccgaca ggcgggccgt    480

cacccggtgc agatcctgat cggggtcgag agcttccttc tgcaggagat cgtcgatcac    540

tatgccgacc gtcaccggct tttgtccgag gagaacagct cgggcttcgt gccgggcgag    600

gccgcggccg cgctgatcgt ggcgccccgg ggcatggcgc ccggtctggc gctgaagggc    660

ctcggcgcgg gccgcgagcc ttcgggtgca ggcggcagcc gcgatgcgcc ggtgacgggc    720

gagggcctca ccgatgcgat ccgcgcggcg ctggcggcgg ccgagatccc gctcttcgac    780

attccgatct ttctcggcga cctgaacggc gagcatttca agttcaagga ggcgatgatc    840

gccacgatgc gcctcgaccg tctgccgccc gagaatgtct cccggcggcc gcggggtcat    900

ccggaacatt ggaacgcgat cgaggggctg ggagagatcg gcgcggcgct gatgcccgcg    960

cagctcggct gggccttcga ggcgtcgcgg agcggccggc tgccgcaggg ccgggcgctg   1020

gccttcgccg gcgaggacga tggcgcacgg gtggcgatcg tcgccgctgc ggcaggagga   1080

cctgtccggt ga                                                       1092


<210> SEQ ID NO 128
<211> LENGTH: 363
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 128

Met Ala Glu Leu Arg Gly Leu Ala Pro Gly Leu Ser Val Val Gly Tyr
1               5                   10                  15

Gly Met Trp Thr Ala Leu Gly Pro Asp Gly Pro Thr Thr Val Ala Gly
            20                  25                  30

Leu Asp Ala Arg Leu Ile Val Ser Gln Ser Gly Asp Leu Arg Glu Pro
        35                  40                  45

Leu Thr Gly Ala Ala Leu Pro Cys Phe Arg Leu Ala Ala Gln His Trp
    50                  55                  60

Trp Ala Gly Pro Ser Phe Leu Ser Glu Met Leu Leu Pro Val Leu Gly
65                  70                  75                  80

Glu Cys Ala Glu Gln Leu Ala Ala Leu Pro Ala Pro Leu Arg Arg Pro
                85                  90                  95

Ala Ser Glu Val Pro Val Leu Ile Ala Val Ala Pro Cys Gly Arg Pro
            100                 105                 110

Ala Arg Pro Asp Asp Leu Glu Ala Arg Leu Leu Ala Glu Leu Glu Ala
        115                 120                 125

Arg Leu Gly Pro Leu Pro Glu Gly Ser Ala Val Val Gly Ala Gly Arg
    130                 135                 140

Val Gly Leu Pro His Leu Ile Ala Arg Ala Ala Arg Gln Ala Gly Arg
```

145 150 155 160

His Pro Val Gln Ile Leu Ile Gly Val Glu Ser Phe Leu Leu Gln Glu
165 170 175

Ile Val Asp His Tyr Ala Asp Arg His Arg Leu Leu Ser Glu Glu Asn
180 185 190

Ser Ser Gly Phe Val Pro Gly Glu Ala Ala Ala Ala Leu Ile Val Ala
195 200 205

Pro Arg Gly Met Ala Pro Gly Leu Ala Leu Lys Gly Leu Gly Ala Gly
210 215 220

Arg Glu Pro Ser Gly Ala Gly Gly Ser Arg Asp Ala Pro Val Thr Gly
225 230 235 240

Glu Gly Leu Thr Asp Ala Ile Arg Ala Ala Leu Ala Ala Ala Glu Ile
245 250 255

Pro Leu Phe Asp Ile Pro Ile Phe Leu Gly Asp Leu Asn Gly Glu His
260 265 270

Phe Lys Phe Lys Glu Ala Met Ile Ala Thr Met Arg Leu Asp Arg Leu
275 280 285

Pro Pro Glu Asn Val Ser Arg Arg Pro Arg Gly His Pro Glu His Trp
290 295 300

Asn Ala Ile Glu Gly Leu Gly Glu Ile Gly Ala Ala Leu Met Pro Ala
305 310 315 320

Gln Leu Gly Trp Ala Phe Glu Ala Ser Arg Ser Gly Arg Leu Pro Gln
325 330 335

Gly Arg Ala Leu Ala Phe Ala Gly Glu Asp Asp Gly Ala Arg Val Ala
340 345 350

Ile Val Ala Ala Ala Ala Gly Gly Pro Val Arg
355 360

<210> SEQ ID NO 129
<211> LENGTH: 1968
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 129

atgaccaacg acctcatccg gcgcagcgac tccgacggga tcgcgcttct gaccctcgcc 60

aacccgccgg tgaacgcgct gagcctcgcg gtgcgccaga ggctcgccgc gctgacggcc 120

gagctcgagg ccgacgagag cgtgcgcgcc gtggtgcttg cggccgaggg ccgggtcttc 180

gtcggcggcg cggacatcgc cgagttcgac cgcccgcccg aggcgccgca cctgcccgat 240

gtgatcgccg ccatcgaggc ctcgcggaag ccgtggatcg cggcgctgaa cggcgcggcc 300

ctcggcggcg gggccgagct tgcgctcggc tgccactacc ggatcttcgc ggataccgcc 360

cggctgggcc tgccggagac gagcctcggc ctcatccccg gcgcgggcgg cacgcagcgc 420

ctgccgcgcc ggatcggcct tgctcccgcc atcgaggtca tcaccgccgg ccgcaccctg 480

tcggccgccg aggcgcggga ggcgggcctt gcggaccgga tcgccgcggg cgagctgatc 540

cccgaggcgc tggccttcgc ccgcaccctc gacggcgccc tgcccctgcc tgcctctgcg 600

gccccgctcg ccgatcccgg gcccgccttc tgggacgagg cccgcgcgcg catcgccagg 660

gcggcccgag gcaatcccgc gcccgccgcg gccctcgaag cgatccgcgc gggcgtggcg 720

gaaggcttcg ccgcgggtct ccgcgccgag cgcgagacct tcctgcggct ccgcgcttcg 780

gacgaagccg cggccctgcg ccatctcttc ttcgccgagc gtgcggccct gcgcccggcc 840

gcccttcgcg gcatcgagcc tgtgcccctc acccgcgcag gcgtgatcgg cggcggcacg 900

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atgggcagcg gcatcgcggc cgccctcgcc gcggccgggc tggaggtgcg tctcactgaa    960

accgggcccg agtcgctcgc ggccggcctc gagcgggtcg aggccatctt cgaggcgcag   1020

gtcaagcgcg ggctgacgga tcgggccggc gcggcggagc ggatggcccg cgtcaccggc   1080

acggtcggtc tcggggcgct ggcggactgc gatctggtga tcgaggcggt cttcgaggat   1140

ctcgccgtca agcgccgggt gttcgaagag ctggtccgtc tttgcgggcc cgaggcgatc   1200

cttgccacca acacctccta cctcgatccc gaacggatcg tggagggcct gccgcacccc   1260

caccgcttca tcgcgctgca tttcttcagc ccggcgcagg tgatgaagct gctcgagatc   1320

gtgccgctgg ccgccaccgc gccgcgcacc ctcgccaccg gcgtcgctct ggcggcgcgg   1380

ctcggcaaga tcccggtaca ggcgggcaac ggcgagggtt tcatcggcaa ccgcatcctc   1440

aagcgctacc gcgccgaggc cgaggctctg ctgctcgcag gagccacccc gaccgagatc   1500

gacgaggcca tgcgcgcctt cggcctcggc atgggtccgt tcgagatgca ggacatggcc   1560

gggctcgaca tcgccttccg cgcgcgggag gccgcccgcg cgctcgggca ggacctgccc   1620

gaaggccccg gagaccggct ggtgcgcgca ggccgcctcg gccgcaagtc gggcggcggc   1680

tggtacgact atgcgccggg cagccgcctt ccccagccgt cgccggaggc agccgctctg   1740

atcgcgcctc tggtgacccc cggcccgcgg ccgagcggca ccgagattgc cgaccgcctc   1800

atcgccgcca tggccgagga aggccaacgg atctgcgacg agggcctcgc gcagagcccc   1860

tcggacatcg atctggtcga ggtgcatggc tacggcttcc cccgtcacaa gggggaccg    1920

atgtttcacg ccgcgcgcaa gacccgaagc cgcacgggcg gagcatga                1968


<210> SEQ ID NO 130
<211> LENGTH: 655
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 130

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

Leu Thr Leu Ala Asn Pro Pro Val Asn Ala Leu Ser Leu Ala Val Arg
            20                  25                  30

Gln Arg Leu Ala Ala Leu Thr Ala Glu Leu Glu Ala Asp Glu Ser Val
        35                  40                  45

Arg Ala Val Val Leu Ala Ala Glu Gly Arg Val Phe Val Gly Gly Ala
    50                  55                  60

Asp Ile Ala Glu Phe Asp Arg Pro Pro Glu Ala Pro His Leu Pro Asp
65                  70                  75                  80

Val Ile Ala Ala Ile Glu Ala Ser Arg Lys Pro Trp Ile Ala Ala Leu
                85                  90                  95

Asn Gly Ala Ala Leu Gly Gly Gly Ala Glu Leu Ala Leu Gly Cys His
            100                 105                 110

Tyr Arg Ile Phe Ala Asp Thr Ala Arg Leu Gly Leu Pro Glu Thr Ser
        115                 120                 125

Leu Gly Leu Ile Pro Gly Ala Gly Gly Thr Gln Arg Leu Pro Arg Arg
    130                 135                 140

Ile Gly Leu Ala Pro Ala Ile Glu Val Ile Thr Ala Gly Arg Thr Leu
145                 150                 155                 160

Ser Ala Ala Glu Ala Arg Glu Ala Gly Leu Ala Asp Arg Ile Ala Ala
                165                 170                 175

Gly Glu Leu Ile Pro Glu Ala Leu Ala Phe Ala Arg Thr Leu Asp Gly
            180                 185                 190
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Ala Leu Pro Leu Pro Ala Ser Ala Ala Pro Leu Ala Asp Pro Gly Pro
        195                 200                 205

Ala Phe Trp Asp Glu Ala Arg Ala Arg Ile Ala Arg Ala Ala Arg Gly
    210                 215                 220

Asn Pro Ala Pro Ala Ala Ala Leu Glu Ala Ile Arg Ala Gly Val Ala
225                 230                 235                 240

Glu Gly Phe Ala Ala Gly Leu Arg Ala Glu Arg Glu Thr Phe Leu Arg
                245                 250                 255

Leu Arg Ala Ser Asp Glu Ala Ala Ala Leu Arg His Leu Phe Phe Ala
            260                 265                 270

Glu Arg Ala Ala Leu Arg Pro Ala Ala Leu Arg Gly Ile Glu Pro Val
        275                 280                 285

Pro Leu Thr Arg Ala Gly Val Ile Gly Gly Gly Thr Met Gly Ser Gly
    290                 295                 300

Ile Ala Ala Ala Leu Ala Ala Ala Gly Leu Glu Val Arg Leu Thr Glu
305                 310                 315                 320

Thr Gly Pro Glu Ser Leu Ala Ala Gly Leu Glu Arg Val Glu Ala Ile
                325                 330                 335

Phe Glu Ala Gln Val Lys Arg Gly Leu Thr Asp Arg Ala Gly Ala Ala
            340                 345                 350

Glu Arg Met Ala Arg Val Thr Gly Thr Val Gly Leu Gly Ala Leu Ala
        355                 360                 365

Asp Cys Asp Leu Val Ile Glu Ala Val Phe Glu Asp Leu Ala Val Lys
    370                 375                 380

Arg Arg Val Phe Glu Glu Leu Val Arg Leu Cys Gly Pro Glu Ala Ile
385                 390                 395                 400

Leu Ala Thr Asn Thr Ser Tyr Leu Asp Pro Glu Arg Ile Val Glu Gly
                405                 410                 415

Leu Pro His Pro His Arg Phe Ile Ala Leu His Phe Phe Ser Pro Ala
            420                 425                 430

Gln Val Met Lys Leu Leu Glu Ile Val Pro Leu Ala Ala Thr Ala Pro
        435                 440                 445

Arg Thr Leu Ala Thr Gly Val Ala Leu Ala Ala Arg Leu Gly Lys Ile
    450                 455                 460

Pro Val Gln Ala Gly Asn Gly Glu Gly Phe Ile Gly Asn Arg Ile Leu
465                 470                 475                 480

Lys Arg Tyr Arg Ala Glu Ala Glu Ala Leu Leu Leu Ala Gly Ala Thr
                485                 490                 495

Pro Thr Glu Ile Asp Glu Ala Met Arg Ala Phe Gly Leu Gly Met Gly
            500                 505                 510

Pro Phe Glu Met Gln Asp Met Ala Gly Leu Asp Ile Ala Phe Arg Ala
        515                 520                 525

Arg Glu Ala Ala Arg Ala Leu Gly Gln Asp Leu Pro Glu Gly Pro Gly
    530                 535                 540

Asp Arg Leu Val Arg Ala Gly Arg Leu Gly Arg Lys Ser Gly Gly Gly
545                 550                 555                 560

Trp Tyr Asp Tyr Ala Pro Gly Ser Arg Leu Pro Gln Pro Ser Pro Glu
                565                 570                 575

Ala Ala Ala Leu Ile Ala Pro Leu Val Thr Pro Gly Pro Arg Pro Ser
            580                 585                 590

Gly Thr Glu Ile Ala Asp Arg Leu Ile Ala Ala Met Ala Glu Glu Gly
        595                 600                 605
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Gln Arg Ile Cys Asp Glu Gly Leu Ala Gln Ser Pro Ser Asp Ile Asp
    610                 615                 620

Leu Val Glu Val His Gly Tyr Gly Phe Pro Arg His Lys Gly Gly Pro
625                 630                 635                 640

Met Phe His Ala Ala Arg Lys Thr Arg Ser Arg Thr Gly Gly Ala
                645                 650                 655


<210> SEQ ID NO 131
<211> LENGTH: 753
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 131

atgatgagca tgatcgacca cggacccgat ccgacccaga ctccgattgc cgtcggcgcc      60

atcggcggca gcggcacccg cgtcgtcgcc cgcatcctca agggggcggg cgtcttcatg     120

gggacgaggc tgaacgagtc ggaagacaat ctggacttca ccgagcgttt ccgccatcgc     180

gaggtgctcg ctttgcccga tggggccttc gaggcgcggc tgcggcagtt cgagggcctg     240

tcgcgcgccg gcatgcgcga ggccgggcag cggcactggg gctggaaaga gcccaacacc     300

catgtggtga tcgaccggat cctcgcggcc tatccgaaga tgcgctatgt ccatctgctg     360

cgcagcgggc tcgacatggc cttctccgcc aaccagcgcc aggcgtggtt ctggggggcct     420

tacttcctcg agcgtcccgt ggccgagccg ccggggccgc gggacatgct ggcctatttc     480

tgcgcggtgc accgccggat cagcgccctg gccgaccggc cggagaaccg tggccgggtg     540

ctgttcctgc agtacgaggc gctctgcgcc cggcccgaag cggagatcgt gcggctgctg     600

gacttcctcg ggctggagcc cgcccagccc gtcgccacgc tggccgccct gatcgcgccc     660

cccgccagca tcggccggca ccgggagcac gatctgtcgg tcttcgatcc ggccgatctg     720

gcctatctca aacagaccca gcccgctccc tga                                  753


<210> SEQ ID NO 132
<211> LENGTH: 250
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 132

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

Ala Val Gly Ala Ile Gly Gly Ser Gly Thr Arg Val Val Ala Arg Ile
            20                  25                  30

Leu Lys Gly Ala Gly Val Phe Met Gly Thr Arg Leu Asn Glu Ser Glu
        35                  40                  45

Asp Asn Leu Asp Phe Thr Glu Arg Phe Arg His Arg Glu Val Leu Ala
    50                  55                  60

Leu Pro Asp Gly Ala Phe Glu Ala Arg Leu Arg Gln Phe Glu Gly Leu
65                  70                  75                  80

Ser Arg Ala Gly Met Arg Glu Ala Gly Gln Arg His Trp Gly Trp Lys
                85                  90                  95

Glu Pro Asn Thr His Val Val Ile Asp Arg Ile Leu Ala Ala Tyr Pro
            100                 105                 110

Lys Met Arg Tyr Val His Leu Leu Arg Ser Gly Leu Asp Met Ala Phe
        115                 120                 125

Ser Ala Asn Gln Arg Gln Ala Trp Phe Trp Gly Pro Tyr Phe Leu Glu
    130                 135                 140

Arg Pro Val Ala Glu Pro Pro Gly Pro Arg Asp Met Leu Ala Tyr Phe
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145                 150                 155                 160

Cys Ala Val His Arg Arg Ile Ser Ala Leu Ala Asp Arg Pro Glu Asn
                165                 170                 175

Arg Gly Arg Val Leu Phe Leu Gln Tyr Glu Ala Leu Cys Ala Arg Pro
            180                 185                 190

Glu Ala Glu Ile Val Arg Leu Leu Asp Phe Leu Gly Leu Glu Pro Ala
        195                 200                 205

Gln Pro Val Ala Thr Leu Ala Ala Leu Ile Ala Pro Pro Ala Ser Ile
    210                 215                 220

Gly Arg His Arg Glu His Asp Leu Ser Val Phe Asp Pro Ala Asp Leu
225                 230                 235                 240

Ala Tyr Leu Lys Gln Thr Gln Pro Ala Pro
                245                 250


<210> SEQ ID NO 133
<211> LENGTH: 7890
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 133

atgccgacag tgaacctgac ctctgccctg accttctccg agggcggcgt gccgcagctc      60

gtcgacccga acatcacgat cacgggcggc ggagccttta ccgaaggcta catcgaattc     120

tcggtcagtt cgcccacggc cggcgacaac ttcagcctga ccagcgccgc caatccgctg     180

gccaacggcg cgatctcgtt cgagaacggc gacgtctatc tcgggaccgg ctcggcccgc     240

gagcggatcg gctcggtcga tgcgaccttc gacggccagg acggccagcc gctgcgcatc     300

ctgttctcga gcccgctgcc gaacgccggc ttcgaggaag gcgaggcgaa ctggaccatc     360

cgcgacgagc aatatggcga caacggcagc gagctgaacc tcgacggcct gcagatcacg     420

ctggccaatg actcggccta cagcggcggc accggcacga ccaacgtcca ggcctccgcc     480

ggcatgacct gggacgggtc ggtgcaggat ggtgcgggcg ttgacggatc gcgcgccctc     540

tatctcggca gcggcggaaa catcgttgcg ggcgatcaga acccggccgg cggctatcag     600

gtcaacggct acggctcgat ccacggcccc tatgccacca gctcggtgat caccgtcgcg     660

cagggtgact cgatctcgct cgactttcag gccgtgggca cgagcgacga ctacgaggtg     720

ttcggcttcc tgcgtcgcgt cgacgccaac ggcaacttcc tgagcaacag cgtcagcagc     780

cccgacaaca tcctgctctt cgcccagcgg ggcgatgaca ccagcgggtg gacgaccatc     840

agcaaggacg gcctgcccgc aggcagctac cggttcgagt tcgtcggcgg cacctatgat     900

ggcacgggcg gcctcgcggt gggctcgaac ctctttgtcg acaacatccg cctgatctcg     960

gccacctcgg tgaacgacag catcgcccag gccatcgccc ggcaggtcgc ctaccagaac    1020

gacgccaatg atgcgccggt cacccgccag atcacggtca cggccgtgga cggcaacggc    1080

atcagcggct cctcctcgaa cggcctgacc ttcgaaggcg agaacgacgc gccgagcctt    1140

gccaacacca cgctcacctc gatcgccgag gacagcagcc ccgccggcca gaccatcgcc    1200

gcagccttcg gcggctcctt ctcggatccc gacaacgcct attcccccac cgactcgatg    1260

gcgggcgtcg tcatcaccgg caatgcggcg accggcgccc aaggcgactg gcagtattcg    1320

accgacggcg gcaccacctg gatctcggtc ggcagcgtga cctcgcagag cgggctcgtg    1380

ctttcctcgg ccacgctgat ccgcttcgaa cccgcgctga actggaacgg cacgcccggc    1440

gcgctgacgc tccatgcgct ggacagcacc tatggcggca gcttcaccag cggcacgacg    1500

gcggtgaacc tcgacacgac cggcgccacc ggcaccggcg cgctcagcca gaacagcgcc    1560
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accggctcga tcaccgtcac cccggtcaac gacgcccccg tcttcaccgc ggccccggtc   1620

gcgctgacgg ttgccgacac cgaggccgtg gacacgccgg ccgcgctcac cggctcgatc   1680

tcggcctccg acctgcatgg cggtgcgccg ggcgaaggcg gcacgctcag ctacggcgtt   1740

cagggcggcg tgtcggccaa cggcttctcg gttctgacgc tgccctacgg cacgctgtcg   1800

gtgaaccagt cgaccggagc ctacagcttc ctgccgaacc ccacggcgct gaacagcctc   1860

gccgagggtg cagaggcgaa cttctccttc acgctcaccg tctcggacgg gcagggcggc   1920

acgcagaccg cgccgctcga catcaccttc accggcgcca acgacgtgcc ggtcgtcagc   1980

gcccagaccg gcacggcggt cgaggcctcg ggtctcaaca acaacgtcgc cggcagcgcg   2040

gccacgggct cgctgctgac cggtccgaat gcggcgaccg atatcgacgg cgacgagatc   2100

tcggtggtgg gtgtgcgcac cggcggccag tccgagaccg gcaccgaagg cgtctggacc   2160

gacggcacga tcacgcttca gggcacctac ggcacgctga cgctgaacga ggacggcagc   2220

tggtcctacg cggccgacga tgacaacccg accgtcgacg gcctgaccgg gccgaccgac   2280

acgctggagg agaccttcac ctacaccgtg acggacgcga acggcgccac cgcgtcgcag   2340

gagctgaccg tcaccatctc gggccgcaac gacgcgctga acgtgtcgag cagcatcggc   2400

accgatatct cgacgggcga ggatgccgac acgcagatcg accttaccgg cctcgtgttc   2460

gaagaccccg atctgggctc ggaaatctac gaattcgccg tggatgcggg ccagggcacg   2520

ctctggaccg aaggtgtgga cgggctgacc gtcaccggca acggaacggg ccagctggtg   2580

ctgaccggct cggccaccgc gatttccgaa tggatcgcgg ccaacgacct gacctaccgc   2640

tcgcccgtgg aaggcagcgg cgccgacacg atcagcctct cctacagcga ggcgggcgcc   2700

gaggtccgca cggcgctcga gtccatcgac gtcgcggtgg acatgatcaa cgacccggcc   2760

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caggtcacct tcctgtcgac cggcaccgct caggtgctga atttcgacgg ggtgcagatg   2880

cagatcgcgg ccggcagcac tgccgccgag attgccgaag ccttcgcggc gcaggagttc   2940

ccgaactgga ccgtcagcct tgacggcgag ggccgggtga cgctgaccgc gaccgccacc   3000

ggcgcgcggc cggacctgac ggcggccgac ttcaccaacg gctcgggcgc cttctcgccg   3060

ctggtcgaga ccaccggcgg caccgacggc agcatcaatt tcaccgcgcg cggaccggcc   3120

atcgccatcc tgccgacgct ggaactgagc gacgtcgaca gcgcgatgat gtcgggcgcc   3180

aaggtcagca tgaccgaagg cctgttcgac aacgggttcg gcacgatcta cgaacggctc   3240

tcgctgtcgg cggaggcgcg ggaattcgcg cagcagaacg gcgtgggcat cagcatcgtg   3300

acgacggccg ctgccggctc ggtcatcacc ttcaccggca tggcctcggc ggaggtctac   3360

gagaccatcc tgcgcggcgt gatctacagc aacaccaacc cgaatgcggt ggcgggcacc   3420

cgccccgtga agatcgaagt gaccgactct gacgggctcg cctcgagcct ctccagcgtc   3480

aacctgacag agggcaacac cgacatcgcc gtcggccagc gcatcttcat caacggcgtg   3540

gacagcggcc aggtcgtctc gatggtgcgc gacgccacca gcttcgtggc cagcggcccg   3600

ctggccgatc tggagccggg tgcggtgctg agcttccatg acggcagcgg tcagcagacc   3660

acggcggttt cggcgggcga cggcacggcc acgatggacg tgaacgtgat ctgggctccc   3720

gtgatcgaca tgaacggcgc cggcgcgggc gatatccacc ggacgaccta catcgagcag   3780

catgccccga tcgccatcgc gaccgccgat gcccgcatcg tcgatcagga aggtctgatc   3840

cgctcgctcg acgtcgtgct gaccaacccg ctcgacaatg tcgaaggttc ggctccggtc   3900
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gaatatctcg gcatctcgaa ggcggtgctg gacgtgctgg cggcccgcgg catcaccatc 3960

ggtgcccatg acggccagtt cgacgccaac ggcaacctga ccggcgccac ctcgatcacc 4020

ttcgcggcgg ccaacggcgc cagcgccacc agcttccaga ttgcgctgcg gggcgtgacc 4080

tatgccaaca tggacgatgc cccggacacc gggacgcgga tcgtgacggc gcagggcacc 4140

gacatggacg gcaacgaggg cctgatctcg cacaccgaga tcaacccgat cgcggtgggc 4200

gacgcgccgg tggcgatcga cagcggcgtg accggctccg aagatgcggg ccatgtcttt 4260

gccgccggag acttcggctt tgccgatccg ctggatggcg gcgcgaacca gctcgcctcg 4320

atcaccatca acagcctgcc cgccacgggc acgctgctcc tgggcggggt cgcggtcgcc 4380

gtgggcaccg tggtcaccct cgcgcagctt caggccggcg cgctgaccta tcagccggtg 4440

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ccggtgaacg atgctccggt cctgccggaa ggcacctccg tcaccggcac cacgatcacc 4620

gaagaccagc agctgaatgc cggtgaactg gtggccgatc tggtcggcgc catgacggat 4680

gtcgatacgg gcgtgcacag cgccacgaac ggcacccagc agggcatcgc ggtttatggc 4740

gcgggctccg aagggttcgg cggcggcacc tggcagtatc gtctcgccgg cggcaccgac 4800

tggatcgacg tcaccctcga tccgggcgag gtcctgctgc tcggtgcgga cgaccgcatc 4860

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ggggcgaccg gcaccgcggg caacgtggtc gcaggcatcg cggggccggg caatgcctcg 4980

aaccgtggcg gcacctcggc cttctccagc aacggcgcct ctgccacggt cgaggtgaca 5040

gctgtcaacg acgcgccgtc gatcagcatg ggcgagggca ataccttcta tgctcgcggc 5100

gaggcggtgg cgctgttctc ggacgagacg ctgcaactga ccgacccgga cgagggcgcg 5160

gcggtaagcc agattgtcat cacgctcgat ggcgagacca cggtcgacaa cgccttcggc 5220

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gaaacggcca ccgagggcgt taccgtcagc ctcgcgctgc agggcgaagg ccagttcgtg 6600

aacgcgcagg aaggcaacga cccgctgacc tcgatcgaga acctgacggg cagcaatcac 6660

gacgacacgc tgatcgggga cgagggcgac aacgtgctct cgggtctcgc gggcaacgac 6720

gtgctggtgg gcggcgcggg caatgacacg ctgctcggcg gtgccggcaa cgacatcgcc 6780

gactacgccg cggcgacggg cggggtgacg gtcaatctgg cgcgtgatgg gcaggcgcag 6840

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gcaaccgccg gtgtcaccgt ggatctctcg ctgcagggtc aggcgcagcg catcagtgcc 7260

gaggaaggca cggatacgct gttctcgatc gagaacatcc tcggcagccg gtatgacgac 7320

cgcctgctgg gcgatgcggg ctccaacttg atcgacggca gtgccggcaa cgacactgcc 7380

atgggtcagg cgggcgagga cctcatcttc ggcggggacg gcaacgacag cctctatggc 7440

aaccaggaca acgacactct ggtcggcggc aacggcaacg actggttgca cggcggtcag 7500

ggcaacgatc tcctggtggg cgatgccggc agcgacaccc tcaacggcgg cgtgggcgac 7560

gatgtgctgg tcgggggtca gggcttcgac cttctgacgg gcggcaccgg ggcggacact 7620

ttcgtcttcg gcagcctcga cagcgcggat gcggatcgga tcaccgattt cgagcagggc 7680

gtcgaccaga tcgtgatcgc cgaccagctg atgtgggcgc tggagaatgc cgagctgaac 7740

ctcgccgatc agatcgtctg gaatgccgag accggcatgc tctccatcga tctcgacgcc 7800

ggggaggcga cccgtctggt ggatcttgct cagatcgatc atgatggaac gctgaacatc 7860

acgatcgacg acttccagtt cctgcgctga 7890

<210> SEQ ID NO 134
<211> LENGTH: 2629
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 134

Met Pro Thr Val Asn Leu Thr Ser Ala Leu Thr Phe Ser Glu Gly Gly
1 5 10 15

Val Pro Gln Leu Val Asp Pro Asn Ile Thr Ile Thr Gly Gly Gly Ala
20 25 30

Phe Thr Glu Gly Tyr Ile Glu Phe Ser Val Ser Ser Pro Thr Ala Gly
35 40 45

Asp Asn Phe Ser Leu Thr Ser Ala Ala Asn Pro Leu Ala Asn Gly Ala
50 55 60

Ile Ser Phe Glu Asn Gly Asp Val Tyr Leu Gly Thr Gly Ser Ala Arg
65 70 75 80

Glu Arg Ile Gly Ser Val Asp Ala Thr Phe Asp Gly Gln Asp Gly Gln

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                 85                  90                  95

Pro Leu Arg Ile Leu Phe Ser Ser Pro Leu Pro Asn Ala Gly Phe Glu
            100                 105                 110

Glu Gly Glu Ala Asn Trp Thr Ile Arg Asp Glu Gln Tyr Gly Asp Asn
        115                 120                 125

Gly Ser Glu Leu Asn Leu Asp Gly Leu Gln Ile Thr Leu Ala Asn Asp
    130                 135                 140

Ser Ala Tyr Ser Gly Gly Thr Gly Thr Thr Asn Val Gln Ala Ser Ala
145                 150                 155                 160

Gly Met Thr Trp Asp Gly Ser Val Gln Asp Gly Ala Gly Val Asp Gly
                165                 170                 175

Ser Arg Ala Leu Tyr Leu Gly Ser Gly Gly Asn Ile Val Ala Gly Asp
            180                 185                 190

Gln Asn Pro Ala Gly Gly Tyr Gln Val Asn Gly Tyr Gly Ser Ile His
        195                 200                 205

Gly Pro Tyr Ala Thr Ser Ser Val Ile Thr Val Ala Gln Gly Asp Ser
    210                 215                 220

Ile Ser Leu Asp Phe Gln Ala Val Gly Thr Ser Asp Asp Tyr Glu Val
225                 230                 235                 240

Phe Gly Phe Leu Arg Arg Val Asp Ala Asn Gly Asn Phe Leu Ser Asn
                245                 250                 255

Ser Val Ser Ser Pro Asp Asn Ile Leu Leu Phe Ala Gln Arg Gly Asp
            260                 265                 270

Asp Thr Ser Gly Trp Thr Thr Ile Ser Lys Asp Gly Leu Pro Ala Gly
        275                 280                 285

Ser Tyr Arg Phe Glu Phe Val Gly Gly Thr Tyr Asp Gly Thr Gly Gly
    290                 295                 300

Leu Ala Val Gly Ser Asn Leu Phe Val Asp Asn Ile Arg Leu Ile Ser
305                 310                 315                 320

Ala Thr Ser Val Asn Asp Ser Ile Ala Gln Ala Ile Ala Arg Gln Val
                325                 330                 335

Ala Tyr Gln Asn Asp Ala Asn Asp Ala Pro Val Thr Arg Gln Ile Thr
            340                 345                 350

Val Thr Ala Val Asp Gly Asn Gly Ile Ser Gly Ser Ser Ser Asn Gly
        355                 360                 365

Leu Thr Phe Glu Gly Glu Asn Asp Ala Pro Ser Leu Ala Asn Thr Thr
    370                 375                 380

Leu Thr Ser Ile Ala Glu Asp Ser Ser Pro Ala Gly Gln Thr Ile Ala
385                 390                 395                 400

Ala Ala Phe Gly Gly Ser Phe Ser Asp Pro Asp Asn Ala Tyr Ser Pro
                405                 410                 415

Thr Asp Ser Met Ala Gly Val Val Ile Thr Gly Asn Ala Ala Thr Gly
            420                 425                 430

Ala Gln Gly Asp Trp Gln Tyr Ser Thr Asp Gly Gly Thr Thr Trp Ile
        435                 440                 445

Ser Val Gly Ser Val Thr Ser Gln Ser Gly Leu Val Leu Ser Ser Ala
    450                 455                 460

Thr Leu Ile Arg Phe Glu Pro Ala Leu Asn Trp Asn Gly Thr Pro Gly
465                 470                 475                 480

Ala Leu Thr Leu His Ala Leu Asp Ser Thr Tyr Gly Gly Ser Phe Thr
                485                 490                 495

Ser Gly Thr Thr Ala Val Asn Leu Asp Thr Thr Gly Ala Thr Gly Thr
            500                 505                 510
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Gly Ala Leu Ser Gln Asn Ser Ala Thr Gly Ser Ile Thr Val Thr Pro
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Val Asn Asp Ala Pro Val Phe Thr Ala Ala Pro Val Ala Leu Thr Val
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Ala Asp Thr Glu Ala Val Asp Thr Pro Ala Ala Leu Thr Gly Ser Ile
545                 550                 555                 560

Ser Ala Ser Asp Leu His Gly Gly Ala Pro Gly Glu Gly Gly Thr Leu
                565                 570                 575

Ser Tyr Gly Val Gln Gly Gly Val Ser Ala Asn Gly Phe Ser Val Leu
            580                 585                 590

Thr Leu Pro Tyr Gly Thr Leu Ser Val Asn Gln Ser Thr Gly Ala Tyr
        595                 600                 605

Ser Phe Leu Pro Asn Pro Thr Ala Leu Asn Ser Leu Ala Glu Gly Ala
    610                 615                 620

Glu Ala Asn Phe Ser Phe Thr Leu Thr Val Ser Asp Gly Gln Gly Gly
625                 630                 635                 640

Thr Gln Thr Ala Pro Leu Asp Ile Thr Phe Thr Gly Ala Asn Asp Val
                645                 650                 655

Pro Val Val Ser Ala Gln Thr Gly Thr Ala Val Glu Ala Ser Gly Leu
            660                 665                 670

Asn Asn Asn Val Ala Gly Ser Ala Ala Thr Gly Ser Leu Leu Thr Gly
        675                 680                 685

Pro Asn Ala Ala Thr Asp Ile Asp Gly Asp Glu Ile Ser Val Val Gly
    690                 695                 700

Val Arg Thr Gly Gly Gln Ser Glu Thr Gly Thr Glu Gly Val Trp Thr
705                 710                 715                 720

Asp Gly Thr Ile Thr Leu Gln Gly Thr Tyr Gly Thr Leu Thr Leu Asn
                725                 730                 735

Glu Asp Gly Ser Trp Ser Tyr Ala Ala Asp Asp Asp Asn Pro Thr Val
            740                 745                 750

Asp Gly Leu Thr Gly Pro Thr Asp Thr Leu Glu Glu Thr Phe Thr Tyr
        755                 760                 765

Thr Val Thr Asp Ala Asn Gly Ala Thr Ala Ser Gln Glu Leu Thr Val
    770                 775                 780

Thr Ile Ser Gly Arg Asn Asp Ala Leu Asn Val Ser Ser Ser Ile Gly
785                 790                 795                 800

Thr Asp Ile Ser Thr Gly Glu Asp Ala Asp Thr Gln Ile Asp Leu Thr
                805                 810                 815

Gly Leu Val Phe Glu Asp Pro Asp Leu Gly Ser Glu Ile Tyr Glu Phe
            820                 825                 830

Ala Val Asp Ala Gly Gln Gly Thr Leu Trp Thr Glu Gly Val Asp Gly
        835                 840                 845

Leu Thr Val Thr Gly Asn Gly Thr Gly Gln Leu Val Leu Thr Gly Ser
    850                 855                 860

Ala Thr Ala Ile Ser Glu Trp Ile Ala Ala Asn Asp Leu Thr Tyr Arg
865                 870                 875                 880

Ser Pro Val Glu Gly Ser Gly Ala Asp Thr Ile Ser Leu Ser Tyr Ser
                885                 890                 895

Glu Ala Gly Ala Glu Val Arg Thr Ala Leu Glu Ser Ile Asp Val Ala
            900                 905                 910

Val Asp Met Ile Asn Asp Pro Ala Val Val Asp Val Asn Gly Ser Val
        915                 920                 925
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Thr Thr Gln Gly Ser Ala Gly Val Ala Glu Val Ala Gln Val Thr Phe
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Leu Ser Thr Gly Thr Ala Gln Val Leu Asn Phe Asp Gly Val Gln Met
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Gln Ile Ala Ala Gly Ser Thr Ala Ala Glu Ile Ala Glu Ala Phe Ala
                965                 970                 975

Ala Gln Glu Phe Pro Asn Trp Thr Val Ser Leu Asp Gly Glu Gly Arg
            980                 985                 990

Val Thr Leu Thr Ala Thr Ala Thr  Gly Ala Arg Pro Asp  Leu Thr Ala
        995                 1000                1005

Ala Asp  Phe Thr Asn Gly Ser  Gly Ala Phe Ser Pro  Leu Val Glu
    1010                 1015                 1020

Thr Thr  Gly Gly Thr Asp Gly  Ser Ile Asn Phe Thr  Ala Arg Gly
    1025                 1030                 1035

Pro Ala  Ile Ala Ile Leu Pro  Thr Leu Glu Leu Ser  Asp Val Asp
    1040                 1045                 1050

Ser Ala  Met Met Ser Gly Ala  Lys Val Ser Met Thr  Glu Gly Leu
    1055                 1060                 1065

Phe Asp  Asn Gly Phe Gly Thr  Ile Tyr Glu Arg Leu  Ser Leu Ser
    1070                 1075                 1080

Ala Glu  Ala Arg Glu Phe Ala  Gln Gln Asn Gly Val  Gly Ile Ser
    1085                 1090                 1095

Ile Val  Thr Thr Ala Ala Ala  Gly Ser Val Ile Thr  Phe Thr Gly
    1100                 1105                 1110

Met Ala  Ser Ala Glu Val Tyr  Glu Thr Ile Leu Arg  Gly Val Ile
    1115                 1120                 1125

Tyr Ser  Asn Thr Asn Pro Asn  Ala Val Ala Gly Thr  Arg Pro Val
    1130                 1135                 1140

Lys Ile  Glu Val Thr Asp Ser  Asp Gly Leu Ala Ser  Ser Leu Ser
    1145                 1150                 1155

Ser Val  Asn Leu Thr Glu Gly  Asn Thr Asp Ile Ala  Val Gly Gln
    1160                 1165                 1170

Arg Ile  Phe Ile Asn Gly Val  Asp Ser Gly Gln Val  Val Ser Met
    1175                 1180                 1185

Val Arg  Asp Ala Thr Ser Phe  Val Ala Ser Gly Pro  Leu Ala Asp
    1190                 1195                 1200

Leu Glu  Pro Gly Ala Val Leu  Ser Phe His Asp Gly  Ser Gly Gln
    1205                 1210                 1215

Gln Thr  Thr Ala Val Ser Ala  Gly Asp Gly Thr Ala  Thr Met Asp
    1220                 1225                 1230

Val Asn  Val Ile Trp Ala Pro  Val Ile Asp Met Asn  Gly Ala Gly
    1235                 1240                 1245

Ala Gly  Asp Ile His Arg Thr  Thr Tyr Ile Glu Gln  His Ala Pro
    1250                 1255                 1260

Ile Ala  Ile Ala Thr Ala Asp  Ala Arg Ile Val Asp  Gln Glu Gly
    1265                 1270                 1275

Leu Ile  Arg Ser Leu Asp Val  Val Leu Thr Asn Pro  Leu Asp Asn
    1280                 1285                 1290

Val Glu  Gly Ser Ala Pro Val  Glu Tyr Leu Gly Ile  Ser Lys Ala
    1295                 1300                 1305

Val Leu  Asp Val Leu Ala Ala  Arg Gly Ile Thr Ile  Gly Ala His
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Asp Gly  Gln Phe Asp Ala Asn  Gly Asn Leu Thr Gly  Ala Thr Ser
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Ile Thr  Phe Ala Ala Ala Asn  Gly Ala Ser Ala Thr  Ser Phe Gln
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Ile Ala  Leu Arg Gly Val Thr  Tyr Ala Asn Met Asp  Asp Ala Pro
    1355                1360                1365

Asp Thr  Gly Thr Arg Ile Val  Thr Ala Gln Gly Thr  Asp Met Asp
    1370                1375                1380

Gly Asn  Glu Gly Leu Ile Ser  His Thr Glu Ile Asn  Pro Ile Ala
    1385                1390                1395

Val Gly  Asp Ala Pro Val Ala  Ile Asp Ser Gly Val  Thr Gly Ser
    1400                1405                1410

Glu Asp  Ala Gly His Val Phe  Ala Ala Gly Asp Phe  Gly Phe Ala
    1415                1420                1425

Asp Pro  Leu Asp Gly Gly Ala  Asn Gln Leu Ala Ser  Ile Thr Ile
    1430                1435                1440

Asn Ser  Leu Pro Ala Thr Gly  Thr Leu Leu Leu Gly  Gly Val Ala
    1445                1450                1455

Val Ala  Val Gly Thr Val Val  Thr Leu Ala Gln Leu  Gln Ala Gly
    1460                1465                1470

Ala Leu  Thr Tyr Gln Pro Val  Ala Asn Val Asn Gly  Glu Gly Val
    1475                1480                1485

Ala Ser  Phe Asp Phe Leu Val  Thr Asp Asn Gly Ser  Leu Ala Asn
    1490                1495                1500

Gly Gly  Gln Thr Thr Ser Thr  Ala Pro Ala Thr Met  Val Ile Asp
    1505                1510                1515

Leu Thr  Pro Val Asn Asp Ala  Pro Val Leu Pro Glu  Gly Thr Ser
    1520                1525                1530

Val Thr  Gly Thr Thr Ile Thr  Glu Asp Gln Gln Leu  Asn Ala Gly
    1535                1540                1545

Glu Leu  Val Ala Asp Leu Val  Gly Ala Met Thr Asp  Val Asp Thr
    1550                1555                1560

Gly Val  His Ser Ala Thr Asn  Gly Thr Gln Gln Gly  Ile Ala Val
    1565                1570                1575

Tyr Gly  Ala Gly Ser Glu Gly  Phe Gly Gly Gly Thr  Trp Gln Tyr
    1580                1585                1590

Arg Leu  Ala Gly Gly Thr Asp  Trp Ile Asp Val Thr  Leu Asp Pro
    1595                1600                1605

Gly Glu  Val Leu Leu Leu Gly  Ala Asp Asp Arg Ile  Arg Phe Ser
    1610                1615                1620

Pro Asp  Gly Glu Asn Ala Thr  Glu Ala Gln Leu Ser  Tyr Tyr Ala
    1625                1630                1635

Trp Asp  Gly Ala Thr Gly Thr  Ala Gly Asn Val Val  Ala Gly Ile
    1640                1645                1650

Ala Gly  Pro Gly Asn Ala Ser  Asn Arg Gly Gly Thr  Ser Ala Phe
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Ser Ser  Asn Gly Ala Ser Ala  Thr Val Glu Val Thr  Ala Val Asn
    1670                1675                1680

Asp Ala  Pro Ser Ile Ser Met  Gly Glu Gly Asn Thr  Phe Tyr Ala
    1685                1690                1695

Arg Gly  Glu Ala Val Ala Leu  Phe Ser Asp Glu Thr  Leu Gln Leu
    1700                1705                1710

Thr Asp  Pro Asp Glu Gly Ala  Ala Val Ser Gln Ile  Val Ile Thr
    1715                1720                1725
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Leu Asp  Gly Glu Thr Thr Val  Asp Asn Ala Phe Gly  Thr Thr Tyr
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Glu Thr  Ile Phe Ser Ala Ser  Gly Ser Thr Phe Val  Ala Gln Ser
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Gly Thr  Glu Leu Thr Ile Ser  Gly Thr Gly Val Ala  Gly Asp Pro
    1760                 1765                 1770

Leu Thr  Ile Ser Gly Ala Gly  Ser Met Glu Asp Tyr  Arg Glu Ala
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Leu Leu  Ser Leu Arg Tyr Glu  Asn Thr Asn Pro Asn  Ala Phe Ala
    1790                 1795                 1800

Gly Asp  Arg Ala Ile Ser Val  Thr Val Thr Asp Glu  Thr Gly Ala
    1805                 1810                 1815

Gly Ser  Ala Pro Thr Asp Phe  Ile Leu Pro Val Glu  Trp Ala Thr
    1820                 1825                 1830

Val Ala  Asp Leu Asn Gly Pro  Ser Gly Glu Gly Arg  Asp His Ser
    1835                 1840                 1845

Ile Thr  Tyr Leu Glu Gly Ser  Gly Ser Gln Ala Ile  Ala Thr Ala
    1850                 1855                 1860

Asp Ala  Glu Met Ile Asp Gln  Asp Gly Asn Thr Val  Glu Val Val
    1865                 1870                 1875

Ile Thr  Leu Glu Asp Ala Val  Asn Gly Ser Ala Glu  Met Leu Phe
    1880                 1885                 1890

Val Asp  Pro Ala Val Leu Pro  Ala Leu Ala Ala Leu  Asn Ile Val
    1895                 1900                 1905

Val Thr  Gly Asn Gly Thr His  Glu Ile Arg Leu Thr  Ser Glu Glu
    1910                 1915                 1920

Gly Val  Asp Pro Thr Asn Phe  Gln Leu Ala Leu Arg  Ala Val Arg
    1925                 1930                 1935

Tyr Val  Asn Ser Ser Thr Ala  Pro Thr Ala Ala Glu  Arg His Val
    1940                 1945                 1950

Thr Val  Ser Ser Thr Asp Ala  Asp Gly Asn Pro Gly  Val Pro Ala
    1955                 1960                 1965

Thr Thr  Val Ile Gly Met Glu  Leu Val Asn Asp Ala  Pro Val Ala
    1970                 1975                 1980

Asp Leu  Ser Ile Ser Tyr Glu  Ala Ser Glu Thr Arg  Asn Pro Leu
    1985                 1990                 1995

Ser Gly  Asp Gln Leu Leu Leu  Asp Gly Thr Leu Asp  Asp Ala Asp
    2000                 2005                 2010

Gly Leu  Gly Pro Asn Pro Pro  Val Ile Glu Trp Leu  Arg Asp Gly
    2015                 2020                 2025

Val Val  Ile Ala Ser Gly Asn  Gly Met Pro Val Tyr  Thr Leu Lys
    2030                 2035                 2040

Pro Ala  Asp Ala Gly His Val  Ile Ser Ala Arg Ile  Thr Tyr Thr
    2045                 2050                 2055

Asp Gly  Glu Gly Asn Leu Glu  Val Ile Asn Val Asp  Gly Pro Ala
    2060                 2065                 2070

Met Val  Gly Leu Asn Leu Glu  Gly Thr Asp Gly Ala  Asp Leu Leu
    2075                 2080                 2085

Ile Gly  Ser Arg Gly Ala Asp  Val Ile Ser Gly Arg  Met Phe Asn
    2090                 2095                 2100

Asp Thr  Leu Met Gly Gly Ala  Gly Asn Asp Ser Leu  Tyr Gly Asn
    2105                 2110                 2115
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Gly Asp  Asp Asp Arg Leu Tyr  Val Asn Glu Gly Asn  Asp Ser Leu
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Tyr Gly  Glu Glu Gly Asn Asp  Trp Leu His Gly Gly  Gln Gly Asp
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Asp Leu  Val Val Gly Gly Asp  Gly Asn Asp Thr Leu  Ala Gly Gly
    2150                 2155                 2160

Leu Gly  Asn Asp Thr Leu Gln  Gly Gly Ala Gly Asn  Asp Thr Ala
    2165                 2170                 2175

Ser Tyr  Glu Thr Ala Thr Glu  Gly Val Thr Val Ser  Leu Ala Leu
    2180                 2185                 2190

Gln Gly  Glu Gly Gln Phe Val  Asn Ala Gln Glu Gly  Asn Asp Pro
    2195                 2200                 2205

Leu Thr  Ser Ile Glu Asn Leu  Thr Gly Ser Asn His  Asp Asp Thr
    2210                 2215                 2220

Leu Ile  Gly Asp Glu Gly Asp  Asn Val Leu Ser Gly  Leu Ala Gly
    2225                 2230                 2235

Asn Asp  Val Leu Val Gly Gly  Ala Gly Asn Asp Thr  Leu Leu Gly
    2240                 2245                 2250

Gly Ala  Gly Asn Asp Ile Ala  Asp Tyr Ala Ala Ala  Thr Gly Gly
    2255                 2260                 2265

Val Thr  Val Asn Leu Ala Arg  Asp Gly Gln Ala Gln  Ile Ile Gly
    2270                 2275                 2280

Ala Asp  Gln Gly Thr Asp Val  Leu Ser Ser Ile Glu  Gly Val Ile
    2285                 2290                 2295

Gly Ser  Ala Phe Asn Asp Ile  Leu Ser Gly Ser Ala  Val Ala Asn
    2300                 2305                 2310

Leu Ile  Phe Gly Gly Asp Gly  Ala Asp Leu Ala Thr  Gly Gly Ala
    2315                 2320                 2325

Gly Asn  Asp Thr Ile Leu Gly  Gly Ala Gly Ser Asp  Ser Leu Tyr
    2330                 2335                 2340

Gly Asn  Leu Gly Asp Asp Leu  Leu Phe Gly Asp Val  Gly Asn Asp
    2345                 2350                 2355

Trp Ile  His Gly Gly Gln Gly  Asn Asp Thr Val Leu  Gly Gly Phe
    2360                 2365                 2370

Gly Asp  Asp Thr Leu Ala Gly  Gly Val Gly Asp Asp  Val Val Asp
    2375                 2380                 2385

Gly Gly  Asp Gly Ile Asp Thr  Val Glu Phe Gln Thr  Ala Thr Ala
    2390                 2395                 2400

Gly Val  Thr Val Asp Leu Ser  Leu Gln Gly Gln Ala  Gln Arg Ile
    2405                 2410                 2415

Ser Ala  Glu Glu Gly Thr Asp  Thr Leu Phe Ser Ile  Glu Asn Ile
    2420                 2425                 2430

Leu Gly  Ser Arg Tyr Asp Asp  Arg Leu Leu Gly Asp  Ala Gly Ser
    2435                 2440                 2445

Asn Leu  Ile Asp Gly Ser Ala  Gly Asn Asp Thr Ala  Met Gly Gln
    2450                 2455                 2460

Ala Gly  Glu Asp Leu Ile Phe  Gly Gly Asp Gly Asn  Asp Ser Leu
    2465                 2470                 2475

Tyr Gly  Asn Gln Asp Asn Asp  Thr Leu Val Gly Gly  Asn Gly Asn
    2480                 2485                 2490

Asp Trp  Leu His Gly Gly Gln  Gly Asn Asp Leu Leu  Val Gly Asp
    2495                 2500                 2505

Ala Gly  Ser Asp Thr Leu Asn  Gly Gly Val Gly Asp  Asp Val Leu
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    2510                2515                2520

Val Gly  Gly Gln Gly Phe Asp  Leu Leu Thr Gly Gly  Thr Gly Ala
    2525                2530                2535

Asp Thr  Phe Val Phe Gly Ser  Leu Asp Ser Ala Asp  Ala Asp Arg
    2540                2545                2550

Ile Thr  Asp Phe Glu Gln Gly  Val Asp Gln Ile Val  Ile Ala Asp
    2555                2560                2565

Gln Leu  Met Trp Ala Leu Glu  Asn Ala Glu Leu Asn  Leu Ala Asp
    2570                2575                2580

Gln Ile  Val Trp Asn Ala Glu  Thr Gly Met Leu Ser  Ile Asp Leu
    2585                2590                2595

Asp Ala  Gly Glu Ala Thr Arg  Leu Val Asp Leu Ala  Gln Ile Asp
    2600                2605                2610

His Asp  Gly Thr Leu Asn Ile  Thr Ile Asp Asp Phe  Gln Phe Leu
    2615                2620                2625

Arg


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<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

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gccaacgtga acggtgaagg ggtcgcctcg ttcgacttcc tcgtgaccga caacggcagc 4500

ctcgccaacg gcggccagac cacctcgacc gctccggcaa ccatggtgat cgacctgacg 4560

ccggtgaacg atgctccggt cctgccggaa ggcacctccg tcaccggcac cacgatcacc 4620

gaagaccagc agctgaatgc cggtgaactg gtggccgatc tggtcggcgc catgacggat 4680

gtcgatacgg gcgtgcacag cgccacgaac ggcacccagc agggcatcgc ggtttatggc 4740

gcgggctccg aagggttcgg cggcggcacc tggcagtatc gtctcgccgg cggcaccgac 4800

tggatcgacg tcaccctcga tccgggcgag gtcctgctgc tcggtgcgga cgaccgcatc 4860

cgcttctcgc cggatggcga gaacgcgacc gaggcgcagc tgtcctacta cgcctgggac 4920

ggggcgaccg gcaccgcggg caacgtggtc gcaggcatcg cggggccggg caatgcctcg 4980

aaccgtggcg gcacctcggc cttctccagc aacggcgcct ctgccacggt cgaggtgaca 5040

gctgtcaacg acgcgccgtc gatcagcatg ggcgagggca ataccttcta tgctcgcggc 5100

gaggcggtgg cgctgttctc ggacgagacg ctgcaactga ccgacccgga cgagggcgcg 5160

gcggtaagcc agattgtcat cacgctcgat ggcgagacca cggtcgacaa cgccttcggc 5220

accacctacg agacgatctt ctcggccagc ggctcgacct tcgtggccca gtcgggcacc 5280

gaactgacca tctcgggcac cggtgtggcg ggcgatccgc tcaccatctc gggggccggg 5340

tcgatggagg actaccgtga ggcgctcctc agcctgcgct acgagaacac caacccgaac 5400

gccttcgcgg gcgaccgggc gatctcggtc acggtgacgg atgagacggg ggcgggctcc 5460

gcgccgacgg acttcatcct gccggtggaa tgggcaacgg tggccgatct caacggtccg 5520

tcgggcgaag gccgcgacca ctcgatcacc tatctcgagg gcagcggcag ccaggccatc 5580

gctacggccg atgccgagat gatcgaccag gacggcaaca ccgtcgaggt cgtcatcacg 5640

ctcgaggatg cggtgaacgg ctcggccgag atgctgttcg tcgatccggc ggtcctgccg 5700

gctctggcgg cgctgaacat cgtggtcacc ggcaacggca cccacgagat ccggctgacg 5760

agcgaggagg gcgtggatcc cacgaacttc cagctggcgc tgcgggccgt gcgttacgtc 5820

aacagctcga ccgcacccac cgcggcggag cgccatgtca cggtctcctc gaccgatgcc 5880

gacggcaacc cgggcgttcc ggccaccacg gtgatcggga tggagctggg tgaacgacgc 5940

accggttgcg gatctctcga tctcctacga ggcgtccgag acccgcaacc cgctgtcggg 6000

cgatcagctg ctgctcgacg gcacgctgga cgatgccgac gggctcgggc cgaacccgcc 6060

ggtcatcgaa tggctgcggg acggtgtggt gatcgcttcg ggcaacggca tgccggtcta 6120

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cacgctgaaa ccggcggatg caggccatgt catcagcgcc cgcatcacct acaccgacgg   6180

tga                                                                 6183


<210> SEQ ID NO 136
<211> LENGTH: 2060
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 136

Met Pro Thr Val Asn Leu Thr Ser Ala Leu Thr Phe Ser Glu Gly Gly
1               5                   10                  15

Val Pro Gln Leu Val Asp Pro Asn Ile Thr Ile Thr Gly Gly Gly Ala
            20                  25                  30

Phe Thr Glu Gly Tyr Ile Glu Phe Ser Val Ser Ser Pro Thr Ala Gly
        35                  40                  45

Asp Asn Phe Ser Leu Thr Ser Ala Ala Asn Pro Leu Ala Asn Gly Ala
    50                  55                  60

Ile Ser Phe Glu Asn Gly Asp Val Tyr Leu Gly Thr Gly Ser Ala Arg
65                  70                  75                  80

Glu Arg Ile Gly Ser Val Asp Ala Thr Phe Asp Gly Gln Asp Gly Gln
                85                  90                  95

Pro Leu Arg Ile Leu Phe Ser Ser Pro Leu Pro Asn Ala Gly Phe Glu
            100                 105                 110

Glu Gly Glu Ala Asn Trp Thr Ile Arg Asp Glu Gln Tyr Gly Asp Asn
        115                 120                 125

Gly Ser Glu Leu Asn Leu Asp Gly Leu Gln Ile Thr Leu Ala Asn Asp
    130                 135                 140

Ser Ala Tyr Ser Gly Gly Thr Gly Thr Thr Asn Val Gln Ala Ser Ala
145                 150                 155                 160

Gly Met Thr Trp Asp Gly Ser Val Gln Asp Gly Ala Gly Val Asp Gly
                165                 170                 175

Ser Arg Ala Leu Tyr Leu Gly Ser Gly Gly Asn Ile Val Ala Gly Asp
            180                 185                 190

Gln Asn Pro Ala Gly Gly Tyr Gln Val Asn Gly Tyr Gly Ser Ile His
        195                 200                 205

Gly Pro Tyr Ala Thr Ser Ser Val Ile Thr Val Ala Gln Gly Asp Ser
    210                 215                 220

Ile Ser Leu Asp Phe Gln Ala Val Gly Thr Ser Asp Asp Tyr Glu Val
225                 230                 235                 240

Phe Gly Phe Leu Arg Arg Val Asp Ala Asn Gly Asn Phe Leu Ser Asn
                245                 250                 255

Ser Val Ser Ser Pro Asp Asn Ile Leu Leu Phe Ala Gln Arg Gly Asp
            260                 265                 270

Asp Thr Ser Gly Trp Thr Thr Ile Ser Lys Asp Gly Leu Pro Ala Gly
        275                 280                 285

Ser Tyr Arg Phe Glu Phe Val Gly Gly Thr Tyr Asp Gly Thr Gly Gly
    290                 295                 300

Leu Ala Val Gly Ser Asn Leu Phe Val Asp Asn Ile Arg Leu Ile Ser
305                 310                 315                 320

Ala Thr Ser Val Asn Asp Ser Ile Ala Gln Ala Ile Ala Arg Gln Val
                325                 330                 335

Ala Tyr Gln Asn Asp Ala Asn Asp Ala Pro Val Thr Arg Gln Ile Thr
            340                 345                 350

Val Thr Ala Val Asp Gly Asn Gly Ile Ser Gly Ser Ser Ser Asn Gly
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        355                 360                 365

Leu Thr Phe Glu Gly Glu Asn Asp Ala Pro Ser Leu Ala Asn Thr Thr
    370                 375                 380

Leu Thr Ser Ile Ala Glu Asp Ser Ser Pro Ala Gly Gln Thr Ile Ala
385                 390                 395                 400

Ala Ala Phe Gly Gly Ser Phe Ser Asp Pro Asp Asn Ala Tyr Ser Pro
                405                 410                 415

Thr Asp Ser Met Ala Gly Val Val Ile Thr Gly Asn Ala Ala Thr Gly
            420                 425                 430

Ala Gln Gly Asp Trp Gln Tyr Ser Thr Asp Gly Gly Thr Thr Trp Ile
        435                 440                 445

Ser Val Gly Ser Val Thr Ser Gln Ser Gly Leu Val Leu Ser Ser Ala
    450                 455                 460

Thr Leu Ile Arg Phe Glu Pro Ala Leu Asn Trp Asn Gly Thr Pro Gly
465                 470                 475                 480

Ala Leu Thr Leu His Ala Leu Asp Ser Thr Tyr Gly Gly Ser Phe Thr
                485                 490                 495

Ser Gly Thr Thr Ala Val Asn Leu Asp Thr Thr Gly Ala Thr Gly Thr
            500                 505                 510

Gly Ala Leu Ser Gln Asn Ser Ala Thr Gly Ser Ile Thr Val Thr Pro
        515                 520                 525

Val Asn Asp Ala Pro Val Phe Thr Ala Ala Pro Val Ala Leu Thr Val
    530                 535                 540

Ala Asp Thr Glu Ala Val Asp Thr Pro Ala Ala Leu Thr Gly Ser Ile
545                 550                 555                 560

Ser Ala Ser Asp Leu His Gly Gly Ala Pro Gly Glu Gly Gly Thr Leu
                565                 570                 575

Ser Tyr Gly Val Gln Gly Gly Val Ser Ala Asn Gly Phe Ser Val Leu
            580                 585                 590

Thr Leu Pro Tyr Gly Thr Leu Ser Val Asn Gln Ser Thr Gly Ala Tyr
        595                 600                 605

Ser Phe Leu Pro Asn Pro Thr Ala Leu Asn Ser Leu Ala Glu Gly Ala
    610                 615                 620

Glu Ala Asn Phe Ser Phe Thr Leu Thr Val Ser Asp Gly Gln Gly Gly
625                 630                 635                 640

Thr Gln Thr Ala Pro Leu Asp Ile Thr Phe Thr Gly Ala Asn Asp Val
                645                 650                 655

Pro Val Val Ser Ala Gln Thr Gly Thr Ala Val Glu Ala Ser Gly Leu
            660                 665                 670

Asn Asn Asn Val Ala Gly Ser Ala Ala Thr Gly Ser Leu Leu Thr Gly
        675                 680                 685

Pro Asn Ala Ala Thr Asp Ile Asp Gly Asp Glu Ile Ser Val Val Gly
    690                 695                 700

Val Arg Thr Gly Gly Gln Ser Glu Thr Gly Thr Glu Gly Val Trp Thr
705                 710                 715                 720

Asp Gly Thr Ile Thr Leu Gln Gly Thr Tyr Gly Thr Leu Thr Leu Asn
                725                 730                 735

Glu Asp Gly Ser Trp Ser Tyr Ala Ala Asp Asp Asp Asn Pro Thr Val
            740                 745                 750

Asp Gly Leu Thr Gly Pro Thr Asp Thr Leu Glu Glu Thr Phe Thr Tyr
        755                 760                 765

Thr Val Thr Asp Ala Asn Gly Ala Thr Ala Ser Gln Glu Leu Thr Val
    770                 775                 780
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Thr Ile Ser Gly Arg Asn Asp Ala Leu Asn Val Ser Ser Ser Ile Gly
785                 790                 795                 800

Thr Asp Ile Ser Thr Gly Glu Asp Ala Asp Thr Gln Ile Asp Leu Thr
                805                 810                 815

Gly Leu Val Phe Glu Asp Pro Asp Leu Gly Ser Glu Ile Tyr Glu Phe
            820                 825                 830

Ala Val Asp Ala Gly Gln Gly Thr Leu Trp Thr Glu Gly Val Asp Gly
        835                 840                 845

Leu Thr Val Thr Gly Asn Gly Thr Gly Gln Leu Val Leu Thr Gly Ser
    850                 855                 860

Ala Thr Ala Ile Ser Glu Trp Ile Ala Ala Asn Asp Leu Thr Tyr Arg
865                 870                 875                 880

Ser Pro Val Glu Gly Ser Gly Ala Asp Thr Ile Ser Leu Ser Tyr Ser
                885                 890                 895

Glu Ala Gly Ala Glu Val Arg Thr Ala Leu Glu Ser Ile Asp Val Ala
            900                 905                 910

Val Asp Met Ile Asn Asp Pro Ala Val Val Asp Val Asn Gly Ser Val
        915                 920                 925

Thr Thr Gln Gly Ser Ala Gly Val Ala Glu Val Ala Gln Val Thr Phe
    930                 935                 940

Leu Ser Thr Gly Thr Ala Gln Val Leu Asn Phe Asp Gly Val Gln Met
945                 950                 955                 960

Gln Ile Ala Ala Gly Ser Thr Ala Ala Glu Ile Ala Glu Ala Phe Ala
                965                 970                 975

Ala Gln Glu Phe Pro Asn Trp Thr Val Ser Leu Asp Gly Glu Gly Arg
            980                 985                 990

Val Thr Leu Thr Ala Thr Ala Thr  Gly Ala Arg Pro Asp  Leu Thr Ala
        995                 1000                1005

Ala Asp  Phe Thr Asn Gly Ser  Gly Ala Phe Ser Pro  Leu Val Glu
    1010                 1015                 1020

Thr Thr  Gly Gly Thr Asp Gly  Ser Ile Asn Phe Thr  Ala Arg Gly
    1025                 1030                 1035

Pro Ala  Ile Ala Ile Leu Pro  Thr Leu Glu Leu Ser  Asp Val Asp
    1040                 1045                 1050

Ser Ala  Met Met Ser Gly Ala  Lys Val Ser Met Thr  Glu Gly Leu
    1055                 1060                 1065

Phe Asp  Asn Gly Phe Gly Thr  Ile Tyr Glu Arg Leu  Ser Leu Ser
    1070                 1075                 1080

Ala Glu  Ala Arg Glu Phe Ala  Gln Gln Asn Gly Val  Gly Ile Ser
    1085                 1090                 1095

Ile Val  Thr Thr Ala Ala Ala  Gly Ser Val Ile Thr  Phe Thr Gly
    1100                 1105                 1110

Met Ala  Ser Ala Glu Val Tyr  Glu Thr Ile Leu Arg  Gly Val Ile
    1115                 1120                 1125

Tyr Ser  Asn Thr Asn Pro Asn  Ala Val Ala Gly Thr  Arg Pro Val
    1130                 1135                 1140

Lys Ile  Glu Val Thr Asp Ser  Asp Gly Leu Ala Ser  Ser Leu Ser
    1145                 1150                 1155

Ser Val  Asn Leu Thr Glu Gly  Asn Thr Asp Ile Ala  Val Gly Gln
    1160                 1165                 1170

Arg Ile  Phe Ile Asn Gly Val  Asp Ser Gly Gln Val  Val Ser Met
    1175                 1180                 1185
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Val Arg  Asp Ala Thr Ser Phe  Val Ala Ser Gly Pro  Leu Ala Asp
    1190                 1195                 1200

Leu Glu  Pro Gly Ala Val Leu  Ser Phe His Asp Gly  Ser Gly Gln
    1205                 1210                 1215

Gln Thr  Thr Ala Val Ser Ala  Gly Asp Gly Thr Ala  Thr Met Asp
    1220                 1225                 1230

Val Asn  Val Ile Trp Ala Pro  Val Ile Asp Met Asn  Gly Ala Gly
    1235                 1240                 1245

Ala Gly  Asp Ile His Arg Thr  Thr Tyr Ile Glu Gln  His Ala Pro
    1250                 1255                 1260

Ile Ala  Ile Ala Thr Ala Asp  Ala Arg Ile Val Asp  Gln Glu Gly
    1265                 1270                 1275

Leu Ile  Arg Ser Leu Asp Val  Val Leu Thr Asn Pro  Leu Asp Asn
    1280                 1285                 1290

Val Glu  Gly Ser Ala Pro Val  Glu Tyr Leu Gly Ile  Ser Lys Ala
    1295                 1300                 1305

Val Leu  Asp Val Leu Ala Ala  Arg Gly Ile Thr Ile  Gly Ala His
    1310                 1315                 1320

Asp Gly  Gln Phe Asp Ala Asn  Gly Asn Leu Thr Gly  Ala Thr Ser
    1325                 1330                 1335

Ile Thr  Phe Ala Ala Ala Asn  Gly Ala Ser Ala Thr  Ser Phe Gln
    1340                 1345                 1350

Ile Ala  Leu Arg Gly Val Thr  Tyr Ala Asn Met Asp  Asp Ala Pro
    1355                 1360                 1365

Asp Thr  Gly Thr Arg Ile Val  Thr Ala Gln Gly Thr  Asp Met Asp
    1370                 1375                 1380

Gly Asn  Glu Gly Leu Ile Ser  His Thr Glu Ile Asn  Pro Ile Ala
    1385                 1390                 1395

Val Gly  Asp Ala Pro Val Ala  Ile Asp Ser Gly Val  Thr Gly Ser
    1400                 1405                 1410

Glu Asp  Ala Gly His Val Phe  Ala Ala Gly Asp Phe  Gly Phe Ala
    1415                 1420                 1425

Asp Pro  Leu Asp Gly Gly Ala  Asn Gln Leu Ala Ser  Ile Thr Ile
    1430                 1435                 1440

Asn Ser  Leu Pro Ala Thr Gly  Thr Leu Leu Leu Gly  Gly Val Ala
    1445                 1450                 1455

Val Ala  Val Gly Thr Val Val  Thr Leu Ala Gln Leu  Gln Ala Gly
    1460                 1465                 1470

Ala Leu  Thr Tyr Gln Pro Val  Ala Asn Val Asn Gly  Glu Gly Val
    1475                 1480                 1485

Ala Ser  Phe Asp Phe Leu Val  Thr Asp Asn Gly Ser  Leu Ala Asn
    1490                 1495                 1500

Gly Gly  Gln Thr Thr Ser Thr  Ala Pro Ala Thr Met  Val Ile Asp
    1505                 1510                 1515

Leu Thr  Pro Val Asn Asp Ala  Pro Val Leu Pro Glu  Gly Thr Ser
    1520                 1525                 1530

Val Thr  Gly Thr Thr Ile Thr  Glu Asp Gln Gln Leu  Asn Ala Gly
    1535                 1540                 1545

Glu Leu  Val Ala Asp Leu Val  Gly Ala Met Thr Asp  Val Asp Thr
    1550                 1555                 1560

Gly Val  His Ser Ala Thr Asn  Gly Thr Gln Gln Gly  Ile Ala Val
    1565                 1570                 1575

Tyr Gly  Ala Gly Ser Glu Gly  Phe Gly Gly Gly Thr  Trp Gln Tyr
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    1580                 1585                 1590

Arg Leu  Ala Gly Gly Thr Asp  Trp Ile Asp Val Thr  Leu Asp Pro
    1595                 1600                 1605

Gly Glu  Val Leu Leu Leu Gly  Ala Asp Asp Arg Ile  Arg Phe Ser
    1610                 1615                 1620

Pro Asp  Gly Glu Asn Ala Thr  Glu Ala Gln Leu Ser  Tyr Tyr Ala
    1625                 1630                 1635

Trp Asp  Gly Ala Thr Gly Thr  Ala Gly Asn Val Val  Ala Gly Ile
    1640                 1645                 1650

Ala Gly  Pro Gly Asn Ala Ser  Asn Arg Gly Gly Thr  Ser Ala Phe
    1655                 1660                 1665

Ser Ser  Asn Gly Ala Ser Ala  Thr Val Glu Val Thr  Ala Val Asn
    1670                 1675                 1680

Asp Ala  Pro Ser Ile Ser Met  Gly Glu Gly Asn Thr  Phe Tyr Ala
    1685                 1690                 1695

Arg Gly  Glu Ala Val Ala Leu  Phe Ser Asp Glu Thr  Leu Gln Leu
    1700                 1705                 1710

Thr Asp  Pro Asp Glu Gly Ala  Ala Val Ser Gln Ile  Val Ile Thr
    1715                 1720                 1725

Leu Asp  Gly Glu Thr Thr Val  Asp Asn Ala Phe Gly  Thr Thr Tyr
    1730                 1735                 1740

Glu Thr  Ile Phe Ser Ala Ser  Gly Ser Thr Phe Val  Ala Gln Ser
    1745                 1750                 1755

Gly Thr  Glu Leu Thr Ile Ser  Gly Thr Gly Val Ala  Gly Asp Pro
    1760                 1765                 1770

Leu Thr  Ile Ser Gly Ala Gly  Ser Met Glu Asp Tyr  Arg Glu Ala
    1775                 1780                 1785

Leu Leu  Ser Leu Arg Tyr Glu  Asn Thr Asn Pro Asn  Ala Phe Ala
    1790                 1795                 1800

Gly Asp  Arg Ala Ile Ser Val  Thr Val Thr Asp Glu  Thr Gly Ala
    1805                 1810                 1815

Gly Ser  Ala Pro Thr Asp Phe  Ile Leu Pro Val Glu  Trp Ala Thr
    1820                 1825                 1830

Val Ala  Asp Leu Asn Gly Pro  Ser Gly Glu Gly Arg  Asp His Ser
    1835                 1840                 1845

Ile Thr  Tyr Leu Glu Gly Ser  Gly Ser Gln Ala Ile  Ala Thr Ala
    1850                 1855                 1860

Asp Ala  Glu Met Ile Asp Gln  Asp Gly Asn Thr Val  Glu Val Val
    1865                 1870                 1875

Ile Thr  Leu Glu Asp Ala Val  Asn Gly Ser Ala Glu  Met Leu Phe
    1880                 1885                 1890

Val Asp  Pro Ala Val Leu Pro  Ala Leu Ala Ala Leu  Asn Ile Val
    1895                 1900                 1905

Val Thr  Gly Asn Gly Thr His  Glu Ile Arg Leu Thr  Ser Glu Glu
    1910                 1915                 1920

Gly Val  Asp Pro Thr Asn Phe  Gln Leu Ala Leu Arg  Ala Val Arg
    1925                 1930                 1935

Tyr Val  Asn Ser Ser Thr Ala  Pro Thr Ala Ala Glu  Arg His Val
    1940                 1945                 1950

Thr Val  Ser Ser Thr Asp Ala  Asp Gly Asn Pro Gly  Val Pro Ala
    1955                 1960                 1965

Thr Thr  Val Ile Gly Met Glu  Leu Gly Glu Arg Arg  Thr Gly Cys
    1970                 1975                 1980
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Gly Ser  Leu Asp Leu Leu Arg  Gly Val Arg Asp Pro  Gln Pro Ala
    1985                 1990                 1995

Val Gly  Arg Ser Ala Ala Ala  Arg Arg His Ala Gly  Arg Cys Arg
    2000                 2005                 2010

Arg Ala  Arg Ala Glu Pro Ala  Gly His Arg Met Ala  Ala Gly Arg
    2015                 2020                 2025

Cys Gly  Asp Arg Phe Gly Gln  Arg His Ala Gly Leu  His Ala Glu
    2030                 2035                 2040

Thr Gly  Gly Cys Arg Pro Cys  His Gln Arg Pro His  His Leu His
    2045                 2050                 2055

Arg Arg
    2060


<210> SEQ ID NO 137
<211> LENGTH: 747
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 137

atgaaccaga tcgatctggc cggccgcgtg gccgtggtga cgggcggcgc gcaggggatc      60

gggcgcgccg tggccgagcg gctgatcgcc tcgggggcgc gggtctgcct gtgggaccgc     120

gacgccgggc gggccgcggc gacggcggcc gaactgggcg ggaacagctt ctttcaggtg     180

gtggatcagg tggatttcac ggcggtaaag gccgccgccg acgccaccga agccacgggc     240

ggccggatcg acatcctgat cgccaacgcg ggcatcgccg gcagcaatgc gccggtcgcc     300

gactacccgg tcgaggaatg gcaccgcatc atcgatatca acctgaacgg tgtcttccat     360

tgctgcaagg cggtggtgcc cggcatgaag gcccacggat acgggcgcat cgtcacggtc     420

gcctcgatcg ccggcaagga aggcaatccc aatgcggccg cctattcggc ctcgaaggcc     480

ggggtcatcg ctttgaccaa atcgctgggc aaggaggtcg ccggccagga tatcgccgtc     540

aattgcgtga ccccggccgc cgcccgcacg cagatcttcg accagatggc gcagagccac     600

atcgactaca tgctgtcgcg catcccgcgc ggccgctttc tggatctgga cgaggccgcg     660

gcgatgatcg cgtggctggc cagtgccgag aacagcttta ccaccggtgc cgtcttcgat     720

ctctccggcg gccgggccac ctattga                                         747


<210> SEQ ID NO 138
<211> LENGTH: 248
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 138

Met Asn Gln Ile Asp Leu Ala Gly Arg Val Ala Val Val Thr Gly Gly
1               5                   10                  15

Ala Gln Gly Ile Gly Arg Ala Val Ala Glu Arg Leu Ile Ala Ser Gly
            20                  25                  30

Ala Arg Val Cys Leu Trp Asp Arg Asp Ala Gly Arg Ala Ala Ala Thr
        35                  40                  45

Ala Ala Glu Leu Gly Gly Asn Ser Phe Phe Gln Val Val Asp Gln Val
    50                  55                  60

Asp Phe Thr Ala Val Lys Ala Ala Ala Asp Ala Thr Glu Ala Thr Gly
65                  70                  75                  80

Gly Arg Ile Asp Ile Leu Ile Ala Asn Ala Gly Ile Ala Gly Ser Asn
                85                  90                  95
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Ala Pro Val Ala Asp Tyr Pro Val Glu Glu Trp His Arg Ile Ile Asp
            100                 105                 110

Ile Asn Leu Asn Gly Val Phe His Cys Cys Lys Ala Val Val Pro Gly
        115                 120                 125

Met Lys Ala His Gly Tyr Gly Arg Ile Val Thr Val Ala Ser Ile Ala
    130                 135                 140

Gly Lys Glu Gly Asn Pro Asn Ala Ala Ala Tyr Ser Ala Ser Lys Ala
145                 150                 155                 160

Gly Val Ile Ala Leu Thr Lys Ser Leu Gly Lys Glu Val Ala Gly Gln
                165                 170                 175

Asp Ile Ala Val Asn Cys Val Thr Pro Ala Ala Ala Arg Thr Gln Ile
            180                 185                 190

Phe Asp Gln Met Ala Gln Ser His Ile Asp Tyr Met Leu Ser Arg Ile
        195                 200                 205

Pro Arg Gly Arg Phe Leu Asp Leu Asp Glu Ala Ala Ala Met Ile Ala
    210                 215                 220

Trp Leu Ala Ser Ala Glu Asn Ser Phe Thr Thr Gly Ala Val Phe Asp
225                 230                 235                 240

Leu Ser Gly Gly Arg Ala Thr Tyr
                245


<210> SEQ ID NO 139
<211> LENGTH: 936
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 139

atgtcggtgg gagtgattgg aaccggcttc gtcggccggg gctgggcgat ctgccttgcc      60

cgggccggcc acgaggtccg gctgtgggat ccggcgcccg acgccgccga ggccgcccgc     120

acctatatcg ccgagatgct gccggatctg gcggccgcgg acctgctggg cggccgcgcc     180

ccggacgcgg tgctggagcg gatccgcgtc gccccggaca tggccaccgc cgtccgcggc     240

gcccgccaca ttcaggaaag cgcccccgag gatctgcttc tgaagaccgc gctcttcgcc     300

gagctcgacg ctctggccga tcccggcgcg gtgatcgcaa gctcctcctc ggcgcttctg     360

ccttcggcct tcaccgaggg gctggcaggg gcgggccgct gcctcgtcgc ccatccggtc     420

aatccgccgc acctcattcc gctggtcgag ctggtgccgg cgccgtggac cgacgaggag     480

acgctggccc ggaccgagac gctcatgcgc gagatcggcc agagcccggt gcggctcgag     540

cgcgaggtgg acggcttcct gctgaaccgg atccaggccg cggtgctcga cgaggccttc     600

cggctggtcg atgcgggcct cgcctcggcc gatgcggtgg atgcctgcct ccgcgacggt     660

ctggcgctgc gctgggtctt catggggccg ttcgagacca tcgacctcaa cgcgcccgag     720

ggcgtgcgcg actatgtcgc ccgctaccag ccgatgttcc gcaggctcac cgacacgatg     780

cgggaaagcg ccgactggtc cggcccggtg ctcgaccgga tcgaggccga ccgccgcgcg     840

cgcctgccgc aggaggcgct gcgcgcccgg cagatgtggc gcgaccgccg gctgatggcg     900

ctcgccgcct tccgccgcca atccctgcaa tcctag                               936


<210> SEQ ID NO 140
<211> LENGTH: 311
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 140

Met Ser Val Gly Val Ile Gly Thr Gly Phe Val Gly Arg Gly Trp Ala
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1               5                   10                  15

Ile Cys Leu Ala Arg Ala Gly His Glu Val Arg Leu Trp Asp Pro Ala
            20                  25                  30

Pro Asp Ala Ala Glu Ala Ala Arg Thr Tyr Ile Ala Glu Met Leu Pro
        35                  40                  45

Asp Leu Ala Ala Ala Asp Leu Leu Gly Gly Arg Ala Pro Asp Ala Val
    50                  55                  60

Leu Glu Arg Ile Arg Val Ala Pro Asp Met Ala Thr Ala Val Arg Gly
65                  70                  75                  80

Ala Arg His Ile Gln Glu Ser Ala Pro Glu Asp Leu Leu Leu Lys Thr
                85                  90                  95

Ala Leu Phe Ala Glu Leu Asp Ala Leu Ala Asp Pro Gly Ala Val Ile
            100                 105                 110

Ala Ser Ser Ser Ser Ala Leu Leu Pro Ser Ala Phe Thr Glu Gly Leu
        115                 120                 125

Ala Gly Ala Gly Arg Cys Leu Val Ala His Pro Val Asn Pro Pro His
    130                 135                 140

Leu Ile Pro Leu Val Glu Leu Val Pro Ala Pro Trp Thr Asp Glu Glu
145                 150                 155                 160

Thr Leu Ala Arg Thr Glu Thr Leu Met Arg Glu Ile Gly Gln Ser Pro
                165                 170                 175

Val Arg Leu Glu Arg Glu Val Asp Gly Phe Leu Leu Asn Arg Ile Gln
            180                 185                 190

Ala Ala Val Leu Asp Glu Ala Phe Arg Leu Val Asp Ala Gly Leu Ala
        195                 200                 205

Ser Ala Asp Ala Val Asp Ala Cys Leu Arg Asp Gly Leu Ala Leu Arg
    210                 215                 220

Trp Val Phe Met Gly Pro Phe Glu Thr Ile Asp Leu Asn Ala Pro Glu
225                 230                 235                 240

Gly Val Arg Asp Tyr Val Ala Arg Tyr Gln Pro Met Phe Arg Arg Leu
                245                 250                 255

Thr Asp Thr Met Arg Glu Ser Ala Asp Trp Ser Gly Pro Val Leu Asp
            260                 265                 270

Arg Ile Glu Ala Asp Arg Arg Ala Arg Leu Pro Gln Glu Ala Leu Arg
        275                 280                 285

Ala Arg Gln Met Trp Arg Asp Arg Arg Leu Met Ala Leu Ala Ala Phe
    290                 295                 300

Arg Arg Gln Ser Leu Gln Ser
305                 310
```

<210> SEQ ID NO 141
<211> LENGTH: 741
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 141

```
gtgaccggtg ggctcctcgt gacgggcggc agcggcgcca tcggtggcgc actctgccgg     60

atcgcggccc ggcagcaccc ggtgtgggtc ggctacggcg cgggggccgg acgggcccgg    120

gcccttgccg ccgagatcac gcaggcgggc ggacgggccg agccgctggc gctgccgctt    180

caggatcccg cagcgctcga gaccgcgctg gcagcacttc ccgagccgcc cgcgtcactc    240

gcgctctgcg cctggcccgc gcccttcgtg gcgcccttcg ggcgtcaggg cgaggatctg    300

gcgcttcagg cggcggcgct tgccggctgt cacgcgctga tcgccacggc ctggcggctc    360
```

tggtggcggc gcgcgggcgg cgggcatgtg ctggccgtcc tgtcggccgc gtccgagccg 420

cccgtggccc gccacatggc cgcctatgtg gcgcagaagg cggcgctgcg cgccctgctc 480

gcggcggccg ccgccgaact ggggcccgcg gggctgcggg tgagcgtggt ggcccccggc 540

ttcgtcgaga cgccgatgct cggcgccttc gacccgcgcc tgctggagcg cgcccgggcc 600

gacgccggag gcaggttcct gtcccctgaa cgcgtggcgc aggcgctcgt cgccgcgctc 660

gacgcaccgc cccccgccgg gacggtgcag gacattcatc tggctgagga ggtggagagc 720

gatgaaaagc aaaccgcttg a 741

<210> SEQ ID NO 142
<211> LENGTH: 246
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 142

```
Met Thr Gly Gly Leu Leu Val Thr Gly Gly Ser Gly Ala Ile Gly Gly
1               5                   10                  15

Ala Leu Cys Arg Ile Ala Ala Arg Gln His Pro Val Trp Val Gly Tyr
            20                  25                  30

Gly Ala Gly Ala Gly Arg Ala Arg Ala Leu Ala Ala Glu Ile Thr Gln
        35                  40                  45

Ala Gly Gly Arg Ala Glu Pro Leu Ala Leu Pro Leu Gln Asp Pro Ala
    50                  55                  60

Ala Leu Glu Thr Ala Leu Ala Ala Leu Pro Glu Pro Pro Ala Ser Leu
65                  70                  75                  80

Ala Leu Cys Ala Trp Pro Ala Pro Phe Val Ala Pro Phe Gly Arg Gln
                85                  90                  95

Gly Glu Asp Leu Ala Leu Gln Ala Ala Ala Leu Ala Gly Cys His Ala
            100                 105                 110

Leu Ile Ala Thr Ala Trp Arg Leu Trp Trp Arg Arg Ala Gly Gly Gly
        115                 120                 125

His Val Leu Ala Val Leu Ser Ala Ala Ser Glu Pro Pro Val Ala Arg
    130                 135                 140

His Met Ala Ala Tyr Val Ala Gln Lys Ala Ala Leu Arg Ala Leu Leu
145                 150                 155                 160

Ala Ala Ala Ala Ala Glu Leu Gly Pro Ala Gly Leu Arg Val Ser Val
                165                 170                 175

Val Ala Pro Gly Phe Val Glu Thr Pro Met Leu Gly Ala Phe Asp Pro
            180                 185                 190

Arg Leu Leu Glu Arg Ala Arg Ala Asp Ala Gly Gly Arg Phe Leu Ser
        195                 200                 205

Pro Glu Arg Val Ala Gln Ala Leu Val Ala Ala Leu Asp Ala Pro Pro
    210                 215                 220

Pro Ala Gly Thr Val Gln Asp Ile His Leu Ala Glu Glu Val Glu Ser
225                 230                 235                 240

Asp Glu Lys Gln Thr Ala
                245
```

<210> SEQ ID NO 143
<211> LENGTH: 996
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 143

atggccgagg ccgacaccga gcgccggccc cacatcccgg tgctgctgcg tcctcttctg 60

```
gccgcggtgg cgccggtcga gggcacatgg ctcgacggca ccttcggggc gggcggttat    120

gcgcggggtc tgctcgaggc gggcgcggac cgggtgatcg gcgtcgaccg cgatccgctc    180

gcgctgaaga tggcctccgg ctgggcgggt gactacggcg accgcctgcg cctcgtggcg    240

ggcaccttct cgcagctcga cagccatgcg ggcgcgcccc tcgacggggt ggtgctcgat    300

ctcggcgtct cctccatgca gctcgatctg gccgaacgcg gcttctcgtt ccagaaggac    360

ggcccgctcg acatgcgcat gagccaagag ggcgaaagcg cggccgatct ggtcaatacc    420

gcctccgagg agacgctggc cgacattctc tatcattatg gcgaggagcg cgcctcgcgc    480

cgcatcgccc gcgccatcgt cgaggcccgc gccgcggcgc ccatcacccg cacgctcgcg    540

ctggccgaga tcgtggcgcg ctgcctgccg cggccgaagc ccggccagat gcacccggcc    600

acccgcagct ttcaggcgat ccgtatcgcg gtgaatgccg aattctcgga actggtcgag    660

gggctcgagg cggccgagcg cgcgctcagg cccggcggcc ggctcgccgt cgtcaccttc    720

cacagcctcg aggaccggat cgtgaaacgg ttcctccagc tccgctcggg cggcgagggg    780

cagggcaacc gctacgcccc cgagacgcgc gccgatgcgc cccgcttcac tcttccgctc    840

cgtcgtgcca tcagcccgga cgaggcggaa ctcgccgaga atccgcgcgc ccggtcggcc    900

cggctgcggg tgggcgtccg gacggacgcc cccgcgggaa aggtcgatcc gcaggcgctc    960

ggcaccccgc tcatcccgaa gaaaggacgc cgctga                              996


<210> SEQ ID NO 144
<211> LENGTH: 331
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 144

Met Ala Glu Ala Asp Thr Glu Arg Arg Pro His Ile Pro Val Leu Leu
1               5                   10                  15

Arg Pro Leu Leu Ala Ala Val Ala Pro Val Glu Gly Thr Trp Leu Asp
            20                  25                  30

Gly Thr Phe Gly Ala Gly Gly Tyr Ala Arg Gly Leu Leu Glu Ala Gly
        35                  40                  45

Ala Asp Arg Val Ile Gly Val Asp Arg Asp Pro Leu Ala Leu Lys Met
    50                  55                  60

Ala Ser Gly Trp Ala Gly Asp Tyr Gly Asp Arg Leu Arg Leu Val Ala
65                  70                  75                  80

Gly Thr Phe Ser Gln Leu Asp Ser His Ala Gly Ala Pro Leu Asp Gly
                85                  90                  95

Val Val Leu Asp Leu Gly Val Ser Ser Met Gln Leu Asp Leu Ala Glu
            100                 105                 110

Arg Gly Phe Ser Phe Gln Lys Asp Gly Pro Leu Asp Met Arg Met Ser
        115                 120                 125

Gln Glu Gly Glu Ser Ala Ala Asp Leu Val Asn Thr Ala Ser Glu Glu
    130                 135                 140

Thr Leu Ala Asp Ile Leu Tyr His Tyr Gly Glu Glu Arg Ala Ser Arg
145                 150                 155                 160

Arg Ile Ala Arg Ala Ile Val Glu Ala Arg Ala Ala Ala Pro Ile Thr
                165                 170                 175

Arg Thr Leu Ala Leu Ala Glu Ile Val Ala Arg Cys Leu Pro Arg Pro
            180                 185                 190

Lys Pro Gly Gln Met His Pro Ala Thr Arg Ser Phe Gln Ala Ile Arg
        195                 200                 205
```

```
Ile Ala Val Asn Ala Glu Phe Ser Glu Leu Val Glu Gly Leu Glu Ala
    210                 215                 220

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

His Ser Leu Glu Asp Arg Ile Val Lys Arg Phe Leu Gln Leu Arg Ser
                245                 250                 255

Gly Gly Glu Gly Gln Gly Asn Arg Tyr Ala Pro Glu Thr Arg Ala Asp
            260                 265                 270

Ala Pro Arg Phe Thr Leu Pro Leu Arg Arg Ala Ile Ser Pro Asp Glu
        275                 280                 285

Ala Glu Leu Ala Glu Asn Pro Arg Ala Arg Ser Ala Arg Leu Arg Val
    290                 295                 300

Gly Val Arg Thr Asp Ala Pro Ala Gly Lys Val Asp Pro Gln Ala Leu
305                 310                 315                 320

Gly Thr Pro Leu Ile Pro Lys Lys Gly Arg Arg
                325                 330


<210> SEQ ID NO 145
<211> LENGTH: 744
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 145

atgaccggac gtctggcagg ccgcaagatc gtcatcaccg gagcaggctc gggcatcggc     60

cgcgagtccg cgcgccagtt cgcgcgcgag gggcgacgc tggcgctgat cgaccgcgac    120

gaggcggcgg cgcaggtgac ggcggacgag acgggggcc atgtcttcgc gctcgacgtg    180

accgacgagg cggcggtcga aaccgtcgtg ggccgcgcgg cggaggcgct cggcggcatc    240

gacgggctgc tcaattcggc gggcatcctg accatgaaga ccgtggacga tatcggcgtc    300

gaggagttcc gccgggtggt ggatgtgaac ctgacgggga ccttcctcgt ctgtcaggcg    360

gcgctgccgt ggctgcgcaa ggagccgaag gccgccatcg tcaacatcgc ctcggcgcag    420

gcgctgctgc cctcgctgac cggctcggcc tatgccgcct cgaaggccgc ggtgatgatg    480

ttctcgaaga gcatcgccaa ggaacttgcc ccggcggtgc gggtgaacat catctgcccg    540

ggggccaccg agacgccgat gaccgatcag ggcgtggcgc ccgacgatgt ggcgggccgc    600

aaggcgctgg ccgcggtcta tgcgatgaac cgtctggccc agcccgagga gatcgcggcg    660

ggcatcctgt tcctgatgtc ggacgaggcc gcggccatca cgggcgtcgc gctggcgatc    720

gacaacggcc gcaccttcca ttga                                           744


<210> SEQ ID NO 146
<211> LENGTH: 247
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 146

Met Thr Gly Arg Leu Ala Gly Arg Lys Ile Val Ile Thr Gly Ala Gly
1               5                   10                  15

Ser Gly Ile Gly Arg Glu Ser Ala Arg Gln Phe Ala Arg Glu Gly Ala
            20                  25                  30

Thr Leu Ala Leu Ile Asp Arg Asp Glu Ala Ala Ala Gln Val Thr Ala
        35                  40                  45

Asp Glu Thr Gly Gly His Val Phe Ala Leu Asp Val Thr Asp Glu Ala
    50                  55                  60
```

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```
Ala Val Glu Thr Val Val Gly Arg Ala Ala Glu Ala Leu Gly Gly Ile
65                  70                  75                  80

Asp Gly Leu Leu Asn Ser Ala Gly Ile Leu Thr Met Lys Thr Val Asp
                85                  90                  95

Asp Ile Gly Val Glu Glu Phe Arg Arg Val Val Asp Val Asn Leu Thr
            100                 105                 110

Gly Thr Phe Leu Val Cys Gln Ala Ala Leu Pro Trp Leu Arg Lys Glu
        115                 120                 125

Pro Lys Ala Ala Ile Val Asn Ile Ala Ser Ala Gln Ala Leu Leu Pro
    130                 135                 140

Ser Leu Thr Gly Ser Ala Tyr Ala Ala Ser Lys Ala Ala Val Met Met
145                 150                 155                 160

Phe Ser Lys Ser Ile Ala Lys Glu Leu Ala Pro Ala Val Arg Val Asn
                165                 170                 175

Ile Ile Cys Pro Gly Ala Thr Glu Thr Pro Met Thr Asp Gln Gly Val
            180                 185                 190

Ala Pro Asp Asp Val Ala Gly Arg Lys Ala Leu Ala Ala Val Tyr Ala
        195                 200                 205

Met Asn Arg Leu Ala Gln Pro Glu Glu Ile Ala Ala Gly Ile Leu Phe
    210                 215                 220

Leu Met Ser Asp Glu Ala Ala Ala Ile Thr Gly Val Ala Leu Ala Ile
225                 230                 235                 240

Asp Asn Gly Arg Thr Phe His
                245


<210> SEQ ID NO 147
<211> LENGTH: 1194
<212> TYPE: DNA
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 147

atgaaccagc agaacacgat ttccgcagct cctgcggaca cgatggccga acgggcccgg     60

gccatcgccc ccctcgtgcg ggccgaggcg caggcctcgg aagagctcgg gacgatgacg    120

cccaaggtgg tgcaggccat caaggaggcg ggcctcttct ggatgctcct cgagcgcaag    180

gtgggcggcg cccaggccga catggccgat tgcatgcgcg cctgggaaga gatcgccgcc    240

gccgacgcct cggccggctg gtcgctgatg gccaactcga caggcaccgc cgttccttac    300

gcctattgca gcgaggaggc ggtggccgag atctacggcg gccccgaact gccgatcatg    360

gccgggatgc tcgggccggg cggctcggcg aaggagaccg agggcgcgct ccacggcagc    420

ggcaaatatc gcttcggcag cggctcgctg catgcgacct ggatcggcgc gggcatgttc    480

gtgatggacg agggcggcat gcgcaagctg cctgacggca gccccgtcgt gcgcgtctgc    540

tggcggccgg cctcggaggt cacgttcgac aatgaatgga acgtgctcgg cctgcgcggc    600

acgggcagcg tcgattacac gctggaggaa gccacgatcc ccgcgggctt ccaccacgag    660

cgcgcggtcc agcgcggcct gcgcgactgg cggctctacg acatcggcat cccgggcctc    720

gcctgtgcgg gccacaccgg ggtggcgctc ggcctgatgc gccgcgcgct ggaagagatc    780

acccgcatcg ccttcggcaa gaagcgcccg gcctatcaga ccgtgctggg cgaccagcag    840

gtcttccgcc acgatttcgc ctatcacgag gcgagctatc acgcggcgcg cgacttcacc    900

ctgcgcttct acgccgagat ccaggagtat ctggaggcgg gcggcgagct cacgcccgcc    960

atgcgcgcgc gcttccggca gaactgcatc tatgtccaca aggtcgcggc cgaggttgtg   1020

cgcttctgct acacgatggg cggctccgag gcgctgcgcg agccgagcga tctcgggcgc   1080
```

```
tgcatgcgcg acatgtatgc cgcgacccag catatcttcg tcgatacgat cgccatgcag   1140

gacatcgcgg tgccgatcct cgccgaatgg agagagcagg ccgccgcgca atga         1194


<210> SEQ ID NO 148
<211> LENGTH: 397
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 148

Met Asn Gln Gln Asn Thr Ile Ser Ala Ala Pro Ala Asp Thr Met Ala
1               5                   10                  15

Glu Arg Ala Arg Ala Ile Ala Pro Leu Val Arg Ala Glu Ala Gln Ala
            20                  25                  30

Ser Glu Glu Leu Gly Thr Met Thr Pro Lys Val Val Gln Ala Ile Lys
        35                  40                  45

Glu Ala Gly Leu Phe Trp Met Leu Leu Glu Arg Lys Val Gly Gly Ala
    50                  55                  60

Gln Ala Asp Met Ala Asp Cys Met Arg Ala Trp Glu Glu Ile Ala Ala
65                  70                  75                  80

Ala Asp Ala Ser Ala Gly Trp Ser Leu Met Ala Asn Ser Thr Gly Thr
                85                  90                  95

Ala Val Pro Tyr Ala Tyr Cys Ser Glu Glu Ala Val Ala Glu Ile Tyr
            100                 105                 110

Gly Gly Pro Glu Leu Pro Ile Met Ala Gly Met Leu Gly Pro Gly Gly
        115                 120                 125

Ser Ala Lys Glu Thr Glu Gly Ala Leu His Gly Ser Gly Lys Tyr Arg
    130                 135                 140

Phe Gly Ser Gly Ser Leu His Ala Thr Trp Ile Gly Ala Gly Met Phe
145                 150                 155                 160

Val Met Asp Glu Gly Gly Met Arg Lys Leu Pro Asp Gly Ser Pro Val
                165                 170                 175

Val Arg Val Cys Trp Arg Pro Ala Ser Glu Val Thr Phe Asp Asn Glu
            180                 185                 190

Trp Asn Val Leu Gly Leu Arg Gly Thr Gly Ser Val Asp Tyr Thr Leu
        195                 200                 205

Glu Glu Ala Thr Ile Pro Ala Gly Phe His His Glu Arg Ala Val Gln
    210                 215                 220

Arg Gly Leu Arg Asp Trp Arg Leu Tyr Asp Ile Gly Ile Pro Gly Leu
225                 230                 235                 240

Ala Cys Ala Gly His Thr Gly Val Ala Leu Gly Leu Met Arg Arg Ala
                245                 250                 255

Leu Glu Glu Ile Thr Arg Ile Ala Phe Gly Lys Lys Arg Pro Ala Tyr
            260                 265                 270

Gln Thr Val Leu Gly Asp Gln Gln Val Phe Arg His Asp Phe Ala Tyr
        275                 280                 285

His Glu Ala Ser Tyr His Ala Ala Arg Asp Phe Thr Leu Arg Phe Tyr
    290                 295                 300

Ala Glu Ile Gln Glu Tyr Leu Glu Ala Gly Gly Glu Leu Thr Pro Ala
305                 310                 315                 320

Met Arg Ala Arg Phe Arg Gln Asn Cys Ile Tyr Val His Lys Val Ala
                325                 330                 335

Ala Glu Val Val Arg Phe Cys Tyr Thr Met Gly Gly Ser Glu Ala Leu
            340                 345                 350
```

```
Arg Glu Pro Ser Asp Leu Gly Arg Cys Met Arg Asp Met Tyr Ala Ala
        355                 360                 365

Thr Gln His Ile Phe Val Asp Thr Ile Ala Met Gln Asp Ile Ala Val
    370                 375                 380

Pro Ile Leu Ala Glu Trp Arg Glu Gln Ala Ala Ala Gln
385                 390                 395


<210> SEQ ID NO 149
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer tpnRL13-2

<400> SEQUENCE: 149

cagcaacacc ttcttcacga                                                20


<210> SEQ ID NO 150
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer tpnRL17-1.

<400> SEQUENCE: 150

aacaagccag ggatgtaacg                                                20


<210> SEQ ID NO 151
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer KCL58.

<400> SEQUENCE: 151

gcattctaga cgaggcctac gattatctgc                                     30


<210> SEQ ID NO 152
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer KCL59.

<400> SEQUENCE: 152

cgataagctt gtcgggtcgt ttaccagaac                                     30


<210> SEQ ID NO 153
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer KCL60.

<400> SEQUENCE: 153

cggaccgttc tgcgaagca                                                 19


<210> SEQ ID NO 154
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer KCL63.

<400> SEQUENCE: 154
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```
ttcaggcgcc gaccgggact                                                  20


<210> SEQ ID NO 155
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer KCL72.

<400> SEQUENCE: 155

tatctcttcg atttcgagca gccc                                             24


<210> SEQ ID NO 156
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer KCL84.

<400> SEQUENCE: 156

atgttgacct cgtcggaatg                                                  20


<210> SEQ ID NO 157
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer KCL85.

<400> SEQUENCE: 157

gcaagaagat caccgacctc                                                  20


<210> SEQ ID NO 158
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer KCL86.

<400> SEQUENCE: 158

tccttgagcc agatgtcgag gat                                              23


<210> SEQ ID NO 159
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer KCL87.

<400> SEQUENCE: 159

aggccttgac caacctgatg aaga                                             24


<210> SEQ ID NO 160
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer KCL88.

<400> SEQUENCE: 160

ttccagctga tgatagagca ccac                                             24


<210> SEQ ID NO 161
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
```

-continued

```
<220> FEATURE:
<223> OTHER INFORMATION: Primer KCL89.

<400> SEQUENCE: 161

tcaccttcgg cgctatttcg atct                                         24


<210> SEQ ID NO 162
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer KCL116.

<400> SEQUENCE: 162

gcctttgtcg ggatggaac                                               19


<210> SEQ ID NO 163
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer ChrR-UP1.

<400> SEQUENCE: 163

gcgccagcat atgagttgag tgag                                         24


<210> SEQ ID NO 164
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer ChrR-DS1.

<400> SEQUENCE: 164

cgtgaatgac aggggtcgcc                                              20
```

What is claimed is:

1. A recombinant microorganism comprising one or more genetic modifications with respect to a corresponding microorganism not comprising the one or more genetic modifications, wherein:

- the one or more genetic modifications comprise at least one of:
  - a genetic modification that reduces the activity of RSP2839 or a homolog thereof with respect to the corresponding microorganism; and
  - a genetic modification that reduces the activity of RSP2840 or a homolog thereof with respect to the corresponding microorganism;
- the recombinant microorganism exhibits enhanced lipid production with respect to the corresponding microorganism; and
- the recombinant microorganism is *Rhodobacter sphaeroides* or a member of the genus *Rhodopseudomonas*.

2. The recombinant microorganism of claim **1**, wherein the recombinant microorganism exhibits enhanced lipid secretion with respect to the corresponding microorganism.

3. The recombinant microorganism of claim **1**, wherein the one or more genetic modifications comprise the genetic modification that reduces the activity of the RSP2839 or homolog thereof and the genetic modification that reduces the activity of the RSP2840 or homolog thereof.

4. The recombinant microorganism of claim **3**, wherein the homolog of RSP2839 is an NtrY and the homolog of RSP2840 is an NtrX.

5. A recombinant microorganism comprising genetic modifications with respect to a corresponding microorganism not comprising the genetic modifications, wherein:

- the genetic modifications comprise:
  - at least one of:
    - a genetic modification that reduces the activity of RSP2839 or a homolog thereof with respect to the corresponding microorganism; and
    - a genetic modification that reduces the activity of RSP2840 or a homolog thereof with respect to the corresponding microorganism; and
  - one or more modifications that reduce the activity of one or more of an acyl-CoA dehydrogenase, an enoyl-CoA hydratase, a 3-hydroxyacyl-CoA dehydrogenase, and a 3-ketoacyl-CoA thiolase and/or increase the activity of one or more of an acyl-CoA synthetase, an acetyl-CoA carboxylase, an acetyl CoA:ACP transacylase, a malonyl CoA:ACP transacylase, a β-ketoacyl-ACP synthase, a β-ketoacyl-ACP reductase, a β-hydroxyacyl-ACP dehydrase, an enoyl-ACP reductase, a glycerol-3-phosphate acyltransferase, and a 1-acylglycerol-3-phosphate acyltransferase with respect to the corresponding microorganism; and
- the recombinant microorganism exhibits enhanced lipid production with respect to the corresponding microorganism.

6. A recombinant microorganism comprising genetic modifications with respect to a corresponding microorganism not comprising the genetic modifications, wherein:

the genetic modifications comprise:

at least one of:

a genetic modification that reduces the activity of RSP2839 or a homolog thereof with respect to the corresponding microorganism; and

a genetic modification that reduces the activity of RSP2840 or a homolog thereof with respect to the corresponding microorganism; and

a genetic modification that reduces the activity of RSP0382 or a homolog thereof with respect to the corresponding microorganism; and

the recombinant microorganism exhibits enhanced lipid production with respect to the corresponding microorganism.

7. The recombinant microorganism of claim **1**, wherein the one or more genetic modifications further comprise one or more recombinant genes configured to express one or more of RSP2144 or a homolog thereof, RSP1091 or a homolog thereof, and RSP1090 or a homolog thereof; a genetic modification that disrupts binding between ChrR and σ^E or homologs thereof; a genetic modification that increases expression of σ^E or a homolog thereof; and/or a genetic modification that eliminates from the microorganism a native ChrR or homolog thereof.

8. The recombinant microorganism of claim **5**, wherein the corresponding microorganism is a non-oleaginous microorganism.

9. The recombinant microorganism of claim **5**, wherein the recombinant microorganism is a bacterium.

10. The recombinant microorganism of claim **5**, wherein the recombinant microorganism is from the genus *Rhodobacter* or the genus *Rhodopseudomonas.*

11. The recombinant microorganism of claim **1**, wherein the recombinant microorganism exhibits at least 2-fold enhanced lipid production with respect to the corresponding microorganism when the recombinant microorganism and the corresponding organism are grown under aerobic conditions.

12. The recombinant microorganism of claim **1**, wherein the recombinant microorganism is capable of producing at least 1 g/L lipid.

13. The recombinant microorganism of claim **1**, wherein the recombinant microorganism is capable of producing lipids in an amount of at least 20% (w/w) dry cell weight.

14. A method for producing a bioproduct comprising:

culturing a recombinant microorganism in a medium for a time sufficient to consume nutrients present in the medium and produce the bioproduct, wherein:

the recombinant microorganism comprises one or more genetic modifications with respect to a corresponding microorganism not comprising the one or more genetic modifications;

the one or more genetic modifications comprise at least one of:

a genetic modification that reduces the activity of RSP2839 or a homolog thereof with respect to the corresponding microorganism; and

a genetic modification that reduces the activity of RSP2840 or a homolog thereof with respect to the corresponding microorganism;

the recombinant microorganism exhibits enhanced lipid production with respect to the corresponding microorganism; and

the bioproduct comprises lipid; and

extracting the lipid from the medium.

15. The method of claim **14**, wherein the one or more genetic modifications comprise at least one of:

a genetic modification that reduces the activity of RSP2839 or a homolog thereof with respect to the corresponding microorganism, wherein the homolog of RSP2839 is an NtrY; and

a genetic modification that reduces the activity of RSP2840 or a homolog thereof with respect to the corresponding microorganism, wherein the homolog of RSP2840 is an NtrX.

16. The recombinant microorganism of claim **5**, wherein the genetic modifications comprise at least one of:

a genetic modification that reduces the activity of RSP2839 or a homolog thereof with respect to the corresponding microorganism, wherein the homolog of RSP2839 is an NtrY; and

a genetic modification that reduces the activity of RSP2840 or a homolog thereof with respect to the corresponding microorganism, wherein the homolog of RSP2840 is an NtrX.

* * * * *