



Supplementary Figure S1 Soft agar plates of chemotaxis motility assay. Compared to 1° cells, secondaries show increased motility in response to chemoattractants such as serine and maltose. *E. coli* MG1655 was used as positive control.

Supplementary Table S1 List of all 638 genes differentially expressed in both *P. luminescens* DJC cells forms. Genes are sorted accordingly to their functional subgroups. Fold changes are given as values of gene expression in 2° cells to 1° cells during exponential (Exp) and stationary growth phase (Stat) with filter criteria ≤ -3 or ≥ 3 ; $p \leq 0.05$. NS, not significant.

Category and locus tag	Gene	Protein(s) or similarity	Protein accession number	Fold change ratio (2°wt/1°wt)	
				Exp	Stat
<u>Metabolism</u>					
Hydroxyphenylacetate (HPA) metabolism					
PluDJC_04995	<i>hpaC</i>	4-hydroxyphenylacetic acid hydroxylase	WP_011145337.1	6.04	NS
PluDJC_05000	<i>hpaB</i>	4-hydroxyphenylacetate 3-monooxygenase, oxygenase component (4-HPA 3-monooxygenase large component) (4-HPA 3-hydroxylase)	WP_011145338.1	8.06	NS
PluDJC_05035	<i>hpaX</i>	4-hydroxyphenylacetate permease	WP_011145344.1	5.99	NS
PluDJC_05040	<i>hpaI</i>	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase	WP_011145345.1	6.21	NS
PluDJC_05045	<i>hpcG</i>	2-oxo-hepta-3-ene-1,7-dioic acid hydratase	WP_011145346.1	5.78	NS
PluDJC_05050	<i>gabD</i>	Succinate-semialdehyde dehydrogenase	WP_011145347.1	5.07	NS
PluDJC_05055		Similarities with probable MFS transporter	WP_011145348.1	4.55	NS
PluDJC_05060	<i>hpcD</i>	5-carboxymethyl-2-hydroxy-muconic acid isomerase	WP_011145349.1	7.97	NS
PluDJC_05065	<i>hpcB</i>	3,4-dihydroxyphenylacetate 2,3-dioxygenase	WP_011145350.1	8.29	NS
PluDJC_05070	<i>hpcC</i>	5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase	WP_011145351.1	7.18	NS

PluDJC_05075	<i>hpaG2</i>	Probable 4-hydroxyphenylacetate catabolism	WP_011145352.1	7.85	NS
PluDJC_05080	<i>hpaG1</i>	Probable 4-hydroxyphenylacetate catabolism	WP_011145353.1	8.81	NS

Arginine degradation and transport

PluDJC_15875		Probable amino acid permease	WP_011147321.1	18.35	-5.37
PluDJC_15880	<i>astE</i>	Succinylglutamate desuccinylase	WP_011147322.1	20.28	NS
PluDJC_15885	<i>astB</i>	Succinylarginine dihydrolase	WP_011147323.1	16.26	NS
PluDJC_15890	<i>astD</i>	Succinylglutamic semialdehyde dehydrogenase	WP_011147324.1	19.39	NS
PluDJC_15895	<i>astA</i>	Arginine N-succinyltransferase (AOST)	WP_011147325.1	23.72	NS
PluDJC_15900	<i>astC</i>	Succinylornithine transaminase (carbon starvation protein C)	WP_011147326.1	21.83	NS
PluDJC_17735	<i>argO</i>	Arginine exporter ArgO	WP_011147779.1	NS	-4.33

Coenzyme B₁₂ biosynthesis

PluDJC_15270	<i>cbiJ</i>	Precorrin-6X reductase	WP_011147209.1	NS	-6.78
PluDJC_15275	<i>cbiH</i>	Precorrin-3B C17-methyltransferase	WP_011147210.1	-4.94	-7.89
PluDJC_15280	<i>cbiG</i>	Cobalamin biosynthesis protein G (CbiG)	WP_011147211.1	-5.57	-12.83
PluDJC_15285	<i>cbiF</i>	Precorrin-4 C11-methyltransferase	WP_011147212.1	-7.68	-17.99
PluDJC_15290	<i>cbiT</i>	Precorrin-8W decarboxylase	WP_011147213.1	-9.10	-42.31
PluDJC_15295	<i>cbiE</i>	Precorrin-6Y C5,15-methyltransferase	WP_011147214.1	-9.89	NS

PluDJC_15300	<i>cbiD</i>	Cobalamin biosynthesis protein CbiD	WP_011147215.1	-15.68	-21.30
PluDJC_15305	<i>cbiC</i>	Precorrin-8X methylmutase (Precorrin isomerase)	WP_011147216.1	-17.76	-16.59
PluDJC_15310	<i>cbiB</i>	Cobalamin biosynthesis protein CbiB	WP_011147217.1	-29.78	-16.67
PluDJC_15315	<i>cbiA</i>	Cobyric acid A,C-diamide synthase	WP_011147218.1	-32.74	-54.19

Other

PluDJC_00870		Amidinotransferase	WP_011144560.1	-19.65	-9.86
PluDJC_00385	<i>acs</i>	Acetyl-coenzyme A synthetase (acetate--COA ligase) (acyl-activating enzyme)	WP_011144480.1	8.78	NS
PluDJC_01315		Probable 4-hydroxyphenylacetic acid hydroxylase, Similar to 4-hydroxyphenylacetate 3-monooxygenase, oxygenase component HpaB	WP_011144645.1	-3.48	NS
PluDJC_01335		Similar to TRP-1 protein encoded by the <i>toxA</i> gene of <i>Burkholderia glumae</i> , methyltransferase involved in toxoflavin biosynthesis	WP_011144649.1	-3.49	-5.26
PluDJC_01965	<i>murQ</i>	N-acetylmuramic acid 6-phosphate etherase	WP_011144789.1	3.74	NS
PluDJC_02315		Aspartate aminotransferase family protein	WP_041380544.1	-6.86	NS
PluDJC_02320		Zinc-binding dehydrogenase	WP_011144860.1	-4.65	NS
PluDJC_02325		HAD family phosphatase	WP_041379890.1	-3.10	NS
PluDJC_02605		Similar to probable acetyltransferase	WP_082302960.1	4.58	NS
PluDJC_03125	<i>ppdA</i>	Prepilin peptidase dependent protein A precursor	WP_011145002.1	14.12	NS
PluDJC_03130	<i>ppdB</i>	Prepilin peptidase dependent protein B precursor	WP_011145003.1	4.54	NS

PluDJC_03240		Serine protease	WP_011145019.1	7.16	NS
PluDJC_03315	<i>prtA</i>	Alkaline metalloprotease precursor PrtA	WP_011145031.1	-8.47	NS
PluDJC_03320	<i>inh</i>	Proteinase inhibitor Inh precursor	WP_041380576.1	-5.00	NS
PluDJC_03325	<i>prtB</i>	ATP-binding protein PrtB	WP_011145033.1	-4.03	NS
PluDJC_03330	<i>prtC</i>	Membrane Fusion Protein PrtC	WP_011145034.1	-5-39	NS
PluDJC_03895		Acyl carrier protein	WP_011145139.1	3.89	NS
PluDJC_04050		HAD family hydrolase	WP_011145169.1	-4.77	NS
PluDJC_04055		Phosphoribosyltransferase	WP_011145170.1	-9.76	NS
PluDJC_04060	<i>hisA2</i>	1-(5-phosphoribosyl)-5-((5-phosphoribosylamino)methylideneamino)imidazole-4-carboxamide isomerase	WP_011145171.1	-12.55	NS
PluDJC_04150	<i>afuA</i>	Periplasmic ferric iron-binding protein AfuA	WP_041379924.1	4.61	NS
PluDJC_04785		Inositol monophosphatase family protein	WP_011145299.1	25.08	NS
PluDJC_04795		Thymidylate kinase	WP_041379942.1	23.69	NS
PluDJC_04810	<i>mltD</i>	Membrane-bound lytic murein transglycosylase D precursor (murein hydrolase D)	WP_011145304.1	NS	-6.05
PluDJC_05135		Similar to salicylate-5-hydroxylase large oxygenase component	WP_011145363.1	-3.88	NS
PluDJC_06375	<i>nagE</i>	PTS system, N-acetylglucosamine-specific IIABC component (EIIABC-NAG) (N-acetylglucosamine-permease IIABC component)	WP_011145641.1	5.14	NS

PluDJC_07100	<i>cydA</i>	Cytochrome D ubiquinol oxidase subunit I (Cytochrome BD-I oxidase subunit I)	WP_011145752.1	NS	3.48
PluDJC_07245		ATP-binding cassette domain-containing protein	WP_011145770.1	6.28	NS
PluDJC_07330	<i>bioA</i>	Adenosylmethionine-8-amino-7-oxononanoate transaminase (DAPA aminotransferase)	WP_011145786.1	3.14	NS
PluDJC_07330	<i>cdd</i>	Cytidine deaminase (Cytidine aminohydrolase) (CDA)	WP_011145844.1	NS	4.43
PluDJC_07490		Lipase family protein	WP_041380011.1	NS	-5.43
PluDJC_07700		Probable dehydrogenase	WP_011145860.1	-7.94	-8.19
PluDJC_08350	<i>pflA</i>	Pyruvate formate-lyase 1 activating enzyme (PFL- activating enzyme)	WP_011145904.1	-7.19	NS
PluDJC_08355	<i>pflB</i>	Formate acetyltransferase I (pyruvate formate- lyase 1)	WP_011145905.1	-12.50	NS
PluDJC_09075		Similar to probable glycosyltransferase	WP_011146040.1	4.57	NS
PluDJC_10180	<i>xyfB</i>	Xylulose kinase	WP_011146221.1	-4.54	NS
PluDJC_10185		Similar to xylitol (sorbitol) dehydrogenase	WP_011146222.1	-3.38	-5.18
PluDJC_10305	<i>sgcA</i>	Putative phosphotransferase enzyme II, A component SgcA	WP_011146240.1	3.87	NS
PluDJC_10310	<i>sgaB</i>	Putative sugar phosphotransferase component II B	WP_041380050.1	3.98	NS
PluDJC_10350		Some similarities with unknown protein YhfS of Escherichia coli	WP_041380051.1	3.11	11.90
PluDJC_10360	<i>fruB</i>	Probable PTS system	WP_011146250.1	4.12	3.48

PluDJC_10365	<i>fruA</i>	Probable PTS sytem	WP_041380052.1	NS	3.38
PluDJC_11035	<i>prsA</i>	Ribose-phosphate pyrophosphokinase (Phosphoribosyl pyrophosphate synthetase)	WP_049789771.1	NS	-5.00
PluDJC_11080		Probable 3-oxoacyl-[acyl-carrier protein] reductase	WP_011146330.1	NS	-9.36
PluDJC_11200	<i>plIA</i>	Lectin A	WP_011146351.1	NS	-12.22
PluDJC_11225	<i>cutC</i>	Copper homeostasis protein CutC	WP_011146355.1	-3.12	NS
PluDJC_11530		Alpha/beta hydrolase	WP_011146414.1	NS	-6.69
PluDJC_11550		Similar to 3-oxoacyl-[acyl-carrier-protein] synthase	WP_011146418.1	-8.71	-4.86
PluDJC_11555		Similar to acyl carrier protein (ACP)	WP_011146419.1	-7.56	NS
PluDJC_11685		Some similarities with diaminobutyric acid aminotransferase	WP_011146443.1	35.28	NS
PluDJC_11690		Similar to hypothetical gamma-butyrobetaine,2- oxoglutarate	WP_082303124.1	25.31	NS
PluDJC_11695		Similar to acetyltransferase	WP_011146446.1	23.26	NS
PluDJC_11705		Probable 2-oxopent-4-dienoate hydratase	WP_011146453.1	NS	-12.09
PluDJC_11710		Similar to the 2-hydroxy-6-keonona-2,4-dienedoic acid hydrolase	WP_011146454.1	-4.35	-22.75
PluDJC_11720	<i>hcaE</i>	3-phenylpropionate dioxygenase alpha subunit (digoxigenin alpha subunit)	WP_011146456.1	NS	-21.76
PluDJC_11725	<i>hcaF</i>	3-phenylpropionate dioxygenase beta subunit (digoxigenin beta subunit)	WP_011146457.1	-3.30	-32.04

PluDJC_11730	<i>hcaC</i>	3-phenylpropionate dioxygenase ferredoxin subunit (digoxigenin ferredoxin subunit)	WP_011146458.1	NS	-29.29
PluDJC_11735	<i>hcaB</i>	2,3-dihydroxy-2,3-dihydrophenylpropionate dehydrogenase	WP_011146459.1	NS	-32.97
PluDJC_11740	<i>mhpB</i>	Similar to 2,3-dihydroxyphenylpropionate 1,2-dioxygenase	WP_011146460.1	NS	-33.64
PluDJC_11745	<i>hcaD</i>	Similar to 3-phenylpropionate dioxygenase ferredoxin-NAD(+) reductase component, putative secreted protein	WP_011146461.1	NS	-25.21
PluDJC_11845	<i>bioD</i>	ATP-dependent dethiobiotin synthetase BioD	WP_011146478.1	-4.50	-25.51
PluDJC_12070	<i>bglA</i>	6-phospho-beta-glucosidase A	WP_011146522.1	NS	-10.08
PluDJC_12090		Glyoxalase	WP_041380079.1	3.59	NS
PluDJC_12115		Some similarities with entry exclusion protein 2 (Exc2)	WP_011146530.1	3.62	NS
PluDJC_12285		Probable siderophore receptor, Similar to the pesticin receptor precursor FuyA	WP_011146558.1	-7.25	NS
PluDJC_12380		Some similarities with acyl-CoA oxidase	WP_011146572.1	NS	-13.15
PluDJC_12405		Some similarities with decarboxylase	WP_041380082.1	10.44	NS
PluDJC_13360	<i>xthA</i>	Exodeoxyribonuclease III (exonuclease III) (EXO III) (AP endonuclease VI)	WP_011146772.1	NS	5.13
PluDJC_13795	<i>aroH</i>	Phospho2-dehydro-3-deoxyheptonate aldolase, trp-sensitive (3-deoxy-D-arabinoheptulosonate 7-phosphate synthase)	WP_011146852.1	-3.19	NS
PluDJC_14120	<i>pip</i>	Proline iminopeptidase (PIP)	WP_011146913.1	6.99	NS

PluDJC_14145	<i>sdaA</i>	L-serine dehydratase 1 (SDH 1)	WP_011146918.1	-3.18	NS
PluDJC_14335		Similar to peptide synthetases like lichenysin synthetase A or bacitracin synthetase	WP_011146954.1	NS	-5.28
PluDJC_14730	<i>pepT</i>	Peptidase T (aminotripeptidase) (tripeptidase)	WP_011147030.1	-4.94	NS
PluDJC_14760		Similar to pyoverdine biosynthesis protein PvcA of <i>Pseudomonas aeruginosa</i>	WP_011147036.1	NS	-58.09
PluDJC_14765		Similar to pyoverdine biosynthesis protein PvcB of <i>Pseudomonas aeruginosa</i>	WP_011147037.1	NS	-297.45
PluDJC_14790	<i>ndh</i>	NADH dehydrogenase	WP_011147041.1	-3.26	NS
PluDJC_14895		NAD(P)-dependent oxidoreductase	WP_011147062.1	3.80	NS
PluDJC_15145		Highly similar to the N-terminal region of siroheme synthase activity	WP_011147184.1	-5.55	NS
PluDJC_15150		Similar to PduX protein	WP_041380147.1	-9.55	NS
PluDJC_15155	<i>cobD</i>	Aminotransferase	WP_041380149.1	-8.61	-3.97
PluDJC_15160		Highly similar to the C-terminal region of siroheme synthase activity	WP_041380961.1	-7.93	-6.32
PluDJC_15170	<i>eutB</i>	Ethanolamine ammonia-lyase heavy chain	WP_011147189.1	NS	-4.49
PluDJC_15175	<i>eutC</i>	Ethanolamine ammonia-lyase light chain	WP_011147190.1	NS	-4.98
PluDJC_15410		unknown, Similar to putative galactosyl transferase or beta-glucosyltransferase	WP_011147235.1	NS	26.38
PluDJC_15530		Dabb family protein	WP_011147256.1	-3.84	NS

PluDJC_15540	<i>paaK</i>	Phenylacetate-coenzyme A ligase (Phenylacetyl-CoA ligase) (PA-CoA ligase)	WP_011147258.1	-3.45	NS
PluDJC_15545		Similar to branched-chain amino acid aminotransferase	WP_011147259.1	-3.27	NS
PluDJC_15550		Some similarities with prephenate dehydratase	WP_011147260.1	-3.49	NS
PluDJC_15555		Carboxymuconolactone decarboxylase family protein	WP_011147261.1	-3.05	NS
PluDJC_15560		Similar to ornithine cyclodeaminase	WP_011147262.1	-3.16	NS
PluDJC_15695	<i>menE</i>	O-succinylbenzoic acid--CoA ligase (OSB-CoA synthetase) (O-succinylbenzoate-CoA synthase)	WP_011147286.1	-3.58	NS
PluDJC_15705	<i>menB</i>	naphthoate synthase (dihydroxynaphthoic acid synthetase) (DHNA synthetase)	WP_011147288.1	-3.53	NS
PluDJC_15710		Similar to putative enzyme YfbB of Escherichia coli	WP_011147289.1	-9.86	NS
PluDJC_15715	<i>menD</i>	menaquinone biosynthesis protein menD	WP_011147290.1	-7.50	-4.04
PluDJC_15825	<i>ackA</i>	Acetate kinase (acetokinase)	WP_011147312.1	-6.63	NS
PluDJC_15830	<i>pta</i>	Phosphate acetyltransferase (phosphotransacetylase)	WP_071824169.1	-5.09	NS
PluDJC_15865		Similar to cysteine desulfurase (NifS protein homolog)	WP_041380178.1	3.17	NS
PluDJC_16320	<i>hutH</i>	Histidine ammonia-lyase (histidase)	WP_011147399.1	8.31	NS
PluDJC_16325	<i>hutU</i>	Urocanate hydratase (urocanase) (imidazolonepropionate hydrolase)	WP_011147400.1	8.82	NS
PluDJC_17465	<i>prpD</i>	2-methylcitrate dehydratase	WP_011147720.1	3.17	NS

PluDJC_17470	<i>prpC</i>	2-methylcitrate synthase (Methylcitrate synthase) (Citrate synthase 2)	WP_011147721.1	5.46	NS
PluDJC_17475	<i>prpB</i>	Probable methylisocitrate lyase (2-methylisocitrate lyase)	WP_011147722.1	7.15	NS
PluDJC_17585		Similar to p-aminobenzoic acid synthase	WP_011147742.1	-4.60	NS
PluDJC_17590		Similar to PapB protein and to chorismate mutase/prephenate dehydrogenase	WP_011147743.1	-4.18	NS
PluDJC_17595		Similar to class II aminotransferase and 5-aminolevulinic acid synthase	WP_011147744.1	-4.94	NS
PluDJC_17600		Similar to putative methylase and with protoporphyrinogen oxidase	WP_011147745.1	-3.97	NS
PluDJC_17605		Similar to N-formimidoyl fortimicin A synthase	WP_011147746.1	-4.25	NS
PluDJC_17655		Some similarities with hemagglutinin/hemolysin-related protein.	WP_011147762.1	6.04	NS
PluDJC_17660	<i>gcvP</i>	glycine dehydrogenase [decarboxylating] (glycine decarboxylase) (glycine cleavage system P-protein)	WP_011147763.1	4.46	NS
PluDJC_17670	<i>gcvT</i>	Aminomethyltransferase (glycine cleavage system T protein)	WP_011147765.1	3.04	NS
PluDJC_17715	<i>rpiA</i>	Ribose 5-phosphate isomerase A (phosphoriboisomerase A)	WP_011147773.1	NS	5.23
PluDJC_17800	<i>pdhR</i>	Pyruvate dehydrogenase complex repressor	WP_011147791.1	-4.23	NS
PluDJC_18080	<i>speA</i>	Biosynthetic arginine decarboxylase (ADC)	WP_011147844.1	-3.59	NS
PluDJC_18090	<i>sprT</i>	Protein SprT	WP_011147847.1	-3.33	NS

PluDJC_18115		Some similarities with DNA primase.	WP_011145462.1	NS	-5.03
PluDJC_18390	<i>abgT</i>	Aminobenzoyl-glutamate transport protein	WP_011147866.1	7.11	NS
PluDJC_18395	<i>abgB</i>	Aminobenzoyl-glutamate utilization protein B	WP_011147867.1	6.15	NS
PluDJC_18400	<i>abgA</i>	Aminobenzoyl-glutamate utilization protein A	WP_011147868.1	6.70	NS
PluDJC_18420		Similar to aminotransferases	WP_011147872.1	5.18	NS
PluDJC_18485	<i>wzc</i>	Tyrosine-protein kinase Wzc	WP_011147884.1	-9.39	NS
PluDJC_18490	<i>wzb</i>	Low molecular weight protein-tyrosine-phosphatase Wzb	WP_011147885.1	-8.00	NS
PluDJC_18810	<i>ppiB</i>	Peptidyl-prolyl cis-trans isomerase B (PPIase B) (rotamase B)	WP_011147946.1	NS	-4.39
PluDJC_19340	<i>ggt</i>	Gamma-glutamyltranspeptidase	WP_011148043.1	6.46	NS
PluDJC_19410		Some similarities with polyketide synthase and peptide synthetase	WP_011148054.1	NS	-6.63
PluDJC_19615	<i>ribB</i>	3,4-dihydroxy-2-butanone 4-phosphate synthase (DHBP synthase)	WP_011148096.1	3.42	NS
PluDJC_20395	<i>genX</i>	Putative lysyl-tRNA synthetase (Lysine-tRNA ligase)	WP_011148239.1	4.46	-4.74
PluDJC_20195		Isocitrate/isopropylmalate dehydrogenase family protein	WP_011148202.1	30.71	NS
PluDJC_20200		Alpha/beta hydrolase	WP_011148203.1	48.49	NS
PluDJC_20205		3-hydroxy-3-methylglutaryl-CoA lyase	WP_011148204.1	43.31	NS
PluDJC_20370		Sel1 repeat family protein	WP_011148234.1	-10.72	NS

PluDJC_20410	<i>frdA</i>	Fumarate reductase flavoprotein subunit	WP_011148241.1	-4.94	-11.96
PluDJC_20415	<i>frdB</i>	Fumarate reductase iron-sulfur protein	WP_011148242.1	NS	-21.02
PluDJC_20420	<i>frdC</i>	Fumarate reductase 15 kDa hydrophobic protein	WP_011148243.1	NS	-14.13
PluDJC_20425	<i>frdD</i>	Fumarate reductase 13 kDa hydrophobic protein	WP_011148244.1	NS	-7.97
PluDJC_20545		Similar to unknown protein and to dihydrodipicolinate reductase	WP_011148266.1	NS	-9.74
PluDJC_20640		GNAT family N-acetyltransferase	WP_011148282.1	-15.08	NS
PluDJC_20645		Similar to the phenylacetyl-CoA ligase (in the phenylacetic acid catabolic pathway)	WP_011148283.1	-21.24	NS
PluDJC_20650		Some similarities with fatty-acyl-CoA reductase	WP_011148284.1	-25.93	NS
PluDJC_20655		Acyl-protein synthase	WP_011148285.1	-48.11	-5.67
PluDJC_20965	<i>lecB-like</i>	Fucose-binding lectin II	WP_011148336.1	NS	-108.18
PluDJC_20980	<i>ppxB</i>	Photopexin B	WP_011148341.1	3.08	NS
PluDJC_21215	<i>iunH</i>	Inosine-uridine preferring nucleoside hydrolase (IU-nucleoside hydrolase) (purine nucleosidase)	WP_011148384.1	4.88	NS
PluDJC_21220		Similar to glycosyltransferase	WP_011148385.1	NS	-5.98
PluDJC_21285	<i>pcp</i>	Pyrrolidone-carboxylate peptidase (5-oxopropyl-peptidase) (Pyroglutamyl-peptidase I) (PGP-I) (Pyrase)	WP_011148398.1	NS	-25.28
PluDJC_21290	<i>pcxpA</i>	LamB/YcsF family protein	WP_041380395.1	NS	-10.98
PluDJC_21295		5-oxoprolinase/urea amidolyase family protein	WP_011148400.1	NS	-10.18
PluDJC_21305	<i>rtcB</i>	Protein RtcB	WP_041381186.1	NS	-6.42

PluDJC_21310		Nucleotidyltransferase domain-containing protein	WP_011148403.1	NS	-9.58
PluDJC_21450		Some similarities with dioxygenase	WP_082303140.1	-3.11	-4.64
PluDJC_21515	<i>uvrA</i>	Exconuclease ABC subunit A	WP_011148440.1	NS	3.69
PluDJC_22270	<i>nrdD</i>	Anaerobic ribonucleoside-triphosphate reductase	WP_011148579.1	-4.95	NS
PluDJC_22275	<i>nrdG</i>	Anaerobic ribonucleoside-triphosphate reductase activating protein (class III anaerobic ribonucleotide reductase small component)	WP_011148580.1	-5.60	NS
PluDJC_22305		Prenyltransferase	WP_041380416.1	-3.53	NS
PluDJC_22310		Some similarities with 3-hydroxy-3-methylglutaryl coenzyme A reductase	WP_011148587.1	-9.05	NS
PluDJC_22315		Similar to phosphoenolpyruvate synthase	WP_049789807.1	-5.70	NS
PluDJC_22380	<i>deaD</i>	Inducible ATP-independent RNA helicase	WP_011148599.1	-3.79	NS
PluDJC_23160	<i>ilvC</i>	Ketol-acid reductoisomerase	WP_011148738.1	-5.93	NS
PluDJC_23375	<i>rpsK</i>	30S ribosomal protein S11	WP_002919257.1	NS	-4.12
PluDJC_23405	<i>rpsE</i>	30S ribosomal protein S5	WP_011148778.1	NS	-3.52
PluDJC_24320		Class I SAM-dependent methyltransferase	WP_041380442.1	-3.83	NS
PluDJC_24355	<i>ppyS</i>	Photopyrone synthase	WP_041380444.1	NS	-16.83
PluDJC_24550		Similar to macrolide-efflux protein	WP_011148938.1	-4.85	NS
PluDJC_24555		Similar to sugar kinase	WP_011148939.1	-4.26	NS

Phage related

PluDJC_00055	Probable tail synthesis	WP_011144422.1	NS	-5.75
PluDJC_00060	Probable tail synthesis	WP_011144423.1	NS	-24.74
PluDJC_00065	Probable essential tail protein; putative tail length determinant	WP_011144424.1	NS	-17.45
PluDJC_00070	Probable tail synthesis	WP_071824073.1	NS	-22.74
PluDJC_00075	Probable tail synthesis	WP_011144426.1	NS	-32.29
PluDJC_00080	Probable tail tube structure	WP_011144427.1	NS	-28.22
PluDJC_00085	Probable tail sheath structure	WP_011144428.1	NS	-33.96
PluDJC_00110	Probable tail fiber synthesis	WP_011144432.1	NS	-10.38
PluDJC_00115	Probable tail fiber synthesis	WP_011144433.1	NS	-20.69
PluDJC_00120	Probable tail fiber synthesis	WP_011144434.1	NS	-17.79
PluDJC_00125	Probable tail baseplate synthesis	WP_011144435.1	NS	-27.17
PluDJC_00130	Probable tail baseplate synthesis	WP_011144436.1	NS	-17.80
PluDJC_00135	Probable tail baseplate synthesis	WP_011144437.1	NS	-20.68
PluDJC_00140	Probable tail baseplate synthesis	WP_011144438.1	NS	-23.18
PluDJC_00145	Probable tail synthesis	WP_011144439.1	NS	-14.75
PluDJC_00170	Putative tail fiber synthesis	WP_041379846.1	NS	-14.76
PluDJC_00175	Putative tail fiber synthesis	WP_049789712.1	NS	-19.72
PluDJC_01385	Phage integrase family	WP_011144659.1	7.46	NS
PluDJC_02265	Some similarities with gp31 protein of bacteriophage	WP_011144849.1	NS	10.49

PluDJC_02270	Some similarities with gp31 protein of bacteriophage	WP_011144850.1	NS	11.21
PluDJC_02275	Some similarities with gp31 protein of bacteriophage	WP_041379889.1	NS	6.08
PluDJC_02280	Some similarities with gp31 protein of bacteriophage	WP_011144852.1	NS	6.15
PluDJC_04185	Some similarities with gp31/30 protein of bacteriophage	WP_011145192.1	NS	5.06
PluDJC_04190	Some similarities with gp31/30 protein of bacteriophage	WP_011145193.1	NS	12.69
PluDJC_04195	Some similarities with gp31/30 protein of bacteriophage	WP_011145194.1	NS	19.59
PluDJC_04220	Some similarities with gp31 protein of bacteriophage	WP_041379929.1	NS	8.33
PluDJC_04225	Some similarities with gp31 protein of bacteriophage	WP_011145197.1	NS	6.17
PluDJC_04230	Some similarities with gp31 protein of bacteriophage	WP_011145198.1	NS	8.94
PluDJC_07380	Some similarities with gp30 protein of Bacteriophage	WP_011145795.1	3.22	8.88
PluDJC_10545	Similar to putative tail fiber protein	WP_011146278.1	NS	-6.28
PluDJC_10860	Some similarities with DNA inversion product	WP_011146290.1	NS	-7.84
PluDJC_10865	Some similarities with putative tail fiber protein of prophage	WP_011146291.1	NS	-6.84

PluDJC_10945	Some similarities with unknown protein from a prophage	WP_011146304.1	NS	-5.13
PluDJC_12220	Probable bacteriophage protein	WP_011146551.1	-3.19	NS
PluDJC_12290	Similar to putative transmembrane protein and signal transducers like Irp8.	WP_011146559.1	-3.36	NS
PluDJC_15090	Probable bacteriophage protein	CAE15331.1	-3.96	NS
PluDJC_15100	Some similarities with bacteriophage protein	WP_011147178.1	NS	-17.37
PluDJC_15105	Similar to bacteriophage tail fiber protein	WP_011147180.1	-3.46	NS
PluDJC_15110	Similar to bacteriophage tail fiber protein	WP_011147181.1	-3.27	NS
PluDJC_15395	Similar to putative phage protein	WP_011147238.1	NS	4.97
PluDJC_15440	Some similarities with putative tail fiber protein	WP_011147239.1	NS	11.92
PluDJC_15445	Similar to putative phage protein	WP_011147240.1	NS	22.37
PluDJC_15450	Similar to putative tail fiber protein from a lambdoid prophage	WP_011147241.1	NS	14.83
PluDJC_15455	Similar to Sc/SvQ protein of Escherichia coli plasmid p15B	WP_011147242.1	NS	21.09
PluDJC_15460	Probable phage protein	WP_011147243.1	NS	33.08
PluDJC_15465	Probable phage protein	WP_011147244.1	NS	15.38
PluDJC_15470	Probable phage protein	WP_011147245.1	NS	27.52
PluDJC_15475	Probable phage protein	WP_011147246.1	NS	22.90
PluDJC_15480	Probable phage protein	WP_011147247.1	NS	31.28

PluDJC_15485	Probable phage protein	WP_011147248.1	NS	33.40
PluDJC_15490	Probable phage protein	WP_011147249.1	NS	21.03
PluDJC_15495	Probable phage protein	WP_011147250.1	NS	20.87
PluDJC_15500	Probable phage protein	WP_011147251.1	NS	23.09
PluDJC_15505	Probable phage protein	WP_011147252.1	NS	10.55
PluDJC_15510	Probable phage protein	WP_011147253.1	NS	14.07
PluDJC_15515	Probable phage protein	WP_011147254.1	NS	16.87
PluDJC_15520	Probable phage protein	WP_011147255.1	5.18	10.97
PluDJC_18800	Some similarities with prophage tail fiber protein	WP_011147944.1	NS	-3.66
PluDJC_21620	Similar to bacteriophage tail fiber assembly protein	WP_041380400.1	-5.30	NS
PluDJC_21625	Some similarities with the N-terminal region of unknown bacteriophage protein	WP_011148460.1	-5.66	NS

Membrane proteins

PluDJC_00380	Highly similar to putative membrane protein Yjch of Escherichia coli	WP_011144479.1	5.74	NS
PluDJC_09035	Probable porin	WP_011146031.1	3.57	NS
PluDJC_10015	Hypothetical transmembrane protein	WP_011146190.1	4.34	NS
PluDJC_10245	Similar to putative PagC-like membrane protein (virulence-related membrane protein) of Escherichia coli O157:H7	WP_011146228.1	NS	9.56

PluDJC_11335	Some similarities with probable membrane protein YdgF of Escherichia coli	WP_011146377.1	NS	16.37
PluDJC_11545	Hypothetical transmembrane protein	WP_011146417.1	-9.96	NS
PluDJC_13455	Hypothetical protein with candidate membrane-spanning segments	WP_011146792.1	4.28	9.43
PluDJC_13830	Hypothetical transmembrane protein	WP_011146859.1	-4.37	NS
PluDJC_15125	Some similarities to membrane protein	WP_011147182.1	NS	19.56
PluDJC_15415	Some similarities with probable membrane protein YbiP of Escherichia coli	CAE15391.1	NS	22.99
PluDJC_21275	Similar to putative membrane protein	WP_011148396.1	NS	-10.30
PluDJC_22250	Putative transmembrane protein	WP_041380415.1	-25.64	NS

Transporter

PluDJC_00375	Probable permease	WP_011144478.1	5.71	NS	
PluDJC_00945	Probable dicarboxylate transporter	WP_011144574.1	6.38	NS	
PluDJC_00950		WP_011144575.1	6.05	NS	
PluDJC_00955		WP_011144576.1	3.51	NS	
PluDJC_01120	<i>feoB</i>	Ferrous iron transport protein B	WP_011144608.1	4.47	NS
PluDJC_01125	<i>feoA</i>	Ferrous iron transport protein A	WP_011144609.1	4.86	11.91
PluDJC_01580	EamA-like transporter family protein	WP_011144696.1	NS	-10.46	
PluDJC_02330	MFS transporter	WP_011144862.1	-3.12	NS	

PluDJC_02935	<i>nhaA</i>	Na(+)/H(+) antiporter 1 (sodium/proton antiporter 1)	WP_011144966.1	NS	4.54
PluDJC_03195		Lipid A ABC transporter ATP-binding protein/permease MsbA	WP_041379908.1	15.46	NS
PluDJC_04800		MFS transporter	WP_011145302.1	16.36	NS
PluDJC_06170	<i>proW</i>	Glycine betaine/L-proline ABC transporter, permease	WP_011145606.1	NS	4.69
PluDJC_06175	<i>proV</i>	Glycine betaine/L-proline ABC transporter, ATP-binding component	WP_011145607.1	NS	3.96
PluDJC_08360	<i>focA</i>	Formate transporter 1 FocA (Formate channel 1)	WP_011145906.1	NS	-10.14
PluDJC_10255	<i>dsdX</i>	Probable D-serine permease	WP_011146230.1	NS	-9.64
PluDJC_10855	<i>aqpZ</i>	Transmembrane water channel, aquaporin Z	WP_011146289.1	-3.30	NS
PluDJC_11703		Probable transporter	WP_082303125.1	NS	-11.39
PluDJC_11750		Probable transporter, Highly similar to oligopeptide-binding protein precursor OppA	WP_011146463.1	NS	-11.68
PluDJC_12400		Highly similar to tyrosine-specific transport system TyrP of Escherichia coli	WP_011146576.1	8.80	NS
PluDJC_12450		Probable transporter, Similar to oligopeptide-binding protein precursor	WP_011146586.1	-7.90	NS
PluDJC_13080	<i>oppF</i>	Oligopeptide ABC transporter	WP_011146712.1	5.50	NS
PluDJC_13085	<i>oppD</i>		WP_011146713.1	5.95	NS
PluDJC_13090	<i>oppC</i>		WP_011146714.1	5.86	NS

PluDJC_13095	<i>oppB</i>		WP_011146715.1	7.05	NS
PluDJC_13100	<i>oppA2</i>	Periplasmic-binding protein precursor OppA2	WP_011146716.1	7.96	NS
PluDJC_13105	<i>oppA1</i>	Periplasmic-binding protein precursor OppA1	WP_011146717.1	3.46	NS
PluDJC_16265	<i>tctC</i>	Probable tricarboxylic tansporte	WP_011147388.1	4.27	NS
PluDJC_16315		Highly similar to amino acid permease (proline-specific permease ProY of Escherichia coli)	WP_011147398.1	7.56	NS
PluDJC_18425		Probable Na ⁺ /H ⁺ antiporter	WP_011147873.1	5.44	NS
PluDJC_18445		Probable magnesium transporter	WP_011147877.1	3.63	NS
PluDJC_18470		Probable amino acid transporter	WP_011147881.1	11.11	NS
PluDJC_18495		Probable polysaccharide transporter	WP_011147886.1	-5.05	-4.50
PluDJC_18795		AEC family transporter	WP_011147943.1	6.71	NS
PluDJC_19770	<i>sstT</i>	Serine/threonine transporter SstT	WP_011148123.1	6.11	NS
PluDJC_21145		APC family permease	WP_011148370.1	NS	11.02
PluDJC_21925		Probable transporter	WP_011148514.1	-5.91	NS
PluDJC_22355		Probable ABC transporter	WP_011148595.1	15.46	NS

Virulence factors

Toxins

PluDJC_04120	<i>tccB3</i>	unknown, probable Insecticidal toxin complex protein TccB3	WP_011145180.1	3.47	NS
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PluDJC_10985		Probable toxin, Some similarities with putative adhesin, invasin and intimin	WP_011146312.1	NS	18.17
PluDJC_20255		Hypothetical insectidal toxins, Some similarities with putative juvenile hormone esterase	WP_011148213.1	NS	-7.05
PluDJC_20260		Hypothetical toxin	WP_011148214.1	NS	-11.71
PluDJC_20375		Putative toxin	WP_011148235.1	-8.38	NS
Antibiotic					
Synthesis					
PluDJC_04515		Some similarities with killer protein of pyocin S3	WP_011145251.1	4.37	17.63
PluDJC_04530		Similar to C-terminal region of klebicin B, pyocin S2 and the killer protein of pyocin S1	WP_071824155.1	4.61	26.04
PluDJC_04540		Similar to killer protein of pyocin S3	WP_082303108.1	11.65	NS
PluDJC_04580		Probable protein involved in antibiotic biosynthesis	WP_011145262.1	-11.29	NS
PluDJC_04585		Probable protein involved in antibiotic biosynthesis	WP_011145263.1	-5.06	NS
PluDJC_04590		Probable protein involved in antibiotic biosynthesis	WP_011145264.1	-4.90	NS
PluDJC_04860		Antibiotic biosynthesis monooxygenase	WP_011145312.1	-6.05	NS
PluDJC_09845		Some high similarities with killer protein of pyocin S3	--	7.84	NS
PluDJC_09855		Probable toxin, Similar to pyocin S2 and S1	--	7.56	NS
PluDJC_11880	<i>sttA</i>	Stilbene A, Similar to histidine ammonia-lyase	WP_011146484.1	-4.95	NS
PluDJC_15990		Probable protein involved in antibiotic biosynthesis	WP_011147343.1	NS	-5.47

PluDJC_16670	Highly similar to proteins involved in antibiotic biosynthesis	WP_011147463.1	-5.58	NS
Resistance				
PluDJC_04520	Similar to colicin / pyocin immunity protein	WP_011145252.1	4.91	29.69
PluDJC_04525		WP_011145253.1	3.64	40.95
PluDJC_04535		WP_011145254.1	4.81	38.58
PluDJC_04545		WP_011145255.1	8.96	NS
PluDJC_04550		WP_011145256.1	8.74	NS
PluDJC_04555		WP_011145257.1	4.52	NS
PluDJC_06645	Similar to metal-dependent hydrolases of the beta-lactamase superfamily II	WP_011145677.1	-10.08	-17.03
PluDJC_09840	Similarities with immunity protein of pyocin S3	WP_011146156.1	6.99	NS
PluDJC_09850	Similar to colicin E2 immunity protein	WP_011146157.1	11.22	NS
PluDJC_20210	Similar to putative transport protein and multidrug resistance protein	WP_011148206.1	25.30	NS
PluDJC_20605	Similar to pyocin S3 immunity protein	WP_011148275.1	3.46	NS
PluDJC_20610		WP_011148276.1	3.73	NS
PluDJC_20615		WP_011148277.1	3.32	NS
PluDJC_20625		WP_011148279.1	NS	8.66
PluDJC_20630		WP_011148280.1	3.46	6.73
PluDJC_21500		MBL fold metallo-hydrolase	WP_011148437.1	NS

LPS

O-antigen biosynthesis

PluDJC_24130	<i>wbO</i>	Predicted sugar 1-phosphate nucleotidyltransferase	WP_011148859.1	NS	9.33
PluDJC_24135	<i>wbQ</i>	Similar to amino or hexapeptide transferase	WP_011148860.1	NS	32.72
PluDJC_24140	<i>wbA</i>	Similar to sugar or UDP-sugar dehydrogenases	WP_011148861.1	-3.34	NS
PluDJC_24205	<i>wbB</i>	Similar to sugar or UDP-sugar dehydrogenases	WP_011148874.1	-3.32	NS
PluDJC_24215	<i>wbC</i>	Similar to amino or hexapeptide transferase	WP_041380434.1	-3.08	NS
PluDJC_24220	<i>wzxB</i>	Putative O-antigen translocase	WP_041380435.1	NS	10.32

Regulators

PluDJC_00050	<i>ogrK</i>	Probable positive regulator of phage P2 late gene transcription	WP_011144421.1	NS	-9.65
PluDJC_00940	<i>uxuR</i>	Uxu operon transcriptional regulator	WP_011144573.1	3.39	NS
PluDJC_01435		CaiF/GrlA family transcriptional regulator	WP_011144669.1	4.81	NS
PluDJC_02000		Putative transcriptional regulator, LysR-family	WP_011144796.1	5.64	NS
PluDJC_02795	<i>arcA</i>	Negative response regulator of genes in aerobic pathways	WP_011144944.1	-3.20	NS
PluDJC_04155	<i>uhpC</i>	Regulatory protein UhpC	WP_082303107.1	4.80	NS
PluDJC_04255	<i>agaR</i>	Putative aga operon transcriptional repressor	WP_011145204.1	3.43	NS
PluDJC_04695	<i>ner-like</i>	Probable transcriptional regulator	WP_011145282.1	41.68	28.05

PluDJC_04840	<i>ner-like</i>	Probable transcriptional regulator	WP_011145309.1	-4.40	NS	
PluDJC_04850		LuxR family transcriptional regulator	WP_011145310.1	15.28	NS	
PluDJC_04865		MarR family transcriptional regulator	WP_011145313.1	-5.49	NS	
PluDJC_05030	<i>hpaA</i>	Regulator of the 4HPA-hydroxylase operon	WP_011145343.1	4.76	NS	
PluDJC_07465		Transcriptional regulator	WP_041380007.1	-3.04	NS	
PluDJC_09555		LuxR family transcriptional regulator	WP_011146094.1	NS	30.76	
PluDJC_10335		MurR/RpiR family transcriptional regulator	WP_011146246.1	3.31	NS	
PluDJC_10355	<i>fimB</i>	Similar to type 1 fimbriae regulatory recombinase protein of Escherichia coli	WP_011146249.1	3.17	7.88	
PluDJC_10415		Transcription regulator, LuxR family (PAS4)	WP_011146260.1	4.45	5.96	
PluDJC_10420			WP_011146261.1	6.52	NS	
PluDJC_10430			WP_011146262.1	4.51	NS	
PluDJC_10435			WP_011146263.1	6.34	NS	
PluDJC_10440			WP_011146264.1	6.48	NS	
PluDJC_10445			WP_011146265.1	5.92	NS	
PluDJC_10450			WP_011146266.1	4.73	NS	
PluDJC_10460			WP_011146267.1	3.65	NS	
PluDJC_12280			AraC family transcriptional regulator	WP_011146557.1	-3.63	NS
PluDJC_13835			AraC family transcriptional regulator	WP_011146860.1	-6.72	NS
PluDJC_16255	<i>tctD</i>	Two-component response regulator	WP_011147386.1	7.16	NS	

PluDJC_18380		Transcriptional regulator LuxR family	WP_011147865.1	NS	8.30
PluDJC_18405	<i>abgR</i>	Putative transcriptional regulator AbgR	WP_011147869.1	3.90	NS
PluDJC_21150		Transcriptional regulator, LuxR family	WP_011148371.1	3.93	NS
PluDJC_20190		RraA family protein	WP_011148201.1	21.51	NS
PluDJC_21240		Transcriptional regulator, HTH-XRE superfamily	WP_011148389.1	469.99	65.30
PluDJC_21265		Transcriptional regulator, HTH-XRE superfamily	WP_011148394.1	-42.73	-49.00
PluDJC_22590	<i>pluR</i>	Transcriptional regulator, LuxR family (PluR)	WP_011148637.1	-3.30	-9.26
PluDJC_23170		Some similarities with probable transcriptional regulator LumQ	WP_011148740.1	-3.74	NS

Adhesion

Fimbrial

PluDJC_01390		Some similarities with type 1 fimbrial protein precursor	WP_011144660.1	11.75	11.64
PluDJC_01395		Putative fimbrial chaperone	WP_011144661.1	6.37	5.18
PluDJC_01400		unknown	WP_011144662.1	7.54	5.23
PluDJC_01405		Similar to putative fimbrial protein	WP_011144663.1	5.92	6.62
PluDJC_01410		unknown	WP_041379865.1	3.97	6.75
PluDJC_01415		Putative fimbrial chaperone	WP_011144665.1	5.58	6.56
PluDJC_01420		Putative fimbrial chaperone	WP_011144666.1	6.55	4.67
PluDJC_01425		Probable export and assembly of type 1 fimbriae	WP_049789718.1	5.73	NS

PluDJC_02045		Probable recombinase involved in the regulation of fimbrial operon	WP_011144805.1	8.70	NS
PluDJC_02510		Some similarities with major fimbrial subunit precursor. Putative secreted protein	WP_011144892.1	-3.65	NS
PluDJC_03915	<i>mrfA</i>	Highly similar to major structural subunit MrpA of <i>Proteus mirabilis</i> - cell adhesion	WP_011145143.1	-40.49	NS
PluDJC_03920	<i>mrfB</i>	MrfB protein, by similarities may function as the terminator for fimbrial assembly.	WP_011145144.1	-25.58	NS
PluDJC_03925	<i>mrfC</i>	Probable export and assembly of type 1 fimbriae	WP_011145145.1	-7.48	NS
PluDJC_03930	<i>mrfD</i>	Highly similar to periplasmic fimbrial chaperone precursor MrpD of <i>Proteus mirabilis</i>	WP_011145146.1	-4.26	NS
PluDJC_03935	<i>mrfX</i>	Fimbrial minor pilin protein precursor	WP_011145147.1	-6.58	NS
PluDJC_03940	<i>mrfE</i>	Minor fimbrial subunit and to MrpE from fimbrial operon	WP_011145148.1	-4.17	NS
PluDJC_03945	<i>mrfF</i>	Minor fimbrial subunit protein MrpF of <i>Proteus mirabilis</i>	WP_011145149.1	-3.85	NS
PluDJC_03950	<i>mrfG</i>	Fimbrial protein MrpG of <i>Proteus mirabilis</i> , a putative minor subunit of the MR/P fimbria, functions as an adhesin responsible for hemagglutination.	WP_011145150.1	-6.09	NS
PluDJC_04005		unknown	WP_011145160.1	NS	-16.63
PluDJC_04010		Putative fimbrial chaperone	WP_011145161.1	NS	-17.27
PluDJC_04015		unknown	WP_011145162.1	NS	-16.77
PluDJC_04020		Putative fimbrial chaperone	WP_011145163.1	NS	-24.51

PluDJC_05115	<i>phfC</i>	Putative fimbrial chaperone	WP_011145359.1	-6.19	NS
PluDJC_05120	<i>phfS</i>	Probable fimbrial adhesin	WP_011144660.1	-4.81	NS

Nonfimbrial

PluDJC_07690		Similar to dictyostelium discoideum calcium-dependent cell adhesion molecule-1	WP_011145858.1	NS	-30.20
PluDJC_13040		Attachment protein	WP_011146704.1	-3.66	NS

Motility and Chemotaxis

Flagella formation

PluDJC_09685	<i>flhD</i>	flagellar transcriptional activator	WP_011146117.1	3.15	NS
PluDJC_09860	<i>flhB</i>	Flagellar biosynthetic protein FlhB	WP_011146159.1	3.41	NS
PluDJC_09950	<i>flgB</i>	Flagellar basal-body rod protein FlgB (Putative proximal rod protein)	WP_011146177.1	6.74	NS
PluDJC_09955	<i>flgC</i>	Flagellar basal-body rod protein FlgC (Putative proximal rod protein)	WP_011146178.1	6.63	NS
PluDJC_09960	<i>flgD</i>	Basal-body rod modification protein FlgD (flagellar protein for the initiation of hook assembly)	WP_011146179.1	5.76	NS
PluDJC_09965	<i>flgE</i>	Flagellar hook protein FlgE	WP_011146180.1	5.35	NS
PluDJC_09970	<i>flgF</i>	Flagellar basal-body rod protein FlgF (Putative proximal rod protein)	WP_011146181.1	4.87	NS
PluDJC_09975	<i>flgG</i>	Flagellar basal-body rod protein FlgG (Distal rod protein)	WP_011146182.1	4.95	NS

PluDJC_09980	<i>flgH</i>	Flagellar L-ring protein precursor (Basal body L-ring protein)	WP_011146183.1	3.26	NS
PluDJC_09985	<i>flgI</i>	Flagellar P-ring protein precursor (Basal body P-ring protein)	WP_011146184.1	3.28	NS
PluDJC_09995	<i>flgK</i>	Flagellar hook-associated protein 1 (HAP1)	WP_011146186.1	8.57	4.53
PluDJC_10000	<i>flgL</i>	Flagellar hook-associated protein 3 (HAP3) (Hook-filament junction protein)	WP_011146187.1	8.92	NS
PluDJC_10085	<i>fliL</i>	Flagellar protein FliL	WP_011146204.1	3.71	NS
PluDJC_10095	<i>fliJ</i>	Flagellar protein FliJ	WP_011146206.1	3.06	NS
PluDJC_10100	<i>fliI</i>	Flagellum-specific ATP synthase	WP_011146207.1	3.31	NS
PluDJC_10110	<i>fliG</i>	Flagellar motor switch protein FliG	WP_011146209.1	3.04	NS
PluDJC_10115	<i>fliF</i>	Flagellar basal-body M-ring protein	WP_011146210.1	4.00	NS
PluDJC_10120	<i>fliE</i>	Flagellar hook-basal body 11K protein FliE	WP_011146211.1	4.75	NS
PluDJC_10140	<i>fliT</i>	Flagellar protein FliT	WP_011146213.1	5.08	NS
PluDJC_10145	<i>fliS</i>	Flagellar protein FliS	WP_011146214.1	8.56	NS
PluDJC_10150	<i>fliD</i>	Flagellar hook-associated protein 2 (HAP2) (Filament cap protein)	WP_011146215.1	15.77	4.21
PluDJC_10155	<i>fliC</i>	Flagellin	WP_011146216.1	25.47	NS

Chemoreceptors

PluDJC_09715	<i>cheD</i>	Methyl-accepting chemotaxis protein I (MCP-I) (Serine chemoreceptor protein) = tsr	WP_011146123.1	5.93	NS
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PluDJC_09720	Similar to methyl-accepting chemotaxis protein I (MCP-I) (Serine chemoreceptor protein)	WP_011146124.1	4.01	NS
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Extracellular and secretion related proteins

Type VI secretion system

PluDJC_01820	Type VI secretion system contractile sheath small subunit	WP_011144761.1	NS	19.73
PluDJC_01970	Highly similar to type VI secretion system tube protein Hcp	WP_011144790.1	8.00	NS
PluDJC_10005	Type VI secretion system tip protein VgrG-like	WP_011146188.1	4.10	4.73
PluDJC_13450	Highly similar to type VI secretion system tube protein Hcp	WP_011146791.1	8.38	18.49
PluDJC_16115	Highly similar to type VI secretion system tube protein Hcp	WP_011147363.1	4.35	NS
PluDJC_16550	Type VI secretion system lipoprotein TssJ-like	WP_011147441.1	4.22	NS
PluDJC_16595	Type VI secretion system tip protein VgrG-like	WP_011147450.1	4.71	NS
PluDJC_16640	Highly similar to type VI secretion system tube protein Hcp	WP_011147458.1	4.19	NS
PluDJC_20795	Highly similar to type VI secretion system tube protein Hcp	WP_011148312.1	8.68	NS
PluDJC_22815	Type VI secretion system baseplate subunit TssF-like	WP_011148673.1	15.73	NS
PluDJC_22820	Type VI secretion system tip protein VgrG-like	WP_011148674.1	13.95	NS

Other

PluDJC_00540		Putative secreted protein	WP_011144510.1	-4.26	-11.47
PluDJC_01210		Unknown, probable hemolysin secretion/activation protein	WP_011144626.1	8.43	NS
PluDJC_02845		Similar to monofunctional chorismate mutase. Putative secreted protein	WP_011144952.1	NS	4.66
PluDJC_03200		HlyD family type I secretion periplasmic adaptor subunit	WP_011145011.1	7.14	NS
PluDJC_05475		Probable hemolysin secretion/activation protein	WP_011145477.1	3.62	NS
PluDJC_05570		Hypothetical secreted protein	WP_011146048.1	NS	13.24
PluDJC_10020		Hypothetical secreted protein	WP_011146191.1	3.20	NS
PluDJC_12275		Probable lipase	WP_011146556.1	7.87	NS
PluDJC_12385		Hypothetical secreted protein	WP_011146573.1	-22.32	NS
PluDJC_15670		Probable hemolysin	WP_011147281.1	9.77	NS
PluDJC_15675		Probable hemolysin secretion/activation protein	WP_011147282.1	7.31	NS
PluDJC_16145	<i>pdl</i>	Lipase	WP_011147368.1	NS	-6.33
PluDJC_16510		Putative secreted protein	WP_011147432.1	3.30	NS
PluDJC_16515		Putative secreted protein	WP_011147433.1	4.59	NS
PluDJC_16575		Putative secreted protein	WP_011147446.1	3.47	NS
PluDJC_16585		Putative secreted protein	WP_011147448.1	4.43	NS

PluDJC_17615		Similar to outer membrane hemolysin activator protein	WP_011147747.1	23.92	NS
PluDJC_21900		Twin-arginine translocation signal domain-containing protein; similar to putative exported protein	WP_011148509.1	NS	-13.32
<u>Other</u>					
PluDJC_01670		Putative AidA protein (quorum-sensing and slow killing of <i>C. elegans</i>)	WP_011144713.1	-101.80	-7.46
PluDJC_01680		Truncated gene. Highly similar in N terminal to VgrG and VgrE related protein of Photorhabdus		8.66	27.93
PluDJC_04355		Truncated gene. Similar to regions of colicin V secretion protein		-54.15	NS
PluDJC_08505		Truncated gene. Some similarities with unknown protein		NS	6.92
PluDJC_08650		Truncated gene. Highly similar to N-term of unknown protein of Photorhabdus		NS	-5.91
PluDJC_09205		Truncated gene, similar to C terminal part of unknown protein		NS	7.47
PluDJC_12460		Similar to chitinase and chitin binding protein precursor	WP_011146588.1	NS	4.43
PluDJC_13025	<i>ompW</i>	Outer membrane protein W precursor	WP_011146701.1	-5.90	-4.86
PluDJC_13840		Some similarities with hypothetical glycine-rich protein	WP_011146861.1	NS	-12.19

PluDJC_14125	<i>yebF</i>	Similar to lipoprotein YebF precursor of Escherichia coli	WP_011146914.1	8.05	NS
PluDJC_14225		Truncated gene. Similar to DNA invertase or putative resolvase		NS	-4.13
PluDJC_16860		Truncated gene. Similar to the N-terminal region of VgrG proteins		3.09	NS
PluDJC_20580		Truncated gene. Highly similar to the N-terminal region of insecticidal toxin complex protein TccZ		3.06	NS
PluDJC_21245	<i>CcdA-like</i>	Similar to CcdA protein which binds to and blocks the activity of CcdB	WP_011148390.1	201.79	NS
PluDJC_21250	<i>CcdB-like</i>	Similarities with the N-terminal region of cytotoxic protein CcdB. Putative truncated protein	WP_011148391.1	26.82	19.37
PluDJC_04125		Type II toxin-antitoxin system HicB family antitoxin	WP_011145181.1	3.28	NS

AI-2 and polyamine related synthesis

PluDJC_03525	<i>metI</i>	D-methionine transport permease protein MetI	WP_011145072.1	-4.25	NS
PluDJC_03530	<i>metN</i>	D-methionine transport ATP-binding protein MetN	WP_011145073.1	-3.86	NS
PluDJC_04305	<i>speD</i>	S-adenosylmethionine decarboxylase proenzyme	WP_011145214.1	NS	6.91
PluDJC_04310	<i>speE</i>	Spermidine synthase (putrescine aminopropyltransferase)	WP_011145215.1	3.55	9.39
PluDJC_06280	<i>gltL</i>	Gutamate/aspartate ABC transporter	WP_011145628.1	6.38	NS
PluDJC_06285	<i>gltK</i>		WP_011145629.1	7.58	NS

PluDJC_06290	<i>gltJ</i>		WP_011145630.1	23.27	NS
PluDJC_06295	<i>gltI</i>		WP_011145631.1	59.42	NS
PluDJC_16065	<i>lsrA</i>	ATP-binding protein of AI-2 transporter	WP_011147354.1	5.47	NS
PluDJC_16070	<i>lsrC</i>	Inner Membrane protein of AI-2 transporter	WP_011147355.1	3.92	NS
PluDJC_16075	<i>lsrD</i>	Inner Membrane protein of AI-2 transporter	WP_011147356.1	3.42	NS
PluDJC_16080	<i>lsrB</i>	Binding Protein of AI-2 transporter	WP_011147357.1	5.72	NS
PluDJC_16085	<i>lsrF</i>	AI-2-processing aldolase	WP_011147358.1	6.12	NS
PluDJC_16090	<i>lsrG</i>	AI-2 processing protein	WP_011147359.1	8.46	NS
PluDJC_18085	<i>metK</i>	S-adenosylmethionine synthetase (methionine adenosyltransferase) (AdoMet synthetase) (MAT)	WP_011147846.1	-4.41	NS
PluDJC_21905	<i>metE</i>	Methionine synthase	WP_011148510.1	-9.11	NS
PluDJC_23675	<i>metF</i>	5,10-methylenetetrahydrofolate reductase	WP_011148819.1	-23.54	NS

Stress response

PluDJC_01585	<i>dppA</i>	Periplasmic dipeptide transport protein precursor DppA	WP_011144697.1	98.34	NS
PluDJC_01590	<i>dppB</i>	Dipeptide transport system permease protein	WP_011144698.1	19.09	NS
PluDJC_01595	<i>dppC</i>	Dipeptide transport system permease protein	WP_011144699.1	14.37	NS
PluDJC_01600	<i>dppD</i>	Dipeptide transport ATP-binding protein DppD	WP_011144700.1	13.76	NS
PluDJC_01605	<i>dppF</i>	Dipeptide transport ATP-binding protein DppF	WP_011144701.1	11.34	NS

PluDJC_07845	<i>cspD</i>	Cold shock-like protein; induced upon starvation or oxidative stress	WP_011145889.1	5.01	NS
PluDJC_10850	<i>usp</i>	Universal stress protein	WP_011146288.1	-4.27	NS
PluDJC_10880	<i>phoH</i>	Phosphate starvation-inducible protein	WP_011146295.1	NS	5.93
PluDJC_18730	<i>cspI</i>	Cold shock-like protein	WP_011147931.1	NS	3.99
PluDJC_22375	<i>cstA</i>	Carbon starvation protein A	WP_011148598.1	NS	4.95

Pigmentation

PluDJC_20685	<i>antI</i>	Anthraquinone biosynthesis	WP_011148290.1	-12.73	-30.02
PluDJC_20690	<i>antH</i>		WP_011148291.1	-12.11	-10.52
PluDJC_20695	<i>antG</i>		WP_011148292.1	-20.86	NS
PluDJC_20700	<i>antF</i>		WP_011148293.1	-30.46	-26.52
PluDJC_20705	<i>antE</i>		WP_011148294.1	-20.61	NS
PluDJC_20710	<i>antD</i>		WP_011148295.1	-35.16	-13.11
PluDJC_20715	<i>antC</i>		WP_011148296.1	-36.69	-15.25
PluDJC_20720	<i>antB</i>		WP_011148297.1	-19.52	-57.15
PluDJC_20725	<i>antA</i>		WP_011148298.1	-19.71	-25.95

CRISPR-Cas

PluDJC_03795	CRISPR-associated cas3-cluster	WP_011145119.1	5.33	4.61
PluDJC_03800		WP_011145120.1	3.96	NS

PluDJC_03805			WP_011145121.1	3.81	NS
PluDJC_03810			WP_011145122.1	4.39	NS
PluDJC_03815			WP_011145123.1	7.67	NS
PluDJC_03820			WP_011145124.1	8.74	NS

Cell clumping

PluDJC_22595	<i>pcfF</i>	Carbamoyl-phosphate synthase subunit	WP_011148638.1	NS	-64.84
PluDJC_22600	<i>pcfE</i>	Efflux transporter	WP_049789808.1	NS	-87.19
PluDJC_22605	<i>pcfD</i>	Carbamoyl transferase, NodU family	WP_011148640.1	NS	-110.61
PluDJC_22610	<i>pcfC</i>	Glycine amidino transferase	WP_011148641.1	NS	-100.05
PluDJC_22615	<i>pcfB</i>	Argininosuccinate synthase	WP_011148642.1	NS	-10.98
PluDJC_22620	<i>pcfA</i>	Cysteine synthase	WP_011148643.1	NS	-10.52

Crystalline inclusions

PluDJC_00865	<i>cipB</i>	Crystalline inclusion protein CipB	WP_011144559.1	NS	-16,21
PluDJC_07765	<i>cipA-like</i>	Similar to crystalline inclusion protein type II (CipA-like protein)	WP_011145872.1	-4.20	-47.76
PluDJC_07770	<i>cipA</i>	Crystalline inclusion protein CipA	WP_011145873.1	-5.01	-27.91

DNA replication, recombination and repair

PluDJC_05285		Probable DNA helicase	WP_011145389.1	NS	9.67
PluDJC_17195	<i>recN</i>	DNA repair protein recN (recombination protein N)	WP_011147558.1	3.43	NS
PluDJC_23045	<i>ISPlu4A</i>	Transposase	WP_011144714.1	NS	-4.01

Bioluminescence

PluDJC_11100	<i>luxC</i>	Fatty acid reductase	WP_011146334.1	NS	-11.56
PluDJC_11105	<i>luxD</i>	Acyl transferase	WP_011146335.1	NS	-10.85

Proteins with unknown function

PluDJC_00425		DUF2282 domain-containing protein	WP_011144488.1	4.55	16.41
PluDJC_00875		Fatty acid desaturase	WP_082303147.1	NS	-6.52
PluDJC_00880		Hypothetical protein	WP_041380490.1	-3.17	NS
PluDJC_00930		Hypothetical protein	CAE12464	4.09	7.15
PluDJC_01045		Hypothetical protein	WP_011144594.1	-3.23	NS
PluDJC_01200		Hypothetical protein	WP_011144624.1	8.26	NS
PluDJC_01205		filamentous hemagglutinin N-terminal domain-containing protein	WP_011144625.1	20.02	NS
PluDJC_01370		Hypothetical protein	WP_011144656.1	85.85	28.50
PluDJC_01375		Hypothetical protein	WP_011144657.1	73.74	32.87
PluDJC_01430		Hypothetical protein	WP_041379866.1	4.90	4.15

PluDJC_01442	Hypothetical protein	WP_041379867.1	4.65	NS
PluDJC_01465	Hypothetical protein	WP_011144675.1	3.50	NS
PluDJC_01470	Hypothetical protein	WP_011144676.1	6.25	NS
PluDJC_01475	Hypothetical protein	WP_011144677.1	6.97	10.93
PluDJC_01480	Hypothetical protein	WP_041380511.1	7.28	12.19
PluDJC_01485	Hypothetical protein	WP_011144680.1	9.86	7.00
PluDJC_01655	Hypothetical protein	WP_011144710.1	-3.18	NS
PluDJC_01915	Hypothetical protein	WP_011144779.1	NS	8.94
PluDJC_01975	Hypothetical protein	WP_011144791.1	NS	18.67
PluDJC_01980	Hypothetical protein	WP_011144792.1	NS	6.34
PluDJC_01990	DUF1240 domain-containing protein	WP_011144794.1	3.32	NS
PluDJC_02610	Hypothetical protein	WP_041379897.1	5.94	NS
PluDJC_02620	DUF692 family protein	WP_011144911.1	23.16	NS
PluDJC_02625	DUF692 family protein	WP_011144912.1	25.75	NS
PluDJC_03205	Hypothetical protein	WP_011145012.1	8.10	NS
PluDJC_03210	Hypothetical protein	WP_011145013.1	7.41	NS
PluDJC_03215	Hypothetical protein	WP_011145014.1	7.55	NS
PluDJC_03220	Hypothetical protein	WP_011145015.1	10.37	NS
PluDJC_03225	Hypothetical protein	WP_011145016.1	9.01	NS
PluDJC_03230	Hypothetical protein	WP_011145017.1	9.69	NS

PluDJC_03235	Hypothetical protein	WP_011145018.1	8.95	NS
PluDJC_03745	Hypothetical protein	WP_011145109.1	-16.23	NS
PluDJC_03755	Hypothetical protein	WP_011145111.1	NS	-11.15
PluDJC_03760	Hypothetical protein	WP_011145112.1	NS	-9.56
PluDJC_03822	Hypothetical protein	WP_011145125.1	5.12	NS
PluDJC_03890	Hypothetical protein	WP_011145138.1	3.24	NS
PluDJC_04360	Hypothetical protein	WP_011145224.1	-9.32	NS
PluDJC_04365	Hypothetical protein	WP_011145225.1	-9.28	-4.60
PluDJC_04370	Hypothetical protein	WP_011145226.1	-11.97	NS
PluDJC_04620	DUF1460 domain-containing protein	WP_011145268.1	3.97	NS
PluDJC_04775	Hypothetical protein	WP_011145297.1	11.71	NS
PluDJC_04780	Hypothetical protein	WP_049789740.1	18.06	NS
PluDJC_04790	Hypothetical protein	WP_011145300.1	29.66	NS
PluDJC_05130	Cupin domain-containing protein	WP_011145362.1	-3.89	NS
PluDJC_05345	Hypothetical protein	WP_011145401.1	3.81	NS
PluDJC_05350	Hypothetical protein	WP_011145402.1	4.49	NS
PluDJC_05765	Hypothetical protein	WP_011145536.1	4.09	NS
PluDJC_06970	DUF2517 family protein	WP_011145728.1	-3.38	NS
PluDJC_07210	DUF2778 domain-containing protein	WP_011145764.1	6.88	NS
PluDJC_07215	Hypothetical protein	WP_011145765.1	7.33	NS

PluDJC_07760	Hypothetical protein	WP_011145871.1	NS	-7.48
PluDJC_08430	Hypothetical protein	WP_011145919.1	3.76	NS
PluDJC_08640	Hypothetical protein	WP_011145958.1	-5.41	NS
PluDJC_09650	Hypothetical protein	WP_011146112.1	NS	-17.24
PluDJC_09810	Cupin domain-containing protein	WP_011146151.1	NS	-13.99
PluDJC_09930	Hypothetical protein	WP_041380044.1	NS	9.55
PluDJC_10010	DUF4123 domain-containing protein	WP_011146189.1	3.59	4.78
PluDJC_10135	DUF2829 domain-containing protein	WP_011146212.1	3.45	NS
PluDJC_10380	Hypothetical protein	WP_011146227.1	7.07	NS
PluDJC_10935	Hypothetical protein	WP_011146302.1	NS	-6.83
PluDJC_11315	Hypothetical protein	WP_011146373.1	NS	-7.28
PluDJC_11320	Hypothetical protein	WP_011146374.1	NS	-33.69
PluDJC_11435	Hypothetical protein	WP_011146396.1	3.49	NS
PluDJC_11795	Hypothetical protein	WP_011146471.1	NS	-23.60
PluDJC_11800	Hypothetical protein	WP_041380075.1	NS	-8.10
PluDJC_12120	DUF1778 domain-containing protein	WP_011146531.1	4.99	NS
PluDJC_12470	Hypothetical protein	WP_011146591.1	-3.52	-6.73
PluDJC_13305	Hypothetical protein	WP_011146757.1	NS	-5.83
PluDJC_13310	Hypothetical protein	WP_011146758.1	NS	10.14
PluDJC_14570	DUF1508 domain-containing protein	WP_011146999.1	5.73	NS

PluDJC_15535	DUF2000 domain-containing protein	WP_011147257.1	-3.81	NS
PluDJC_15660	Hypothetical protein	WP_011147279.1	4.25	NS
PluDJC_15840	Hypothetical protein	WP_011147314.1	NS	-23.01
PluDJC_15870	Hypothetical protein	WP_011147320.1	3.17	NS
PluDJC_15950	Hypothetical protein	WP_011147332.1	4.71	NS
PluDJC_15985	Hypothetical protein	WP_011147342.1	-4.94	-19.84
PluDJC_16530	Hypothetical protein	WP_041380212.1	3.17	NS
PluDJC_16535	Hypothetical protein	WP_011147438.1	3.72	NS
PluDJC_16672	Hypothetical protein	CAE15638.1	-12.76	NS
PluDJC_17315	Hypothetical protein	WP_011147688.1	3.08	NS
PluDJC_17565	Hypothetical protein	WP_011147738.1	-3.81	NS
PluDJC_17570	Hypothetical protein	WP_011147739.1	-3.62	NS
PluDJC_17717	Hypothetical protein	WP_071824132.1	3.88	NS
PluDJC_17720	Hypothetical protein	WP_011147775.1	3.25	5.55
PluDJC_18740	Hypothetical protein	WP_011147933.1	NS	-5.46
PluDJC_18745	Hypothetical protein	WP_011147934.1	NS	-6.34
PluDJC_18790	Hypothetical protein	WP_011147942.1	9.11	NS
PluDJC_19930	Hypothetical protein	WP_011148153.1	4.47	NS
PluDJC_20185	Hypothetical protein	WP_011148200.1	14.18	NS
PluDJC_20205	Hypothetical protein	CAE16455	39.72	NS

PluDJC_20910	Hypothetical protein	WP_011148329.1	-3.80	NS
PluDJC_20985	Hypothetical protein	WP_011148342.1	15.17	NS
PluDJC_21445	Hypothetical protein	WP_011148427.1	NS	-20.72
PluDJC_21635	DUF1266 domain-containing protein	WP_011148462.1	NS	-7.04
PluDJC_21745	Hypothetical protein	WP_011148483.1	NS	-23.02
PluDJC_22280	Hypothetical protein	WP_011148581.1	-5.63	NS
PluDJC_22285	DUF1471 domain-containing protein	WP_011148582.1	-9.61	NS
PluDJC_22825	DUF4123 domain-containing protein	WP_011148675.1	11.85	6.13
PluDJC_22830	Hypothetical protein	WP_011148676.1	9.31	9.76
PluDJC_22835	Hypothetical protein	WP_011148677.1	13.03	NS
PluDJC_22840	Hypothetical protein	WP_011148678.1	18.81	NS
PluDJC_22845	PAAR domain-containing protein	WP_011148679.1	12.30	NS
PluDJC_22850	Hypothetical protein	WP_011148680.1	16.67	NS
PluDJC_22855	Hypothetical protein	WP_011148681.1	14.87	NS
PluDJC_22860	Hypothetical protein	WP_011148682.1	7.00	NS
PluDJC_22865	Hypothetical protein	WP_011148683.1	4.55	NS
PluDJC_22870	Hypothetical protein	WP_011148684.1	3.03	NS
PluDJC_23645	DUF4879 domain-containing protein	WP_011148816.1	-3.22	-5.26
PluDJC_24500	Hypothetical protein	WP_011148929.1	NS	4.35
PluDJC_24590	Hypothetical protein	WP_011148944.1	NS	-14.41

PluDJC_24605	Hypothetical protein	WP_011148947.1	NS	-7.21
PluDJC_24610	Hypothetical protein	WP_011148948.1	-4.19	-7.24