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A Glimpse into the Proteome of Phototrophic Bacterium

Rhodobacter capsulatus

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Abstract

A first glimpse into the proteome of *Rhodobacter capsulatus* revealed more than 450 [with over 210 cytoplasmic and 185 extracytoplasmic known as well as 55 unknown] proteins that are identified with high degree of confidence using nLC-MS/MS analyses. The accumulated data provide a solid platform for ongoing efforts to establish the proteome of this species and the cellular locations of its constituents. They also indicate that, at least 40 of the identified proteins, which were annotated in genome databases as unknown hypothetical proteins, correspond to predicted translation products that are indeed present in cells under the growth conditions used in this work. In addition, matching the identification labels of the proteins reported between the two available *R. capsulatus* genome databases (ERGO-light with *RRCxxxxx* and NT05 with *NT05RCxxxx* numbers) indicated that eleven such proteins are listed only in the latter database.

Introduction

The Gram negative, purple non-sulfur facultative phototrophic bacterium *Rhodobacter capsulatus* is a model organism that is intensely studied for various aspects of major metabolic pathways such as photosynthesis and respiration (Zannoni 1995; Hunter, Daldal et al. 2009). Using this species, which exhibits highly versatile growth modes including anoxygenic light (*i. e.*, photosynthesis), anoxygenic dark (*i. e.* anaerobic respiration) and oxygenic (*i. e.*, light independent aerobic respiration) metabolisms, physiologically relevant cellular responses to the availability of light or oxygen can be examined at the molecular level (Hunter, Daldal et al. 2009). Indeed, a complete definition of the presence, regulation and biogenesis of various cellular components in response to the changing environmental conditions greatly benefits from global analyses approaches, including transcriptomic and proteomic studies (Park et al. 2005; Wasinger 2006). Thus, along with the transcriptional studies, availability of qualitative and quantitative description of *R. capsulatus* proteomes under defined growth conditions is extremely invaluable. Towards this end, we have initiated an effort to define the complete proteome of this species (Onder et al. 2008), and we present here a first glimpse to this developing protein identification dataset.

Materials and Methods

Wild type *R. capsulatus* strain MT1131 was grown under respiratory growth condition in enriched MPYE (mineral-peptone-yeast extracts) medium (Daldal, Chen et al. 1986), under standard culture conditions (1 L medium in 2 L flask, shaken at approximately 150 rpm at 35°C in dark for approximately 36 hrs) (Myllykallio, Jenney et al. 1997). Cells were harvested by centrifugation at 4°C (5000 × g, 20 min), washed with ice cold 20 mM Tris-HCl, pH 8.0, and gently resuspended in cold extraction buffer consisting of 1 mg/ml of

polymyxin B sulfate, 20 mM Tris-HCl, 250 mM NaCl, [pH 8.0] (5 ml/g of wet cells) (Ren and Thony-Meyer 2001; Onder, Turkarslan et al. 2008). The suspension was gently stirred for 1 hour at 4 °C and centrifuged at 10,000 × g for 20 min at 4 °C. The supernatant was carefully transferred into a clean tube, re-centrifuged at 150,000 × g for 2 hours at 4 °C and saved as the periplasmic fractions at −20 °C. Polymyxin treated cells pellets were then resuspended in 50 mM MOPS, 100 mM KCl (pH 8.0) buffer and processed using a French pressure cell, as described earlier (Onder, Turkarslan et al. 2008). After centrifugation for 2 hrs at 45,000 rpm, supernatants (*i. e.*, cytoplasmic fractions) and pellets (*i. e.*, membrane fractions) were processed separately for analyses of their protein contents.

Soluble or periplasmic proteins were precipitated with trichloroacetic (TCA)/acetone (20% w/v), washed twice with ice-cold acetone to remove residual TCA, and dried under vacuum. Pellets were resuspended in two dimensional-gel electrophoresis (2D-GE) sample solubilization buffer (SSB: 8 M urea, 4% CHAPS, 40 mM Tris, 0.2% Bio-Lyte-pH 3–10, 65 mM DTT) at room temperature until complete solubilization. For 2D-GE, samples containing 300 µg of solubilized proteins were applied to an 18 cm, pH 4–7 immobilized pH gradient (IPG) strips (Bio-Rad), and following a 12 hours passive rehydration, isoelectrofocusing (IEF) was carried out by using PROTEAN IEF Cell (Bio-Rad) at 20 °C at a maximum of 7000 V for 15–18 hours, and the strips thus prepared were kept frozen at −20 °C until use. For the second dimension sodium dodecylsulfate-polyacrylamide gel electrophoresis (SDS-PAGE), IPG strips were reduced with 1% w/v dithiothreitol (DTT) and alkylated with 2.5% w/v iodoacetamide at room temperature, both prepared in equilibration buffer consisting of 50 mM Tris-HCl, pH 8.8, 6 M urea, 30% v/v glycerol, 2% SDS and 0.02% bromophenol blue. After equilibration, the IPG strips were layered on top of the second dimension resolving gel slabs and overlaid with a solution of molten 0.5% agarose in SDS electrophoresis buffer. The second dimension Laemmli-type SDS-PAGE was carried out using 11% gels without any stacking at 40 mA per gel in a Protean II XL cell (Bio-Rad), and gels were stained with colloidal coomassie brilliant blue (Neuhoff, Stamm et al. 1990). Spots or bands were manually excised from gels and subjected to in-gel trypsin digestions (Onder, Yoon et al. 2006). Tryptic peptide extracts were analyzed using a nanoLC-MS/MS set up (LCQ Deca XP Plus mass spectrometer from Thermo Scientific, coupled to an Ultimate Nano liquid chromatography system from DIONEX). Tryptic peptide mixtures were first loaded onto a µ-precolumn (C18, 5 µm, 100 Å, 300 µm i.d. × 5 mm) (DIONEX), and washed for 4 min at a flow rate of 0.25 µl/min with the LC buffer A, then transferred onto an analytical C18-nanocapillary HPLC column (DIONEX, Acclaim PepMap100, C18 column (75 µm i.d. by 150 mm) with a 3 µm particle size and a 100 Å pore diameter for fractionation. A fused silica tip with 8-µm aperture (New Objective, Woburn, MA) was used for nanospray ionization of peptides eluting from the column. Mass spectra were analyzed using the DTA generation and SEQUEST search algorithms within Bioworks 3.3 software (Thermo Scientific) and *R. capsulatus* protein databases (ERGO Light from <http://www.ergo-light.com> or in-house available NT05 data bases). The following parameters were used for SEQUEST analyses: as appropriate trypsin or GluC were selected as the proteolytic enzymes, with trypsin cleavage only after arginine and lysine was allowed, and the number of maximal internal (missed) cleavage sites was set to 2–4. Mass tolerance for precursor and fragment ions was 2.0–2.5 and 1.0, respectively. Methionine oxidation and cysteine carbamidomethylation were set as variable modification with maximum modification set to 2, and default setting was used for all other variables. Matching peptides were filtered according to correlation scores (X_{Corr} at least 1.5, 2.0 and 2.5 for +1, +2 and +3 charged peptides, respectively, and $\Delta C_N > 0.1$) to give high confidence of protein identification, and proteins were considered as significant only when at least two peptides were identified with the SEQUEST filter settings mentioned above. The *R. capsulatus* proteins thus identified were examined with bioinformatic tools. Prediction softwares SignalP (version 3.0) (Bendtsen, Nielsen et al. 2004)

(<http://www.cbs.dtu.dk/services/SignalP/>) and PSORTb (version 2.0) (Gardy, Laird et al. 2005) (<http://www.psorth.org/psorth/>) were used to predict the likely sub-cellular localization of identified proteins.

Results and Discussion

A long-term objective of this study is the establishment of a comprehensive proteomic reference database for *R. capsulatus* under different growth conditions. This physiological proteomics will then establish an important step to enable detailed analyses of major metabolic pathways of this organism extending from photosynthesis to respiration. To this end, we use modern proteomic approaches involving 1D- and 2D-GE combined with liquid chromatography and tandem mass spectrometry techniques. In addition, as comprehensive proteome analyses are often limited by physiological constraints and technical issues, to maximize the number of proteins identified, to reduce the sample complexity and also to detect low abundance proteins, we prepare overlapping subproteomes of periplasmic, cytoplasmic and membrane fractions of *R. capsulatus* cells grown under different conditions, and analyze these samples as described in Materials and Methods. These analyses identified so far more than over 450 *R. capsulatus* proteins that are grouped into different cellular function categories listed in Table 1. Tentative sub-cellular localizations of these proteins are also indicated using the PSORTb v 2.0 prediction software trained on bacterial protein sub-cellular localization prediction (Gardy, Laird et al. 2005). Of these proteins, 218 are predicted to be cytoplasmic and 187 are assigned to be exported proteins. Among the latter extracytoplasmic proteins, 52 and 94 of them are considered to be periplasmic and integral membrane proteins, respectively. Clearly, the predictive analysis is highly successful as for only 53 out of the 450 identified proteins a cellular localization could not be attributed reliably using PSORTb program. Moreover, global distributions of the identified proteins into different cellular function categories are also analyzed, and the results are presented as a pie chart. Even though the available data set is not yet exhaustive, it appears that “Energy Metabolism” and “Transport and Binding Proteins” categories are among the most populated groups of proteins with 82 and 79 members, respectively. Remarkably, while a large fraction of the identified proteins correspond to proteins of known functions, yet 49 of them have undefined roles, and among the latter group 41 of them were initially annotated as hypothetical proteins in either or both (ERGO-light with *RRCxxxxx* and NT05 with *NT05RCxxxx* numbers) of *R. capsulatus* genome databases (Table 1). Our data establish that these translation products are indeed real, and searches for defining their functions can now be initiated on firm grounds. We believe that data set that is under construction is of great value for rapid progress of current and future studies focused on *Rhodobacter* species (Du et al. 2008). This ever-growing data set is providing a platform onto which we can build future qualitative and quantitative comparisons for various cellular components under defined physiological conditions. A current example to the point is illustrated by one of our recent studies where a portion of our accumulated proteomics data of *R. capsulatus*, once combined with standard in-depth biochemical and molecular genetic approaches, yielded exquisite understanding in detailed molecular terms of an unusual physiological situation simply detected by a growth phenotype (Onder, Turkarslan et al. 2008). We believe that establishment of a comprehensive proteomic data for *R. capsulatus* species, like in many other cases, will be invaluable to provide much needed impetus for understanding the global biology of this organism with a “systems” level organization.

Acknowledgments

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Figure 1.

Representative 1D- and 2D-gel analyses of *R. capsulatus* protein samples. **A.** Periplasmic fraction proteins of *R. capsulatus* were separated by 2D-GE, with pH 4–7 IPG and SDS–PAGE, as first and second dimensions. **B.** Chromatophore membranes of *R. capsulatus* were separated on 1D-GE using SDS PAGE. In both cases, protein samples were prepared as described in Materials and Methods, gels were stained with colloidal coomassie blue and protein spots or bands were excised and trypsin digested for identification by nano-LC-MS/MS.

Table 1

Complete list of *R. capsulatus* proteins identified by nLC-MS/MS analyses. Identified proteins are categorized according to their predominant function as reported in the current literature (ref). Protein names, enzyme commission (EC) numbers, gene acronyms, ERGO-light (*RRCxxxx*) and NT05 (*NT05RRCxxxx*) identification numbers are indicated. Sub-cellular localization of each protein was predicted by PSORTb and SignalP analyses, and C, EC, P, IM, OM and M were used to designate cytoplasmic, extracytoplasmic, periplasmic, inner membrane and membrane proteins, respectively.

Protein Name	EC Number	Gene Name	ERGO*	NT05*	Location
AMINO ACID BIOSYNTHESIS					
<i>Aromatic amino acid family</i>					
Ornithine cyclodeaminase, Ocd	4.3.1.12	<i>arcB</i>	RRC00632	NT05RRC2206	C
Tryptophan synthase beta subunit, TrpB	4.2.1.20	<i>trpB</i>	RRC01000	NT05RRC2658	C
Tryptophan synthase alpha subunit, TrpA	4.2.1.20	<i>trpA</i>	RRC00192	NT05RRC3179	C
Aromatic-aminoacid aminotransferase, AroA (aroA)	2.6.1.57	<i>tyrB</i>	RRC01763	NT05RRC3527	C
<i>Aspartate family</i>					
Dihydrodipicolinate synthase	4.2.1.52	<i>dapA</i>	RRC02939	NT05RRC0396	C
Aspartokinase (Aspartate kinase)	2.7.2.4	<i>lysC</i>	RRC02984	NT05RRC0439	C
5,10-Methylenetetrahydrofolate reductase	1.5.1.20	<i>metF</i>	RRC03981	NT05RRC0510	C
5-Methylenetetrahydrofolate homocysteine methyltransferase/Methionine synthase I	2.1.1.13	<i>metH</i>	RRC01233	NT05RRC2273	C
Threonine synthase, ThrC	4.2.99.2	<i>thrC</i>	RRC00242	NT05RRC3231	C
<i>Glutamate family</i>					
Glutamate synthase NADPH large chain, NADPH-Gogat	1.4.1.13	<i>glrA</i>	RRC04596	NT05RRC0170	C
Glutamate synthase NADPH small chain, NADPH-Gogat	1.4.1.13	<i>glrD</i>	RRC03219	NT05RRC0172	C
Argininosuccinate synthase	6.3.4.5	<i>argG</i>	RRC03172	NT05RRC0219	C
Glutamate N-acetyl transferase/Arginine biosynthesis bifunctional protein, ArgJ	2.3.1.35/2.3.1.1	<i>argJ</i>	RRC04654	NT05RRC0229	C
N-acetyl-gamma-glutamyl-phosphate reductase, ArgC	1.2.1.38	<i>argC</i>	RRC03917	NT05RRC0575	C
Pyrroline-5-carboxylate reductase	1.5.1.2	<i>proC</i>	RRC04153	NT05RRC1196	C
Glutamine synthetase, GlnA	6.3.1.2	<i>glnA</i>	RRC03526	NT05RRC1748	C
Acetyltransferase/gnat family	2.3.1.-		RRC01355	NT05RRC2400	
<i>Histidine family</i>					
Imidazole glycerol phosphate synthase, cyclase subunit, HisF	4.1.3.-	<i>hisF</i>	RRC04158	NT05RRC1201	C

Protein Name	EC Number	Gene Name	ERGO*	NT05*	Location
Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase	5.3.1.16	<i>hisA</i>	RRC04159	NT05RC1202	C
Imidazole glycerol phosphate synthase, glutamine amidotransferase subunit, HisH	2.4.2.-	<i>hisH</i>	RRC04493	NT05RC1232	C
Histidinol dehydrogenase, HisD	1.1.1.23	<i>hisD</i>	RRC01022	NT05RC2681	C
<i>Pyruvate family</i>					
3-Isopropylmalate dehydrogenase	1.1.1.85	<i>leuB</i>	RRC03293	NT05RC0087	C
Ketol-acid reductoisomerase/2-Dehydropanoate 2-reductase	1.1.1.86	<i>ilvC</i>	RRC02733	NT05RC1266	C
<i>Serine family</i>					
Cysteine synthase A, CysK	2.5.1.47	<i>cysK</i>	RRC00998	NT05RC2657	
O-acetylhomoserine thiol-lyase (O-acetylhomoserinesulphydrylase)/Homocysteine synthase	2.5.1.49/4.2.99.8	<i>metY</i>	RRC00762	NT05RC2915	C
Cysteine synthase (O-acetylserine sulphydrylase)/O-acetylserine thiol-lyase, CSase	2.5.1.47/4.2.99.8		RRC00087	NT05RC3089	
Phosphoserine aminotransferase	2.6.1.52	<i>serC</i>	RRC05753	NT05RC3593	CM
BIOSYNTHESIS OF COFACTORS, PROSTHETIC GROUPS, AND CARRIERS					
<i>Chlorophyll and bacteriochlorophyll</i>					
Light-independent protochlorophyllide reductase, iron-sulfur ATP-binding protein	1.18.-.-	<i>bchlL</i>	RRC02850	NT05RC0691	C
Bacteriochlorophyll synthase 33 kDa chain/Geranylgeranyl/bacteriochlorophyllide synthase	2.5.1.-	<i>bchG</i>	RRC02841	NT05RC0700	CM
Bacteriochlorophyll-geranylgeranyl reductase	1.3.1.-	<i>bchlP</i>	RRC02839	NT05RC0702	CM
Magnesium chelatase ATPase subunit I	6.6.1.1	<i>bchlI</i>	RRC02835	NT05RC0706	C
2-Desacetyl-2-hydroxyethyl bacteriochlorophyllide A dehydrogenase, BchC	1.-.-.-	<i>bchC</i>	RRC02826	NT05RC0715	CM
Chlorophyllide reductase 35 kDa protein, BchA(XYZ)	1.18.-.-	<i>bchA</i>	RRC02825	NT05RC0716	C
<i>Folic acid</i>					
MoxR-like ATPase/AAA_3 ATPase			RRC04552	NT05RC0619	C
5-methyltetrahydrofolate corrinoid iron sulfur protein methyltransferase/Dihydropteroate synthase, Dhps	1.2.99.2	<i>acsE</i>	RRC03586	NT05RC1686	C
Para-aminobenzoate synthetase component I, PabB	4.1.3.-/6.3.5.8	<i>pabB</i>	RRC01115	NT05RC2770	C
Methylenetetrahydrofolate dehydrogenase (NADP+)/Methylenetetrahydrofolate cyclohydrolase/Bifunctional protein, FdhD	1.5.1.5/3.5.4.9	<i>fdhD</i>	RRC00338	NT05RC3327	C
<i>Glutathione and analogs</i>					
Glutathione synthetase	6.3.2.3	<i>gshB</i>	RRC04009	NT05RC0483	C
<i>Heme, porphyrin, and cobalamin</i>					
Ferrochelatase	4.99.1.1	<i>hemH</i>	RRC04666	NT05RC0206	C

Protein Name	EC Number	Gene Name	ERGO*	NT05*	Location
Cobaltochelatase subunit, CobS	6.6.1.2	<i>cobS</i>	RRC01954	NT05RC0874	C
Uroporphyrinogen decarboxylase	4.1.1.37	<i>hemE</i>	RRC04134	NT05RC1222	CM
Porphobilinogen deaminase	2.5.1.61	<i>hemC</i>	RRC04136	NT05RC1223	C
5-aminolevulinic acid synthase	2.3.1.37	<i>hemA</i>	RRC04400	NT05RC1506	CM
Delta-aminolevulinic acid dehydratase	4.2.1.24	<i>hemB</i>	RRC06033	NT05RC1890	
Precorrin-8X methylmutase/Precorrin isomerase, HBAsynthase	5.4.1.2	<i>cobH</i>	RRC00650	NT05RC2138	C
Cobalamin biosynthesis protein, CobD		<i>cobD</i>	RRC00706	NT05RC2147	CM
Nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase, CobT	2.4.2.21	<i>cobT</i>	RRC00590	NT05RC2151	C
<i>Menaquinone and ubiquinone</i>					
3-Demethylubiquinone 3-methyltransferase	2.1.1.64	<i>ubiG</i>	RRC03170	NT05RC0221	C
Ubiquinone biosynthesis protein AARF/2-Polyprenylphenol 6-hydroxylase		<i>ubiB</i>	RRC03386	NT05RC3680	CM
<i>Pantothenate and coenzyme A</i>					
Pantoate-beta-alanine Ligase	6.3.2.1	<i>panC</i>	RRC02990	NT05RC0445	C
<i>Pyridine nucleotides</i>					
UDP-sugar diphosphatase/5'-Nucleotidase	3.6.1.45/3.1.3.5	<i>ushA</i>	RRC01089	NT05RC2743	P
<i>Riboflavin, FMN, and FAD</i>					
Riboflavin biosynthesis protein, RibF	2.7.1.26/2.7.7.2	<i>ribF</i>	RRC00565	NT05RC2178	C
Riboflavin biosynthesis protein, RibAB/GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase	3.5.4.25/4.1.2.-	<i>ribAB</i>	RRC00220	NT05RC3210	C
<i>Thiamine</i>					
Thiamin-phosphate pyrophosphorylase	2.5.1.3	<i>thiE</i>	RRC06023	NT05RC1674	C
<i>Other</i>					
Iron-sulfur cluster assembly ATP-dependent transporter, SufC		<i>sufC</i>	RRC01541	NT05RC1963	C, CM
CELL ENVELOPE					
<i>Biosynthesis and degradation of murein sacculus and peptidoglycan</i>					
Glucose-1-phosphate thymidyltransferase	2.7.7.24	<i>rfbA</i>	RRC03209	NT05RC0184	C
dTDP-4-dehydrohamnose reductase	1.1.1.133	<i>rfbD</i>	RRC03208	NT05RC0185	EC
dTDP-glucose-4,6-dehydratase	4.2.1.46	<i>rfbB</i>	RRC03206	NT05RC0187	EC

Protein Name	EC Number	Gene Name	ERGO*	NT05*	Location
dTDP-4-dehydrothamnose 3,5-epimerase (reductase)	5.1.3.13	<i>rfbC</i>	RRC03205	NT05RC0188	EC
Glucans biosynthesis protein, MdoG		<i>mdoG</i>	RRC04027	NT05RC0391	P
Soluble lytic murein transglycosylase	3.2.1.-	<i>slt</i>	RRC02941	NT05RC0397	P
Cell elongation specific D,D-transpeptidase/Peptidoglycan glycosyltransferase	2.4.1.129	<i>ftsI</i>	RRC04232	NT05RC0836	C, CM
UDP-N-acetylglucosamine-N-acetylmuramyl-pentapeptide-pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	2.4.1.227	<i>murG</i>	RRC04656	NT05RC0856	CM
Peptidoglycan-binding domain 1 protein			RRC02722	NT05RC1256	EC
D-alanyl-D-alanine serine-type carboxypeptidase	3.4.16.4		RRC02699	NT05RC1306	CM
UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase, GlnU	2.7.7.23/2.3.1.157	<i>glnU</i>	RRC04347	NT05RC1565	C
Alanine racemase, Alr	5.1.1.1	<i>alr</i>	RRC03627	NT05RC1640	C
Succinoglycan biosynthesis transport protein, ExoP	2.7.1.112	<i>exoP</i>	RRC01472	NT05RC2037	CM
D-alanyl-D-alanine carboxypeptidase (D-alanyl-D-alanine-endopeptidase)/Penicillin-binding protein 4, PBP-4		<i>dacB</i>	RRC01098	NT05RC2752	C
Peptidoglycan-associated lipoprotein/OmpA-MotB family protein			RRC04613	NT05RC3334	OM
Membrane-bound lytic murein transglycosylase B	3.2.1.-	<i>mltB</i>	RRC05698	NT05RC3538	CM, P
Other					
Competence lipoprotein/Tetratricopeptide TPR_2 repeat protein		<i>comL</i>	RRC01947	NT05RC0865	M
CELLULAR PROCESSES					
Adaptations to atypical conditions					
Transcriptional regulator/Methionine-R-sulfoxide reductase	1.8.4.-	<i>mstB</i>	RRC00410	NT05RC3399	EC
Cell division					
Cell division ATP-binding protein, FtsE	3.6.3.-	<i>ftsE</i>	RRC00317	NT05RC3307	CM
Chemotaxis and motility					
Flagellar hook protein, FlgE		<i>flgE</i>	RRC00713	NT05RC0007	OM
Flagellar hook-associated protein 1, FlgK		<i>flgK</i>	RRC00714	NT05RC0008	OM
Flagellar hook-associated protein 3, FlgL		<i>flgL</i>	RRC00715	NT05RC0009	OM
Flagellar biosynthetic protein, FlhA		<i>flhA</i>	RRC03323	NT05RC0057	CM
Methyl-accepting chemotaxis sensory transducer			RRC04109	NT05RC1237	CM
Methyl-accepting chemotaxis protein, McpA		<i>mcpA</i>	RRC01082	NT05RC2737	CM
Flagellin protein		<i>fliC</i>	RRC03417	NT05RC3674	P

Protein Name	EC Number	Gene Name	ERGO*	NT05*	Location
<i>Detoxification</i>					
Dihæm cytochrome c551 peroxidase	1.11.1.5	<i>ccpA</i>	RRC00728	NT05RC0020	P
Glutathione peroxidase	1.11.1.9	<i>gpx</i>	RRC02811	NT05RC0730	P
Phosphinothricin N-acetyltransferase/gnat family	2.3.1.-	<i>pat</i>	RRC04226	NT05RC0842	
NAD-dependent aldehyde dehydrogenase	1.1.1.1	<i>adh</i>	RRC04460	NT05RC1433	C
Catalase/peroxidase, HPI	1.11.1.6/1.11.1.7	<i>katG</i>	RRC03460	NT05RC1815	
Beta-lactamase/hypothetical protein	3.5.2.6		RRC00641	NT05RC2200	CM
Beta-lactamase family protein/putative beta-lactamase	3.5.2.6	<i>bla</i>	RRC00550	NT05RC2365	P
Superoxide dismutase (Fe)	1.15.1.1	<i>sodB</i>	RRC01365	NT05RC2413	
Toluene tolerance protein, Ttg2D		<i>ttg2D</i>	RRC01770	NT05RC3534	
Peroxiredoxin, AhpC/Glutaredoxin domain protein	1.11.1.15	<i>ahpC</i>	RRC05718	NT05RC3559	
<i>Pathogenesis</i>					
Virulence-associated protein E			RRC00816	NT05RC2862	
Iron-regulated protein frpC/Rhizobiocin, RzcA		<i>frpC/rzcA</i>	RRC00341	NT05RC3330	EC
<i>Toxin production and resistance</i>					
Bicyclomycin resistance protein/Drug resistance transporter, Bcr			RRC02414	NT05RC1893	M
Iron-regulated protein, FrpC/Bifunctional hemolysin-adenylate cyclase (cyclolysin), AC-HLY		<i>frpC</i>	RRC01135	NT05RC2792	EC
CENTRAL INTERMEDIARY METABOLISM					
<i>Amino sugars</i>					
N-acetylglucosamine-6-phosphate deacetylase	3.5.1.25	<i>nagA</i>	RRC05751	NT05RC3592	
<i>Nitrogen fixation</i>					
Nitrogenase Iron Protein	1.18.6.1	<i>nifH</i>	RRC03785	NT05RC0610	C
Iron-sulfur cluster assembly NifU domain protein	1.18.6.1	<i>nifU</i>	RRC00380	NT05RC3369	C
Nitrogenase cofactor biosynthesis protein, NifB	1.18.6.1	<i>nifB</i>	RRC03905	NT05RC3406	C
Nitrogenase MoFe cofactor biosynthesis protein, NifE	1.18.6.1	<i>nifE</i>	RRC00431	NT05RC3420	C
<i>Nitrogen metabolism</i>					
Nitrogen regulatory protein P-II		<i>glnB</i>	RRC03527	NT05RC1747	C
<i>Polyamine biosynthesis</i>					

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Agmatinase	3.5.3.11	<i>speB</i>	RRC03474	NT05RC1799	C
Arginase, RocF	3.5.3.1	<i>rocF</i>	RRC00631	NT05RC2207	C
One-carbon metabolism					
Trimethylamine methyltransferase family protein, MtdB		<i>mttB</i>	RRC02448	NT05RC1856	CM
2-Hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase or acyltransferase	3.7.1.-	<i>bphD</i>	RRC01136	NT05RC2793	C
Phosphorus compounds					
Bacterial phosphonate metabolism protein, PhnI		<i>phnI</i>	RRC04121	NT05RC1247	C
Sulfur metabolism					
Nitrilotriacetate monooxygenase component B	1.14.13.-	<i>ntaB</i>	RRC00711	NT05RC0005	C
3'(2'),5'-bisphosphate nucleotidase	3.1.3.7	<i>cysQ</i>	RRC05208	NT05RC0131	C, CM
Other					
Succinate-semialdehyde dehydrogenase [NADP ⁺], Ssdh	1.2.1.16	<i>gabD</i>	RRC02976	NT05RC0431	C
Methylmalonyl-CoA mutase alpha subunit	5.4.99.2	<i>mutB</i>	RRC02025	NT05RC0954	
S-adenosylmethionine synthetase	2.5.1.6	<i>metK</i>	RRC01795	NT05RC1167	C
Gamma-aminobutyrate aminotransferase/Aminotransferase class-III	2.6.1.19/2.6.1.18		RRC01241	NT05RC2282	C
Exopolyphosphatase/Pyrophosphate phosphohydrolase family II	3.6.1.11	<i>ppx</i>	RRC00932	NT05RC2590	C
Acetate-CoA ligase, AcsA	6.2.1.1	<i>acsA</i>	RRC01093	NT05RC2746	CM
DNA METABOLISM					
DNA replication, recombination, and repair					
DNA Polymerase III beta chain	2.7.7.7	<i>dnaN</i>	RRC00708	NT05RC0002	C
ATP-dependent DNA helicase II, PcrA	3.6.1.-	<i>pcrA</i>	RRC04357	NT05RC1555	
Replicative DNA helicase	3.6.1.-	<i>dnaB</i>	RRC03626	NT05RC1641	C
NAD-dependent DNA ligase, LigA	6.5.1.2	<i>ligA</i>	RRC03535	NT05RC1737	C
Single-stranded DNA-binding protein, Ssb/Helix-destabilizing protein		<i>ssb</i>	RRC02420	NT05RC1887	C
DNA polymerase I, Pol I	2.7.7.7	<i>polI</i>	RRC00937	NT05RC2594	C
DNA primase	2.7.7.-	<i>dnaG</i>	RRC00201	NT05RC3187	C
Primosomal protein N'		<i>priA</i>	RRC00361	NT05RC3351	C
Exodeoxyribonuclease III	3.1.11.2	<i>exoDNase_III</i>	RRC00493	NT05RC3477	

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DNA mismatch repair protein, MutS		<i>mutS</i>	RRC05797	NT05RC3643	CM
ENERGY METABOLISM					
Amino acids and amines					
Adenosylhomocysteinase	3.3.1.1	<i>ahcY</i>	RRC03330	NT05RC0050	C
Serine hydroxymethyl transferase	2.1.2.1	<i>glyA</i>	RRC03001	NT05RC0457	C
Alanine dehydrogenase	1.4.1.1	<i>ald</i>	RRC03987	NT05RC0504	C
Tyrosine phenol-lyase/Beta-tyrosinase	4.1.99.2	<i>tlp</i>	RRC03952	NT05RC0536	CM
Sarcosine oxidase beta subunit/FAD dependent oxidoreductase	1.5.3.1	<i>soxB</i>	RRC03939	NT05RC0550	CM
Aminomethyltransferase/Glycine cleavage system T protein	2.1.2.10	<i>gcvT</i>	RRC03644	NT05RC1190	C
Methylmalonate-semialdehyde dehydrogenase (acylating)	1.2.1.27	<i>mmxA</i>	RRC03635	NT05RC1631	C
Propanediol utilization protein, PduB		<i>pduB</i>	RRC01267	NT05RC2309	
Tyrosine phenol-lyase/Beta-tyrosinase	4.1.99.2	<i>tpl</i>	RRC01364	NT05RC2411	C
Sarcosine oxidase gamma subunit	1.5.3.1	<i>soxG</i>	RRC01367	NT05RC2415	
Sarcosine oxidase alpha subunit	1.5.3.1	<i>soxA</i>	RRC01368	NT05RC2416	C
Sarcosine oxidase beta subunit	1.5.3.1	<i>soxB</i>	RRC01370	NT05RC2418	C
Aminotransferase, DegT/DmrJ/EryC1/StrS family			RRC00767	NT05RC2910	
LMW-protein-tyrosine-phosphatase, PTPase/Small, acidic phosphotyrosine protein phosphatase (PY protein phosphatase)	3.1.3.48	<i>ptpA</i>	RRC00274	NT05RC3261	
D-alanine aminotransferase (D-aspartate aminotransferase)/D-amino acid aminotransferase/D-amino acidtransaminase, DaaT	2.6.1.21	<i>daat</i>	RRC01700	NT05RC3299	C
Ornithine cyclodeaminase	4.3.1.12	<i>arcB</i>	RRC05768	NT05RC3610	C
Anaerobic					
Trimethylamine-N-oxide reductase 1, TMAO reductase 1	1.7.2.3		RRC05612	NT05RC2976	P
ATP-proton motive force interconversion					
ATP synthase subunit I b chain	3.6.3.14	<i>ATP_synth_b</i>	RRC04287	NT05RC0776	EC
ATP synthase F1 beta subunit, AtpD	3.6.1.34	<i>atpD</i>	RRC00103	NT05RC3105	C
ATP synthase F1 alpha subunit, AtpA	3.6.1.34	<i>atpA</i>	RRC00106	NT05RC3107	C
ATP synthase F1 delta subunit, AtpH	3.6.1.34	<i>atpH</i>	RRC00107	NT05RC3108	C
Biosynthesis and degradation of polysaccharides					
Anhydromuramoyl-peptide exo-beta-N-acetylglucosaminidase	3.2.1.-	<i>nagZ</i>	RRC01974	NT05RC0895	C

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Periplasmic beta-glucosidase (Gentiobiase) (Cellobiase)/Beta-D-glucoside glucosylhydrolase	3.2.1.21	<i>bgIX</i>	RRC01186	NT05RC2528	P
Electron transport					
Glutaryl-CoA dehydrogenase, Gcd	1.3.99.7	<i>gcd</i>	RRC04664	NT05RC0023	C
Electron transfer flavoprotein alpha or large subunit (alpha-Etf or EtfI)		<i>alpha-etf</i>	RRC03239	NT05RC0149	
Electron transfer flavoprotein beta or small subunit (beta-Etf or EtfS)		<i>beta-etf</i>	RRC03238	NT05RC0150	
Oxidoreductase, FAD-binding/Homologous to D-amino acid dehydrogenase/Glycine oxidase family			RRC02945	NT05RC0400	
Electron transfer flavoprotein-ubiquinone oxidoreductase. EFT-Qo (Electron-transferring-flavoprotein dehydrogenase)	1.5.5.1	<i>EFT-Qo</i>	RRC03955	NT05RC0533	
Sulfide-quinone reductase, Sqr	1.8.5.-	<i>sqr</i>	RRC04245	NT05RC0820	CM, P
Cytochrome c oxidase, cbb3-type, subunit I	1.9.3.1	<i>ccoN</i>	RRC04162	NT05RC1206	CM
Cytochrome c oxidase, cbb3-type, subunit II monoheme subunit	1.9.3.1	<i>ccoO</i>	RRC04163	NT05RC1207	CM
Cytochrome c oxidase, cbb3-type, subunit III, diheme subunit	1.9.3.1	<i>ccoP</i>	RRC04165	NT05RC1209	CM
Cytochrome c2		<i>cycA</i>	RRC02712	NT05RC1293	P
NADH-quinone oxidoreductase chain D	1.6.5.3	<i>nuoD</i>	RRC02454	NT05RC1585	C
NADH-quinone oxidoreductase chain E	1.6.5.3	<i>nuoE</i>	RRC02455	NT05RC1586	CM
Acyl-CoA dehydrogenase family member 8, Acad-8/Isobutyryl-coa dehydrogenase/activator-recruited cofactor 42 kDa component, Arc-42	1.3.99.2		RRC02499	NT05RC1630	C
Ferredoxin-NADP reductase	1.18.1.2	<i>fpr</i>	RRC03609	NT05RC1659	C
N-ethylmaleimide reductase/Xenobiotic reductase, XenB	1.7.1.-	<i>xenB</i>	RRC03600	NT05RC1668	
Cytochrome c551 peroxidase/cytochrome c peroxidase, Ccp	1.11.1.5	<i>ccpA</i>	RRC03475	NT05RC1798	P
Thiol-disulfide Isomerase/Thioredoxin, redoxin domain protein			RRC02397	NT05RC1909	
Cytochrome P450 like protein			RRC01166	NT05RC2544	C
Cytochrome c-type cyt cy		<i>cycY</i>	RRC00961	NT05RC2616	CM, P
Ubiquinol-cytochrome c reductase iron-sulfur subunit, PetA	1.10.2.2	<i>petA</i>	RRC00780	NT05RC2896	CM
Ubiquinol-cytochrome c reductase cytochrome b subunit, PetB	1.10.2.2	<i>petB</i>	RRC00781	NT05RC2897	CM
Ubiquinol-cytochrome c reductase Cytochrome c1 subunit, PetC	1.10.2.2	<i>petC</i>	RRC00779	NT05RC2898	CM
Ferredoxin I, FdI		<i>fdI</i>	RRC00758	NT05RC2920	C
Cytochrome c-type biogenesis protein CcmH (Ccl2)		<i>ccl2/ccmH</i>	RRC00287	NT05RC3273	CM, P
Cytochrome P450 family protein	1.14.15.3		RRC00405	NT05RC3394	C
Sulfide dehydrogenase (flavocytochrome c)/FAD-dependent pyridine nucleotide-disulphide oxidoreductase	1.8.2.-	<i>fccB</i>	RRC00443	NT05RC3435	EC
Fermentation					
Phosphate acetyltransferase/Phosphate butyryltransferase	2.3.1.8/2.3.1.19	<i>pta</i>	RRC01951	NT05RC0870	C

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<i>Glycolysis/gluconeogenesis</i>					
Phosphoenolpyruvate-protein phosphotransferase, PtsP	2.7.3.9	<i>ptsP</i>	RRC02985	NT05RC0440	C
Triosephosphate isomerase	5.3.1.1	<i>tpiA</i>	RRC03602	NT05RC1666	C
Fructose-bisphosphate aldolase type I	4.1.2.13	<i>fba</i>	RRC03492	NT05RC1781	C
Phosphoglycerate kinase	2.7.2.3	<i>pgk</i>	RRC03491	NT05RC1782	C
Enolase/Phosphopyruvate hydratase	4.2.1.11	<i>eno</i>	RRC03484	NT05RC1789	C
Fructose-bisphosphate aldolase, class II, Calvin cycle subtype	4.1.2.13	<i>fba</i>	RRC02394	NT05RC1912	C
Glyceraldehyde 3-phosphate dehydrogenase B	1.2.1.12	<i>gap</i>	RRC02393	NT05RC1913	C
Glyceraldehyde-3-phosphate dehydrogenase, type I Gap	1.2.1.12	<i>gap</i>	RRC04329	NT05RC2258	C
Fructose-bisphosphate aldolase, putative aldolase, YneB	4.1.2.13	<i>yneB</i>	RRC00008	NT05RC3011	CM
L-lactate dehydrogenase (FMN-linked) [cytochrome]/(S)-2-hydroxy-acid oxidase	1.1.2.3/1.3.15	<i>lldD</i>	RRC00194	NT05RC3180	
<i>Pentose phosphate pathway</i>					
Ribose 5-phosphate isomerase A	5.3.1.6	<i>rpiA</i>	RRC01215	NT05RC2502	C
Ribulose-phosphate 3-epimerase/Pentose-5-phosphate 3-epimerase	5.1.3.1	<i>rpe</i>	RRC00013	NT05RC3016	CM
Fructose-1,6-bisphosphatase, class II GlpX	3.1.3.11	<i>glpX</i>	RRC00208	NT05RC3195	CM
Transaldolase, putative	2.2.1.2		RRC00360	NT05RC3349	C
<i>Photosynthesis</i>					
Light-harvesting protein B-870, alpha chain		<i>puhA</i>	RRC02820	NT05RC0721	P
Light-harvesting protein B-800/850, alpha chain		<i>pucA</i>	RRC02342	NT05RC2651	P
Light-harvesting protein B-800/850, gamma chain		<i>pucE</i>	RRC00994	NT05RC2653	CM
Photosynthetic reaction center H subunit		<i>pulhA</i>	RRC02853	NT05RC0688	CM
Photosynthetic reaction center L subunit		<i>puhL</i>	RRC02819	NT05RC0722	CM
Photosynthetic reaction center M subunit		<i>puhM</i>	RRC02818	NT05RC0723	CM
<i>Sugars</i>					
Xylose Isomerase	5.3.1.5	<i>xyIA</i>	RRC00720	NT05RC0014	C
Xylulose kinase	2.7.1.17	<i>xyIB</i>	RRC00721	NT05RC0015	C
Nucleoside-diphosphate-sugar epimerase			RRC03125	NT05RC0264	CM
Phosphoglycolate phosphatase, Gph	3.1.3.18	<i>gph</i>	RRC02398	NT05RC1908	
Phosphoribulokinase I	2.7.1.19	<i>cbhP</i>	RRC02391	NT05RC1915	C

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Ribulose biphosphate carboxylase large chain 2	4.1.1.39	<i>rbcL</i>	RRC02395	NT05RC1911	C
Phosphoglucomutase/Glucose phosphomutase, Pgm	5.4.2.2	<i>pgm</i>	RRC02387	NT05RC1919	C
TCA cycle					
Malate dehydrogenase, NAD-dependent	1.1.1.37	<i>mdh</i>	RRC02795	NT05RC0747	C
Succinyl-CoA synthetase beta chain	6.2.1.5	<i>sucC</i>	RRC02793	NT05RC0750	C
Succinyl-CoA synthetase alpha chain	6.2.1.5	<i>sucD</i>	RRC02792	NT05RC0751	C
Isocitrate dehydrogenase, NADP-dependent	1.1.1.42	<i>idh2</i>	RRC01533	NT05RC1971	C
Aconitate hydratase	4.2.1.3	<i>acnA</i>	RRC04337	NT05RC2248	C
FATTY ACID AND PHOSPHOLIPID METABOLISM					
Biosynthesis					
CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	2.7.8.5	<i>pgsA</i>	RRC02959	NT05RC0413	CM
MaoC domain protein dehydratase		<i>maoC</i>	RRC02782	NT05RC0761	C
Dehydrogenase with MaoC-like domain			RRC02783	NT05RC0761	C
Putative phosphatidylserine decarboxylase homolog	4.1.1.65	<i>psd</i>	RRC04174	NT05RC0957	CM
Acyl-CoA thioesterase I precursor/Lipolytic enzyme, G-D-S-L family	3.1.2-	<i>acatI</i>	RRC04139	NT05RC1226	P
Malonyl-CoA-[acyl-carrier-protein] transacylase, FabD	2.3.1.39	<i>fabD</i>	RRC03525	NT05RC1749	
3-Oxoacyl-[acyl-carrier protein] synthase, FabF	2.3.1.179	<i>fabF</i>	RRC03521	NT05RC1754	C
Enoyl-[acyl-carrier protein] reductase (NADH)	1.3.1.9	<i>fabI</i>	RRC01406	NT05RC2453	C
3-Oxoacyl-(acyl-carrier protein) reductase/Short-chain dehydrogenase/reductase, SDR	1.1.1.100	<i>fabG</i>	RRC01189	NT05RC2525	C
Enoyl-[acyl-carrier-protein] reductase [NADH] (NADH-dependent enoyl-ACP reductase)	1.3.1.9		RRC05546	NT05RC2794	C
3-oxoacyl-[acyl-carrier-protein] synthase II, FabF		<i>fabF</i>	RRC01138	NT05RC2795	C
Beta-hydroxyacyl-(acyl-carrier-protein) dehydratase, FabA	4.2.1.60	<i>fabA</i>	RRC01139	NT05RC2796	C
3-Hydroxyacyl-CoA dehydrogenase type-2, type II HADH/3-Hydroxy-2-methylbutyryl-CoA Dehydrogenase	1.1.1.35	<i>hadh</i>	RRC00129	NT05RC3126	C
Degradation					
Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit b, Oxt b	2.8.3.5	<i>scoB</i>	RRC00248	NT05RC3237	C
Other					
Acetyl-CoA acetyltransferase/Acetoacetyl-CoA thiolase	2.3.1.9	<i>Acat</i>	RRC00329	NT05RC3317	C
PROTEIN FATE					
Degradation of proteins, peptides, and glycopeptides					

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Secreted protease C precursor	3.4.24.-		RRC03223	NT05RC0167	EC
Peptidase T, PepT	3.4.11.-	<i>pepT</i>	--	NT05RC0370	C
Peptidase, M20/M25/M40 family	3.5.1.14		RRC04401	NT05RC1505	C
N-acyl-L-amino acid amidohydrolase/Hippuricase	3.5.1.14		RRC02444	NT05RC1861	C
ATP-dependent protease La/ATP-dependent endopeptidase, Lon	3.4.21.53		RRC01049	NT05RC2706	C
Leucyl/phenylalanyl-tRNA-protein transferase	2.3.2.-	<i>aat</i>	RRC01073	NT05RC2731	CM
ATP-dependent endopeptidase clp proteolytic subunit, ClpP	3.4.21.92	<i>clpP</i>	RRC01078	NT05RC2735	CM
Oligoendopeptidase F, putative	3.4.24.-	<i>pepF</i>	RRC00748	NT05RC2930	C
<i>Protein and peptide secretion and trafficking</i>					
Protein-export chaperone, SecB		<i>secB</i>	RRC00736	NT05RC0029	C
Protein secretion ABC efflux permease and ATP-binding protein/Type I secretion processing peptidase			RRC03199	NT05RC0194	CM
Preprotein translocase, SecA subunit		<i>secA</i>	RRC03160	NT05RC0231	C
Peptidase M16 domain protein/Zinc protease	3.4.99.-		RRC03108	NT05RC0280	CM
Peptidase M16 domain protein/Insulinase family Zinc protease	3.4.99.-		RRC03107	NT05RC0281	EC
60 kDa inner membrane insertion protein, YidC		<i>yidC</i>	RRC03045	NT05RC0360	CM
General secretion pathway protein D/Type II and III secretion system protein		<i>gspD</i>	RRC03968	NT05RC0522	OM
SecY stabilizing Integral membrane protein		<i>secY</i>	RRC01986	NT05RC0911	CM
Hemin import ATP-binding protein, HmuV/Transporter		<i>hmuV</i>	RRC04502	NT05RC1071	C, CM
Preprotein translocase, YajC subunit		<i>yajC</i>	RRC02443	NT05RC1862	CM
Survival protein, SurA/PpiC-type peptidyl-prolyl cis-trans isomerase	5.2.1.8	<i>surA</i>	--	NT05RC2819	EC
Microcin-processing peptidase 2 protein, TldD		<i>tldD</i>	RRC00243	NT05RC3232	M
Tol system periplasmic component, YbgF/tetratricopeptide TPR_2		<i>ybgF</i>	RRC05669	NT05RC3333	EC
Outer membrane lipoprotein carrier protein, LolA		<i>lolA</i>	RRC00485	NT05RC3469	EC
Type I secretion adaptor protein (HlyD family)/RTX secretion protein D		<i>type_I_hlyD</i>	RRC05697	NT05RC3537	C, CM
<i>Protein folding and stabilization</i>					
PpiC-type peptidyl-prolyl cis-trans isomerase	5.2.1.8		--	NT05RC0230	OM
Chaperone protein, DnaK		<i>dnaK</i>	RRC03154	NT05RC0235	C
Thiol:disulfide interchange protein DsbA (DsbA oxidoreductase)		<i>dsbA</i>	RRC03149	NT05RC0240	EC
Peptidyl-prolyl cis-trans isomerase, cyclophilin type			RRC03490	NT05RC1783	P
Peptidyl-prolyl cis-trans isomerase, PPIase/Rotamase/Cyclophilin/Cyclosporin A-bindingprotein, CYP B	5.2.1.8	<i>cypB</i>	RRC03489	NT05RC1784	CM

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Outer membrane protein thiol:disulfide interchange protein DsbA-like		<i>dsbA</i>	RRC03455	NT05RC1820	EC
Trigger Factor, PPIase, Tig	5.2.1.8	<i>tig</i>	RRC00692	NT05RC2098	C
Putative peptidyl-prolyl cis-trans isomerase	5.2.1.8		RRC01410	NT05RC2457	
Endopeptidase, DegP/Periplasmic serine protease	3.4.21.-	<i>degP</i>	RRC01208	NT05RC2508	P
10 kDa chaperonin, GroES		<i>groS</i>	RRC00934	NT05RC2591	C
60 kDa chaperonin, GroEL		<i>groL</i>	RRC00935	NT05RC2592	C
ATP-dependent chaperone, ClpB		<i>clpB</i>	RRC05711	NT05RC3551	C
Co-chaperone, GrpE		<i>grpE</i>	RRC05796	NT05RC3642	C
Protein modification and repair					
Carboxyl-processing protease (Tail specific protease)	3.4.21.102		RRC03302	NT05RC0077	CM
Universal stress family protein		<i>uspA</i>	RRC02802	NT05RC0740	C
Universal stress protein UspA and related nucleotide-binding domain protein		<i>uspA</i>	RRC04161	NT05RC1205	C
Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase			RRC01014	NT05RC2673	
Leucyl aminopeptidase	3.4.11.1	<i>pepA</i>	RRC04532	NT05RC2823	C
Protein-L-isopartate o-methyltransferase	2.1.1.77	<i>PcmI</i>	RRC00264	NT05RC3250	C
Other					
Von Willebrand factor type A domain protein/CBBO			RRC03776	NT05RC0600	C
PROTEIN SYNTHESIS					
Ribosomal proteins: synthesis and modification					
LSU ribosomal protein, L12 (L7/L12)		<i>rplL</i>	RRC03083	NT05RC0305	C
SSU ribosomal protein, S3		<i>rpsC</i>	RRC03069	NT05RC0320	C
LSU ribosomal protein, L14		<i>rplN</i>	RRC03064	NT05RC0325	C
LSU ribosomal protein, L6		<i>rplG</i>	RRC03059	NT05RC0330	C
SSU ribosomal protein, S5		<i>rpsE</i>	RRC03057	NT05RC0332	C
SSU ribosomal protein, S13		<i>rpsM</i>	RRC03051	NT05RC0339	C
SSU ribosomal protein, S11		<i>rpsK</i>	RRC03050	NT05RC0340	C
LSU ribosomal protein, L19 (or L31)		<i>rplM</i>	RRC03026	NT05RC0377	C
SSU ribosomal protein, S1		<i>rpsA</i>	RRC01790	NT05RC1173	C
SSU ribosomal protein, S2		<i>rpsB</i>	RRC02403	NT05RC1903	C
LSU ribosomal protein, L9		<i>rplI</i>	RRC00691	NT05RC2101	C

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Translation factors					
Translation elongation factor Tu		<i>tuf</i>	RRC03808	NT05RC0153	C
Protein translation elongation factor G (EF-G)		<i>fusA</i>	RRC02509	NT05RC0311	C
Protein translation elongation factor Tu (EF-TU)		<i>tuf</i>	RRC03235	NT05RC0312	C
Protein translation elongation factor Tu (EF-TU)		<i>tuf</i>	RRC03808	NT05RC0312	C
Translation Elongation and release factor G (GTPase)		<i>GTPase</i>	RRC04353	NT05RC1559	C
Peptide chain release factor 2, RF-2		<i>prfB</i>	RRC02481	NT05RC1613	C
Protein translation elongation factor Ts (EF-Ts)		<i>tsf</i>	RRC02402	NT05RC1904	C
Bacterial peptide chain release factor 3 (RF-3), PflC		<i>prfC</i>	RRC06068	NT05RC2425	C
tRNA and rRNA base modification					
Aspartyl/glutamyl-tRNA amidotransferase subunit A	6.3.5.-	<i>gata</i>	RRC00798	NT05RC2879	CM
Aspartyl/glutamyl-tRNA amidotransferase subunit B (Asp/Glu-ADT subunit B)	6.3.5.-	<i>gatB</i>	RRC01959	NT05RC0880	C
D-Tyrosyl-tRNA deacylase, Did	3.1.-.-	<i>did</i>	RRC00975	NT05RC2630	C
tRNA aminoacylation					
Tryptophanyl-tRNA synthetase	6.1.1.2	<i>trpS</i>	RRC04002	NT05RC0490	C
Aspartyl-tRNA synthetase	6.1.1.12	<i>aspS</i>	RRC03937	NT05RC0553	C
Seryl-tRNA synthetase	6.1.1.11	<i>serS</i>	RRC04397	NT05RC1510	C, CM
Prolyl-tRNA synthetase		<i>proRS</i>	--	NT05RC2575	C
Phenylalanyl-tRNA synthetase, beta subunit	6.1.1.20	<i>pheT</i>	RRC06104	NT05RC3289	C
PURINES, PYRIMIDINES, NUCLEOSIDES, AND NUCLEOTIDES					
Nucleotide and nucleoside interconversions					
Adenylate Kinase (ATP-AMP transphosphorylase)/Nucleoside-diphosphate kinase	2.7.4.3/2.7.4.6	<i>adk</i>	RRC03052	NT05RC0338	C
Nucleoside diphosphate kinase, Ndk/NDP kinase/Nucleoside-2-P kinase	2.7.4.6	<i>ndk</i>	RRC03479	NT05RC1794	C
Purine ribonucleotide biosynthesis					
GMP synthase [glutamine-hydrolyzing]	6.3.5.2	<i>guaA</i>	RRC00895	NT05RC1941	C
Formyltetrahydrofolate deformylase	3.5.1.10	<i>purU</i>	RRC01205	NT05RC2511	
Pyrimidine ribonucleotide biosynthesis					
Carbamoyl-phosphate synthase, large subunit	6.3.5.5	<i>carB</i>	RRC03938	NT05RC0552	CM, P

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Orotate phosphoribosyltransferase	2.4.2.10	<i>pyrE</i>	RRC03625	NT05RC1642	C
Dihydropyrimidine dehydrogenase [NADP+] beta subunit/dihydroorotate dehydrogenase family protein	1.3.1.2	<i>DPYD</i>	RRC00991	NT05RC2646	C
<i>Salvage of nucleosides and nucleotides</i>					
Adenine phosphoribosyltransferase, Apt	2.4.2.7	<i>apt</i>	RRC01698	NT05RC3227	C
Purine nucleotide phosphorylase	2.4.2.1		RRC00387	NT05RC3376	C
<i>2'-Deoxyribonucleotide metabolism</i>					
Pyrimidine-specific ribonucleoside hydrolase, RihA/Cytidine/uridine-specific hydrolase	3.2.-.-	<i>rihA</i>	RRC03481	NT05RC1792	C
<i>Other</i>					
Nucleoside-binding protein/Bmp family protein			RRC04244	NT05RC0821	EC
Xanthine dehydrogenase, small subunit	1.17.1.4	<i>xdhA</i>	RRC04239	NT05RC0827	C
REGULATORY FUNCTIONS					
<i>DNA interactions</i>					
Transcriptional regulator, LuxR family		<i>luxR</i>	RRC03806	NT05RC0343	C
Cell cycle transcriptional regulator, CtrA/Response regulator Soka		<i>ctrA</i>	RRC03536	NT05RC1736	C
Transcriptional regulatory protein BaeR, Alkaline phosphatase synthesis		<i>baeR</i>	RRC00026	NT05RC3031	C
<i>Protein interactions</i>					
Regulatory protein, SenC(PtrC)		<i>senC/prrC/scoI</i>	RRC03336	NT05RC0044	CM
Phosphohistidine phosphatase, SixA/Phosphoglycerate mutase family protein	3.1.3.-	<i>sixA</i>	RRC04024	NT05RC0354	
Protease activity modulator		<i>hflK</i>	RRC01212	NT05RC2505	
<i>Small molecule interactions</i>					
Diguanylate cyclase/phosphodiesterase with PAS/PAC and GAF sensor	2.7.7.65		RRC00149	NT05RC3141	C
<i>Two-component systems</i>					
Two component response regulator (winged helix family)			--	NT05RC0276	C
<i>Other</i>					
Response regulator/ggdef domain protein			RRC06082	NT05RC2762	
Phosphate transport system regulatory protein, PhoU		<i>phoU</i>	RRC05801	NT05RC3647	C

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SIGNAL TRANSDUCTION					
<i>Two-component systems</i>					
Methyl-accepting chemotaxis sensory transducer, McpA		<i>mcpA</i>	RRC04620	NT05RC1409	CM
Sensory transduction histidine protein kinase	2.7.3.-		RRC05028	NT05RC1570	CM
Methyl-accepting chemotaxis protein, McpC		<i>mcpC</i>	RRC03579	NT05RC1694	CM
Sensory transduction protein kinase	2.7.3.-		RRC01105	NT05RC2760	
Two-component response sensory transduction histidine kinase, potential phosphate regulatory protein			RRC06094	NT05RC2997	C
Two component system integral membrane signal transduction histidine kinase	2.7.3.-		RRC00027	NT05RC3032	CM
TRANSCRIPTION					
<i>Degradation of RNA</i>					
Polyribonucleotide nucleotidyltransferase/Polynucleotidylphosphorylase, PNPase	2.7.7.8		RRC03090	NT05RC0297	C
Ribonuclease E, RNase E	3.1.4.-	<i>RNaseEG</i>	RRC05484	NT05RC2263	C
Translation initiation inhibitor/Endoribonuclease L-PSP			RRC05722	NT05RC3562	CM
<i>DNA-dependent RNA polymerase</i>					
DNA-directed RNA polymerase beta subunit	2.7.7.6	<i>rpoB</i>	RRC03082	NT05RC0306	C
DNA-directed RNA polymerase beta' subunit	2.7.7.6	<i>rpoC</i>	RRC03080	NT05RC0307	C
DNA-directed RNA polymerase, alpha subunit	2.7.7.6	<i>rpoA</i>	RRC03049	NT05RC0341	C
<i>Transcription factors</i>					
Sigma 54 modulation protein/ribosomal protein S30EA or factor Y		<i>rpoX</i>	RRC03265	NT05RC0121	C
Transcription elongation factor, GreA		<i>greA</i>	RRC03954	NT05RC0534	C
Transcriptional regulator, LysR family		<i>lysR</i>	RRC03919	NT05RC0572	C
Transcription elongation factor, NusA/N utilization substance protein A		<i>nusA</i>	RRC03167	NT05RC224	C
<i>Other</i>					
Putative AraC family transcriptional regulator			RRC04375	NT05RC1537	CM
TRANSPORT AND BINDING PROTEINS					
<i>Amino acids, peptides and amines</i>					
Transporter/import inner membrane translocase, subunit Tim44 homolog		<i>Sec?</i>	RRC00738	NT05RC0031	CM
Oligopeptide-binding protein, OppA/Extracellular solute-binding protein, family 5		<i>oppA</i>	RRC03230	NT05RC0161	P

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Glutamate/glutamine/aspartate/asparagine-binding protein, BztA		<i>bztA</i>	RRC03799	NT05RC0350	P
Glutamine-binding protein/Extracellular solute-binding protein, family 3			RRC04018	NT05RC0474	P
Type II secretion system protein E			RRC03965	NT05RC0525	CM, P
Putative lysine-arginine-ornithine or histidine binding periplasmic protein			RRC02872	NT05RC0650	P
Oligopeptide-binding Protein OppA/Extracellular solute-binding protein family		<i>oppA</i>	RRC02807	NT05RC0735	CM, P
Dipeptide-binding protein/Extracellular solute-binding protein, family			RRC01964	NT05RC0885	P
Dipeptide transport ATP-binding protein, DppD/Oligopeptide transport ATP-binding protein, OppD		<i>oppD</i>	RRC01967	NT05RC0888	C, CM
Glycine betaine/L-proline transport system binding protein, ProX		<i>proX</i>	RRC02010	NT05RC0936	
Spermidine/putrescine ABC transporter ATP-binding subunit			RRC02709	NT05RC1297	C, CM
Putative polyamine ABC transporter, periplasmic polyamine-binding protein			RRC02708	NT05RC1298	EC
Polyamine ABC transporter, permease protein			RRC02707	NT05RC1299	CM
Probable phosphatidylinositol-4-phosphate-5-kinase			RRC04081	NT05RC1419	EC
ABC Polyamine/Opine/Phosphonate transporter, periplasmic ligand binding protein			RRC04469	NT05RC1423	EC
ABC transporter ATP-binding protein/Methionine import ATP-binding protein, MetN		<i>metN</i>	RRC03629	NT05RC1638	CM
Leucine-, Isoleucine-, Valine-, Threonine and Alanine-binding Protein/Extracellular ligand-binding receptor		<i>braC</i>	RRC00901	NT05RC1935	P
Putrescine transport ATP-binding protein, PotG		<i>potG</i>	RRC01528	NT05RC1977	C
Putrescine transport system permease protein, PotI		<i>potI</i>	RRC01527	NT05RC1978	CM
Spermidine/putrescine transport system permease protein, PotB/Binding-protein-dependent inner membrane transport component		<i>potB</i>	RRC01526	NT05RC1979	CM
Spermidine/putrescine-binding protein/Extracellular solute-binding protein, family 1			RRC01245	NT05RC2286	P
Taurine ABC transporter, periplasmic taurine-binding protein			RRC01299	NT05RC2343	EC
Spermidine/Putrescine-binding periplasmic protein			RRC01326	NT05RC2370	P
Oligopeptide-binding protein, OppA		<i>oppA</i>	RRC01333	NT05RC2377	P
Branched-chain amino acid ABC transporter, ATP-binding protein, LivF		<i>livF</i>	RRC01157	NT05RC2553	C, CM
His/Glu/Gln/Arg/opine family ABC transporter/Periplasmic His/Glu/Gln/Arg/opine family-binding protein			RRC00775	NT05RC2902	P
Spermidine/putrescine-binding protein, ABC polyamine transporter, periplasmic substrate-binding protein			RRC00091	NT05RC3093	P
Branched-chain amino acid aminotransferase	2.6.1.42		RRC00377	NT05RC3367	C
ABC transporter, Cyd cysteine exporter family permease/ATP-binding protein, CydC		<i>cydC</i>	RRC00404	NT05RC3393	CM
ABC branched amino acid transporter family, periplasmic substrate-binding subunit			RRC05738	NT05RC3577	EC
ABC branched amino acid transporter family, ATPase subunit			RRC05739	NT05RC3578	C, CM
Anions					

Protein Name	EC Number	Gene Name	ERGO*	NT05*	Location
Molybdate ABC transporter, periplasmic molybdate-binding protein		<i>modA</i>	RRC03762	NT05RC0585	P
Molybdate ABC transporter, ATP-binding protein, ModC		<i>modC</i>	RRC03907	NT05RC0587	C, CM
Thiosulfate-binding protein			--	NT05RC2870	P
Membrane protein MosC, major facilitator superfamily MFS_1		<i>mosC</i>	RRC00195	NT05RC3181	CM
Phosphate transport ATP-binding protein, PstB		<i>pstB</i>	RRC05802	NT05RC3648	C, CM
Phosphate ABC transporter, permease protein, PstA		<i>pstA</i>	RRC05803	NT05RC3649	CM
ABC phosphate transporter, inner membrane subunit, PstC		<i>pstC</i>	RRC03394	NT05RC3650	CM
Phosphate-Binding Periplasmic Protein			RRC03395	NT05RC3651	P
<i>Carbohydrates, organic alcohols, and acids</i>					
D-xylose ABC transporter, D-xylose-binding protein		<i>xyfF</i>	RRC00724	NT05RC0018	P
Mannitol-binding protein/Trap dicarboxylate transporter, Dctp subunit			RRC04462	NT05RC1431	EC
Alpha-glucoside-binding protein/ABC alpha-glucoside transporter, periplasmic substrate-binding protein		<i>algE</i>	RRC03427	NT05RC1851	EC
Alpha-glucoside transport ATP-binding protein, AgIK		<i>algK</i>	RRC03422	NT05RC1855	C, CM
Fructose binding periplasmic protein, FrcB		<i>frcB</i>	--	NT05RC2111	P
Sorbitol-binding protein/Potential maltose-binding protein			RRC00677	NT05RC2114	EC
ABC sugar transporter, periplasmic binding protein/D-Galactose-binding/Ribitol-binding protein			RRC02337	NT05RC2476	P
Mannitol-binding protein			RRC01191	NT05RC2524	EC
Ribose ABC transporter, D-ribose-binding protein			RRC01127	NT05RC2784	P
Ribose transport ATP-binding protein RbsA/ABC transporter, carbohydrate uptake transporter-2 (CUT2) family		<i>rbsA</i>	RRC01129	NT05RC2786	C, CM
C4-dicarboxylate-binding periplasmic protein			RRC00169	NT05RC3156	P
<i>Cations and iron carrying compounds</i>					
Manganese transport protein, MntH		<i>mntH</i>	RRC03871	NT05RC0626	CM
Iron (III) Dicitrate-binding periplasmic protein		<i>fecB</i>	RRC04484	NT05RC1088	EC
Outer membrane siderophore receptor/TonB-dependent siderophore receptorR		<i>fhu</i>	RRC04402	NT05RC1504	OM
Sensor protein, KdpD	2.7.3.-	<i>kdpD</i>	RRC01313	NT05RC2357	CM
Transporter/TrkA-C domain protein			--	NT05RC2388	CM
TonB-system energizer ExbB/TolQ protein		<i>exbB</i>	RRC01434	NT05RC2479	CM
2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase/short-chain dehydrogenase/reductase, SDR	1.3.1.28	<i>entA</i>	RRC01183	NT05RC2531	C
25 kD Outer-membrane immunogenic protein/Rhizobioicin, RzcA		<i>rzcA</i>	RRC01603	NT05RC2572	OM
Iron-regulated protein, FrpC		<i>frpC</i>	RRC01604	NT05RC2573	EC

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Iron-regulated protein FrpC/poly(beta-D-mannuronate) C5 epimerase 3 (Mannuronanepimerase 3)		<i>frpC</i>	RRC00309	NT05RC3297	EC
Porins					
Porin			RRC03116	NT05RC0272	OM
Other					
Putative membrane protein			RRC03140	NT05RC0250	CM
Acetyltransferase/MobC protein	2.3.1.-	<i>mobC</i>	RRC02973	NT05RC0428	CM
Acriflavin resistance plasma membrane protein B		<i>acrB</i>	RRC02995	NT05RC0450	CM
Acriflavin resistance periplasmic protein			RRC02881	NT05RC0641	P
Periplasmic component of efflux system/HlyD family protein			RRC02879	NT05RC0643	CM, P
ABC transporter, substrate-binding protein, aliphatic sulphonates/Taurine-Binding Periplasmic Protein			RRC06012	NT05RC1459	EC
ABC transporter ATP-binding protein			RRC04420	NT05RC1484	CM
Transporter			RRC04392	NT05RC1517	CM
ABC transporter, fused ATPase and inner membrane subunit			RRC01360	NT05RC2407	CM
Putative transport protein, YidE/Integral membrane protein with TrkA domains		<i>yidE</i>	RRC01177	NT05RC2535	CM
Oligopeptide-binding protein/extracellular solute-binding protein, family 5			RRC00960	NT05RC2615	EC
ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic component, TauA		<i>tauA</i>	RRC00984	NT05RC2639	EC
Iron(III)-binding periplasmic protein			RRC01044	NT05RC2700	P
Thiamin/thiamin pyrophosphate ABC transporter, thiamin/thiamin pyrophosphate-binding protein, ThiB		<i>thiB</i>	RRC01667	NT05RC2825	P
Acriflavin resistance protein E/Efflux transporter, RND family, MFP subunit			RRC00805	NT05RC2872	CM, P
Acriflavin resistance plasma membrane protein			RRC00803	NT05RC2873	CM
TolB protein		<i>tolB</i>	RRC00346	NT05RC3335	P
ABC transporter, periplasmic substrate-binding protein			RRC00383	NT05RC3372	P
UNCLASSIFIED					
Role category not yet assigned					
Myo-inositol-1(or 4)-monophosphatase (1-1-Pase)	3.1.3.25		RRC03984	NT05RC0507	C
Myo-inositol-1(or 4)-monophosphatase family protein	3.1.3.25		RRC01989	NT05RC0915	EC
Lipoprotein, putative			RRC01112	NT05RC2767	EC
Inositol monophosphatase/ADP-ribosylglycolhydrolase, CysQ Protein	3.1.3.25		RRC00266	NT05RC3253	
UNKNOWN FUNCTION					

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General					
Filament-A precursor (Peptidase M23B)		<i>flaA</i>	RRC03301	NT05RC0078	C, CM
Putative iojap protein family homolog			RRC03298	NT05RC0081	C
Pentapeptide repeat family protein			RRC04445	NT05RC1451	EC
Outer membrane protein E/Membrane protein involved in aromatic hydrocarbon degradation			RRC01502	NT05RC2007	OM
HYPOTHETICAL PROTEINS					
Conserved Domain proteins					
ErfK/YbiS/YciS/YnhG family protein			RRC02993	NT05RC0448	
Conserved hypothetical protein			RRC03927	NT05RC0563	
Conserved hypothetical protein			RRC03926	NT05RC0564	
Conserved hypothetical membrane spanning protein			RRC02854	NT05RC0687	CM
Conserved hypothetical protein			RRC02456	NT05RC1587	
Hypothetical cytosolic protein of unknown function			RRC02483	NT05RC1615	C
Hypothetical protein/GfdT protein			RRC03541	NT05RC1732	C
Conserved hypothetical membrane associated protein			RRC03520	NT05RC1755	C, CM
Hypothetical Membrane Associated Protein/Invasion associated family protein			RRC00884	NT05RC1952	EC
Hypothetical protein			RRC01494	NT05RC2016	
Conserved hypothetical cytosolic protein			RRC00597	NT05RC2240	C
Hypothetical Exported Protein			RRC01358	NT05RC2405	EC
Hypothetical membrane associated protein/pyrrolo-quinoline quinone			RRC01359	NT05RC2406	CM
Hypothetical protein			--	NT05RC2634	
Hypothetical protein/lipoprotein, putative			RRC01128	NT05RC2785	
Hypothetical membrane spanning protein of unknown function			RRC06091	NT05RC2994	CM
Conserved hypothetical protein			RRC06095	NT05RC3026	
Conserved hypothetical protein, Phage Minor Tail Protein			RRC02354	NT05RC3046	CM
Hypothetical protein			RRC05643	NT05RC3064	C
Hypothetical cytosolic protein, prophage Lp2 protein			RRC00072	NT05RC3071	CM
Conserved hypothetical protein			--	NT05RC3075	
Conserved hypothetical Protein			RRC00313	NT05RC3301	C
Conserved hypothetical protein/Permease			RRC00389	NT05RC3378	EC
Conserved hypothetical protein			RRC00393	NT05RC3382	EC

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Conserved hypothetical cytosolic protein			RRC00413	NT05RC3402	C
Conserved hypothetical Exported Protein			RRC01759	NT05RC3524	CM, P
Conserved hypothetical protein			RRC03402	NT05RC3658	P
Conserved Hypothetical proteins					
Conserved hypothetical (transglutaminase-like) protein			RRC03327	NT05RC0053	
Conserved hypothetical cytosolic protein			RRC03249	NT05RC0139	C
Conserved hypothetical protein/Glucose-1-phosphate adenylyltransferase	2.7.7.27		--	NT05RC0925	
OmpA family hypothetical protein			RRC03674	NT05RC0952	EC
Conserved hypothetical protein/Aminomethyltransferase	2.1.2.10		RRC03662	NT05RC0993	C
Conserved hypothetical protein			RRC01788	NT05RC1175	
Hypothetical Cytosolic Protein			RRC03645	NT05RC1186	
Hypothetical protein			RRC02694	NT05RC1315	
Conserved hypothetical protein			RRC02685	NT05RC1327	
Conserved hypothetical protein			RRC06004	NT05RC1351	EC
Outer membrane protein/Inner membrane lipoprotein YiaD		<i>yiaD</i>	RRC00951	NT05RC2605	OM
Hypothetical Membrane Spanning Protein			RRC01102	NT05RC2757	CM
Conserved hypothetical Exported Protein (<i>Mucoidy inhibitor A</i>)			RRC01654	NT05RC2839	EC
Conserved hypothetical Exported Protein			RRC03610	NT05RC2917	CM, P
GTP-binding protein/conserved hypothetical protein			RRC00370	NT05RC3360	C