

ID	AC	Δ hrpG	hrpB Δ	WT pAM5	WTpBBL12	hrpB Δ pBBL1	Gene	Description	Class
RS0001	RS06178			-0.30 0.04		-1.09 0.00	rpmH	50S RIBOSOMAL PROTEIN L34	III.C.2
RS0002	RS01824			-0.57 0.01		-1.52 0.01	rnvA	RIBONUCLEASE P PROTEIN COMPONENT	II.A.2
RS0003	RS01825		0.38 0.04	-0.38 0.05		-1.06 0.00		CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RS0004	RS01826				0.89 0.00	-0.58 0.02	yidC	TRANSMEMBRANE COG0706, Preprotein translocase subunit YidC	IV.E.2
RS0005	RS01827		0.46 0.02				thdF	THIOPHENE AND FURAN OXIDATION PROTEIN	IV.G.4
RS0006	RS01828		0.73 0.03					COG4551, Predicted protein tyrosine phosphatase	V.I.C
RS0007	RS01829							HYPOTHETICAL PROTEIN	VI.B
RS0008	RS01830			-0.33 0.01			rpsU	30S RIBOSOMAL SUBUNIT PROTEIN S21	III.C.2
RS0009	RS01831							DRUG EFFLUX LIPOPROTEIN	IV.D
RS0010	RS01832			-0.22 0.01	1.88 0.02		acrB	TRANSMEMBRANE ACRIFLAVIN RESISTANCE PROTEIN	IV.D
RS0011	RS01833					0.69 0.04	acrA	ACRIFLAVIN RESISTANCE LIPOPROTEIN A PRECURSOR	IV.G.2
RS0012	RS01834			-0.54 0.00	-0.91 0.02	1.24 0.00	acrR	TRANSCRIPTION REGULATOR ACRA B OPERON REPRESSOR	IV.G.2
RS0013	RS01835			-0.44 0.00	1.43 0.01			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RS0014	RS01836		-0.90 0.00				gor	OXIDOREDUCTASE GLUTATHIONE REDUCTASE	I.B.6
RS0015	RS01837	-0.51 0.01	0.63 0.02	-0.74 0.00				CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RS0016	RS01838			-0.30 0.01			serA	OXIDOREDUCTASE D-3-PHOSPHOGLYCERATE DEHYDROGENASE	I.A.10
RS0017	RS01839		1.06 0.00		1.46 0.00		pckA	PHOSPHOENOLPYRUVATE CARBOXYKINASE	I.F.13
RS0018	RS01840			-0.99 0.00		-2.06 0.00		TRANSCRIPTION REGULATOR RESPONSE REGULATOR	V.I.A
RS0019	RS01841			-0.82 0.00	-1.37 0.00	-1.94 0.00		CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RS0020	RS01842		1.25 0.00	-0.87 0.01				COG3622, Hydroxypruvate isomerase	I
RS0021	RS01843							TRANSCRIPTION REGULATOR TRANSMEMBRANE SENSOR HISTIDINE KINASE	V.I.A
RS0022	RS01844			-0.82 0.00	-1.01 0.01	-1.24 0.00	cstA	TRANSMEMBRANE CARBON STARVATION PROTEIN A	IV.F
RS0023	RS01845			-1.06 0.00	-1.21 0.00			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RS0024	RS01846		1.34 0.00	-1.31 0.00	-0.85 0.01			SIGNAL PEPTIDE	V.I.C
RS0025	RS01848				0.81 0.00	0.72 0.04	phaP2	POLYHYDROXYBUTYRATE GRANULE-ASSOCIATED PROTEIN (PHASIN) PHAP2	II.B
RS0026	RS01849		0.72 0.00				metW	METHIONINE BIOSYNTHESIS PROTEIN METW	I.A.12
RS0027	RS01850						metX	HOMOSERINE O-ACETYLTRANSFERASE	I.A.12
RS0028	RS01851			-0.72 0.05			gabD1	OXIDOREDUCTASE SUCCINATE-SEMIALDEHYDE DEHYDROGENASE	I.F.18
RS0029	RS01852			-1.43 0.00		1.83 0.00	goaG	4-AMINOBUTYRATE AMINOTRANSFERASE	I.F.18
RS0030	RS01853							TRANSCRIPTION REGULATOR	V.I.A
RS0031	RS01854			-0.64 0.00	-0.42 0.04			TRANSCRIPTION REGULATOR	V.I.A
RS0032	RS01855				-1.32 0.00			COG1011, Hydrolase	II
RS0033	RS01856	-0.77 0.02	0.91 0.04		0.99 0.01		argB	ACETYLGLUTAMATE KINASE	I.A.17
RS0034	RS01857				0.91 0.01			TRANSCRIPTION REGULATOR ECF-FAMILY RNA POLYMERASE SIGMA FACTOR I	V.I.C
RS0035	RS01858	0.34 0.02		-0.61 0.00		1.27 0.00		CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RS0036	RS01859							SIGNAL PEPTIDE	VI.D
RS0037	RS01860			-0.49 0.03		1.78 0.05		HYPOTHETICAL PROTEIN	VI.D
RS0038	RS01861		0.47 0.01	-0.68 0.01		0.90 0.03		TRANSMEMBRANE	V.I.C
RS0039	RS01862				0.40 0.05			TRANSCRIPTION REGULATOR TRANSMEMBRANE SENSOR HISTIDINE KINASE	V.I.A
RS0040	RS01863				2.43 0.00			TRANSCRIPTION REGULATOR RESPONSE REGULATOR	V.I.A
RS0041	RS01864		-1.92 0.00	2.19 0.03	2.43 0.00			HYPOTHETICAL PROTEIN	VI.D
RS0042	RS01865		1.12 0.03			-1.45 0.00	hslU	HEAT SHOCK PROTEIN CHAPERONE	IV.F.1
RS0043	RS01866					-0.72 0.00	hslV	HEAT SHOCK PROTEIN	II.A.4
RS0044	RS01867			-0.53 0.02				ABC TRANSPORTER SUBSTRATE-BINDING PERIPLASMIC PROTEIN (BBP)	IV.D
RS0045	RS01868		1.01 0.02	-0.93 0.00				COG0523, GTPase	V.I.C
RS0046	RS01869						dkxA	DNAX SUPPRESSOR PROTEIN	II.B.8
RS0047	RS01870			-1.36 0.00				COG0523, GTPase	V.I.C
RS0048	RS01871			-0.94 0.00				TRANSCRIPTION REGULATOR	V.I.A
RS0049	RS01872			-0.41 0.00				3-CARBOXYMUCONATE CYCLASE	I
RS0050	RS01873	-0.60 0.04		-1.01 0.00				OXIDOREDUCTASE COG0277, FAD/FMN-containing dehydrogenase	I
RS0051	RS01874		1.47 0.01	-1.08 0.00				COG1092, Predicted SAM-dependent methyltransferase	I
RS0052	RS01875		0.47 0.05	-0.41 0.00				SITE SPECIFIC INTEGRASE/RECOMBINASE	V.D
RS0053	RS01876		0.81 0.00	-0.46 0.01	0.94 0.02			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RS0054	RS01877				0.53 0.03		gatB	GLU-TRNAGLN AMIDOTRANSFERASE SUBUNIT B	II.D.1
RS0055	RS01878							SIGNAL PEPTIDE COG0412, Dienelactone hydrolase and related enzymes	I
RS0056	RS01879			-0.51 0.04				LIPOPROTEIN	V.I.C
RS0057	RS01880						gatA	GLU-TRNA (GLN) AMIDOTRANSFERASE (SUBUNIT A)	II.D.1
RS0058	RS01881			-0.27 0.05			gatC	GLUTAMYL-TRNA GLN AMIDOTRANSFERASE SUBUNIT C	III.C.2
RS0059	RS01882				0.76 0.01		mreB	ROD SHAPE-DETERMINING PROTEIN	III.B.3
RS0060	RS01883						mreC	TRANSMEMBRANE ROD SHAPE-DETERMINING PROTEIN MREC	III.B.3
RS0061	RS01884		0.69 0.00				mreD	TRANSMEMBRANE ROD SHAPE-DETERMINING PROTEIN MRED	III.B.3
RS0062	RS05767			-0.55 0.00	-1.14 0.03			TRANSMEMBRANE SUBSTRATE-BINDING PROTEIN	III.B.3
RS0063	RS05768						mdrB	TRANSMEMBRANE ROD SHAPE-DETERMINING PROTEIN (RODA PROTEIN)	IV.A
RS0064	RS05769							LONG-CHAIN-FATTY-ACID-CoA LIGASE	I.I.1
RS0065	RS02244			-0.63 0.00				TRANSCRIPTION REGULATOR	V.I.A
RS0066	RS02245		0.98 0.01	-0.61 0.04	0.81 0.00		topB	DNA TOPOISOMERASE III	II.B.8
RS0067	RS02246		1.05 0.05	-0.67 0.00				THIOREDOXIN	II.B.7
RS0068	RS02247				-0.75 0.03		smf	SMF PROTEIN (COG0758 Predicted Rossmann fold nucleotide-binding protein involv	VI.C
RS0069	RS02271		0.53 0.05			-0.39 0.02		SIGNAL PEPTIDE	V.I.C
RS0070	RS02248		0.34 0.01	-0.40 0.04	-0.52 0.04	-0.58 0.04	def	POLYPEPTIDE DEFORMYLASE	II.B.7
RS0071	RS02249		1.06 0.01	-0.40 0.00				TRANSMEMBRANE	V.I.C
RS0072	RS02250		0.62 0.00				fmt	METHIONYL-TRNA FORMYLTRANSFERASE	II.D.1
RS0073	RS02251		-1.26 0.00	1.87 0.00	1.91 0.00			TRANSMEMBRANE TRANSPORTER	IV.D
RS0074	RS02252				-0.71 0.01		htpX	TRANSMEMBRANE METALLOPROTEASE ZINC	II.A.4
RS0075	RS02273	-0.82 0.02		-0.30 0.01			rrmB	RNA METHYLTRANSFERASE (SUN PROTEIN)	II.B.6
RS0076	RS02253		0.44 0.05	-0.61 0.00		-0.04 0.04		SIGNAL PEPTIDE PROLINE RICH PROTEIN	V.I.C
RS0077	RS02275			-0.75 0.02				TRANSCRIPTION REGULATOR TWO COMPONENT SENSOR HISTIDINE KINASE	V.I.A
RS0078	RS02276			-0.51 0.00				TRANSCRIPTION REGULATOR TWO COMPONENT RESPONSE REGULATOR	V.I.A
RS0079	RS02277			-0.42 0.01				TRANSMEMBRANE	V.I.D
RS0080	RS02254			-0.32 0.02	-0.24 0.05			TRANSMEMBRANE	V.I.D
RS0081	RS02255				-1.35 0.03			TRANSCRIPTION REGULATOR COG1737, Transcriptional regulator	V.I.A
RS0082	RS02256							COG161, Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	I
RS0083	RS02257			0.15 0.05				CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RS0084	RS02258							ABC TRANSPORTER AMINO-ACID-BINDING PERIPLASMIC PROTEIN (BBP)	IV.D.2
RS0085	RS02259		0.32 0.03	-0.31 0.05			cca	tRNA NUCLEOTIDYLTRANSFERASE	II.D.1
RS0086	RS02260			-0.25 0.05			gstA	GLUTATHIONE S-TRANSFERASE	II.B.7
RS0087	RS02261		0.45 0.05					OXIDOREDUCTASE NADH-UBIQUINONE OXIDOREDUCTASE	I.H
RS0088	RS02278						slt	TRANSMEMBRANE SOLUBLE LYTIC MUREIN TRANSLYCOSYLASE PRECURSOR	III.B.3
RS0089	RS02262			-0.43 0.03				COG0212, 5-formyltetrahydrofolate cyclo-ligase	I
RS0090	RS02263			0.82 0.00		-0.88 0.01		TRANSCRIPTION REGULATOR COG3070, Regulator of competence-specific genes	V.I.A
RS0091	RS02264			-0.45 0.02		-0.80 0.01	metF	OXIDOREDUCTASE 5,10-METHYLENETETRAHYDROFOLATE REDUCTASE	I.A.12
RS0092	RS02279					-0.69 0.05		TRANSMEMBRANE	V.I.C
RS0093	RS02265			-0.63 0.00		-1.52 0.00	ahcY	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE I	V.F
RS0094	RS02282		0.48 0.03	-0.40 0.05				TRANSMEMBRANE LIPOPROTEIN	VI.D
RS0095	RS02285							CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RS0096	RS06003		-2.44 0.00	3.20 0.00	1.32 0.00			HYPOTHETICAL PROTEIN	VI.D
RS0097	RS02267		1.02 0.05					TRANSMEMBRANE ALKALINE PHOSPHATASE LIPOPROTEIN	I.F.20
RS0098	RS02280			-0.60 0.03				SIGNAL PEPTIDE ALKALINE PHOSPHATASE	I.F.20
RS0099	RS02268							SIGNAL PEPTIDE	VI.B
RS0100	RS02611			-0.33 0.04			thiD	BIFUNCTIONAL PROTEIN: HYDROXY-PHOSPHOMETHYLPIRIMIDINE KINASE	II.B.8
RS0101	RS02270							TRANSMEMBRANE LIPOPROTEIN	V.I.C
RS0102	RS05630		-1.54 0.00	1.62 0.01	-1.01 0.01			CALCIUM BINDING HEMOLYSIN	IV.G.3
RS0104	RS00975	-0.75 0.01		-0.55 0.05				HEMOLYSIN-TYPE CALCIUM-BINDING PROTEIN	IV.G.3
RS0105	RS01614							HYPOTHETICAL PROTEIN	V.I.D
RS0106	RS01696		0.38 0.03					SIGNAL PEPTIDE	V.I.D
RS0107	RS00977			-0.61 0.01		2.08 0.00		CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RS0108	RS00978						thiE1	THIAMINE-PHOSPHATE PYROPHOSPHORYLASE	I.B.8
RS0109	RS00979			-0.35 0.03	-1.03 0.01		thiG	THIF PROTEIN THIAMINE BIOSYNTHESIS	I.B.8
RS0111	RS00981			-0.36 0.04			thiS	Sulfur transfer protein ThiS	I.B.8
RS0112	RS00982				-1.16 0.05	-0.60 0.02		OXIDOREDUCTASE D-AMINO ACID OXIDASE FLAVOPROTEIN	I

RSc0113	RS00983				-0.56	0.00			-1.60	0.00	thiC	THIAMINE BIOSYNTHESIS PROTEIN THI C THIAMINE BIOSYNTHESIS	I.B.8
RSc0114	RS00984											OXIDOREDUCTASE DIOXYGENASE related to 2-nitropropane dioxygenase	I
RSc0115	RS00985			0.79	0.00				1.83	0.02		HEMAGGLUTININ-RELATED AUTOTRANSPORTER PROTEIN	III.A
RSc0116	RS00986	0.50	0.01			-1.00	0.00					CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0117	RS00987					-0.52	0.04					CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0118	RS00988					-0.71	0.00					CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0119	RS00989					-0.59	0.00		1.22	0.00		CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0120	RS00990											HYPOTHETICAL/UNKNOWN	V.I.C
RSc0121	RS00991					-0.42	0.04					ACETYLTRANSFERASE	V.I.C
RSc0122	RS00992			0.42	0.01	-0.52	0.00					OXIDOREDUCTASE ACYL-COA DEHYDROGENASE	I
RSc0123	RS00993			0.32	0.04	-0.67	0.00					ABC TRANSPORTER SUBSTRATE-BINDING PERIPLASMIC PROTEIN (PBP)	I.V.D
RSc0124	RS00994					-0.44	0.02					OXIDOREDUCTASE COG2303, Choline dehydrogenase and related flavoproteins	I
RSc0125	RS00995											CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0126	RS00996			-1.40	0.05							TRANSCRIPTION REGULATOR COG2944, Transcriptional regulator	V.I.A
RSc0127	RS00997			-0.86	0.05							HYPOTHETICAL/UNKNOWN	V.I.D
RSc0128	RS00998					0.96	0.01					HEMAGGLUTININ-RELATED PROTEIN	V.I.C
RSc0129	RS00999					-0.20	0.03					TRANSCRIPTION REGULATOR	V.I.A
RSc0130	RS01000					-0.56	0.01					GLUTATHIONE S-TRANSFERASE	I.I.B.7
RSc0131	RS01001											TRANSMEMBRANE COG3448, CBS-domain-containing membrane protein	V.I.A
RSc0132	RS01002											LIPOPROTEIN	V.I.C
RSc0133	RS01003					-0.49	0.00					TRANSCRIPTION REGULATOR	I
RSc0134	RS01004											CONSERVED HYPOTHETICAL PROTEIN	V.I.A
RSc0135	RS01005					-0.46	0.00		-0.64	0.00	metK	S-ADENOSYLMETHIONINE SYNTHETASE	I.F
RSc0136	RS01006											TRANSMEMBRANE ACYLTRANSFERASE	I.I.B
RSc0137	RS01049											ACYLTRANSFERASE	I.I.B
RSc0138	RS01008					0.65	0.04				dapF	DIAMINOPIMELATE EPIMERASE	I.A.13
RSc0139	RS01009											CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0140	RS01010											OROTATE PHOSPHORIBOSYLTRANSFERASE	I.D.1
RSc0141	RS01011					-0.29	0.02					EXODEOXYRIBONUCLEASE III	I.I.A.1
RSc0142	RS01012					-0.44	0.03					TRANSMEMBRANE	V.I.C
RSc0143	RS01013					-0.60	0.00					OXIDOREDUCTASE N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE REDUCTASE	I.A.17
RSc0144	RS01014					-0.70	0.03					CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0145	RS01015					-0.58	0.05					TRANSCRIPTION REGULATOR	V.I.A
RSc0146	RS01016											TRANSMEMBRANE COG0330, Membrane protease subunit, stomatin/prohibitin hom	I.I.A.4
RSc0147	RS01017			0.63	0.00	-0.56	0.00					TRANSMEMBRANE LIPOPROTEIN	V.I.C
RSc0148	RS01018					-0.75	0.01					SIGNAL PEPTIDE HYPOTHETICAL	V.I.B
RSc0149	RS01019											HYPOTHETICAL/UNKNOWN	V.I.D
RSc0150	RS01020					-0.57	0.01					TRANSCRIPTION REGULATOR	V.I.A
RSc0151	RS01021					-0.74	0.02	-0.44	0.03			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0152	RS01022					-1.73	0.02	-1.63	0.00			TRANSMEMBRANE	V.I.C
RSc0153	RS01023					-0.68	0.00					LIPOPROTEIN	V.I.D
RSc0154	RS01024											SIGNAL PEPTIDE COG0501, Zn-dependent protease with chaperone function	I.I.A.4
RSc0155	RS01025											TRANSMEMBRANE TRANSPORT protein	I.V.D
RSc0156	RS01026											CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0157	RS01027			0.40	0.03	-0.27	0.02					OXIDOREDUCTASE COG1028, Dehydrogenases with different specificities (related t	I
RSc0158	RS01028											HYPOTHETICAL PROTEIN	I.F
RSc0159	RS01029					-1.24	0.00					ARGINASE	I.I.3
RSc0160	RS01030					-1.33	0.00					ACETYLMETHYLAMINE AMINOTRANSFERASE	I.I.3
RSc0161	RS01031					0.81	0.01					TRANSCRIPTION REGULATOR	V.I.A
RSc0162	RS01032											OXIDOREDUCTASE TRANSMEMBRANE ALDEHYDE DEHYDROGENASE	I
RSc0163	RS01033					-1.59	0.00	0.91	0.00	-1.71	0.00	TRANSCRIPTION REGULATOR	V.I.A
RSc0164	RS01034					-1.64	0.00			-1.17	0.00	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0165	RS01035					-0.87	0.00					ABC TRANSPORTER ATP-BINDING PROTEIN	I.V.D
RSc0166	RS01036			0.58	0.04	-0.44	0.00					ABC TRANSPORTER ABC-type multidrug transport system, permease component	I.V.D
RSc0167	RS01037											Outer membrane channel lipoprotein	I.V.D
RSc0168	RS01038					0.59	0.01	-0.88	0.00			SIGNAL PEPTIDE	V.I.C
RSc0169	RS01039					1.19	0.01	-0.51	0.00			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0170	RS01040					1.13	0.01					COG0451, Nucleoside-diphosphate-sugar epimerase	I
RSc0171	RS01042					0.53	0.03					TRANSMEMBRANE	V.I.C
RSc0172	RS01043											OXIDOREDUCTASE COG0300, Short-chain dehydrogenases of various substrate spe	I
RSc0173	RS01044					1.97	0.04					TRANSMEMBRANE COG0277, FAD/FMN-containing dehydrogenase	I
RSc0174	RS01045					0.73	0.02	-0.24	0.04			TRANSMEMBRANE PROTEIN WITH COG0382, 4-hydroxybenzoate polyphenyltransf	I
RSc0175	RS01046					-0.62	0.02					OXIDOREDUCTASE COG1893, Ketopantoate reductase	I
RSc0176	RS01047					-0.20	0.01					COG0037, Predicted ATPase of the PP-loop superfamily implicated in cell cycle contr	I.V.A
RSc0177	RS01048					-0.55	0.01					LIPOPROTEIN	V.I.C
RSc0178	RS00609					0.58	0.00			0.98	0.02	UDP-N-ACETYLGALUCOSAMINE PYROPHOSPHORYLASE	I.F.10
RSc0179	RS00610					0.53	0.00					GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE	I.F.8
RSc0180	RS00611											COG0589, Universal stress protein UspA and related nucleotide-binding proteins	V.I.C
RSc0181	RS00612											PSEUDOGENE (ALCOHOL DEHYDROGENASE C-TERMINAL FRAGMENT)	V.I.C
RSc0182	RS00613											PSEUDOGENE (ALCOHOL DEHYDROGENASE N-TERMINAL FRAGMENT)	V.I.C
RSc0183	RS00614					1.38	0.00	1.90	0.01			TRANSMEMBRANE	V.I.C
RSc0184	RS00615											Signal-transduction protein containing a CBS domain	V.I.A
RSc0185	RS00616					-0.24	0.05					COG0589, Universal stress protein UspA and related nucleotide-binding proteins	V.I.C
RSc0186	RS00617											Universal stress protein UspA and related nucleotide-binding proteins	V.I.C
RSc0187	RS00618											COG2823, Periplasmic or secreted lipoprotein	V.I.C
RSc0188	RS00619											COG0716, Flavodoxin	I
RSc0189	RS00621											HYPOTHETICAL PROTEIN	V.I.B
RSc0190	RS00622											COG2823, Periplasmic or secreted lipoprotein	V.I.C
RSc0191	RS00623					-1.12	0.05					TRANSCRIPTION REGULATOR	V.I.A
RSc0192	RS00624											TRANSCRIPTION REGULATOR TRANSMEMBRANE TWO COMPONENT SYSTEM	V.I.A
RSc0193	RS00625											TRANSCRIPTION REGULATOR RESPONSE REGULATOR	V.I.A
RSc0194	RS00626											HYPOTHETICAL PROTEIN	V.I.D
RSc0195	RS00627											OXIDOREDUCTASE ZINC-DEPENDENT ALCOHOL DEHYDROGENASE	I
RSc0196	RS00628											OXIDOREDUCTASE RIBONUCLEOTIDE REDUCTASE, alpha subunit	I
RSc0197	RS00629					-1.14	0.02	-0.49	0.02			SIGNAL PEPTIDE CYTOCHROME C1	I.G.1
RSc0198	RS00630							-0.85	0.03			SIGNAL PEPTIDE CYTOCHROME C	I.G.1
RSc0199	RS00631							-0.77	0.01			TRANSMEMBRANE	V.I.C
RSc0200	RS00632											TRANSMEMBRANE CYTOCHROME B561 CYTOCHROME	I.G.1
RSc0201	RS00633											SMALL HEAT SHOCK PROTEIN	I.V.F.1
RSc0202	RS00634											COG1236, Exonuclease of the beta-lactamase fold involved in RNA processing	I.I.B.6
RSc0203	RS00635											RIBOSE-PHOSPHATE PYROPHOSPHOKINASE	I.D.2
RSc0204	RS00636											CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0205	RS00637					-1.39	0.05					THYMIDINE/PYRIMIDINE-NUCLEOSIDE PHOSPHORYLASE	I.F.1
RSc0206	RS00638							0.40	0.05	-0.74	0.01	TRANSCRIPTION REGULATOR	V.I.A
RSc0207	RS00639									-0.77	0.05	SIGNAL PEPTIDE COG1073, Hydrolase of the alpha/beta superfamily	I.I
RSc0208	RS00640											TRANSMEMBRANE TRANSPORTER	I.V.D
RSc0209	RS00641											TRANSMEMBRANE	V.I.D
RSc0210	RS00642											TRANSCRIPTION REGULATOR	V.I.A
RSc0211	RS00643											TRANSMEMBRANE	V.I.D
RSc0212	RS00644							-0.45	0.00	0.87	0.01	ASPARTATE RACEMASE	I.A.15
RSc0213	RS00645							-0.77	0.03			GLUTAMINE AMIDOTRANSFERASE	I.D.2
RSc0214	RS00646											TRANSCRIPTION REGULATOR	V.I.A
RSc0215	RS00647											OXIDOREDUCTASE COG1028, Dehydrogenases with different specificities (related t	I
RSc0216	RS00648											TRANSMEMBRANE TRANSPORT PROTEIN	I.V.D
RSc0217	RS00649							-1.19	0.00	4.10	0.00	OXIDOREDUCTASE COG0667, Oxidoreductase (related to aryl-alcohol dehydrogena	I
RSc0218	RS00650							-0.87	0.03	3.20	0.00	HYPOTHETICAL/UNKNOWN	V.I.D
RSc0219	RS00651							-1.02	0.00			COG1254, ACYLPHOSPHATASE	I.H
RSc0220	RS00652							-0.68	0.02			COG4101, Predicted mannose-6-phosphate isomerase	I.F.4
RSc0221	RS00653											TRANSMEMBRANE COG1752, Esterase of the alpha-beta hydrolase superfamily	I
RSc0222	RS00654					-1.91	0.00	-1.83	0.01			TRANSCRIPTION REGULATOR SIGMA-54 INTERACTING PROTEIN	I.I.B.6
RSc0223	RS00655							-1.23	0.00	-1.32	0.00	HYPOTHETICAL/UNKNOWN	V.I.D
RSc0224	RS00656							-0.91	0.00	-0.37	0.00	TRANSMEMBRANE	V.I.C
RSc0225	RS00657							-0.80	0.00			COG3541, Nucleotidyltransferase	I.D

RSc0226	RS00658									rtcA	RNA 3'-TERMINAL PHOSPHATE CYCLASE	II.B.6
RSc0227	RS06016	0,64	0,00	-0,45	0,00						REMNANT OF A AVRPM1A1/AVRPP1A1 GENE HOMOLOG	VI.B
RSc0228	RS00660										REMNANT OF A AVRPM1A1/AVRPP1A1 GENE HOMOLOG	VI.B
RSc0229	RS00661	0,42	0,00	-0,55	0,00						TRANSCRIPTION REGULATOR COG1167, Transcriptional regulators containing a DVI	VI.A
RSc0230	RS00663			-0,58	0,04						TRANSMEMBRANE	VI.C
RSc0231	RS00662		-0,54	0,03		1,15	0,00				TRANSMEMBRANE (HOMOSERINE/HOMOSERINE LACTONE) EFFLUX PROTEIN	IV.D.2
RSc0232	RS00664	1,16	0,01	-1,13	0,00	1,89	0,00	4,53	0,00		HYPOTHETICAL PROTEIN	VI.B
RSc0233	RS00665										TRANSMEMBRANE INTEGRAL MEMBRANE PROTEIN	VI.C
RSc0234	RS00666			-0,90	0,00	-0,96	0,02				TRANSCRIPTION REGULATOR	VI.A
RSc0235	RS00667										CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc0236	RS00668		0,39	0,02	-0,65	0,02	1,53	0,01			SIGNAL PEPTIDE HYPOTHETICAL/UNKNOWN	VI.D
RSc0237	RS00669										METHYLMALONYL-CoA MUTASE	I
RSc0238	RS00670			-1,06	0,01		1,31	0,00			TRANSMEMBRANE PUTATIVE PERMEASE	IV.D
RSc0239	RS00671										COG1574, Predicted metal-dependent hydrolase with the TIM-barrel fold	II
RSc0240	RS00672										TRANSMEMBRANE	VI.C
RSc0241	RS00673		-0,71	0,03							TRANSMEMBRANE	VI.C
RSc0242	RS00674										COG1335, Amidase related to nicotinamidase	II
RSc0243	RS00675					-0,96	0,05				TRANSCRIPTION REGULATOR TRANSCRIPTIONAL REGULATOR	VI.A
RSc0244	RS00676		0,68	0,00	-0,77	0,00					OXIDOREDUCTASE 3-HYDROXYBUTYRYL-CoA DEHYDROGENASE	II
RSc0245	RS00677		-3,22	0,00	3,59	0,00	3,16	0,00		paaH1	TYPE III EFFECTOR RIBP	VI.E
RSc0246	RS00678									ripB	CALCIUM BINDING HEMOLYSIN	IV.G.3
RSc0247	RS00679		0,65	0,04	-0,86	0,00	-0,96	0,01		tISRso6	ISRS06-TRANSPOSASE ORFA	VI.B
RSc0248	RS00680		0,68	0,05	-0,29	0,00				tISRso6	ISRS06-TRANSPOSASE ORFB	VI.B
RSc0249	RS00683				-0,38	0,04					CALCIUM BINDING HEMOLYSIN	IV.G.3
RSc0250	RS00684										CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc0251	RS00685		-1,29	0,02	1,16	0,00					SIGNAL PEPTIDE	VI.D
RSc0253	RS00688										COG0384 PREDICTED EPIMERASE (PHENAZINE BIOSYNTHESIS PROTEIN)	I
RSc0254	RS00689				-0,55	0,00	0,71	0,03			TRANSMEMBRANE	VI.C
RSc0255	RS00690				-0,65	0,00					COG2070, Dioxxygenases related to 2-nitropropane dioxxygenase	I
RSc0256	RS00691				-0,84	0,00					HALOACETATE DEHALOGENASE H-1	II.A
RSc0257	RS00692		-4,07	0,00	6,98	0,00	5,13	0,00		dehH	ANKYRIN REPEAT HARBORING PROTEIN	VI.B
RSc0258	RS00693										BETA LACTAMASE	IV.G.4
RSc0259	RS00694										COG3133, Fe-S protein	VI.C
RSc0260	RS00695										CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc0261	RS00696		0,53	0,05							CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc0262	RS00697		-0,53	0,01							OXIDOREDUCTASE COG0111, Phosphoglycerate dehydrogenase and related dehyd	I
RSc0263	RS00698										HYPOTHETICAL PROTEIN	VI.D
RSc0264	RS00699		0,32	0,03							HYPOTHETICAL PROTEIN	VI.B
RSc0265	RS05771										COG4770, Acetyl/propionyl-CoA carboxylase, alpha subunit	I
RSc0266	RS03233		0,56	0,05						bioB	BIOTIN SYNTHASE	II.B.15
RSc0267	RS03234				-0,72	0,03	-0,34	0,03			ENOYL-CoA HYDRATASE	I.A.4
RSc0268	RS03235										SIGNAL PEPTIDE COG0412, Dienelactone hydrolase and related enzymes	I
RSc0269	RS03236		0,81	0,00	-0,34	0,03					COG4799, Acetyl-Coa carboxylase, carboxyltransferase component (subunits alpha &	I
RSc0270	RS03237				-0,26	0,01	0,88	0,04			CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc0271	RS03238		0,70	0,05							COG0637, Phosphatase/phosphohexomutase	I
RSc0272	RS03239										COG0607, Rhodanese-related sulfurtransferase	I
RSc0273	RS03240		0,95	0,04							2-HYDROXYCHROMENE-2-CARBOXYLATE ISOMERASE	II.A
RSc0274	RS03241		-1,05	0,01				0,76	0,00		OXIDOREDUCTASE ACYL CoA DEHYDROGENASE	I
RSc0275	RS03242		0,72	0,02							OXIDOREDUCTASE COG0300, Short-chain dehydrogenases of various substrate spe	I
RSc0276	RS03243										ACETYL-CoA ACETYLTRANSFERASE (ACETOACETYL-CoA THIOLASE)	II.1
RSc0277	RS03244		0,70	0,02							CARBONIC ANHYDRASE	I.F.18
RSc0278	RS03245				-0,26	0,00				aceK	TRANSMEMBRANE MULTIFUNCTIONAL ENZYME : ISOCITRATE DEHYDROGENA	I.F.17
RSc0279	RS03246										OXIDOREDUCTASE ACYL-CoA DEHYDROGENASE	II.3
RSc0280	RS03247				-0,51	0,00					TRANSCRIPTION REGULATOR	VI.A
RSc0281	RS03248		1,00	0,01							COG0491, Zn-dependent hydrolases, including glyoxylases	II
RSc0282	RS03249										CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc0283	RS03250				-0,36	0,00					ABC TRANSPORTER COG0614, ABC-type Fe3+-hydroxamate transport system, peri	IV.D.5
RSc0284	RS03251				-0,41	0,00					OXIDOREDUCTASE COG0300, Short-chain dehydrogenases of various substrate spe	I
RSc0285	RS03252				-0,40	0,00					SIGNAL PEPTIDE THIOL-DISULFIDE INTERCHANGE PROTEIN	II.B.7
RSc0286	RS03253		0,60	0,04	-0,37	0,01	0,59	0,02		dsbA1	TRANSMEMBRANE Cell division protein FtsN	IV.A
RSc0287	RS03254										ARGINYL-TRNA SYNTHETASE (ARGININE--TRNA LIGASE)	II.D.1
RSc0288	RS03255				-0,42	0,04		0,61	0,00		CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc0289	RS03256				-0,70	0,01					TRANSCRIPTION REGULATOR TRANSMEMBRANE SENSOR KINASE VSRA	I.E.1
RSc0290	RS03257		-0,31	0,01	-0,34	0,04					COG5510 : Predicted small secreted protein	III.A
RSc0291	RS03258				-0,51	0,00					TRANSCRIPTION REGULATOR	VI.A
RSc0292	RS03259				-0,52	0,00					TRANSCRIPTION REGULATOR RESPONSE REGULATOR	I.E.1
RSc0293	RS03260				-0,45	0,01	1,13	0,00	2,70	0,00	SIGNAL PEPTIDE	VI.D
RSc0294	RS03261									metHb	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (MII	A.12
RSc0295	RS03262		0,41	0,01	-0,38	0,05				metHa	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (MII	A.12
RSc0296	RS03263				-0,66	0,01	-0,66	0,02	1,52	0,02	COG0607, Rhodanese-related sulfurtransferase	I
RSc0297	RS03264				-1,66	0,00	-1,94	0,00			CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc0298	RS03265		0,32	0,03			-1,11	0,05		pcaD2	B-KETOADIPATE ENOL-LACTONE HYDROLASE	II.A
RSc0299	RS03266		0,88	0,01	-0,27	0,05	0,91	0,04			SIGNAL PEPTIDE PROLIN-RICH PROTEIN	VI.C
RSc0300	RS03267				-0,35	0,00					TRANSCRIPTION REGULATOR	VI.A
RSc0301	RS03268		1,75	0,01	-0,34	0,02					OXIDOREDUCTASE COG0179, 2-keto-4-pentenolate hydratase/2-oxohepta-3-ene-1,7	I
RSc0302	RS03269				-1,17	0,00					TRANSCRIPTION REGULATOR	VI.A
RSc0303	RS03270				-1,52	0,00	-1,62	0,01			CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc0304	RS03271		0,65	0,02							ENOYL-CoA HYDRATASE	II.A
RSc0305	RS03272				0,45	0,04	1,53	0,00			CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc0306	RS03273										COG1752, Esterase of the alpha-beta hydrolase superfamily	I
RSc0307	RS03274				-0,58	0,00					GLUTATHIONE PEROXIDASE	II.B.7
RSc0308	RS03275		0,43	0,01	-0,55	0,04					CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc0309	RS03276										CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc0310	RS03277										SIGNAL PEPTIDE	VI.C
RSc0311	RS03278				-0,39	0,01	-0,61	0,02			TRANSCRIPTION REGULATOR TRANSCRIPTION REGULATION ACCESSORY FA	VI.A
RSc0312	RS03279										BIFUNCTIONAL PROTEIN: BIOTIN OPERON REPRESSOR AND BIOTIN-[ACETYL	I.B.15
RSc0313	RS03280		0,41	0,02				-0,48	0,04	birA	ABC TRANSPORTER COG0767, ABC-type transport system involved in resistance to	IV.D
RSc0314	RS03281										ABC TRANSPORTER COG1127, ABC-type transport system involved in resistance to	IV.D
RSc0315	RS03282		0,59	0,01							ABC TRANSPORTER COG1463, ABC-type transport system involved in resistance to	IV.D
RSc0316	RS03283						-0,65	0,04			ABC TRANSPORTER COG3218, ABC-type uncharacterized transport system, auxilia	IV.D
RSc0317	RS03284	0,47	0,02		-0,50	0,02					TRANSMEMBRANE	VI.C
RSc0318	RS03285						-0,75	0,03			HYPOTHETICAL PROTEIN	VI.D
RSc0319	RS03286									plcN	SIGNAL PEPTIDE NON-HEMOLYTIC PHOSPHOLIPASE C (PHOSPHATIDYLCHOLI	I.1
RSc0320	RS03287		1,15	0,02	-0,60	0,00	-1,80	0,00			SIGNAL PEPTIDE	VI.C
RSc0321	RS03288		-2,23	0,00	3,22	0,00	2,95	0,00			HYPOTHETICAL PROTEIN	VI.D
RSc0322	RS03289				-0,65	0,02					LIPOIC ACID SYNTHETASE (LIP-SYN) (LIPOATE SYNTHASE)	I.B.13
RSc0323	RS03290				-0,58	0,00					LIPOATE-PROTEIN LIGASE B	I.B.13
RSc0324	RS03291				-0,54	0,00		1,12	0,00	lipB	HYPOTHETICAL PROTEIN	VI.B
RSc0325	RS03292				-0,65	0,01					TRANSCRIPTION REGULATOR	VI.A
RSc0326	RS03293				-0,27	0,01					CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc0327	RS03294				-0,52	0,01					TRANSMEMBRANE PENICILLIN-BINDING PROTEIN (D-ALANYL-D-ALANINE CARE	IV.A
RSc0328	RS03295		0,46	0,02				-0,49	0,05	dac	TRANSMEMBRANE COG2945, Hydrolase of the alpha/beta superfamily	II
RSc0329	RS03296		0,38	0,02	-0,44	0,00					FERREDOXIN 2FE-2S	I.G.1
RSc0330	RS03297		0,38	0,01	-1,24	0,00					TRANSMEMBRANE C4-DICARBOXYLATE TRANSPORT PROTEIN	IV.D.3
RSc0331	RS03298						-1,69	0,02		dctA1	TRANSCRIPTION REGULATOR C4-DICARBOXYLATE TRANSPORT SENSOR KIN/	IV.D.3
RSc0332	RS03299						-0,47	0,02		dctB2	TRANSCRIPTION REGULATOR C4-DICARBOXYLATE TRANSPORT RESPONSE R	IV.D.3
RSc0333	RS03300				-0,82	0,01					TRANSMEMBRANE COG0526, Thiol-disulfide isomerase and thioredoxins	II.B.7
RSc0334	RS03301				-0,66	0,00	-0,60	0,04			COG2110, Phosphatase homologous to the C-terminal domain of histone macroH2A	VI.C
RSc0335	RS03302				-0,49	0,01					TRANSMEMBRANE	VI.C
RSc0336	RS03303				-0,72	0,00					SIGNAL PEPTIDE	VI.D
RSc0337	RS03304				-0,88	0,01					OXIDOREDUCTASE POLYPHENOL OXIDASE B PRECURSOR (CATECHOL OXIDA	I.A.4
RSc0338	RS03305				-0,54	0,03					COG0606, ATPase with chaperone activity	II.B.7

RSc0339	RSc03306			-0.57	0.00			0.74	0.00	TRANSMEMBRANE	VI.C			
RSc0340	RSc03307					0.67	0.01	0.57	0.02	CONSERVED HYPOTHETICAL PROTEIN	VI.C			
RSc0341	RSc03308			-0.39	0.01	-1.51	0.02			SIGNAL PEPTIDE	VI.C			
RSc0342	RSc03309									glrK TRANSCRIPTION REGULATOR NITROGEN REGULATORY PROTEIN P-II	IA.18			
RSc0343	RSc03310			-0.45	0.01					amtB TRANSMEMBRANE AMMONIUM TRANSPORTER	IF.18			
RSc0344	RSc03311									CONSERVED HYPOTHETICAL PROTEIN	VI.C			
RSc0345	RSc03312							-1.85	0.04	gshB GLUTATHIONE SYNTHETASE	IB.6			
RSc0346	RSc03313			-0.53	0.04					COG2893, Phosphotransferase system, mannose/fructose-specific component IIA	IV.D.3			
RSc0347	RSc03314									pstH PHOSPHOCARRIER PROTEIN HPR (phosphohistidinoprotein-hexose phosphotransf	IV.D.3			
RSc0348	RSc03315	0.68	0.02		0.55	0.03				pslI TRANSMEMBRANE PHOSPHOENOLPYRUVATE-PROTEIN PHOSPHOTRANSFER	IV.D.3			
RSc0349	RSc03316			-1.63	0.00	-1.44	0.00	-0.80	0.02	bfd BACTERIOFERRITIN-ASSOCIATED FERREDOXIN	IV.F.1			
RSc0350	RSc03317			-0.24	0.02	-0.78	0.00	-0.78	0.00	bfr BACTERIOFERRITIN BFR (CYTOCHROME B-1) (CYTOCHROME B-557)	IV.F.1			
RSc0351	RSc03318				0.64	0.01				thiF TRANSMEMBRANE THIIF PROTEIN	IB.8			
RSc0352	RSc03319				0.34	0.02				TRANSMEMBRANE COG0793, Periplasmic protease	IA.4			
RSc0353	RSc03320				-0.46	0.00		0.81	0.00	gpmA PHOSPHOGLYCERATE MUTASE 1 (PHOSPHOGLYCEROMUTASE 1)	I.H.8			
RSc0354	RSc03321									TRANSMEMBRANE COG0607, Rhodanese-related sulfurtransferase	I			
RSc0355	RSc03322									grxC GLUTAREDOXIN 3 (GRX3)	IB.6			
RSc0356	RSc03323				0.50	0.03				secB PROTEIN-EXPORT PROTEIN SECB	IV.E.2			
RSc0357	RSc03324				1.07	0.00				OXIDOREDUCTASE GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD(P)+)	I.H.3			
RSc0358	RSc03326									yibK TRNA/RRNA METHYLTRANSFERASE	IB.6			
RSc0359	RSc03327									COMPETENCE PROTEIN F-RELATED PROTEIN	IV.E			
RSc0360	RSc03328				0.89	0.04				bioC BIOTIN SYNTHESIS PROTEIN (METHYLTRANSFERASE)	IB.15			
RSc0361	RSc03329	0.39	0.04		0.39	0.02		0.87	0.00	TRANSMEMBRANE	VI.C			
RSc0362	RSc03330				0.74	0.00		0.82	0.01	COX236, Predicted Zn-dependent peptidases	II.3			
RSc0363	RSc03331				0.67	0.05		1.23	0.00	COX0612, Predicted Zn-dependent peptidases	II.3			
RSc0364	RSc03332							1.11	0.00	COG0742, N6-adenine-specific methylase	II.B.8			
RSc0365	RSc03333				0.81	0.00		0.75	0.02	PHOSPHOPANTETHEINE ADENYLYLTRANSFERASE (PANTETHEINE- PHOSPH	III.A.1			
RSc0366	RSc03334				0.34	0.00	-0.30	0.03		FERREDOXIN	I.G.1			
RSc0367	RSc03335				0.57	0.00				SIGNAL PEPTIDE	VI.C			
RSc0368	RSc03336									COG1660, Predicted P-loop-containing kinase	VI.C			
RSc0369	RSc03337									SIGNAL PEPTIDE	VI.C			
RSc0370	RSc03338				0.72	0.04				PTS2, Predicted Zn-dependent peptidases	II.3			
RSc0371	RSc03339				1.08	0.05	-0.52	0.02		COG0612, Predicted Zn-dependent peptidases	II.3			
RSc0372	RSc03340				0.91	0.00	-0.31	0.00		COG0742, N6-adenine-specific methylase	II.B.8			
RSc0373	RSc03341				0.44	0.00	-0.67	0.00	0.72	0.03	1.22	0.00	LIPOPROTEIN	VI.C
RSc0374	RSc03342						-0.49	0.00					rpoH TRANSCRIPTION REGULATOR RNA POLYMERASE SIGMA H (SIGMA-32) FACTO	I.E.1
RSc0375	RSc03343						-0.76	0.05					TRANSMEMBRANE SIGNAL TRANSDUCTION PROTEIN GGDEF DOMAIN	VI.A
RSc0376	RSc03344												COG1765, Redox protein, regulator of disulfide bond formation	II.B.7
RSc0377	RSc03345												PIRIN-RELATED PROTEIN	VI.C
RSc0378	RSc03346				0.35	0.01							trpD3 ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE	IA.6
RSc0379	RSc03347				0.33	0.05	-0.35	0.02					nasD ABC TRANSPORTER NITRATE ATP-BINDING PROTEIN	IV.D.1
RSc0380	RSc03348												nasE ABC TRANSPORTER NITRATE TRANSMEMBRANE PROTEIN	IV.D.1
RSc0381	RSc03349												nasF NITRATE TRANSPORTER	IV.D.1
RSc0382	RSc03350												TRANSCRIPTION REGULATOR RESPONSE REGULATOR	VI.A
RSc0383	RSc03351												OXIDOREDUCTASE COG0179, 2-keto-4-pentenolate hydratase / 2-oxohepta-3-ene-1	I
RSc0384	RSc03352												mhpD OXIDOREDUCTASE COG0179, 2-keto-4-pentenolate hydratase / 2-oxohepta-3-ene-1	I
RSc0385	RSc03353												gslB GLUTATHIONE S-TRANSFERASE	II.B.7
RSc0386	RSc03354				0.44	0.01							ftsY TRANSMEMBRANE COG1279, LysE-type efflux permease	IV.D
RSc0387	RSc03355				0.66	0.03							CELL DIVISION PROTEIN	IV.A
RSc0388	RSc03356						-0.61	0.00	0.73	0.05			SIGNAL PEPTIDE	VI.C
RSc0389	RSc03357						-0.43	0.00					COG0612, Predicted Zn-dependent peptidases	II.3
RSc0390	RSc03358				1.02	0.01	-0.51	0.01					SIGNAL PEPTIDE	VI.C
RSc0391	RSc03359						-0.51	0.00					COG0742, N6-adenine-specific methylase	II.B.8
RSc0392	RSc03360						-1.05	0.00	-0.80	0.00			kdtB PHOSPHOPANTETHEINE ADENYLYLTRANSFERASE (PANTETHEINE- PHOSPHA	III.A.1
RSc0393	RSc03361						-0.76	0.00	-2.25	0.00			FERREDOXIN	I.G.1
RSc0394	RSc03362												SIGNAL PEPTIDE	VI.C
RSc0395	RSc03363												pth PEPTIDYL-TRNA HYDROLASE	II.D.1
RSc0396	RSc03364				0.88	0.02			-0.77	0.05			rplY 50S RIBOSOMAL SUBUNIT PROTEIN L25	III.C.2
RSc0397	RSc03365						-0.36	0.00					prsA RIBOSE-PHOSPHATE PYROPHOSPHOKINASE	ID.2
RSc0398	RSc03366												ipk ISOPENYLYL MONOPHOSPHATE KINASE (4-CYTIDINE-5'-DIPHOSPHO-2-C-ME	IF
RSc0399	RSc03367						-0.56	0.01	1.26	0.01			lolB COG3017, Outer membrane lipoprotein involved in outer membrane biogenesis	III.B.2
RSc0400	RSc03368				0.37	0.01	-0.49	0.00					mutM TRANSMEMBRANE	VI.C
RSc0401	RSc03369						-0.40	0.00	-0.42	0.05			FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE	II.B.8
RSc0402	RSc03370												COG0699, Predicted GTPase (dynammin-related)	VI.C
RSc0403	RSc03371												mutY AVG-SPECIFIC ADENINE GLYCOSYLASE	II.B.8
RSc0404	RSc03372												CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc0405	RSc03373												COG1660, Predicted P-loop-containing kinase	VI.C
RSc0406	RSc03374												SIGNAL PEPTIDE	VI.C
RSc0407	RSc03375												ptsK HPR KINASE AND PHOSPHATASE	IF
RSc0408	RSc03376												TRANSCRIPTION REGULATOR NITROGEN REGULATORY IIA PROTEIN (ENZYME	I.E.1
RSc0409	RSc03377												ptsN SIGMA-54 MODULATION PROTEIN	I.E.1
RSc0410	RSc03378				0.69	0.01							rpoN1 TRANSCRIPTION REGULATOR RNA POLYMERASE SIGMA N (SIGMA 54) FACTO	I.E.1
RSc0411	RSc03379												ABC TRANSPORTER ATP-BINDING PROTEIN	IV.D
RSc0412	RSc03380												SIGNAL PEPTIDE	VI.C
RSc0413	RSc03381												TRANSMEMBRANE	VI.C
RSc0414	RSc03382												yrbI 3-DEOXY-D-MANNO-OCTULOSONATE 8-PHOSPHATE (KDO 8-P)PHOSPHATASE	II.B.2
RSc0415	RSc03383												COG0794, Predicted sugar phosphate isomerase involved in capsule formation	III.B
RSc0416	RSc03384												TRANSMEMBRANE GLUTATHIONE-REGULATED POTASSIUM-EFFLUX SYSTEM	IV.D.4
RSc0417	RSc03385												CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc0418	RSc03386												COG0693, Intracellular protease/amidase	II
RSc0419	RSc03387												apt ADENINE PHOSPHORIBOSYLTRANSFERASE (APRT)	IF.1
RSc0420	RSc03388												TRANSMEMBRANE TRANSPORT PROTEIN	IV.D
RSc0421	RSc03389												TRANSMEMBRANE	VI.C
RSc0422	RSc03390												uvrA1 ABC TRANSPORTER EXCINUCLEASE ABC SUBUNIT A (DNA REPAIR ATP-BINDI	II.B.8
RSc0423	RSc03392												TRANSMEMBRANE MULTIDRUG-EFFLUX TRANSPORTER	IV.D
RSc0424	RSc03393												ssb SINGLE-STRAND BINDING PROTEIN (HELIX-DESTABILIZING PROTEIN)	II.B.8
RSc0425	RSc03394												REMNANT OF A TRANSPOSASE	VI.A
RSc0426	RSc03395												SIGNAL PEPTIDE	VI.C
RSc0427	RSc03396												COG4706, 3-hydroxylacyl-(acyl carrier protein) dehydratase	I
RSc0428	RSc03397												CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc0429	RSc03398												3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE (BETA- KETOACYL-ACP SYII	IB.1
RSc0430	RSc03399												TRANSMEMBRANE Polysaccharide deacetylase	II.4
RSc0431	RSc0400												TRANSMEMBRANE COG4258, Predicted exporter	VI.C
RSc0432	RSc0401												SIGNAL PEPTIDE	VI.B
RSc0433	RSc0402												COG4261 - Predicted acyltransferase	I
RSc0434	RSc0403												COG0365, Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases	I
RSc0435	RSc0404												TRANSMEMBRANE	VI.C
RSc0436	RSc0405												COG0236, Acyl carrier protein	I
RSc0437	RSc0406												OXIDOREDUCTASE 3-OXOACYL-[ACYL-CARRIER-PROTEIN] REDUCTASE	IB.1
RSc0438	RSc0407												COG0463, Glycosyltransferase	I
RSc0439	RSc0408												SIGNAL PEPTIDE	VI.C
RSc0440	RSc0409												SIGNAL PEPTIDE	VI.C
RSc0441	RSc0410												LIPASE/ESTERASE	II.1
RSc0442	RSc0411												SIGNAL PEPTIDE	VI.B
RSc0443	RSc0412												gntK THERMORESISTANT GLUCONOKINASE (GLUCONATE KINASE 2)	IF.4
RSc0444	RSc0413												TRANSMEMBRANE FATTY-ACID-COA LIGASE	II.1
RSc0445	RSc0414												SIGNAL PEPTIDE GLYCIN-RICH PROTEIN	VI.C
RSc0446	RSc0415												SIGNAL PEPTIDE	VI.C
RSc0447	RSc0416												SIGNAL PEPTIDE COG3271, Predicted double-glycine peptidase	II.3
RSc0448	RSc0417												LIPOPROTEIN	VI.B
RSc0449	RSc0418												CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc0450	RSc0419												CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc0451	RSc0420												TRANSMEMBRANE THREONINE AMONIA-LYASE (THREONINE DEHYDRATASE, I	IA.2
RSc0452	RSc0421												TRANSMEMBRANE ATP-SENSITIVE INWARD RECTIFIER POTASSIUM CHANNEL IV	IV.D

RSc0451	RS04451			-0.91	0.00	-1.33	0.00		TRANSMEMBRANE	V.I.D		
RSc0452	RS04450			1.85	0.00				TRANSMEMBRANE	V.I.C		
RSc0453	RS04448			-0.54	0.04				TRANSMEMBRANE	V.I.C		
RSc0454	RS04446								OXIDOREDUCTASE COG0247, Fe-S OXIDOREDUCTASE AND COG0277, FAD/FM1			
RSc0455	RS04445								COG0537, Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydroly			
RSc0456	RS04444								ABC TRANSPORTER ATP-BINDING TRANSPORT PROTEIN	I.V.D		
RSc0457	RS04443			-0.44	0.01	0.60	0.00		CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSc0458	RS04441					-0.68	0.00	-0.27	0.04	ubiE	I.B.5	
RSc0459	RS04440			-0.70	0.00	-0.54	0.04		TRANSMEMBRANE	V.I.C		
RSc0460	RS04439			-0.45	0.01			-1.61	0.01	CONSERVED HYPOTHETICAL PROTEIN	V.I.C	
RSc0461	RS04437			-0.72	0.03				TRANSMEMBRANE UBIQUINONE BIOSYNTHESIS PROTEIN	I.B.5		
RSc0462	RS04436		0.71	0.04					CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSc0463	RS04434		0.85	0.01	-0.49	0.00			TRANSMEMBRANE SODIUM/SOLUTE SYMPORTER	I.V.D		
RSc0464	RS04433		0.49	0.01	-0.34	0.00		-0.36	0.04	CONSERVED HYPOTHETICAL PROTEIN	V.I.C	
RSc0465	RS04432				-0.51	0.01	-0.64	0.03	-0.45	0.04	TRANSMEMBRANE	V.I.C
RSc0466	RS04431		0.90	0.00	-0.35	0.01				aspS	I.I.D.1	
RSc0467	RS04430				-0.57	0.02				TRANSMEMBRANE	V.I.C	
RSc0468	RS04429				-0.46	0.00				ntpA	I.F.9	
RSc0469	RS04427				-0.53	0.00		-0.73	0.01	COG3568, Metal-dependent hydrolase	I.I	
RSc0470	RS04425									COG1502, Phosphatidylserine/phosphatidylglycerophosphate/cardioliipin synthases ar	I	
RSc0471	RS04424		0.73	0.02	-0.49	0.03				COG4670, Acyl CoA:acetate/3-ketoacid CoA transferase	I	
RSc0472	RS04423		0.99	0.00	-1.42	0.00				TRANSCRIPTION REGULATOR	V.I.A	
RSc0473	RS04422		0.77	0.01	-0.72	0.00	-0.89	0.00		OXIDOREDUCTASE ACYL-CoA DEHYDROGENASE	I.I.1	
RSc0474	RS04421		0.90	0.01	-0.48	0.01				OXIDOREDUCTASE 3-HYDROXYACYL-CoA DEHYDROGENASE	I.I.1	
RSc0475	RS04420		0.80	0.01	-0.56	0.00				ACETYL-CoA ACYLTRANSFERASE	I.C	
RSc0476	RS04419									ENOYL-CoA HYDRATASE	I.I.4	
RSc0477	RS04418				-0.79	0.00				COG1607, Acyl-CoA hydrolase	I.I	
RSc0478	RS04417				-0.66	0.01				ABC TRANSPORTER COMPOSITE ATP-BINDING TRANSMEMBRANE PROTEIN	I.V.D	
RSc0479	RS04416				-0.47	0.01				TRANSCRIPTION REGULATOR	V.I.A	
RSc0480	RS04415		0.49	0.01	-0.36	0.04				gdhA	I.A.19	
RSc0481	RS04394		0.36	0.05	-0.54	0.00	0.82	0.00		ABC TRANSPORTER AMINO-ACID-BINDING PERIPLASMIC PROTEIN (PBP)	I.V.D	
RSc0482	RS04391		0.72	0.00	-0.36	0.00	0.95	0.03		ABC TRANSPORTER GLUTAMATE/ASPARTATE TRANSMEMBRANE PROTEIN	I.V.D.2	
RSc0483	RS04390		0.88	0.00	-0.27	0.02			-1.31	0.01	ABC TRANSPORTER GLUTAMATE/ASPARTATE TRANSMEMBRANE PROTEIN	I.V.D.2
RSc0484	RS04389				-0.41	0.00			-0.88	0.00	ABC TRANSPORTER GLUTAMATE/ASPARTATE TRANSPORT ATP-BINDING PRO	I.V.D.2
RSc0485	RS04388				-0.79	0.00	-0.89	0.00		COG0121, Predicted glutamine amidotransferase	I	
RSc0486	RS05749				-0.30	0.01				ttuD2	I.I.4	
RSc0487	RS05822		1.20	0.01						DIHYDROOROTASE	I.D.1	
RSc0488	RS05751									CONSERVED HYPOTHETICAL PROTEIN	V.I.C	
RSc0489	RS05752		0.59	0.03	-0.63	0.00	-0.64	0.00		COG1765, Predicted redox protein, regulator of disulfide bond formation	I.I.B.7	
RSc0490	RS05035								-1.05	0.01	50S RIBOSOMAL PROTEIN L13	I.II.C.2
RSc0491	RS05034		0.88	0.03					-0.98	0.04	30S RIBOSOMAL PROTEIN S9	I.II.C.2
RSc0492	RS05033				-0.49	0.00			-0.94	0.00	TRANSMEMBRANE	V.I.C
RSc0493	RS05032				-0.42	0.01				ccmA	I.II.B	
RSc0494	RS05030				-0.22	0.01			-0.97	0.00	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0495	RS05029				-0.63	0.00				COG2377, Predicted molecular chaperone distantly related to HSP70-fold metallopro	I.I.B.7	
RSc0496	RS05028		0.82	0.05	-0.17	0.05	1.21	0.01		tyrS	I.I.D.1	
RSc0497	RS05026		0.52	0.04			0.89	0.01		COG1490, D-Tyr-IRNAtyr deacylase	I.I.D.1	
RSc0498	RS05025									HYPOTHETICAL PROTEIN	V.I.D	
RSc0499	RS05023								-0.97	0.02	gpmB	I.I.H.8
RSc0500	RS05022		0.75	0.05			0.88	0.02		PHOSPHOGLYCERATE MUTASE 2	I.I.H.8	
RSc0501	RS05021									rolB	I.I.H.8	
RSc0502	RS05020				-0.73	0.00				HOLLIDAY JUNCTION DNA HELICASE	I.I.H.8	
RSc0503	RS05019				-0.44	0.01				glpQ	I.I.F.11	
RSc0504	RS05018								-1.20	0.00	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE, PERIPLASMIC PROTEIN	I.I.H.8
RSc0505	RS05017									purH	I.I.D.2	
RSc0506	RS05006				-0.52	0.00				TRANSMEMBRANE BIFUNCTIONAL PROTEIN : PHOSPHORIBOSYLAMINOIMIDAZI	I.I.C	
RSc0507	RS05000									TRANSCRIPTION REGULATOR FACTOR-FOR-INVERSION-STIMULATION PROTEI	I.I.C	
RSc0508	RS04999								-0.39	0.01	COG0042, tRNA-dihydrouridine synthase	I.I.D.1
RSc0509	RS04998									TRANSMEMBRANE AMINO ACID DEHYDROGENASE	I.I.3	
RSc0510	RS04997								0.68	0.00	OXIDOREDUCTASE 2-OCTAPRENYL-6-METHOXYPHENOL HYDROXYLASE	I.I.H.3
RSc0511	RS04996		0.51	0.02						pepP	I.I.A.4	
RSc0512	RS04995				-0.52	0.02	0.99	0.00		TRANSMEMBRANE SIGNAL TRANSDUCTION PROTEIN EAL - GGDEF DOMAINS	V.I.A	
RSc0513	RS04992				1.01	0.01				COG1208, Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysacc	V.I.C	
RSc0514	RS04986		0.47	0.01						TRANSMEMBRANE	V.I.C	
RSc0515	RS04980				-0.32	0.02				TRANSMEMBRANE COG1296, Predicted branched-chain amino acid permease (azal	I.V.D.2	
RSc0516	RS04977				-0.35	0.02			-0.93	0.00	COG3178, Predicted phosphotransferase related to Ser/Thr protein kinases	V.I.C
RSc0517	RS04975				-0.38	0.01				TRANSMEMBRANE ORGANIC SOLVENT TOLERANCE PROTEIN	I.V.F.1	
RSc0518	RS04973				-0.21	0.02				PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (ROTAMASE C)	I.V.B	
RSc0519	RS04969									pdxA	I.B.10	
RSc0520	RS04961		0.88	0.02						ksgA	I.V.G.2	
RSc0521	RS04960									DIMETHYLADENOSINE TRANSFERASE (16S RRNA DIMETHYLASE)	V.I.C	
RSc0522	RS04959				-0.32	0.05				TRANSMEMBRANE	I.F.17	
RSc0523	RS04957		0.72	0.00						gloA	I.I	
RSc0524	RS04944		1.24	0.00					-0.74	0.00	LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE)	I.I
RSc0525	RS04943				-0.30	0.00				COG1451, Predicted metal-dependent hydrolase	I.I	
RSc0526	RS04942									TRANSMEMBRANE PHOSPHATE ACYLTRANSFERASE	I	
RSc0527	RS04941		1.13	0.00	-0.73	0.00	-0.88	0.03		COG0241, Histidinol phosphatase and related phosphatases	I	
RSc0528	RS04940		0.49	0.02	-0.60	0.00				glyS	I.I.D.1	
RSc0529	RS04939									GLYCYL-TRNA SYNTHETASE BETA CHAIN	V.I.C	
RSc0530	RS04938									SIGNAL PEPTIDE	V.I.C	
RSc0531	RS04937								1.07	0.03	GLYCYL-TRNA SYNTHETASE ALPHA CHAIN	I.I.D.1
RSc0532	RS04936									Int	I.I.D.1	
RSc0533	RS04935									TRANSMEMBRANE APOLIPOPROTEIN N-ACYLTRANSFERASE	I.V.F.1	
RSc0534	RS04933		0.46	0.03	-0.71	0.01				COG4535, Putative Mg2+ and Co2+ transporter	I.V.D	
RSc0535	RS04931		0.92	0.04						COG0319, Predicted metal-dependent hydrolase	I.I	
RSc0537	RS04929				-1.04	0.00				phoH	I.V.F.1	
RSc0538	RS04928				-1.23	0.01				COG0621, 2-methylthioadenine synthetase	I.I.B.7	
RSc0539	RS04927				-0.50	0.01	-0.41	0.00	-0.50	0.00	SIGNAL PEPTIDE	V.I.C
RSc0540	RS04926		0.90	0.03						OXIDOREDUCTASE COG3380, Predicted NAD/FAD-dependent oxidoreductase	I	
RSc0541	RS04925		1.04	0.01	-1.65	0.00				TRANSMEMBRANE LIPOPROTEIN	V.I.C	
RSc0542	RS04924									SIGNAL PEPTIDE	V.I.B	
RSc0543	RS04923				-0.67	0.00				TRANSMEMBRANE SHORT-CHAIN DEHYDROGENASE	I.I	
RSc0544	RS04922				-0.35	0.00				OXIDOREDUCTASE TRANSMEMBRANE ACYL-CoA DEHYDROGENASE	I.I	
RSc0545	RS04921				-0.67	0.04				TRANSCRIPTION REGULATOR	V.I.A	
RSc0546	RS04920									CONSERVED HYPOTHETICAL PROTEIN	V.I.C	
RSc0547	RS04919									OXIDOREDUCTASE	I.I	
RSc0548	RS04918									TRANSMEMBRANE	V.I.C	
RSc0549	RS04917								-0.59	0.05	TRANSMEMBRANE SUGAR TRANSPORTER	I.V.D.3
RSc0550	RS04916		0.39	0.05	-0.70	0.01				TRANSCRIPTION REGULATOR TRANSMEMBRANE SENSOR HISTIDINE KINASE	V.I.A	
RSc0551	RS04915								-0.59	0.02	TRANSCRIPTION REGULATOR RESPONSE REGULATOR	V.I.A
RSc0552	RS04913				-0.36	0.01				recA	I.II.B.8	
RSc0553	RS04912				-0.47	0.02	-1.23	0.02	-1.74	0.00	DNA STRAND EXCHANGE AND RECOMBINATION PROTEIN	V.I.A
RSc0554	RS04911								-1.54	0.00	REGULATORY PROTEIN RECX	V.I.C
RSc0555	RS04910								-1.68	0.00	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0556	RS04909		1.17	0.04						sucC	I.II.6	
RSc0557	RS04908				-0.65	0.02				sucD	I.II.6	
RSc0558	RS04907		0.79	0.01	-0.29	0.00				TRANSMEMBRANE COG0861, Membrane protein TerC, possibly involved in tellurium	I.II.B.1	
RSc0559	RS04906		0.84	0.02	-0.62	0.00				SIGNAL PEPTIDE TYPE 4 FIMBRIAL PILIN-LIKE PROTEIN	I.II.A.2	
RSc0560	RS04905				-0.41	0.03				SIGNAL PEPTIDE TYPE 4 FIMBRIAL PILIN	I.II.A.2	
RSc0561	RS04904		0.98	0.01						TRANSMEMBRANE COG3307, Lipid A core - O-antigen ligase and related enzymes	I.II.A.1	
RSc0562	RS04903				-0.56	0.00				MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN C	I.II.12	
										SIGNAL PEPTIDE COG4783, Putative Zn-dependent protease, contains TPR repeats	I.II.A.4	
										CONSERVED HYPOTHETICAL PROTEIN	V.I.C	

RSc0678	RS01583		0,77	0,00					pyrB	ASPARTATE CARBAMOYLTRANSFERASE (CATALYTIC CHAIN)	I.D.1		
RSc0679	RS01584		0,58	0,00	-0,25	0,00		-0,59	pyrX	DIHYDROOROTASE-LIKE PROTEIN	I.D.1		
RSc0680	RS01585	-0,31	0,04					-0,70	plsC	TRANSMEMBRANE 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE	II.B.1		
RSc0681	RS01586		0,48	0,01					apaH	BIS(5'-NUCLEOSYL)-TETRAPHOSPHATASE (SYMMETRICAL)	I.F.1		
RSc0682	RS01587		0,58	0,00	-0,26	0,00	0,77	0,00	rfbB	DTDP-GLUCOSE 4,6-DEHYDRATASE	I.F.10		
RSc0683	RS01588		0,80	0,00			0,45	0,02	rfbD	OXIDOREDUCTASE DTDP-4-DEHYDRORHAMNOSE REDUCTASE	I.F.10		
RSc0684	RS01589		0,50	0,04	-0,36	0,01	0,61	0,03	rfbA	GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE	I.F.10		
RSc0685	RS01590		1,02	0,00	-0,37	0,00			rfbC	DTDP-4-DEHYDRORHAMNOSE 3,5-EPIMERASE	I.F.10		
RSc0686	RS01591				-0,52	0,00					TRANSMEMBRANE LIPOPOLYSACCHARIDE O-SIDE CHAIN BIOSYNTHESIS PRO	II.B.2	
RSc0687	RS01592		0,39	0,00	-0,46	0,04			rfbF	DTDP-RHAMNOSYL TRANSFERASE RFBF	II.B.2		
RSc0688	RS01593		0,57	0,05						GLYCOSYL TRANSFERASE	II.B.2		
RSc0689	RS01594				-0,25	0,02			wecA	TRANSMEMBRANE UNDECAPRENYL PHOSPHATE N-ACETYLGLUCOSAMINYLTHI	II.B.2		
RSc0690	RS01595		0,50	0,04	-0,39	0,00				TRANSMEMBRANE	V.I.C		
RSc0691	RS01596		0,48	0,02	-0,30	0,00				PHOSPHOMANNOMUTASE OR PHOSPHOGLUCOMUTASE	I.F.18		
RSc0692	RS01597		0,67	0,00	-0,32	0,01			rfaC1	LIPOPOLYSACCHARIDE HEPTOSYLTRANSFERASE	II.B.2		
RSc0693	RS01598						-1,04	0,02	kdtA	TRANSMEMBRANE 3-DEOXY-D-MANNO-OCTULOSONIC-ACID TRANSFERASE	II.B.2		
RSc0694	RS01599				-0,70	0,01	-0,98	0,05		TRANSMEMBRANE COG3187, Heat shock protein	II.B.7		
RSc0695	RS01600							-0,99		ABC TRANSPORTER PORIN (OMP)	I.V.D		
RSc0696	RS01601		0,81	0,00						COG0607, Rhodanese-related sulfurtransferase	I		
RSc0697	RS01602		0,65	0,03			0,71	0,02	pcm	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE	II.B.7		
RSc0698	RS01603		0,35	0,00	-0,64	0,01		1,02		TRANSCRIPTION REGULATOR	V.I.A		
RSc0699	RS01604				-0,48	0,01				OXIDOREDUCTASE COG0727: Predicted Fe-S-cluster oxidoreductase	I		
RSc0700	RS01605				0,38	0,00				TRANSMEMBRANE	V.I.C		
RSc0701	RS01606				-0,33	0,02			bacA	TRANSMEMBRANE BACITRACIN RESISTANCE PROTEIN PUTATIVE UNDECAPRI	IV.G.2		
RSc0702	RS01607	-0,45	0,05							OXIDOREDUCTASE COG1902, NADH:flavin oxidoreductases	I		
RSc0703	RS01608		0,77	0,05						COG0220, Predicted S-adenosylmethionine-dependent methyltransferase	V.I.C		
RSc0704	RS01609		0,52	0,01						COG0388, Predicted amidohydrolase	V.I.C		
RSc0705	RS01610				0,76	0,00				TRANSMEMBRANE	V.I.D		
RSc0706	RS05147		0,32	0,03	-0,53	0,00				CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSc0707	RS05146				-0,87	0,01				HYPOTHETICAL PROTEIN	V.I.D		
RSc0708	RS05145		0,78	0,01	-0,68	0,01			ubiD	3-OCTAPRENYL-4-HYDROXYBENZOATE CARBOXY-LYASE (POLYPRENYL P-HY)	I.B.5		
RSc0709	RS05144						1,02	0,00		TRANSMEMBRANE TRANSGLYCOSYLASE	V.I.B		
RSc0710	RS05143				0,54	0,01				AMINOTRANSFERASE	I.F.14		
RSc0711	RS05142		0,49	0,02	-0,11	0,02	0,89	0,05	nusB	TRANSCRIPTION REGULATOR N UTILIZATION SUBSTANCE PROTEIN B (TRANS	II.B.6		
RSc0712	RS05141								ribH	RIBOFLAVIN SYNTHASE (BETA CHAIN) : 6,7-DIMETHYL-8-RIBITYLLUMAZINE SY	I.B.7		
RSc0713	RS05140		0,35	0,03	-0,34	0,01	-0,71	0,00	ribAB	RIBOFLAVIN BIOSYNTHESIS BIFUNCTIONAL PROTEIN : GTP CYCLOHYDROLASE	I.B.7		
RSc0714	RS05139								ribE	RIBOFLAVIN SYNTHASE (ALPHA CHAIN)	I.B.7		
RSc0715	RS05138								ribD	OXIDOREDUCTASE RIBOFLAVIN BIOSYNTHESIS BIFUNCTIONAL PROTEIN RIBD	I.B.7		
RSc0716	RS05137				-0,78	0,01				TRANSMEMBRANE TYPE 4 FIMBRIAL PILIN RELATED PROTEIN	III.A.2		
RSc0717	RS05136									SIGNAL PEPTIDE TYPE-4 FRIMBRIAL PILIN-RELATED PROTEIN	III.A.2		
RSc0718	RS05135				-0,44	0,03				TRANSMEMBRANE TYPE 4 FIMBRIAL BIOGENESIS PROTEIN PILY1-RELATED PFI	III.A.2		
RSc0719	RS05134				0,94	0,00				SIGNAL PEPTIDE TYPE 4 FIMBRIAL BIOGENESIS PILX-RELATED PROTEIN	III.A.2		
RSc0720	RS05133	-3,07	0,00	-1,35	0,00	1,81	0,00	1,45	0,03	TRANSMEMBRANE TYPE 4 FIMBRIAL BIOGENESIS PROTEIN PILW-RELATED PRI	III.A.2		
RSc0721	RS05132									TRANSMEMBRANE	V.I.D		
RSc0722	RS05131									TRANSMEMBRANE TYPE 4 FIMBRIAL PILIN RELATED PROTEIN	III.A.2		
RSc0723	RS05130		0,38	0,02						TRANSMEMBRANE TYPE-4 FIMBRIAL PILIN-RELATED PROTEIN	III.A.2		
RSc0724	RS05129				-0,55	0,01	1,64	0,05		SIGNAL PEPTIDE TYPE-4 FIMBRIAL BIOGENESIS PLY1-RELATED PROTEIN	III.A.2		
RSc0725	RS05128				-0,40	0,00		-0,39	0,02	TRANSMEMBRANE TYPE 4 FIMBRIAL BIOGENESIS PROTEIN PILX-RELATED PR	III.A.2		
RSc0726	RS05127		-0,61	0,00	-0,20	0,01	1,40	0,00		TRANSMEMBRANE TYPE 4 FIMBRIAL BIOGENESIS PROTEIN PILW RELATED PR	III.A.2		
RSc0727	RS05126				-0,67	0,04				TRANSMEMBRANE TYPE-4 FIMBRIAL BIOGENESIS PILV-RELATED PROTEIN	III.A.2		
RSc0728	RS05125				-0,67	0,00	0,72	0,04		COG1327, Predicted transcriptional regulator, consists of a Zn-ribbon and ATP-cone	V.I.A		
RSc0729	RS05124				-0,96	0,00	1,12	0,01	0,99	0,02	glyA1	SERINE HYDROXYMETHYLTRANSFERASE	I.A.11
RSc0730	RS05123		0,43	0,04						OXIDOREDUCTASE	I		
RSc0731	RS05122				-0,66	0,01				THIOESTERASE	I		
RSc0732	RS05121				-0,56	0,01			tolI	TRANSMEMBRANE TOLQ-RELATED TRANSPORT PROTEIN	IV.E		
RSc0733	RS05120				-0,62	0,00			tolR	TRANSMEMBRANE TOLR-RELATED PROTEIN TRANSPORT	IV.E		
RSc0734	RS05119				-0,74	0,00			tolA	TRANSMEMBRANE TOLA-RELATED TRANSPORT PROTEIN	IV.E		
RSc0735	RS05118				-0,60	0,00	0,42	0,05	tolB	TOLB -RELATED TRANSPORT PROTEIN	IV.E		
RSc0736	RS05117				-0,47	0,00			pal	PEPTIDOGLYCAN-ASSOCIATED LIPOPROTEIN PRECURSOR	III.B.3		
RSc0737	RS05116				-0,30	0,00				TRANSMEMBRANE	V.I.C		
RSc0738	RS05115				-0,30	0,04				SIGNAL PEPTIDE COG0603, Predicted PP-loop superfamily ATPase	V.I.C		
RSc0739	RS05114		0,44	0,01				-0,69	0,02	TRANSMEMBRANE	V.I.C		
RSc0740	RS05113		0,56	0,02				0,99	0,00	TRANSMEMBRANE	V.I.D		
RSc0741	RS05112		0,45	0,05	-0,67	0,02	-0,82	0,00	che	TRANSCRIPTION REGULATOR CHEMOTAXIS RESPONSE REGULATOR PROTEI	IV.C		
RSc0742	RS05111		0,68	0,01	-1,10	0,00			cheZ2	CHEMOTAXIS PROTEIN CHEZ	IV.C		
RSc0743	RS05110		0,53	0,00	-0,39	0,01			aroG2	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE, PHE-SENSITIVE (DA	I.A.5		
RSc0744	RS05109				-0,51	0,00				DNA/RNA NON-SPECIFIC ENDONUCLEASE	I.A		
RSc0745	RS05108									COG3613, Nucleoside 2-deoxyribosyltransferase	I		
RSc0746	RS05107		0,66	0,01					tauD	OXIDOREDUCTASE ALPHA-KETOGLUTARATE-DEPENDENT TAURINE DIOXYGE	II.1.2		
RSc0747	RS05106									CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSc0748	RS05105				-0,36	0,03	-1,03	0,05	-0,69	0,00	ABC TRANSPORTER COG0390, ABC-type uncharacterized transport system, perme	IV.D	
RSc0749	RS05104				-0,33	0,02				ABC TRANSPORTER ATP-BINDING PROTEIN	IV.D		
RSc0750	RS05103				-1,20	0,00				TRANSMEMBRANE	IV.B		
RSc0751	RS05102				-0,80	0,00				CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSc0752	RS05101				-0,41	0,00				TRANSMEMBRANE	V.I.C		
RSc0753	RS05100									TRANSMEMBRANE	V.I.C		
RSc0754	RS05099				-0,27	0,02	-0,59	0,02		OXIDOREDUCTASE ANTIOXIDANT PROTEIN (PEROXIDASE)	IV.G.4		
RSc0755	RS05098									TRANSMEMBRANE COG2252, Permeases	IV.D		
RSc0756	RS05097		0,62	0,02					gcdH	OXIDOREDUCTASE GLUTARYL-CoA DEHYDROGENASE	II.3		
RSc0757	RS05096									TRANSCRIPTION REGULATOR	V.I.A		
RSc0758	RS05095				0,34	0,01			kynA	OXIDOREDUCTASE Tryptophan 2,3-dioxygenase	II.3		
RSc0759	RS05094				0,43	0,01			kynU	KYNURENINASE	II.3		
RSc0760	RS05093								kynB	KYNURENINE FORMIDASE	II.3		
RSc0761	RS05092				-0,77	0,00				TRANSCRIPTION REGULATOR	V.I.A		
RSc0762	RS05091		0,85	0,03	-0,43	0,02				CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSc0763	RS05090		0,24	0,05						OXIDOREDUCTASE MONOOXYGENASE	I		
RSc0764	RS05089	-0,54	0,04		-0,65	0,04			msrA	OXIDOREDUCTASE PEPTIDE METHIONINE SULFOXIDE REDUCTASE	IV.B		
RSc0765	RS05088									CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSc0766	RS05087				-0,80	0,00			cfa2	CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE	I.C		
RSc0767	RS05086		0,75	0,05					pdxH1	OXIDOREDUCTASE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (PNP/PMP OXIDA	I.B.10		
RSc0768	RS05151									HYPOTHETICAL PROTEIN	V.I.D		
RSc0769	RS05085		0,84	0,01						HYDROLASE GLYCOSIDASE	II.4		
RSc0770	RS05084				-1,00	0,01				OXIDOREDUCTASE TRANSMEMBRANE DEHYDROGENASE (SMALL SUBUNIT)	I		
RSc0771	RS05083									OXIDOREDUCTASE TRANSMEMBRANE DEHYDROGENASE (LARGE SUBUNIT)	I		
RSc0772	RS05082									SIGNAL PEPTIDE OXIDOREDUCTASE DEHYDROGENASE (CYTOCHROME C SUE	I.G.1		
RSc0773	RS05081								asmA	TRANSMEMBRANE COG2982, Uncharacterized protein involved in outer membrane	IV.C		
RSc0774	RS05080									TRANSMEMBRANE COG1179, Dinucleotide-utilizing enzyme involved in molybdopter	I.B		
RSc0775	RS05079		0,80	0,00	0,32	0,02			katGb	OXIDOREDUCTASE PEROXIDASE/CATALASE (CATA PROTEIN)	IV.G.4		
RSc0777	RS05077									COG2703, Hemerythrin	IV.D.5		
RSc0778	RS05076				-0,28	0,05				COG3531, Predicted protein-disulfide isomerase	II.B.6		
RSc0779	RS05075		0,82	0,01						THIOREDOXIN	I.B.6		
RSc0780	RS05058				-0,57	0,03			fadD2	LONG-CHAIN-FATTY-ACID-CoA LIGASE	II.1.1		
RSc0781	RS05057									SIGNAL PEPTIDE ANKYRIN REPEAT HARBORING PROTEIN	V.I.C		
RSc0782	RS05056				-0,78	0,01	-0,44	0,02		COG3703, Uncharacterized protein involved in cation transport	IV.D.4		
RSc0783	RS05055				-0,94	0,05				TRANSMEMBRANE	IV.D		
RSc0784	RS05054		0,48	0,01					fkpA	FKBP-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE)(IMMUNOPHIL	IV.B		
RSc0785	RS05053		0,66	0,01						CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSc0786	RS05051				-0,94	0,00				CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSc0787	RS05050				-0,63	0,03				TRANSMEMBRANE	V.I.C		
RSc0788	RS05049						0,49	0,02		TRANSMEMBRANE	V.I.C		
RSc0789	RS05048		0,50	0,05				-0,25	0,04	CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSc0790	RS05047		0,76	0,00						SIGNAL PEPTIDE	V.I.C		

RSc0791	RS05046			-0.35	0.00	0.84	0.00	glnS	GLUTAMINYL-tRNA SYNTHETASE	II.D.1					
RSc0792	RS05045								CONSERVED HYPOTHETICAL PROTEIN	V.I.C					
RSc0793	RS05044	1.60	0.00	-0.60	0.00				TRANSMEMBRANE	V.I.C					
RSc0794	RS05043	1.60	0.02	-0.85	0.02				TRANSMEMBRANE	V.I.C					
RSc0795	RS05042	0.54	0.04	-0.34	0.01				TRANSMEMBRANE	V.I.C					
RSc0796	RS05041	0.68	0.04	-0.39	0.02			alaS	TRANSMEMBRANE COG1804, Predicted acyl-CoA transferases/carnitine dehydratase I	II.D.1					
RSc0797	RS05040	0.43	0.02			-0.77	0.03		ALANYL-tRNA SYNTHETASE	II.D.1					
RSc0798	RS05039			-0.64	0.00				PURINE NUCLEOSIDE PERMEASE	IV.D.6					
RSc0799	RS05038	0.40	0.02	-0.40	0.02				PURINE NUCLEOSIDE PERMEASE	IV.D.6					
RSc0800	RS05037					-1.93	0.05		SIGNAL PEPTIDE FERRISIDEROPHORE RECEPTOR	IV.D.5					
RSc0801	RS05036	0.70	0.02	-1.05	0.00				TRANSMEMBRANE LIPOPROTEIN	V.I.C					
RSc0802	RS05031								TRANSMEMBRANE COG0330, Membrane protease subunit, stomatin/prohibitin homc	II.A.4					
RSc0803	RS05027	-0.62	0.02	-0.54	0.00				TRANSMEMBRANE COG1030, Membrane-bound serine protease (ClpP class)	II.A.4					
RSc0804	RS05024			-0.62	0.00				TRANSCRIPTION REGULATOR	V.I.A					
RSc0805	RS05064	-0.59	0.00	0.88	0.00				CONSERVED HYPOTHETICAL PROTEIN	V.I.C					
RSc0806	RS05016								ALDOLASE	I					
RSc0807	RS05015								TAUTOMERASE (4-OXALOCROTONATE TAUTOMERASE)	II.A					
RSc0808	RS05014	0.55	0.02					ItaA	LOW SPECIFICITY L-THREONINE ALDOLASE	II.A.11					
RSc0809	RS05013			-0.53	0.00				HYDROLASE	II					
RSc0810	RS05012			-0.39	0.02	-0.71	0.01		COG0425, Predicted redox protein, regulator of disulfide bond formation	II.B.7					
RSc0811	RS05011							sirA	OXIDOREDUCTASE SULFITE:CYTOCHROME C OXIDOREDUCTASE (SUBUNIT B)	II.F.3					
RSc0812	RS05010			1.40	0.00	2.45	0.00	sorB	OXIDOREDUCTASE SULFITE:CYTOCHROME C OXIDOREDUCTASE (SUBUNIT A)	II.F.3					
RSc0813	RS05009	0.51	0.00	0.49	0.00	0.73	0.02	sorAb	OXIDOREDUCTASE SULFITE:CYTOCHROME C OXIDOREDUCTASE (SUBUNIT A)	II.F.3					
RSc0814	RS05008			-0.83	0.00				TRANSMEMBRANE COG1280, Threonine efflux protein	IV.D.2					
RSc0815	RS05007			-1.18	0.00				TRANSMEMBRANE	V.I.B					
RSc0816	RS05006								TRANSCRIPTION REGULATOR COG1733, Transcriptional regulator	V.I.A					
RSc0817	RS05005			-0.48	0.00			gstD	GLUTATHIONE S-TRANSFERASE	II.B.7					
RSc0818	RS05004								COG4305, Endoglucanase C-terminal domain/subunit and related proteins	II.A.3					
RSc0819	RS05003			1.52	0.00				COG5485, Ester cyclase	I					
RSc0820	RS05179	1.53	0.04						TRANSCRIPTION REGULATOR	V.I.A					
RSc0821	RS05178								NADPH NITROREDUCTASE	I					
RSc0822	RS05171								CONSERVED HYPOTHETICAL PROTEIN	V.I.B					
RSc0823	RS05169			-0.89	0.00	-2.07	0.01		HYPOTHETICAL PROTEIN	V.I.D					
RSc0824	RS05166			-1.73	0.02	2.39	0.00		CONSERVED HYPOTHETICAL PROTEIN	V.I.C					
RSc0825	RS06018	-1.32	0.05	-2.16	0.00	3.98	0.00		HYPOTHETICAL PROTEIN	V.I.D					
RSc0826	RS05162			-1.73	0.00	3.60	0.00		TYPE III EFFECTOR PROTEIN POPP1	V.I.E					
RSc0827	RS05161							popP1	CONSERVED HYPOTHETICAL PROTEIN	V.I.C					
RSc0830	RS05157								CONSERVED HYPOTHETICAL PROTEIN	V.I.C					
RSc0831	RS05156			-0.34	0.01	-2.37	0.02	secA2	Preprotein translocase subunit SecA (ATPase, RNA helicase) - related protein	IV.E.2					
RSc0832	RS05155			-0.52	0.00				HYPOTHETICAL PROTEIN	V.I.D					
RSc0833	RS04994			-1.17	0.01				HYPOTHETICAL PROTEIN	V.I.B					
RSc0834	RS04993								HYPOTHETICAL PROTEIN	V.I.B					
RSc0835	RS04991								CONSERVED HYPOTHETICAL PROTEIN	V.I.C					
RSc0836	RS04990			-0.63	0.00				CONSERVED HYPOTHETICAL PROTEIN	V.I.C					
RSc0837	RS04989								CONSERVED HYPOTHETICAL PROTEIN	V.I.C					
RSc0838	RS04988			-1.01	0.04				HYPOTHETICAL PROTEIN	V.I.D					
RSc0839	RS04987			-0.70	0.00				BACTERIOPHAGE-RELATED PROTEIN	V.D					
RSc0840	RS04985			-2.87	0.03				CONSERVED HYPOTHETICAL PROTEIN	V.I.C					
RSc0841	RS04984								CONSERVED HYPOTHETICAL PROTEIN	V.I.C					
RSc0842	RS05150			-1.04	0.00	-1.40	0.00		HYPOTHETICAL PROTEIN	V.I.D					
RSc0844	RS04982								COG0863, DNA modification methylase	II.B.8					
RSc0845	RS04981								COG0863, DNA modification methylase	II.B.8					
RSc0846	RS04979								HYPOTHETICAL PROTEIN	V.I.D					
RSc0847	RS04978								HYPOTHETICAL PROTEIN	V.I.B					
RSc0848	RS04976	0.54	0.05						CONSERVED HYPOTHETICAL PROTEIN	V.I.C					
RSc0849	RS04974								CONSERVED HYPOTHETICAL PROTEIN	V.I.C					
RSc0850	RS04972			-0.56	0.00		0.90	0.02	CONSERVED HYPOTHETICAL PROTEIN	V.I.C					
RSc0851	RS04971			-0.51	0.03				HYPOTHETICAL PROTEIN	V.I.D					
RSc0852	RS04970			-1.88	0.03	0.60	0.03	0.47	0.01	BACTERIOPHAGE-RELATED PROTEIN	V.D				
RSc0853	RS04968			-0.72	0.03				BACTERIOPHAGE-RELATED PROTEIN	V.D					
RSc0854	RS04967								HYPOTHETICAL PROTEIN	V.I.D					
RSc0855	RS04966					0.55	0.01		HYPOTHETICAL PROTEIN	V.I.D					
RSc0856	RS04965								HYPOTHETICAL PROTEIN	V.I.D					
RSc0857	RS04964								BACTERIOPHAGE-RELATED PROTEIN	V.D					
RSc0858	RS04963								BACTERIOPHAGE-RELATED PROTEIN	V.D					
RSc0859	RS04962			-1.00	0.02				BACTERIOPHAGE-RELATED PROTEIN	V.D					
RSc0860	RS04958			-1.14	0.01				BACTERIOPHAGE-RELATED PROTEIN	V.D					
RSc0861	RS04956								HYPOTHETICAL PROTEIN	V.I.D					
RSc0862	RS04955								SIGNAL PEPTIDE	V.I.D					
RSc0863	RS04954								CONSERVED HYPOTHETICAL PROTEIN	V.I.C					
RSc0864	RS04952								CONSERVED HYPOTHETICAL PROTEIN	V.I.C					
RSc0865	RS04953								HYPOTHETICAL PROTEIN	V.I.D					
RSc0866	RS04951								HYPOTHETICAL PROTEIN	V.I.B					
RSc0867	RS04950			0.55	0.02		-0.56	0.05	TRANSCRIPTION REGULATOR HNS-LIKE PROTEIN	V.I.A					
RSc0868	RS04882			-3.39	0.00	4.25	0.00	2.87	0.00	popP2	TYPE III EFFECTOR PROTEIN POPP2	V.I.E			
RSc0869	RS04946								BACTERIOPHAGE CYTOSINE-SPECIFIC METHYLTRANSFERASE	II.B.8					
RSc0870	RS04945								HYPOTHETICAL PROTEIN	V.I.B					
RSc0871	RS04877			-0.33	0.00	-0.57	0.05	-0.19	0.02	PLASMID STABILITY-LIKE PROTEIN	V.B				
RSc0872	RS04874					-0.89	0.00	-0.51	0.01	CONSERVED HYPOTHETICAL PROTEIN	V.I.C				
RSc0873	RS04872								TRANSMEMBRANE BACTERIOPHAGE-RELATED PROTEIN	V.D					
RSc0874	RS04870								TRANSMEMBRANE	V.I.D					
RSc0875	RS04868								CONSERVED HYPOTHETICAL PROTEIN	V.I.C					
RSc0876	RS04866								CONSERVED HYPOTHETICAL PROTEIN	V.I.C					
RSc0877	RS04865								HYPOTHETICAL PROTEIN	V.I.D					
RSc0878	RS04864								HYPOTHETICAL PROTEIN	V.I.D					
RSc0879	RS04863					-0.56	0.05		TRANSMEMBRANE	V.I.B					
RSc0880	RS04862			-0.42	0.03				CONSERVED HYPOTHETICAL PROTEIN	V.I.C					
RSc0881	RS04861								TRANSMEMBRANE	V.I.C					
RSc0882	RS04860								TRANSMEMBRANE	V.I.C					
RSc0883	RS04859								LYSOZYME (ENDOLYSIN)	II.A.4					
RSc0884	RS04858								CONSERVED HYPOTHETICAL PROTEIN	V.I.C					
RSc0885	RS04857			-0.45	0.01				CONSERVED HYPOTHETICAL PROTEIN	V.I.C					
RSc0886	RS04856			1.11	0.00	-0.60	0.02		CONSERVED HYPOTHETICAL PROTEIN	V.I.C					
RSc0887	RS04855								HEMAGGLUTININ-RELATED PROTEIN	V.I.C					
RSc0888	RS04850			-0.61	0.00				ACTIVATION/SECRETION PROTEIN	IV.E.2					
RSc0889	RS04841								COG3677, Transposase and inactivated derivatives	V.A					
RSc0890	RS04839			-1.50	0.01				BACTERIOPHAGE RELATED PROTEIN	V.D					
RSc0891	RS04522					-1.26	0.00		SITE-SPECIFIC INTEGRASE/RECOMBINASE	V					
RSc0892	RS04521								PHAGE-RELATED PROTEIN	V.D					
RSc0893	RS04520			-1.35	0.00	3.00	0.00	2.22	0.00	TRANSPOSAE	V.A				
RSc0894	RS05563			-7.01	0.00	7.46	0.00	4.88	0.00	SIGNAL PEPTIDE	V.I.C				
RSc0895	RS04524			-1.47	0.00	-4.10	0.00	3.88	0.00	2.98	0.00	-1.36	0.00	HYPOTHETICAL PROTEIN	V.I.B
RSc0896	RS04519					-0.55	0.01			TRANSMEMBRANE	V.I.C				
RSc0897	RS04518					-0.33	0.00			COG0546, Phosphatase	I				
RSc0898	RS04517								3-DEMETHYLBUBIQUINONE-9 3-METHYLTRANSFERASE	I.B.5					
RSc0899	RS04516			-0.46	0.03			0.80	0.01	TRANSMEMBRANE OUTER MEMBRANE LIPOPROTEIN	III.B.2				
RSc0900	RS04515			0.37	0.00	-0.25	0.05	0.51	0.02	SIGNAL PEPTIDE COG2885, Outer membrane protein and related peptidoglycan-ass	III.B.2				
RSc0901	RS04514	-0.38	0.05	0.56	0.01					DNA GYRASE (SUBUNIT A)(TYPE II TOPOISOMERASE)	II.B.8				
RSc0902	RS04513					-0.48	0.00			SIGNAL PEPTIDE	V.I.C				
RSc0903	RS04512	-0.24	0.03	0.30	0.00			-0.70	0.00	serC	PHOSPHOSERINE AMINOTRANSFERASE (PSAT)	II.A.10			
RSc0904	RS04511			0.71	0.01	-0.38	0.00		-0.66	0.04	pheA	BIFUNCTIONAL PROTEIN: CHORISMATE MUTASE AND PREPHENATE DEHYDR.	II.F.14		
RSc0905	RS04510			0.67	0.00					hisC2	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE	II.A.4			

RSc0906	RS04509	0.49	0.01	-0.59	0.00	-0.68	0.03	tyrA	OXIDOREDUCTASE PREPHENATE DEHYDROGENASE	I.A.7
RSc0907	RS04508	0.77	0.00	-0.29	0.01			aroA	3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE (EPSP SYNTHASE)	I.A.5
RSc0908	RS04507	0.89	0.01	-0.28	0.04			cmk	CYTIDYLATE KINASE	I.D.1
RSc0909	RS04506	0.45	0.02	-0.30	0.01	0.80	0.00	rpsA	30S RIBOSOMAL SUBUNIT PROTEIN S1	III.C.2
RSc0910	RS04505							ihfB	INTEGRATION HOST FACTOR BETA-SUBUNIT (IHFB-BETA)	V.D
RSc0911	RS04504			-0.42	0.00				TRANSMEMBRANE	V.I.C
RSc0912	RS04503			-0.42	0.02				TRANSMEMBRANE COG2956, Predicted N-acetylglucosaminyl transferase	II
RSc0913	RS04502			-0.73	0.01	-1.37	0.00	ugd	OXIDOREDUCTASE UDP-GLUCOSE 6-DEHYDROGENASE (UDG PROTEIN)	III.A.1
RSc0914	RS04501			-0.63	0.04			rfaE	ADP-HEPTOSE SYNTHASE	II.B.2
RSc0915	RS04500					-0.44	0.01	rfaD	ADP-L-GLYCERO-D-MANNO-HEPTOSE-6-EPIMERASE	I.B
RSc0916	RS04499			-0.79	0.00	-0.53	0.04		SIGNAL PEPTIDE	V.I.C
RSc0917	RS04497							cysM	CYSTEINE SYNTHASE B (CSASE B)	I.A.9
RSc0918	RS04496							mltB	MEMBRANE-BOUND LYTIC MUREIN TRANSGLYCOSYLASE B	III.B.3
RSc0919	RS04494	0.88	0.03						COG0123, Deacetylase, including acetoin utilization protein	I
RSc0920	RS04495								ABC TRANSPORTER ATP-BINDING PROTEIN	IV.D
RSc0921	RS04492					-1.72	0.00		ABC TRANSPORTER TRANSMEMBRANE PROTEIN	IV.D
RSc0922	RS04493					-1.56	0.00		ABC TRANSPORTER COG1464, ABC-type metal ion transport system, periplasmic cy	IV.D.5
RSc0923	RS04491					-0.56	0.00		ELECTRON TRANSFER FLAVOPROTEIN (BETA-SUBUNIT)	I.G.1
RSc0924	RS04490			-0.49	0.01			etfB	ELECTRON TRANSFER FLAVOPROTEIN (ALPHA-SUBUNIT)	I.G.1
RSc0925	RS04489							etfA	ELECTRON TRANSFER FLAVOPROTEIN (ALPHA-SUBUNIT)	I.G.1
RSc0926	RS04488							dadA	OXIDOREDUCTASE ACYL-CoA DEHYDROGENASE	I
RSc0927	RS04487			-0.68	0.00			lrp	SIGNAL PEPTIDE OXIDOREDUCTASE INNER MEMBRANE-BOUND D-AMINO ACID	I.I.3
RSc0928	RS04486			-0.41	0.03				TRANSCRIPTION REGULATOR LEUCINE-RESPONSIVE REGULATORY DNA-BINDING	I.E.1
RSc0929	RS04485			-0.54	0.00				COG1533, DNA repair photolyase	II.B.8
RSc0930	RS04484			-0.53	0.00				TRANSMEMBRANE	V.I.C
RSc0931	RS04483			-1.15	0.00				TRANSMEMBRANE	V.I.D
RSc0932	RS04482			-1.37	0.00				SIGNAL PEPTIDE	V.I.F
RSc0933	RS04481			-0.44	0.02			rpsP	OXIDOREDUCTASE COG2133, Glucose/sorbose dehydrogenase	III.C.2
RSc0934	RS04480			-0.46	0.00			rimM	30S RIBOSOMAL SUBUNIT PROTEIN S16 (DNA-BINDING CATION-DEPENDENT	III.C.1
RSc0935	RS04479			-0.45	0.03	0.78	0.00	trmB	16S RRNA PROCESSING PROTEIN	II.D.1
RSc0936	RS04478			-0.43	0.01			trmB	tRNA (GUANINE-N1)-METHYLTRANSFERASE	III.C.1
RSc0937	RS04477			-0.35	0.01			rplS	50S RIBOSOMAL SUBUNIT PROTEIN L19	III.C.2
RSc0938	RS04475			-0.51	0.00				COG0494, NTP pyrophosphohydrolase including oxidative damage repair enzymes	V.I.C
RSc0939	RS04472			-0.47	0.05	-0.97	0.01		TRANSMEMBRANE COBALAMIN BIOSYNTHESIS COBD-RELATED PROTEIN	I.B.3
RSc0940	RS04469			0.46	0.03				CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0941	RS04465								COG1162, Predicted GTPase	V.I.C
RSc0942	RS04464			-0.32	0.00				TRANSMEMBRANE INTEGRAL MEMBRANE PROTEASE	I.A.4
RSc0943	RS04462							orn	OLIGORIBONUCLEASE	II.A.2
RSc0944	RS04461							mog	MOLYBDOCHETALASE IN MOLYBDOPTERIN BIOSYNTHESIS	I.B.12
RSc0945	RS04460								CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0946	RS04449			-0.44	0.01			pmbA	PMB A PROTEIN (TLDE PROTEIN)	II.B.7
RSc0947	RS04447			-0.46	0.01	0.69	0.02	folA	OXIDOREDUCTASE DIHYDROFOLATE REDUCTASE	I.F
RSc0948	RS04442			-0.46	0.00			thyA	THYMIDYLATE SYNTHASE (TRANSLATION REGULATION REPRESSOR RNA-BINDING	I.F.2
RSc0949	RS04438			-0.71	0.00				AMINO-ACID DEHYDRATASE	I.A
RSc0950	RS04435								TRANSMEMBRANE COG0861, Membrane protein TerC	III.B.1
RSc0951	RS04428								CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0952	RS04426			-0.60	0.00	0.57	0.05		HYPOTHETICAL PROTEIN	V.I.B
RSc0953	RS04413			-1.26	0.00	-1.56	0.00		ATP-DEPENDENT RNA HELICASE	II.B.6
RSc0954	RS04412					-1.04	0.01		TRANSMEMBRANE	V.I.D
RSc0955	RS04411			-0.65	0.00	-0.42	0.05		HYPOTHETICAL PROTEIN	V.I.D
RSc0956	RS04410			-0.58	0.02	-1.16	0.04		TRANSMEMBRANE	V.I.D
RSc0957	RS04409			-1.46	0.00				HYPOTHETICAL PROTEIN	V.I.D
RSc0958	RS04407			-1.41	0.00				HYPOTHETICAL PROTEIN	V.I.D
RSc0959	RS04408			-1.38	0.00	-0.55	0.04		VGR-RELATED PROTEIN	V.I.C
RSc0960	RS04406			-1.29	0.00				TRANSMEMBRANE	V.I.C
RSc0961	RS04405			-0.76	0.02				CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0962	RS04402			-1.40	0.00	-1.79	0.00		CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0963	RS04401			-0.88	0.00	-0.61	0.04		TRANSCRIPTION REGULATOR BACTERIOPHAGE DNA-BINDING PROTEIN	V.D
RSc0964	RS04403			-1.58	0.02				HYPOTHETICAL PROTEIN	V.I.D
RSc0965	RS04404			-0.70	0.00	-1.42	0.01		TRANSCRIPTION REGULATOR BACTERIOPHAGE TRANSCRIPTIONAL ACTIVATOR	V.D
RSc0966	RS04400			-0.52	0.00				HYPOTHETICAL PROTEIN	V.I.D
RSc0967	RS04399								CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0968	RS04398			-0.45	0.03	-1.07	0.01		CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0969	RS04395								CP4-LIKE INTEGRASE	V.A
RSc0970	RS04396								TRANSMEMBRANE	V.I.C
RSc0971	RS04393			-1.24	0.02	1.14	0.00		SIGNAL PEPTIDE	V.I.D
RSc0972	RS04392					-0.47	0.01		HYPOTHETICAL PROTEIN	V.I.B
RSc0973	RS04319			-0.77	0.02				CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0974	RS04318			-1.67	0.00	-1.81	0.00		ABC TRANSPORTER AMINO-ACID-BINDING PERIPLASMIC PROTEIN (PBP)	IV.D.2
RSc0975	RS04385								TRANSMEMBRANE	V.I.D
RSc0976	RS04316								ABC TRANSPORTER ATP-BINDING PROTEIN	IV.D
RSc0977	RS04315			-0.63	0.01			parE	DNA TOPOISOMERASE IV (SUBUNIT B)	II.B.8
RSc0978	RS04314								SIGNAL PEPTIDE TRANSGLYCOSYLASE	V.I.B
RSc0979	RS04313			0.89	0.02			parC	DNA TOPOISOMERASE IV (SUBUNIT A)	II.B.8
RSc0980	RS04312			1.07	0.03				TRANSMEMBRANE	V.I.C
RSc0981	RS04311			1.51	0.01				TRANSMEMBRANE	V.I.C
RSc0982	RS04310			-0.68	0.02			ltdP	TRANSMEMBRANE L-LACTATE PERMEASE	IV.D.3
RSc0983	RS04309			-0.66	0.00	-0.91	0.05		TRANSMEMBRANE	V.I.C
RSc0984	RS04308			-0.58	0.00				CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0985	RS04307							gstE	GLUTATHIONE S-TRANSFERASE	II.B.7
RSc0986	RS04306								TRANSCRIPTION REGULATOR COG1167, Transcriptional regulators containing a D	VI.A
RSc0987	RS04305			0.39	0.02				COG0251, Translation initiation inhibitor	II.B.7
RSc0988	RS04304			-0.45	0.00				TRANSMEMBRANE	V.I.C
RSc0989	RS04303								COG2872, Predicted metal-dependent hydrolases related to alanyl-tRNA synthetase	II.I
RSc0990	RS04302			-0.58	0.01				TRANSCRIPTION REGULATOR	V.I.A
RSc0991	RS04301					0.62	0.00	hptG	CHAPERONE (HEAT SHOCK PROTEIN HTPG)	IV.B
RSc0992	RS04300							mug	COG3663, G:T/U mismatch-specific DNA glycosylase	II.B.8
RSc0993	RS04299			-0.59	0.00	-1.19	0.05	gstF	TRANSMEMBRANE GLUTATHIONE S-TRANSFERASE WITH COG3832 (Uncharacter	II.B.7
RSc0994	RS04298								TRANSCRIPTION REGULATOR TRANSCRIPTIONAL REGULATORY DNA-BINDING	V.I.A
RSc0995	RS04297			0.63	0.03				TRANSMEMBRANE	V.I.C
RSc0996	RS04296								COG0421, Spermidine synthase	I.F.15
RSc0997	RS04295					0.86	0.01		CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc0998	RS04294			-0.34	0.00				COG1670, Acetyltransferase	I
RSc0999	RS04293								COG0714, MoxR-like ATPase	V.I.C
RSc1000	RS04292			0.15	0.01	0.56	0.00		SIGNAL PEPTIDE PERIPLASMIC CYTOCHROME TYPE-C OXIDOREDUCTASE	I.G.1
RSc1001	RS04291			0.58	0.01	0.58	0.01		SIGNAL PEPTIDE PERIPLASMIC CYTOCHROME TYPE-C OXIDOREDUCTASE	I.G.1
RSc1002	RS04290								CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1003	RS04289			0.84	0.01				TRANSMEMBRANE	V.I.C
RSc1004	RS04288			-0.43	0.03	0.86	0.00		CARBOXYPEPTIDASE	II.A.4
RSc1005	RS04287			0.46	0.00	-0.37	0.00		COG0778, Nitroreductase	I
RSc1006	RS04286			-0.41	0.00	-0.44	0.05	nth	ENDONUCLEASE III	I.A.1
RSc1007	RS04285								FERREDOXIN [4Fe-4S]	I.G.1
RSc1008	RS04284					-0.69	0.01		TRANSCRIPTION REGULATOR	V.I.A
RSc1009	RS04280			-0.43	0.01			phaZ	POLY(DL-3-HYDROXYBUTYRATE) DEPOLYMERASE	I.A
RSc1010	RS04277							tyrB	AROMATIC-AMINO-ACID AMINOTRANSFERASE	II.A
RSc1011	RS04272							uvrB	EXONUCLEASE ABC SUBUNIT B (SOS RESPONSE EXCISION NUCLEASE DNA	III.B.8
RSc1012	RS04269					-0.73	0.03		TRANSMEMBRANE SITE-SPECIFIC RECOMBINASE	V.A
RSc1013	RS04266					-3.20	0.00		RIBOKINASE	I
RSc1014	RS04264			0.83	0.03				TRANSCRIPTION REGULATOR TRANSCRIPTIONAL REGULATORY DNA-BINDING	V.I.A
RSc1015	RS04262			0.54	0.00	-0.54	0.01		ABC TRANSPORTER RIBOSE ABC TRANSPORTER, PERMEASE PROTEIN	IV.D.3
RSc1016	RS04260					-1.22	0.02		ABC TRANSPORTER RIBOSE ABC TRANSPORTER, ATP-BINDING PROTEIN	IV.D.3
RSc1017	RS04257			-0.27	0.03	-0.56	0.02		ABC TRANSPORTER RIBOSE ABC TRANSPORTER, PERIPLASMIC RIBOSE-BIND	IV.D.3
RSc1018	RS04257			-0.53	0.00	-1.08	0.00		TRANSCRIPTION REGULATOR COG1959, Transcriptional regulator	V.I.A

RSc1019	RS04253								iscS	Cysteine sulfinate desulfinase / cysteine desulfurase	I
RSc1020	RS04249								iscU	IRON-BINDING PROTEIN	I.H
RSc1021	RS04236								iscA	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1022	RS04245									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1023	RS04234								hscB	CHAPERONE PROTEIN	IV.B
RSc1024	RS04231								hscA	CHAPERONE PROTEIN	IV.B
RSc1025	RS04229								fdx	FERREDOXIN [2FE-2S]	I.G.1
RSc1026	RS04227									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1027	RS04225									TRANSMEMBRANE	V.I.C
RSc1028	RS04223								lysS	LYSYL-TRNA SYNTHETASE	I.I.D.1
RSc1029	RS04221									OXIDOREDUCTASE SHORT-CHAIN ALCOHOL DEHYDROGENASE	I
RSc1030	RS05824								prfB	PEPTIDE CHAIN RELEASE FACTOR 2 (RF-2)	II.B.7
RSc1031	RS04219								pncB	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (NAPRTASE)	I.B
RSc1032	RS04218									TRANSMEMBRANE	V.I.C
RSc1033	RS04217									TRANSMEMBRANE COG1055, Na ⁺ /H ⁺ antiporter NhaD and related arsenite permease	IV.D
RSc1034	RS04216									OXIDOREDUCTASE COG1052, Lactate dehydrogenase and related dehydrogenases	IV
RSc1035	RS04215									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1036	RS04214									TRANSMEMBRANE	V.I.C
RSc1037	RS04213								moeA1	MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN	I.B.12
RSc1038	RS04212								mobA	MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN A (PROT)	I.B.12
RSc1039	RS04211								moeA	MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN A	I.B.12
RSc1040	RS04210								me	RIBONUCLEASE E (RNASE E)	III.A.2
RSc1041	RS04757								riuC	RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C	III.C.1
RSc1042	RS04208									PHOSPHOGLYCOLATE PHOSPHATASE	I.I.4
RSc1043	RS04207									COG2146, Ferredoxin subunits of nitrite reductase and ring-hydroxylating dioxygenase	I
RSc1044	RS04206									TRANSMEMBRANE PROTEASE	II.A.4
RSc1045	RS04205									TRANSMEMBRANE COG0313, Methyltransferase	V.I.C
RSc1046	RS04204									COG0424, Nucleotide-binding protein implicated in inhibition of septum formation	IV.A
RSc1047	RS04197									COG1399, Predicted metal-binding, possibly nucleic acid-binding protein	V.I.C
RSc1048	RS04194								rpmF	50S RIBOSOMAL SUBUNIT PROTEIN L32	III.C.2
RSc1049	RS04184								plsX	FATTY ACID/PHOSPHOLIPID BIOSYNTHESIS ENZYME	I
RSc1050	RS04180								fabH	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE III	I.B.1
RSc1051	RS04178								fabD	MALONYL COA-[ACYL-CARRIER-PROTEIN] TRANSACYLASE	I.B.1
RSc1052	RS04176								fabG1	OXIDOREDUCTASE 3-OXOACYL-[ACYL-CARRIER-PROTEIN] REDUCTASE	I.B.1
RSc1053	RS04175								acpP	ACYL CARRIER PROTEIN	I.B.1
RSc1054	RS04165								fabF1	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE II	I.B.1
RSc1055	RS04163								rpoE1	TRANSCRIPTION REGULATOR RNA POLYMERASE SIGMA-E FACTOR (SIGMA-2)	II.B.6
RSc1056	RS04161								rseA	TRANSCRIPTION REGULATOR TRANSMEMBRANE SIGMA-E FACTOR NEGATIVE	II.B.6
RSc1057	RS04159								rseB	TRANSCRIPTION REGULATOR SIGMA-E FACTOR REGULATORY PROTEIN (NEG)	II.B.6
RSc1058	RS04156									SIGNAL PEPTIDE PERIPLASMIC PROTEASE	II.A.4
RSc1059	RS04149									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1060	RS04148								lepA	GTP-BINDING ELONGATION FACTOR	II.B.7
RSc1061	RS04147								lepB	TRANSMEMBRANE SIGNAL PEPTIDASE I (SPASE I)	II.B.7
RSc1062	RS04145									TRANSMEMBRANE	V.I.C
RSc1063	RS04144								mc	RIBONUCLEASE III (RNASE III)	II.A.2
RSc1064	RS04143								era	GTP-BINDING PROTEIN	IV.A
RSc1065	RS04139								recO	DNA REPAIR PROTEIN RECO (RECOMBINATION PROTEIN O)	II.B.8
RSc1066	RS04138								pdxJ	PYRIDOXAL PHOSPHATE BIOSYNTHETIC PROTEIN	I.B
RSc1067	RS04136								acpS	HOLO-[ACYL-CARRIER-PROTEIN] SYNTHASE	I.B.1
RSc1068	RS04135									HEXOSAMINIDASE	II.I.4
RSc1069	RS04133								efp	ELONGATION FACTOR P	II.B.7
RSc1070	RS04117									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1071	RS04116								uvrC	EXCINUCLEASE ABC SUBUNIT C (SOS RESPONSE DNA REPAIR PROTEIN)	II.A.1
RSc1072	RS04115								pgsA	TRANSMEMBRANE CDP-DIACYLGLYCEROL--GLYCEROL-3-PHOSPHATE 3-PHO	II.B.1
RSc1073	RS04114									TRANSCRIPTION REGULATOR TWO-COMPONENT SYSTEM RESPONSE REGUL	V.I.C
RSc1074	RS04113									SIGNAL PEPTIDE	V.I.C
RSc1075	RS04112									TRANSCRIPTION REGULATOR TWO-COMPONENT SYSTEM SENSOR HISTIDINE	V.I.A
RSc1076	RS04111									TRANSCRIPTION REGULATOR TWO-COMPONENT SYSTEM RESPONSE REGUL	V.I.A
RSc1077	RS04110									TRANSMEMBRANE	V.I.C
RSc1078	RS04109									TRANSCRIPTION REGULATOR TRANSCRIPTIONAL REGULATORY DNA-BINDING	V.I.A
RSc1079	RS04108								gudD1	GLUCARATE DEHYDRATASE	I.I.4
RSc1080	RS04107								exuT2	TRANSMEMBRANE HEXURONATE TRANSPORTER	IV.D
RSc1081	RS04106									GLUCOSIDASE	I
RSc1082	RS04105									OUTER MEMBRANE PORIN	III.B.2
RSc1083	RS04104									COG2017, GALACTOSE MUTAROTASE AND RELATED ENZYMES	I
RSc1084	RS04103									TRANSMEMBRANE COG3203, Outer membrane protein (porin)	III.B.2
RSc1085	RS04102								nagL	GLUTATHIONE S-TRANSFERASE	II
RSc1086	RS04101								nagK	ISOMERASE-DECARBOXYLASE HOMOLOG	II
RSc1087	RS04100								nagI	OXIDOREDUCTASE GENTISATE 1,2-DIOXYGENASE	II
RSc1088	RS04099								nagAb	OXIDOREDUCTASE Ferredoxin subunit of a ring-hydroxylating dioxygenase	II
RSc1089	RS04098								nagH	OXIDOREDUCTASE SALICYLATE-5-HYDROXYLASE SMALL OXYGENASE COMP	II
RSc1090	RS04097								nagG	OXIDOREDUCTASE SALICYLATE-5-HYDROXYLASE LARGE OXYGENASE COMP	II
RSc1091	RS04096								nagAa	OXIDOREDUCTASE FERREDOXIN OXIDOREDUCTASE	II
RSc1092	RS04095									TRANSCRIPTION REGULATOR TRANSCRIPTIONAL REGULATORY DNA-BINDING	V.I.A
RSc1093	RS04094								pcaK	TRANSMEMBRANE 4-HYDROXYBENZOATE TRANSPORTER	IV.D.3
RSc1094	RS04084									TRANSCRIPTION REGULATOR TRANSCRIPTIONAL REGULATORY DNA-BINDING	V.I.A
RSc1095	RS04073									TRANSMEMBRANE COG0679, Predicted permease	IV.D
RSc1096	RS04070								aspC	ASPARTATE AMINOTRANSFERASE	I.A.15
RSc1097	RS04067									TRANSCRIPTION REGULATOR	V.I.A
RSc1098	RS04066									TRANSCRIPTION REGULATOR TRANSCRIPTIONAL REGULATORY DNA-BINDING	V.I.A
RSc1099	RS04061								sda2a	INACTIVATED L-SERINE AMONYA-LYASE, L-SERINE DEHYDRATASE 2 (L-SERIN	I.I.3
RSc1100	RS04059								sda2b	INACTIVATED L-SERINE AMONYA-LYASE, L-SERINE DEHYDRATASE 2 (L-SERIN	I.I.3
RSc1101	RS04056								soxB2	OXIDOREDUCTASE SARCOSINE OXIDASE (BETA SUBUNIT)	II
RSc1102	RS04055								soxD2	OXIDOREDUCTASE SARCOSINE OXIDASE (DELTA SUBUNIT)	II
RSc1103	RS04054								soxA2	OXIDOREDUCTASE SARCOSINE OXIDASE (ALPHA SUBUNIT)	II
RSc1104	RS04053								soxG2	OXIDOREDUCTASE SARCOSINE OXIDASE (GAMMA SUBUNIT)	II
RSc1105	RS04050								folB2	DIHYDRONEOPTERIN ALDOLASE	I.B.14
RSc1106	RS04039								purU3	FORMYLTETRAHYDROFOLATE DEFORMYLASE	I.D.2
RSc1107	RS04032									TRANSMEMBRANE PSEUDOGENE (ABC TRANSPORTER N-TERMINAL FRAGME	V.I.D
RSc1108	RS04035									TRANSCRIPTION REGULATOR TRANSCRIPTIONAL REGULATORY DNA-BINDING	V.I.A
RSc1109	RS04024									PSEUDOGENE (DEHYDROGENASE FRAGMENT)	V.I.D
RSc1110	RS04021									TRANSCRIPTION REGULATOR TRANSCRIPTIONAL REGULATORY DNA-BINDING	V.I.A
RSc1111	RS04015									TRANSMEMBRANE	V.I.C
RSc1112	RS04011									TRANSCRIPTION REGULATOR	V.I.A
RSc1113	RS04007									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1114	RS04006								fdxA	FERREDOXIN	I.G.1
RSc1115	RS05755								recJ	SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE	II.A.1
RSc1116	RS05756									SIGNAL PEPTIDE HYPOTHETICAL PROTEIN	V.I.B
RSc1117	RS05757									TRANSMEMBRANE LIPOPROTEIN RELEASING SYSTEM PROTEIN	IV.E.2
RSc1118	RS05758								loID	ABC TRANSPORTER LIPOPROTEIN RELEASING SYSTEM ATP-BINDING PROTEI	IV.E.2
RSc1119	RS04635									DEOXYRIBONUCLEASE	II.A.1
RSc1120	RS04634									TRANSMEMBRANE COG2333, Predicted hydrolase (metallo-beta-lactamase superfa	II
RSc1121	RS04633									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1122	RS04632									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1123	RS04630									COG1305, Transglutaminase-like enzyme, putative cysteine protease	I
RSc1124	RS04629									COG3484, Predicted proteasome-type protease	II.A.4
RSc1125	RS04628									COG0596, Hydrolase or acyltransferase (alpha/beta hydrolase superfamily)	I
RSc1126	RS04627								pyrG	CTP SYNTHASE	I.D.1
RSc1127	RS04626								kdsA	2-DEHYDRO-3-DEOXYPHOSPHOCTONATE ALDOLASE	III.A.1
RSc1128	RS04625									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1129	RS04624								eno	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)	I.H.8
RSc1130	RS04623									TRANSMEMBRANE COG2919, Septum formation initiator	IV.A

RSc1131	RS04622			-0.53	0.00				TRANSMEMBRANE	VI.C
RSc1132	RS04621	0.69	0.00					-0.62	REDOX REGULATED MOLECULAR CHAPERONE HEAT-SHOCK-LIKE PROTEIN	IV.B
RSc1133	RS04620								COG0663, Carbonic anhydrase/acyltransferase	I
RSc1134	RS04619								CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc1135	RS04618			-0.98	0.00	-1.24	0.01		COG0596, Hydrolase or acyltransferase (alpha/beta hydrolase superfamily)	I
RSc1136	RS04617					-0.83	0.00		CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc1137	RS04616			0.76	0.02				CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc1138	RS04615			-0.33	0.01	-0.61	0.04		OXIDOREDUCTASE COG1748: Saccharopine dehydrogenase and related proteins	I
RSc1139	RS04614								OXIDOREDUCTASE THIOREDOXIN REDUCTASE	II.F.2
RSc1140	RS04613			-0.54	0.00				COG0613, Predicted metal-dependent phosphoesterase	I
RSc1141	RS04612								COG0009, Translation factor	II.B.7
RSc1142	RS04611	0.52	0.01					-1.13	TRANSMEMBRANE COG1994, Zn-dependent protease	II.A.4
RSc1143	RS04610	0.63	0.03	-0.30	0.00				TRYPHOPHANYL-TRNA SYNTHETASE (SYW PROTEIN)	II.D.1
RSc1144	RS04609					-0.92	0.00	-0.61	CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc1145	RS04756			-0.46	0.00			-0.19	CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc1146	RS04607			-0.48	0.04	-0.64	0.03	-0.74	DIHYDRODIPICOLINATE SYNTHASE	II.A.13
RSc1147	RS04606			-0.49	0.01			-0.78	TRANSMEMBRANE	VI.C
RSc1148	RS04604	0.66	0.01						COG1235, Metal-dependent hydrolase of the beta-lactamase superfamily I	II
RSc1149	RS04602			-0.64	0.00	-0.59	0.01		CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc1150	RS04601								FKBP-TYPE PEPTIDYL-PROLYL CIS- TRANS ISOMERASE (ROTAMASE)	IV.B
RSc1151	RS04600					0.42	0.04		TRANSMEMBRANE	VI.C
RSc1152	RS04599								DNA MISMATCH REPAIR PROTEIN	II.B.8
RSc1153	RS04598								TRANSCRIPTION REGULATOR	VI.A
RSc1154	RS04597			-0.44	0.05				TRANSMEMBRANE TRANSMEMBRANE EFFLUX PROTEIN	IV.D
RSc1155	RS04596	0.33	0.05						OXIDOREDUCTASE COG0656, Aldo/keto reductases, related to diketoglucuronate reductase	I
RSc1156	RS04595								TRANSMEMBRANE METHYL-ACCEPTING CHEMOTAXIS TRANSDUCER PROTEIN IV.C	IV.C
RSc1157	RS04594	-0.55	0.01	1.25	0.00				TRANSMEMBRANE METHYL-ACCEPTING CHEMOTAXIS TRANSDUCER PROTEIN IV.C	IV.C
RSc1158	RS04593			-1.93	0.00				CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc1159	RS04592					-0.83	0.01		COG0518, GMP synthase - Glutamine amidotransferase domain	II.D
RSc1160	RS04755			-0.61	0.03	-0.28	0.05		TRANSCRIPTION REGULATOR	VI.A
RSc1161	RS04590					-0.56	0.00		INHOSITOL MONOPHOSPHATASE (EXTRAGENIC SUPPRESSOR PROTEIN)	II.B.6
RSc1162	RS04589								TRNA/RRNA METHYLTRANSFERASE	II.B.6
RSc1163	RS04585								O-ACETYL SERINE SYNTHASE (SERINE ACETYLTRANSFERASE)	II.A.9
RSc1164	RS04581	0.45	0.01			-0.92	0.00		UDP-2,3-DIACYLGLUCOSAMINE HYDROLASE	II.B.2
RSc1165	RS04579	0.35	0.02						PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B (PPIASE B) (ROTAMASE B)(CYBP)	IV.B
RSc1166	RS04578			-0.50	0.00	0.39	0.02		SIGNAL PEPTIDE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (PPIASE A)(ROTIV)	II.B
RSc1167	RS04577					0.53	0.04		SIGNAL PEPTIDE TPR DOMAIN PROTEIN	VI.B
RSc1168	RS04576								CYSTEINYL-TRNA SYNTHETASE (SYC PROTEIN)	II.D.1
RSc1169	RS04560	0.48	0.00			0.69	0.01		COG0122, 3-methyladenine DNA glycosylase/8-oxoguanine DNA glycosylase	II.B.8
RSc1170	RS04559			-0.68	0.04				ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE (ALPHA SUB)	II.B.1
RSc1171	RS04558	0.72	0.00	-0.31	0.02	-0.37	0.05	-2.51	CELL CYCLE PROTEIN	IV.A
RSc1172	RS04754							0.89	ASPARTATE KINASE	II.A.13
RSc1173	RS04555								OXIDOREDUCTASE ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE [NADH]	II.B.1
RSc1174	RS04551			-0.50	0.00				ABC TRANSPORTER SUBSTRATE-BINDING PERIPLASMIC PROTEIN (PBP)	IV.D
RSc1175	RS04550							0.49	ABC TRANSPORTER TRANSMEMBRANE PROTEIN	IV.D
RSc1176	RS04549	0.63	0.03						ABC TRANSPORTER TRANSMEMBRANE PROTEIN	IV.D
RSc1177	RS04548			-0.51	0.00			-0.44	ABC TRANSPORTER ATP-BINDING PROTEIN	IV.D
RSc1178	RS04543	0.51	0.02						TRANSMEMBRANE COG0791, Cell wall-associated hydrolase	II.B
RSc1179	RS04541			-0.37	0.04			-0.86	TRANSMEMBRANE COG1752, Esterase of the alpha-beta hydrolase superfamily	I
RSc1180	RS05712					-0.56	0.02		GLUTAMATE-IRNA SYNTHETASE (CATALYTIC SUBUNIT)(SYE PROTEIN)	II.D.1
RSc1181	RS05713			-0.38	0.00				TRANSMEMBRANE COG0534, Na ⁺ -driven multidrug efflux pump	IV.D
RSc1182	RS05714			-0.41	0.05			-0.95	TRANSMEMBRANE COG1807, 4-amino-4-deoxy-L-arabinose transferase and related	II.B
RSc1183	RS05715			-0.44	0.02				50S RIBOSOMAL SUBUNIT PROTEIN L31	III.C.2
RSc1184	RS05716	0.65	0.03	-0.78	0.00				SIGNAL PEPTIDE	VI.D
RSc1185	RS05717			-0.93	0.00			1.21	CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc1186	RS05718			-0.80	0.00				TRANSCRIPTION REGULATOR	VI.A
RSc1187	RS05719	0.60	0.00	-0.27	0.02			-0.84	TRANSCRIPTION REGULATOR SIGMA-54 INTERACTING PROTEIN	VI.A
RSc1188	RS05720	0.47	0.05	-0.56	0.00				TRANSCRIPTION TERMINATION FACTOR RHO (HELICASE)	II.B.6
RSc1189	RS05721								THIOREDOXIN 1 (REDOX FACTOR)	II.B.6
RSc1190	RS05722	1.48	0.03						COG3893, Inactivated superfamily I helicase AND COG2887, RecB family exonuclease	II.B.8
RSc1191	RS05723	0.56	0.01						ATP-dependent exoDNase (exonuclease V) beta subunit (contains helicase and exon)	II.B.8
RSc1192	RS05724	0.76	0.03						DNA POLYMERASE III (SUBUNITS TAU AND GAMMA)	II.B.8
RSc1193	RS05725	0.53	0.01			-0.50	0.05		CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc1194	RS05726	0.48	0.02	-0.11	0.04	0.42	0.05		HYPOTHETICAL PROTEIN	VI.D
RSc1195	RS05727								DNA REPAIR DNA RECOMBINATION ZINC-FINGER PROTEIN RECR	II.B.8
RSc1196	RS05728					-0.46	0.04		CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc1197	RS05729							3.06	TRANSCRIPTION REGULATOR DNA-BINDING TRANSCRIPTIONAL REGULATORY	VI.A
RSc1198	RS05730	-0.35	0.02						OXIDOREDUCTASE COG1804, Acyl-CoA transferases/carnitine dehydratase	I
RSc1199	RS02665	0.64	0.00	-0.44	0.04	0.91	0.01		ABC TRANSPORTER COG0715, ABC-type nitrate/sulfonate/bicarbonate transport sys	IV.D
RSc1200	RS02669	0.65	0.01						ABC TRANSPORTER COG1116, ABC-type nitrate/sulfonate/bicarbonate transport sys	IV.D
RSc1201	RS02672			-0.20	0.05				ABC TRANSPORTER COG0600, ABC-type nitrate/sulfonate/bicarbonate transport sys	IV.D
RSc1202	RS02674	-1.58	0.04	-1.55	0.00	-1.85	0.00		TRANSCRIPTION REGULATOR	VI.A
RSc1203	RS02677	-1.11	0.04	-1.11	0.00				OXIDOREDUCTASE FLAVOPROTEIN NADH-DEPENDENT	II.F
RSc1204	RS02681			-1.14	0.00				OXIDOREDUCTASE	I
RSc1205	RS02685	0.37	0.05	-0.53	0.00	0.42	0.04		STATIONARY-PHASE SURVIVAL PROTEIN	IV.G
RSc1206	RS02686			-0.62	0.00	-0.92	0.03	-0.85	COG2518, Protein-L-isoaspartate carboxylmethyltransferase	II.B.7
RSc1207	RS02688			-0.31	0.04				LIPOPROTEIN	VI.C
RSc1208	RS02691			-0.57	0.01				TRANSCRIPTION REGULATOR RNA POLYMERASE SIGMA S (SIGMA-38) FACTOR	II.E.1
RSc1209	RS02696	0.91	0.01						COG3568, Metal-dependent hydrolase	II
RSc1210	RS02699								RNA METHYLTRANSFERASE	II.B.6
RSc1211	RS02703	0.61	0.01			0.51	0.03	-0.45	TRANSMEMBRANE	VI.C
RSc1212	RS02704	0.42	0.03					-0.93	NUCLEOSIDE-DIPHOSPHATE KINASE PROTEIN	II.D.2
RSc1213	RS02705	0.34	0.04	-0.41	0.00			-0.32	COG0820, Fe-S-cluster redox enzyme	I
RSc1214	RS02709			-0.34	0.00				TYPE 4 FIMBRIAL BIOGENESIS PROTEIN	II.A.2
RSc1215	RS02710			-0.47	0.00				TRANSMEMBRANE	VI.C
RSc1216	RS02790	0.51	0.01					-0.63	COG0821, GcpE enzyme involved in the deoxyxylulose pathway of isoprenoid biosyn	I
RSc1217	RS02712								HISTIDINE-TRNA SYNTHETASE	II.D.1
RSc1218	RS02713	0.48	0.02	-0.28	0.01			-0.52	TRANSMEMBRANE	VI.C
RSc1219	RS02721								TRANSMEMBRANE COG1520, FOG: WD40-like repeat	VI.C
RSc1220	RS02722			-0.23	0.04	-0.75	0.02		COG1160, GTPase	VI.C
RSc1221	RS02723	0.51	0.03	-0.56	0.00			-0.96	HOST FACTOR-I PROTEIN	VI.D
RSc1222	RS02724			-0.68	0.00				COG2262, GTPase	VI.C
RSc1223	RS02730	0.51	0.01					-0.41	TRANSMEMBRANE COG0330, Membrane protease subunits, stomatin/prohibitin hor	II.B.7
RSc1224	RS02731			-0.48	0.00				TRANSMEMBRANE SERINE PROTEASE	VI.A
RSc1225	RS02732	0.63	0.02						TRANSMEMBRANE	VI.C
RSc1226	RS02733					-0.41	0.01		COG3705, ATP phosphoribosyltransferase involved in histidine biosynthesis	II.A.4
RSc1227	RS02734								ADENYLOSUCCINATE SYNTHETASE	II.D.2
RSc1228	RS02735	0.66	0.02					-0.66	NUCLEOTIDE PHOSPHORIBOSYLTRANSFERASE	II.F.9
RSc1229	RS02736	0.51	0.02						EXORIBONUCLEASE RNase R (VACB PROTEIN)	II.A.2
RSc1230	RS02737								TRNA/RRNA METHYLTRANSFERASE PROTEIN	II.B.6
RSc1231	RS02738					1.48	0.00		COG0846, NAD-dependent protein deacetylase	II.B.6
RSc1232	RS02791	0.91	0.01	-0.34	0.04			-0.95	TRANSALDOLASE	II.F.19
RSc1233	RS02740								RIBOSE 5-PHOSPHATE ISOMERASE	II.F.19
RSc1234	RS02741			0.35	0.00				TRANSMEMBRANE COG1953, Cytosine/uracil/thiamine/allantoin permease	IV.D
RSc1235	RS02742					-1.34	0.01	-1.13	TRANSMEMBRANE METHYL-ACCEPTING CHEMOTAXIS PROTEIN	IV.C
RSc1236	RS02744								CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc1237	RS02745			-0.99	0.02				OUTER MEMBRANE PROTEIN (PORIN)	III.B.2
RSc1238	RS02746			-0.43	0.04				MYO-INOSITOL CATABOLISM PROTEIN	II.A
RSc1239	RS02747								MYO-INOSITOL CATABOLISM PROTEIN	II.A
RSc1240	RS02748								ACETOLACTATE SYNTHASE	II.A
RSc1241	RS02749								TRANSFERASE KINASE	II.A
RSc1242	RS02750								SIGNAL PEPTIDE RHIZOPINE-BINDING PROTEIN PRECURSOR	II.A
									ABC TRANSPORTER SUGAR ATP-BINDING PROTEIN	IV.D.3

RSc1356	RS04638								ripG	TYPE III EFFECTOR PROTEIN GALA6	V.I.E
RSc1357	RS04639	-3.02	0.00	-4.22	0.00	4.62	0.00	4.71	0.00	LRR-GALA FAMILY TYPE III EFFECTOR PROTEIN (GALA 7)	V.I.C
RSc1358	RS04640								aceA	ISOCITRATE LYASE	I.F.17
RSc1359	RS04641	0.64	0.05	-0.33	0.05	0.49	0.00	0.78	0.04	COG589, Universal stress protein UspA and related nucleotide-binding proteins	I.V.G
RSc1360	RS04642									TRANSCRIPTION REGULATOR	V.I.A
RSc1361	RS04643									TRANSMEMBRANE	V.I.D
RSc1362	RS04644									COG1011, Predicted hydrolase	I.I
RSc1363	RS04645									MALATE SYNTHASE A (MSA OR MASY PROTEIN)	I.F.17
RSc1364	RS04646									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1365	RS04647									TRANSMEMBRANE MULTIDRUG RESISTANCE-LIKE EFFLUX PROTEIN	I.V.D.7
RSc1366	RS04648									ACYL-COA-BINDING PROTEIN	I.V.D.7
RSc1367	RS04650									TRANSMEMBRANE COG1214, Inactive homolog of metal-dependent proteases, puta	V.I.C
RSc1368	RS04651									ACETYLTRANSFERASE	I
RSc1369	RS04652									COG1573, Uracil-DNA glycosylase	I.I.B.8
RSc1370	RS04653									TRANSMEMBRANE	V.I.C
RSc1371	RS04748									ALANINE RACEMASE	I.A.3
RSc1372	RS04749									ATP-DEPENDENT PROTEASE, DNA REPAIR (ATP-BINDING DNA-BINDING) PROTI	I.II.A.4
RSc1373	RS04656									OXIDOREDUCTASE TRANSMEMBRANE DISULFIDE BOND FORMATION PROTI	I.II.B.7
RSc1374	RS04657									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1375	RS04658									TRANSMEMBRANE COG1804, Predicted acyl-CoA transferases/carnitine dehydratas	I
RSc1376	RS04659									ABC TRANSPORTER ATP-BINDING PROTEIN	I.V.D
RSc1377	RS04660									TRANSCRIPTION REGULATOR	V.I.A
RSc1378	RS04661									L-ASPARAGINASE PRECURSOR	I
RSc1379	RS04662									ABC TRANSPORTER ATP-BINDING PROTEIN	I.V.D
RSc1380	RS04663									ABC TRANSPORTER SUBSTATE-BINDING PERIPLASMIC PROTEIN (PBP)	I.V.D
RSc1381	RS04750									ABC TRANSPORTER TRANSMEMBRANE PROTEIN	I.V.D
RSc1382	RS04665									ABC TRANSPORTER TRANSMEMBRANE PROTEIN	I.V.D
RSc1383	RS04666									COG3191, L-aminopeptidase/D-esterase	I.II.A.4
RSc1384	RS04667									COG2362, D-aminopeptidase	I.II.A.4
RSc1385	RS04668									TRANSMEMBRANE LIPOPROTEIN	V.I.D
RSc1386	RS04669									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1387	RS04670									GTP CYCLOHYDROLASE I	I.B.14
RSc1388	RS04671									METHYLASE/METHYLTRANSFERASE	I.II.B.8
RSc1389	RS04672									COG1437, Adenylate cyclase, class 2 (thermophilic)	I
RSc1390	RS04673									SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE	I.A.13
RSc1391	RS04674									COG1393, Arsenate reductase and related proteins	I
RSc1392	RS04675									TRANSMEMBRANE	V.I.C
RSc1393	RS04676									2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE	I.A.13
RSc1394	RS04677									SUCCINYLDIAMINOPIMELATE AMINOTRANSFERASE	I.A.13
RSc1395	RS05759									TRANSMEMBRANE	V.I.C
RSc1396	RS05760									TRANSMEMBRANE COG5096, Predicted hydrolases or acyltransferases (alpha/beta)	I
RSc1397	RS05762									TRANSMEMBRANE	V.I.C
RSc1398	RS05294									DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [NAD+])	I.II.B.8
RSc1399	RS05293									POLYPEPTIDE DEFORMYLASE	I.II.B.7
RSc1400	RS05292									TRANSMEMBRANE	V.I.C
RSc1401	RS05291									HYPOTHETICAL PROTEIN	V.I.B
RSc1402	RS05290									PROTEIN-PII URIDYLTRANSFERASE	I.A.18
RSc1403	RS05289									METHIONINE AMINOPEPTIDASE	I.II.B.7
RSc1404	RS05288									30S RIBOSOMAL PROTEIN S2	I.II.C.2
RSc1405	RS05287									ELONGATION FACTOR TS (EF-TS)	I.II.B.7
RSc1406	RS05286									URIDYLATE KINASE	I.F.9
RSc1407	RS05285									RIBOSOME RECYCLING FACTOR (RIBOSOME RELEASING FACTOR)	I.II.B.7
RSc1408	RS05284									UNDECAPRENYL PYROPHOSPHATE SYNTHETASE	I.II.B.3
RSc1409	RS05283									TRANSMEMBRANE PHOSPHATIDATE CYTIDYLTRANSFERASE	I.II.1
RSc1410	RS05282									OXIDOREDUCTASE 1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERA	I.II.B.5
RSc1411	RS05281									TRANSMEMBRANE COG0750, Predicted membrane-associated Zn-dependent prote	I.II.A.4
RSc1412	RS05280									SIGNAL PEPTIDE COG4775, Outer membrane protein	I.II.B.2
RSc1413	RS05279									TRANSMEMBRANE COG2825, OUTER MEMBRANE PROTEIN	I.II.B.2
RSc1414	RS05278									UDP-3-O-3-HYDROXYMYRISTOYL GLUCOSAMINE N-ACYLTRANSFERASE	I.II.A.1
RSc1415	RS05277									3R-HYDROXYMYRISTOYL-ACYL CARRIER PROTEIN DEHYDRATASE	I.II.A.1
RSc1416	RS05276									ACYL-ACYL-CARRIER-PROTEIN-UDP-N-ACETYLGUCOSAMINE O-ACYLTRANS	I.II.A.1
RSc1417	RS05275									LIPID-A-DISACCHARIDE SYNTHASE	I.II.A.1
RSc1418	RS05274									RIBONUCLEASE HII	I.II.A.2
RSc1419	RS05273									COG566, rRNA methylases	I.II.C.1
RSc1420	RS05272									ATP-BINDING PROTEIN	V.I.C
RSc1421	RS05271									PHOSPHOENOLPYRUVATE SYNTHASE	I.F.13
RSc1422	RS05270									TRANSMEMBRANE COG1585, Membrane protein implicated in regulation of membra	I.II.B.1
RSc1423	RS05269									TRANSMEMBRANE COG0330, Membrane protease subunits, stomatin/prohibitin hor	I.II.B.1
RSc1424	RS05268									tmRNA-BINDING PROTEIN (SMALL PROTEIN B)	I.V.B
RSc1425	RS05267									COG2867, Oligoketide cyclase/lipid transport protein	I
RSc1426	RS05266									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1427	RS05265									TRANSMEMBRANE	V.I.C
RSc1428	RS05264									TRANSMEMBRANE	V.I.C
RSc1429	RS05263									OXIDOREDUCTASE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE	I.D.2
RSc1430	RS05261									TRANSMEMBRANE	V.I.C
RSc1431	RS05262									GMP SYNTHASE GLUTAMINE-HYDROLYZING (GLUTAMINE AMIDOTRANSFERA	I.D.2
RSc1432	RS05734									TRANSCRIPTION REGULATOR	V.I.A
RSc1433	RS05735									TRANSMEMBRANE	V.I.D
RSc1440	RS03867									TRANSCRIPTION REGULATOR TRANSCRIPTIONAL REGULATORY DNA-BINDING	I.II.4
RSc1441	RS03866									OXIDOREDUCTASE PROTOCATECHUATE 3,4-DIOXYGENASE (BETA CHAIN)	I.I.4
RSc1442	RS03865									OXIDOREDUCTASE PROTOCATECHUATE 3,4-DIOXYGENASE (ALPHA CHAIN)	I.I.4
RSc1443	RS03864									2H PHOSPHOESTERASE (2'-5' RNA LIGASE)	I.II.B.6
RSc1444	RS03863									COG3531, Predicted protein-disulfide isomerase	I.II.B.7
RSc1445	RS03862									TRANSMEMBRANE COG2814, Arabinose efflux permease	I.V.D.3
RSc1446	RS03861									TRANSCRIPTION REGULATOR HIPA PROTEIN	I.II.B.3
RSc1447	RS03860									TRANSCRIPTION REGULATOR	V.I.A
RSc1448	RS03859									COG2513, PEP phosphonmutase and related enzymes	I
RSc1449	RS03858									COG0602, Organic radical activating enzymes	I.II.B.7
RSc1450	RS03857									6-PYRUVOYL TETRAHYDROBIOPTERIN SYNTHASE	I
RSc1451	RS03856									COG0590, Cytosine/adenosine deaminase	I
RSc1452	RS03855									TRANSMEMBRANE	V.I.C
RSc1453	RS03854									ABC TRANSPORTER ATP-BINDING PROTEIN	I.V.D
RSc1454	RS03853									SIGNAL PEPTIDE	V.I.D
RSc1455	RS03852									PROLINE-RICH PROTEIN	V.I.B
RSc1456	RS03851									OXIDOREDUCTASE BETAINE ALDEHYDE DEHYDROGENASE (BADH)	I.F
RSc1457	RS03850									COG3313, Predicted Fe-S protein	V.I.C
RSc1458	RS03849									COG3387, Glucoamylase and related glycosyl hydrolases	I.II.3
RSc1459	RS03848									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1460	RS03847									TRANSMEMBRANE METHYL-ACCEPTING CHEMOTAXIS TRANSDUCER PROTEIN	I.V.C
RSc1461	RS03846									TRANSMEMBRANE TRANSPORTER PROTEIN	I.V.D
RSc1462	RS03845									SIGNAL PEPTIDE COG0451, Nucleoside-diphosphate-sugar epimerase	I
RSc1463	RS03844									COG1975: Xanthine and CO dehydrogenases maturation factor	I.II.B.7
RSc1464	RS03843									TRANSMEMBRANE	V.I.C
RSc1465	RS03842									COG3552, Protein containing von Willebrand factor type A (vWA) domain	V.I.B
RSc1466	RS03841									COG0714 : MoxR- like ATPase	V.I.C
RSc1467	RS03840									OXIDOREDUCTASE COG1319, Aerobic-type carbon monoxide dehydrogenase, mid	I
RSc1468	RS03839									OXIDOREDUCTASE COG1529, Aerobic-type carbon monoxide dehydrogenase, large	I
RSc1469	RS03838									OXIDOREDUCTASE COG2080, Aerobic-type carbon monoxide dehydrogenase, smal	I
RSc1470	RS03837									HYPOTHETICAL PROTEIN	V.I.D
RSc1471	RS03836									SIGNAL PEPTIDE CREA PROTEIN	V.I.C
RSc1472	RS03835									TRANSCRIPTION REGULATOR	V.I.A
RSc1473	RS03834									TRANSMEMBRANE MULTIDRUG RESISTANCE-LIKE PROTEIN	I.V.D.7

RSc1591	RS03953			-0.95	0.00			hpaI1	OXIDOREDUCTASE 2,4-DIHYDROXYHEPT-2-ENE-1,7-DIOIC ACID ALDOLASE	I.I.4
RSc1592	RS03954			-1.08	0.00				TRANSCRIPTION REGULATOR	V.I.A
RSc1593	RS03955							xthA	EXODEOXYRIBONUCLEASE III	I.I.A.1
RSc1594	RS03956			-0.38	0.03			codA	CYTOSINE DEAMINASE (CYTOSINE AMINOHYDROLASE)	I.F.9
RSc1595	RS03957		0.53	0.01				prfC	OLIGOPEPTIDASE A (OPDA PROTEIN)	I.I.A.4
RSc1596	RS03958							folD	OXIDOREDUCTASE BIFUNCTIONAL PROTEIN : METHYLENETETRAHYDROFOLATE	I.B.14
RSc1597	RS03959		0.31	0.04	-0.41	0.03			TRANSCRIPTION REGULATOR RESPONSE REGULATOR	V.I.A
RSc1598	RS03960								TRANSCRIPTION REGULATOR TWO-COMPONENT TRANSMEMBRANE SENSOR	V.I.A
RSc1599	RS03961								HYPOTHETICAL PROTEIN	V.I.D
RSc1600	RS03962		0.89	0.03	-0.57	0.01		aceE	OXIDOREDUCTASE PYRUVATE DEHYDROGENASE E1 COMPONENT	I.H.7
RSc1601	RS03963		0.78	0.00	-0.65	0.01		aceF	DIHYDROLIPOAMIDE ACETYLTRANSFERASE COMPONENT OF PYRUVATE DEH	I.H.7
RSc1602	RS03964		0.77	0.01	-0.68	0.00			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1603	RS03965		1.12	0.00	-0.70	0.00		lpdA	DIHYDROLIPOAMIDE DEHYDROGENASE (E3 COMPONENT OF PYRUVATE AND	I.H.7
RSc1604	RS03966				-0.68	0.00			TRANSMEMBRANE	V.I.D
RSc1605	RS03967								TRANSMEMBRANE	V.I.D
RSc1606	RS03969		0.39	0.05				phaP1	POLYHYDROXYBUTYRATE GRANULE-ASSOCIATED PROTEIN (PHASIN) PHAP1	I.I.B
RSc1607	RS03968		0.60	0.05	-0.49	0.03			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1608	RS03971								TRANSMEMBRANE	V.I.C
RSc1609	RS03972								OXIDOREDUCTASE	V.I.C
RSc1610	RS03973				-0.50	0.00			D-ALANYL-D-ALANINE- ENDOPEPTIDASE (PENICILLIN-BINDING PROTEIN)	I.V.A
RSc1611	RS03974								TRANSCRIPTION REGULATOR	V.I.A
RSc1612	RS03975		1.25	0.02					CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1613	RS03976								IRON-SULFUR BINDING PROTEIN	V.I.C
RSc1614	RS03977		-0.99	0.01	1.28	0.00			HYPOTHETICAL PROTEIN	V.I.D
RSc1615	RS03978								TRANSMEMBRANE	V.I.B
RSc1616	RS03979								TRANSMEMBRANE	V.I.D
RSc1617	RS03980				-0.84	0.00			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1618	RS03981				-0.38	0.05		aat	LEUCYL(PHENYLALANYL-TRNA--PROTEIN TRANSFERASE	I.I.A.4
RSc1619	RS03982								HYPOTHETICAL PROTEIN	V.I.B
RSc1620	RS03983				-0.67	0.00		pyrD	OXIDOREDUCTASE DIHYDROOROTATE DEHYDROGENASE	I.D.1
RSc1621	RS03984				-0.60	0.00			TRANSMEMBRANE	V.I.D
RSc1622	RS03985							kup2	TRANSMEMBRANE POTASSIUM UPTAKE PROTEIN	I.V.D.4
RSc1623	RS03986		1.07	0.04	-0.53	0.02			TRANSMEMBRANE	V.I.D
RSc1624	RS03987				-0.42	0.03		tex	TRANSCRIPTION ACCESSORY PROTEIN	V.I.C
RSc1625	RS03988				-0.70	0.00			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1626	RS03989								CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1627	RS03990								ATP-DEPENDENT DNA HELICASE-RELATED PROTEIN	I.I.B.8
RSc1628	RS03991								TRANSMEMBRANE	V.I.C
RSc1629	RS03992							rluD	RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE D	I.II.C.1
RSc1630	RS03993				-0.45	0.03			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1631	RS03994		0.57	0.00	-0.38	0.03			CONSERVED HYPOTHETICAL PROTEIN	V.I.D
RSc1632	RS03995		0.63	0.04				phbC	TRANSMEMBRANE POLY-BETA-HYDROXYBUTYRATE POLYMERASE	I.I.B
RSc1633	RS03996							phbA	ACETYL-COA ACETYLTRANSFERASE (ACETOACETYL-COA THIOLEASE)	I.I.B
RSc1634	RS03997							phbB	OXIDOREDUCTASE ACETOACETYL-COA REDUCTASE	I.I.B
RSc1635	RS03998								CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1636	RS03999		1.54	0.00					CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1637	RS05826		0.48	0.01	-0.35	0.01		bktB	BETA-KETOTHIOLASE	I.I.B
RSc1638	RS04012								SIGNAL PEPTIDE	V.I.D
RSc1639	RS04013				0.65	0.00		metC	CYSTATHIONINE BETA-LYASE (CYSTEINE LYASE)	I.A.12
RSc1640	RS04014		-0.61	0.02	1.26	0.01		serB	PHOSPHOSERINE PHOSPHATASE	I.A.10
RSc1641	RS04016							argE	ACETYLMORNITHINE DEACETYLASE (ACETYLMORNITHINASE)	I.A.17
RSc1642	RS04017		0.77	0.00				mfd	TRANSCRIPTION-REPAIR COUPLING FACTOR	I.I.B.6
RSc1643	RS04018		0.92	0.02					CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1644	RS04019		0.61	0.00					CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1645	RS04020							ahpD	ANTIOXIDANT PROTEIN	I.V.G.4
RSc1646	RS04022							ahpC2	OXIDOREDUCTASE ALKYL HYDROPEROXIDE REDUCTASE (SUBUNIT C)	I.V.G.4
RSc1647	RS04023		0.62	0.01				risS	TRANSCRIPTION REGULATOR OXIDATIVE STRESS RESISTANCE TWO-COMP	I.V.G.4
RSc1648	RS04025				-0.38	0.00		risA	TRANSCRIPTION REGULATOR OXIDATIVE STRESS RESISTANCE TWO-COMP	I.V.G.4
RSc1649	RS04026				-0.68	0.00			TRANSMEMBRANE	V.I.D
RSc1650	RS04027								SIGNAL PEPTIDE	V.I.B
RSc1651	RS04028				-0.19	0.00			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1652	RS04029		0.73	0.01	-0.48	0.00		criB	PHYTOENE SYNTHASE	I
RSc1653	RS04030		0.66	0.00	-0.43	0.00			TRANSMEMBRANE TRANSPORT/EFFLUX PROTEIN	I.V.D
RSc1654	RS04031								TRANSMEMBRANE DRUG EFFLUX PROTEIN	I.V.D
RSc1655	RS04034				-0.27	0.04			INTEGRASE/RECOMBINASE	V.A
RSc1656	RS04036								HYPOTHETICAL PROTEIN	V.I.B
RSc1657	RS04037								HYPOTHETICAL PROTEIN	V.I.B
RSc1658	RS04038								JAMM ISOPEPTIDASE	V.I.B
RSc1659	RS04040								HYPOTHETICAL PROTEIN	V.I.D
RSc1660	RS04041								HYPOTHETICAL PROTEIN	V.I.D
RSc1661	RS04042		-0.88	0.03					HYPOTHETICAL PROTEIN	V.I.D
RSc1662	RS04043				-0.54	0.04			HYPOTHETICAL PROTEIN	V.I.D
RSc1663	RS04044								HYPOTHETICAL PROTEIN	V.I.D
RSc1664	RS04045								HYPOTHETICAL PROTEIN	V.I.D
RSc1665	RS04046								HYPOTHETICAL PROTEIN	V.I.D
RSc1666	RS04047								TRANSMEMBRANE	V.I.D
RSc1667	RS04048				-1.23	0.01			HYPOTHETICAL PROTEIN	V.I.D
RSc1668	RS04049								HYPOTHETICAL PROTEIN	V.I.D
RSc1669	RS04051								TRANSMEMBRANE	V.I.D
RSc1670	RS04057		0.79	0.00	-0.68	0.00			HYPOTHETICAL PROTEIN	V.I.D
RSc1671	RS04060				-1.01	0.00			HYPOTHETICAL PROTEIN	V.I.D
RSc1672	RS04062				-0.52	0.03			TRANSCRIPTION REGULATOR	V.I.A
RSc1673	RS04063								HYPOTHETICAL PROTEIN	V.I.D
RSc1674	RS04064								HYPOTHETICAL PROTEIN	V.I.D
RSc1675	RS04066		-0.68	0.01	-0.44	0.00			TRANSMEMBRANE	V.I.D
RSc1676	RS04065								TRANSMEMBRANE	V.I.D
RSc1677	RS04069								HYPOTHETICAL PROTEIN	V.I.D
RSc1678	RS04071								HYPOTHETICAL PROTEIN	V.I.D
RSc1679	RS04072								PHAGE PHI-105 HOLIN-LIKE PROTEIN	V.D
RSc1680	RS04075								TRANSMEMBRANE	V.I.D
RSc1681	RS04076								TRANSMEMBRANE	V.I.D
RSc1682	RS04077								PHAGE PHI-105 ORF25-LIKE PROTEIN	V.D
RSc1683	RS04077		-1.53	0.03	1.49	0.01			PHAGE PHI-105 ORF26-LIKE PROTEIN	V.D
RSc1684	RS04078								PHAGE PHI-C31 GP36-LIKE PROTEIN	V.D
RSc1685	RS04079								BACTERIOPHAGE-RELATED PROTEIN	V.D
RSc1686	RS04080								phage HK022 GP9-RELATED PROTEIN	V.D
RSc1687	RS04081								HYPOTHETICAL PROTEIN	V.I.B
RSc1688	RS04082								HYPOTHETICAL PROTEIN	V.I.B
RSc1689	RS04083								HYPOTHETICAL PROTEIN	V.I.B
RSc1690	RS04086								PHAGE HK97 TAIL LENGTH TAPE MEASURE-RELATED PROTEIN	V.D
RSc1691	RS04087								PHAGE HK97 GP17-RELATED PROTEIN	V.D
RSc1692	RS04088								HYPOTHETICAL PROTEIN	V.I.B
RSc1693	RS04089								TAIL FIBER ASSEMBLY PROTEIN HOMOLOG	V.D
RSc1694	RS04090								PHAGE HK022 GP18-RELATED PROTEIN	V.D
RSc1695	RS04091								PHAGE HK022 GP19-RELATED PROTEIN	V.D
RSc1696	RS04092								PHAGE HK022 GP20-RELATED PROTEIN	V.D
RSc1697	RS04093				-0.51	0.00			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1698	RS02885				-0.46	0.01			BACTERIOPHAGE PROTEIN	V.I.D
RSc1699	RS02888		0.74	0.05	-0.43	0.05			BACTERIOPHAGE PROTEIN	V.D
RSc1700	RS02889								BACTERIOPHAGE ENDOLYSIN	V.D
RSc1701	RS02890								TRANSMEMBRANE LIPOPROTEIN	V.I.D
RSc1702	RS02891				-0.55	0.00			TRANSMEMBRANE	V.I.D
RSc1703	RS02892								SIGNAL PEPTIDE BACTERIOPHAGE-RELATED PROTEIN	V.D
RSc1704	RS02893				-0.41	0.00		ISRso1:	ISRso18-TRANSPOSASE	V.A

RSc1933	RS03502			-0.73	0.01					TRANSMEMBRANE PHAGE-RELATED PROTEIN	V.D		
RSc1934	RS03503			-1.29	0.02			-1.91	0.03	BACTERIOPHAGE PROTEIN	V.D		
RSc1935	RS03504		-1.17	0.00	1.21	0.00				BACTERIOPHAGE PROTEIN	V.D		
RSc1936	RS03505			-1.55	0.00			-1.19	0.05	BACTERIOPHAGE PROTEIN	V.D		
RSc1937	RS03506			-1.94	0.00			-1.92	0.00	BACTERIOPHAGE PROTEIN	V.D		
RSc1938	RS03507			-2.57	0.00			-0.90	0.04	BACTERIOPHAGE PROTEIN	V.D		
RSc1939	RS03508									TERMINASE (ATPase SUBUNIT) RELATED PROTEIN	V.D		
RSc1940	RS03509									TERMINASE (ATPase SUBUNIT) RELATED PROTEIN	V.D		
RSc1941	RS03510									BACTERIOPHAGE PROTEIN	V.D		
RSc1942	RS03511			-2.08	0.00					CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSc1943	RS03513			-2.26	0.00				1.33	0.03	TRANSMEMBRANE	V.I.C	
RSc1944	RS03512			-1.51	0.00					VGR-RELATED PROTEIN	V.I.C		
RSc1945	RS03514									HYPOTHETICAL PROTEIN	V.I.D		
RSc1946	RS03515									HYPOTHETICAL PROTEIN	V.I.D		
RSc1947	RS03518								1.23	0.00	HYPOTHETICAL PROTEIN	V.I.D	
RSc1948	RS03519			-0.62	0.00			-0.51	0.01	0.59	0.03	HYPOTHETICAL PROTEIN	V.I.D
RSc1949	RS03521											TRANSMEMBRANE GLYCINE-RICH PROTEIN	V.I.D
RSc1950	RS03524			-2.82	0.02							TRANSMEMBRANE METHYL-ACCEPTING CHEMOTAXIS TRANSDUCER	I.V.C
RSc1951	RS03525			0.57	0.05							TRANSMEMBRANE SOLUTE:NA+ SYMPORTER PERMEASE	I.V.D.4
RSc1952	RS03526			0.36	0.05			-0.25	0.05			ACETYL-COENZYME A SYNTHETASE	I.C
RSc1953	RS03527							-0.50	0.00			TRANSMEMBRANE	V.I.C
RSc1954	RS03528			0.39	0.03			-0.41	0.01			TRANSMEMBRANE COG2862, Predicted membrane protein	V.I.C
RSc1955	RS03529											FUMARATE HYDRATASE	I.H.6
RSc1956	RS03530											GLUTAMATE RACEMASE	III.B.3
RSc1957	RS03531		0.73	0.00								TRANSMEMBRANE GLUTAMATE SYMPORT PROTEIN	I.V.D.2
RSc1958	RS03532							-0.63	0.01			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1959	RS03533							-0.44	0.02			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1960	RS03534							-0.93	0.00			TRANSCRIPTION REGULATOR TRANSCRIPTIONAL REGULATORY DNA-BINDING	V.I.A
RSc1961	RS03535							-1.28	0.00			COG0464, ATPases of the AAA+ class	V.I.C
RSc1962	RS03536							-1.65	0.00			TRANSMEMBRANE	V.I.D
RSc1963	RS03537			-0.41	0.02			-1.58	0.00			TRANSMEMBRANE TONB PROTEIN	III.B.1
RSc1964	RS03538			0.34	0.03			-1.78	0.00			TRANSMEMBRANE BIOPOLYMER TRANSPORT PROTEIN	I.V.D
RSc1965	RS03539							-1.68	0.00			TRANSMEMBRANE BIOPOLYMER TRANSPORT PROTEIN	I.V.D
RSc1966	RS03540							-1.79	0.00			HEMIN UPTAKE PROTEIN	I.V.D.5
RSc1967	RS03541			0.35	0.05					1.02	0.00	GLCG PROTEIN	V.I.C
RSc1968	RS03542									0.76	0.05	TRANSMEMBRANE	V.I.C
RSc1969	RS03543							-0.94	0.00			TRANSMEMBRANE	V.I.C
RSc1970	RS03544							-0.75	0.00			HYPOTHETICAL PROTEIN	V.I.D
RSc1971	RS03545							-0.54	0.00			POLYHYDROXYBUTYRATE GRANULE-ASSOCIATED PROTEIN (PHASIN) PHAP3	II.B
RSc1972	RS03546									0.44	0.04	TRANSMEMBRANE OSMOTICALLY INDUCIBLE LIPOPROTEIN B1	I.V.F.2
RSc1973	RS03547											ABC TRANSPORTER ATP-BINDING PROTEIN	I.V.D
RSc1974	RS03548							-0.52	0.01			ABC TRANSPORTER TRANSMEMBRANE PERMEASE PROTEIN	I.V.D
RSc1975	RS03549							-0.47	0.01			AMIDOPHOSPHORIBOSYLTRANSFERASE	I.D.2
RSc1976	RS03550			0.62	0.00			-0.31	0.01			TRANSMEMBRANE COLICIN V PRODUCTION PROTEIN	V.C
RSc1977	RS03551											TRANSMEMBRANE	V.I.B
RSc1978	RS03552											BIFUNCTIONAL PROTEIN: FOLYLPOLYGLUTAMATE SYNTHASE AND DIHYDROF	I.B.14
RSc1979	RS03553									-0.38	0.01	ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE (SUBUNIT B)	I.C
RSc1980	RS03554		0.31	0.02								TRYPTOPHAN SYNTHASE (ALPHA CHAIN)	I.A.6
RSc1981	RS03555							0.26	0.00			DNA-METHYLTRANSFERASE (DNA-MODIFICATION METHYLASE)	II.B.8
RSc1982	RS03556											TRYPTOPHAN SYNTHASE (BETA CHAIN)	I.A.6
RSc1983	RS03412											N-(5'-PHOSPHORIBOSYL)ANTHRANILATE ISOMERASE	I.A.6
RSc1984	RS03413							0.27	0.03			TRNA PSEUDOURIDINE SYNTHASE	II.D.1
RSc1985	RS03414		1.00	0.03				-0.38	0.00			TRANSMEMBRANE TYPE IV PILUS ASSEMBLY FimV-RELATED PROTEIN	III.A.2
RSc1986	RS03415							-0.38	0.01			OXIDOREDUCTASE ASPARTATE-SEMIALDEHYDE DEHYDROGENASE	I.A
RSc1987	RS03416									0.58	0.05	OXIDOREDUCTASE 3-ISOPROPYLMALATE DEHYDROGENASE	I.A.1
RSc1988	RS03417							1.03	0.00			3-ISOPROPYLMALATE DEHYDRATASE (SMALL SUBUNIT)	I.A.1
RSc1989	RS03557							0.47	0.00			3-ISOPROPYLMALATE DEHYDRATASE (LARGE SUBUNIT)	I.A.1
RSc1990	RS03558											CITRATE SYNTHASE	I.H.6
RSc1991	RS03559							1.00	0.00			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc1992	RS03560							1.13	0.02			OXIDOREDUCTASE SUCCINATE DEHYDROGENASE (IRON-SULFUR PROTEIN S)	I.H.6
RSc1993	RS03561											OXIDOREDUCTASE SUCCINATE DEHYDROGENASE (FLAVOPROTEIN SUBUNIT)	I.H.6
RSc1994	RS03562							0.84	0.01			OXIDOREDUCTASE TRANSMEMBRANE SUCCINATE DEHYDROGENASE (HYDR)	I.H.6
RSc1995	RS03563							0.69	0.04			OXIDOREDUCTASE TRANSMEMBRANE SUCCINATE DEHYDROGENASE (CYTOC)	I.H.6
RSc1996	RS03564											TRANSCRIPTION REGULATOR	V.I.A
RSc1997	RS03565							-0.89	0.00			OXIDOREDUCTASE MALATE DEHYDROGENASE	I.H.6
RSc1998	RS03566							0.83	0.00			COG2031, Citrate lyase beta subunit	I
RSc1999	RS03567							-0.80	0.01			CARBOXYVINYL-CARBOXYPHOSPHONATE PHOSPHORYLMUTASE	I.I.4
RSc2000	RS03568							0.93	0.01			SIGNAL PEPTIDE	V.I.C
RSc2001	RS03569							0.46	0.04			PRPD PROTEIN	I.I.4
RSc2002	RS03570											ACONITATE HYDRATASE	I.H.6
RSc2003	RS03571							1.13	0.02			SIGNAL PEPTIDE	V.I.D
RSc2004	RS03572											CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc2005	RS03573							-0.80	0.00			ABC TRANSPORTER COG0747, ABC-type dipeptide transport system, periplasmic c	I.V.D.2
RSc2006	RS03574							0.64	0.02			TRANSMEMBRANE LIPOPROTEIN	V.I.C
RSc2007	RS03575							0.53	0.04			COG2866, Predicted carboxypeptidase	I
RSc2008	RS03576							0.64	0.00			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc2009	RS03577											CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc2010	RS03578							0.48	0.05			COG0436, Aspartate/tyrosine/aromatic aminotransferase	I
RSc2011	RS03579											GLUTATHIONE S-TRANSFERASE	II.B.7
RSc2012	RS03580							0.31	0.04			OXIDOREDUCTASE 3-HYDROXYBUTYRYL-COA DEHYDROGENASE	I.I.4
RSc2013	RS03581											ENOYL-COA HYDRATASE	I.I.4
RSc2014	RS03582							-0.71	0.02			COG0406, Fructose-2,6-bisphosphatase	I
RSc2015	RS03583							-0.48	0.02			COG3173, Predicted aminoglycoside phosphotransferase	V.I.C
RSc2016	RS03584							-0.68	0.00			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc2017	RS03585							-0.57	0.00			TRANSCRIPTION REGULATOR	V.I.A
RSc2018	RS03586							-0.51	0.01			SIGNAL PEPTIDE COG2050, Uncharacterized protein, possibly involved in aromatic c	V.I.C
RSc2019	RS03587							0.60	0.05			OXIDOREDUCTASE ACYL-CoA DEHYDROGENASE	I
RSc2020	RS03588											GLUTATHIONE-S-TRANSFERASE	II.B.7
RSc2021	RS03589							-0.65	0.00			TRANSMEMBRANE COG2020, Putative protein-S-isoprenylcysteine methyltransferas	II.B.7
RSc2022	RS03590									-0.98	0.03	HYPOTHETICAL PROTEIN	V.I.D
RSc2023	RS03591							0.45	0.05			TRANSMEMBRANE COG1279, LysE-type efflux permease	I.V.D
RSc2024	RS03592							-2.10	0.01			TRANSMEMBRANE COG3239, Fatty acid desaturase	I
RSc2025	RS03593							-0.78	0.00			HYPOTHETICAL PROTEIN	V.I.D
RSc2026	RS03598							0.32	0.01			HYPOTHETICAL PROTEIN	V.I.D
RSc2027	RS03594							-1.18	0.05			HYPOTHETICAL PROTEIN	V.I.D
RSc2028	RS03599											HYPOTHETICAL PROTEIN	V.I.D
RSc2029	RS03595							1.26	0.02			UREASE ACCESSORY PROTEIN	I.F.5
RSc2030	RS03600							1.11	0.00			UREASE ACCESSORY PROTEIN UREJ	I.F.5
RSc2031	RS03601											UREASE ACCESSORY PROTEIN UREK	I.F.5
RSc2032	RS02789							0.48	0.01			UREASE (ALPHA SUBUNIT)	I.F.5
RSc2033	RS02962							0.67	0.00			UREASE (BETA SUBUNIT)	I.F.5
RSc2034	RS03028							0.64	0.02			TRANSMEMBRANE UREASE ACCESSORY PROTEIN UREJ	I.F.5
RSc2035	RS03029											UREASE (GAMMA SUBUNIT)	I.F.5
RSc2036	RS03030							0.89	0.01			UREASE ACCESSORY PROTEIN UREK	I.F.5
RSc2037	RS03602											ABC TRANSPORTER ATP-BINDING PROTEIN	I.V.D
RSc2038	RS03603							-1.76	0.02			ABC TRANSPORTER ATP-BINDING PROTEIN	I.V.D
RSc2039	RS03604											TRANSMEMBRANE PERMEASE TRANSPORTER PROTEIN	I.V.D
RSc2040	RS03605							-0.94	0.02			TRANSMEMBRANE PERMEASE TRANSPORTER PROTEIN	I.V.D
RSc2041	RS03606							-0.67	0.04			ABC TRANSPORTER COG0683, ABC-type branched-chain amino acid transport syst	I.V.D
RSc2042	RS03607							-0.65	0.02			COG2030, Acyl dehydratase	I
RSc2043	RS03608							0.33	0.05			COG2030, Acyl dehydratase	I
RSc2044	RS03609											OXIDOREDUCTASE ACYL-COA DEHYDROGENASE	I.I.1
RSc2045	RS03610		0.87	0.03				0.70	0.00			OXIDOREDUCTASE ACYL-COA DEHYDROGENASE	I

RSc2159	RS01443			-0.64	0.01	-0.81	0.01	rph	RIBONUCLEASE PH (TRNA NUCLEOTIDYLTRANSFERASE)	II.A.2			
RSc2160	RS01442					-0.65	0.03		COG0127, Xanthosine triphosphate pyrophosphatase	I			
RSc2161	RS01441	0.89	0.01	-0.51	0.01				OXIDOREDUCTASE COG0635, Coproporphyrinogen III oxidase and related Fe-S oxidase	II.B.1			
RSc2162	RS01439								COG1234, Metal-dependent hydrolases of the beta-lactamase superfamily III	II			
RSc2163	RS01438			-0.34	0.01		1.36	0.00	CONSERVED HYPOTHETICAL PROTEIN	V.I.C			
RSc2164	RS01436			-0.23	0.03	0.56	0.02		SIGNAL PEPTIDE	V.I.B			
RSc2165	RS01434							pcp1	PYRROLIDONE-CARBOXYLATE PEPTIDASE (5-OXOPROLYL-PEPTIDASE)	II.F.14			
RSc2166	RS01617			-0.63	0.01	-1.17	0.01		SIGNAL PEPTIDE COG1638, TRAP-type C4-dicarboxylate transport system, periplasmic	IV.D.3			
RSc2167	RS01432	-0.57	0.05	1.02	0.03	0.83	0.00		TRANSMEMBRANE	V.I.C			
RSc2168	RS01431			0.38	0.01		0.45	0.03	TRANSMEMBRANE	V.I.C			
RSc2169	RS01430					0.46	0.04		CONSERVED HYPOTHETICAL PROTEIN	V.I.C			
RSc2170	RS01429			0.68	0.01				COG1984, Allophanate hydrolase subunit 2	II			
RSc2171	RS01428								COG2049, Allophanate hydrolase subunit 1	II			
RSc2172	RS01427								TRANSMEMBRANE DRUG TRANSPORT PROTEIN	IV.D			
RSc2173	RS01426			-0.40	0.05				ABC TRANSPORTER SUGAR ATP BINDING PROTEIN	IV.D.3			
RSc2174	RS01425								ABC TRANSPORTER TRANSMEMBRANE PROTEIN	IV.D			
RSc2175	RS01424			0.85	0.02				ABC TRANSPORTER TRANSMEMBRANE PROTEIN	IV.D			
RSc2177	RS01422								LIPOPROTEIN	V.I.C			
RSc2178	RS01421								HYPOTHETICAL PROTEIN	V.I.D			
RSc2179	RS01420					0.53	0.01		TRANSMEMBRANE	V.I.B			
RSc2180	RS01419			0.90	0.00		-1.86	0.00	TRANSMEMBRANE	V.I.D			
RSc2181	RS01418								HYPOTHETICAL PROTEIN	V.I.B			
RSc2182	RS01417								HYPOTHETICAL PROTEIN	V.I.D			
RSc2183	RS01416					-0.51	0.02		CONSERVED HYPOTHETICAL PROTEIN	V.I.C			
RSc2184	RS01415			0.71	0.00	-0.28	0.05		OXIDOREDUCTASE NADPH:QUINONE REDUCTASE, ZETA-CRYSTALLIN HOMOLOG I	I.G.1			
RSc2185	RS01414	-0.48	0.00	0.47	0.01		0.48	0.01	METHYLGLYOXAL SYNTHASE	IV.D.18			
RSc2186	RS01413			0.42	0.05	-0.42	0.00		OXIDOREDUCTASE COG1028, Dehydrogenases with different specificities (related to)	I			
RSc2187	RS01412			0.89	0.00				TRANSMEMBRANE	V.I.C			
RSc2188	RS01411					0.45	0.01	0.92	0.03	upp	URACIL PHOSPHORIBOSYLTRANSFERASE	I.F.1	
RSc2189	RS01410			0.56	0.01		0.75	0.01	COG0433, PREDICTED ATPase	V.I.C			
RSc2190	RS01409			-1.34	0.01	1.79	0.00		CONSERVED HYPOTHETICAL PROTEIN	V.I.C			
RSc2191	RS01408			0.74	0.00			-0.30	0.01	purD	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE	I.D.2	
RSc2192	RS01407	0.51	0.04			-0.36	0.04		OXIDOREDUCTASE COPROPORPHYRINOGEN III OXIDASE, AEROBIC	II.B.4			
RSc2193	RS01406					-0.38	0.00		COG1057, Nicotinic acid mononucleotide adenyllyltransferase	I			
RSc2194	RS01405					-0.26	0.03		CONSERVED HYPOTHETICAL PROTEIN	V.I.C			
RSc2195	RS01404								CONSERVED HYPOTHETICAL PROTEIN	V.I.C			
RSc2196	RS01403					-0.47	0.00		COG0424, Nucleotide-binding protein implicated in inhibition of septum formation	IV.A			
RSc2197	RS01402					-0.24	0.02		RIBONUCLEASE G (RNASE G) (CYTOPLASMIC AXIAL FILAMENT PROTEIN)	IV.A			
RSc2198	RS01401								CONSERVED HYPOTHETICAL PROTEIN	V.I.C			
RSc2199	RS01400					-0.37	0.02	0.78	0.02	COG128, Uncharacterized conserved protein	V.I.C		
RSc2200	RS01399			-1.95	0.00	2.19	0.00		ABC TRANSPORTER PROTEIN ABC-TYPE MULTIDRUG TRANSPORT SYSTEM, I	IV.D			
RSc2201	RS01398					-0.27	0.03		SIGNAL PEPTIDE COG1216, Glycosyltransferase	I			
RSc2202	RS01397							-0.55	0.04		GLYCOSYL TRANSFERASE	II.B	
RSc2203	RS01396								COG1216, Glycosyltransferase	II.B.2			
RSc2204	RS01395			0.80	0.05	-0.38	0.01		TRANSMEMBRANE LIPOPOLYSACCHARIDE O-ANTIGEN LIGASE	II.B.2			
RSc2205	RS01394					-0.41	0.00		DNA POLYMERASE III (ALPHA CHAIN)	II.B.8			
RSc2206	RS01393						2.13	0.02	COG1054, Predicted sulfurtransferase	I.F.3			
RSc2207	RS01392					-0.91	0.00	0.44	0.04	COG0655, Multimeric flavodoxin WrbA	V.I.C		
RSc2208	RS01391	-1.58	0.01			-2.16	0.00		PIRIN-RELATED PROTEIN	V.I.C			
RSc2209	RS01390	-1.73	0.00			-0.57	0.00		TRANSCRIPTION REGULATOR TRANSCRIPTIONAL REGULATOR	IV.A			
RSc2210	RS01389					-0.52	0.00		COG0008, Glutamyl- and glutaminyl-tRNA synthetases	II.D.1			
RSc2211	RS01388					-0.50	0.01		ATP-DEPENDENT RNA HELICASE	II.B.7			
RSc2212	RS01387								CONSERVED HYPOTHETICAL PROTEIN	V.I.C			
RSc2213	RS01386			0.56	0.01			-1.13	0.05	rhiE2	TRANSCRIPTION REGULATOR TRANSCRIPTIONAL REGULATOR	IV.A	
RSc2214	RS01385								COG0491, Zn-dependent hydrolase	II			
RSc2215	RS01384						0.43	0.05	TRANSCRIPTION REGULATOR RNA POLYMERASE SIGMA D (SIGMA-70) FACTOR I	E.1			
RSc2216	RS01383			0.34	0.02	-0.33	0.03		DNA PRIMASE	II.B.8			
RSc2217	RS01382			0.41	0.05			-1.12	0.05	dnaG	CONSERVED HYPOTHETICAL PROTEIN	V.I.C	
RSc2218	RS01381					-0.46	0.05		TRANSMEMBRANE COG2081, Flavoprotein	V.I.C			
RSc2219	RS01380								O-SIALOGLYCOPROTEIN ENDOPEPTIDASE	II.A.4			
RSc2220	RS01379					-0.76	0.00		CONSERVED HYPOTHETICAL PROTEIN	V.I.C			
RSc2221	RS01378					-0.40	0.01		1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE	IV.F.18			
RSc2222	RS01377			0.46	0.02	-0.47	0.02		GERANYLTRANSFERASE (FARNESYL-DIPHOSPHATE SYNTHASE)	I.B.5			
RSc2223	RS01376					-0.51	0.00	0.43	0.02	xseB	EXODEXOXYRIBONUCLEASE SMALL SUBUNIT	II.A.1	
RSc2224	RS01375			0.62	0.01			-0.81	0.00		OXIDOREDUCTASE COG4638, Phenylpropionate dioxygenase and related ring-hydroxylase	V.I.C	
RSc2225	RS01374					-0.32	0.02		TRANSMEMBRANE	V.I.C			
RSc2226	RS01373								THIOSULFATE SULFURTRANSFERASE	I.F.3			
RSc2227	RS01372							-0.94	0.02	sseA	TRANSMEMBRANE COG0428, Predicted divalent heavy-metal cations transporter	IV.D.4	
RSc2228	RS01371					-0.60	0.02		COG0412, Dienelactone hydrolase and related enzymes	I			
RSc2229	RS01370							-0.27	0.04	ndh	OXIDOREDUCTASE NADH DEHYDROGENASE, MEMBRANE FLAVOPROTEIN FACTOR I	H.3	
RSc2230	RS01369					-0.27	0.04		DNA POLYMERASE I	II.B.8			
RSc2231	RS01368								COG1611, Rossmann fold nucleotide-binding protein	V.I.C			
RSc2232	RS01367					-0.38	0.02		TRANSMEMBRANE	V.I.B			
RSc2233	RS01366			0.72	0.02				HOMOSERINE KINASE	II.A.12			
RSc2234	RS01365					-0.39	0.04	-0.41	0.05	thrB	TRANSMEMBRANE	V.I.C	
RSc2235	RS01364								DNA HELICASE II	II.B.8			
RSc2236	RS01363			0.44	0.00				VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE)	II.D.1			
RSc2237	RS01362			0.65	0.00				UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE	II.A			
RSc2238	RS01361							-0.12	0.00	galU1	TRANSMEMBRANE	V.I.C	
RSc2239	RS01360					-0.70	0.00		-1.06	0.02	infA2	TRANSLATION INITIATION FACTOR IF-1	II.B.7
RSc2240	RS01359					-1.17	0.00		CONSERVED HYPOTHETICAL PROTEIN	V.I.C			
RSc2241	RS01318			0.89	0.03	-0.46	0.03		COG2342, Extracellular endo alpha-1,4 polygalactosaminidase or related polysaccharidase	II.A.3			
RSc2242	RS01317	-0.77	0.04			-1.61	0.00		OXIDOREDUCTASE 4-HYDROXYBENZOATE 3-MONOXYGENASE	II.A			
RSc2243	RS01316					-0.68	0.03		TRANSCRIPTION REGULATOR	V.I.A			
RSc2244	RS01315			-1.06	0.00	1.71	0.00	1.00	0.03	pobB	ABC TRANSPORTER SUBSTRATE-BINDING PERIPLASMIC PROTEIN	IV.D	
RSc2245	RS01314								ABC TRANSPORTER ATP-BINDING PROTEIN	IV.D			
RSc2246	RS01313								ABC TRANSPORTER ATP-BINDING PROTEIN	IV.D			
RSc2247	RS01312					-0.57	0.03		ABC TRANSPORTER TRANSMEMBRANE PROTEIN	IV.D			
RSc2248	RS01311								ABC TRANSPORTER TRANSMEMBRANE PROTEIN	IV.D			
RSc2249	RS01310					-0.94	0.00	-0.99	0.01	pcaC	4-CARBOXYMUCONOLACTONE DECARBOXYLASE	II.A	
RSc2250	RS01309					-0.49	0.00		TRANSMEMBRANE B-KETOADIPATE ENOL-LACTONE HYDROLASE	II.A			
RSc2251	RS01308			0.46	0.01	-0.50	0.02	-0.88	0.03	pcaB	3-CARBOXY-CIS,CIS-MUCONATE CYCLOISOMERASE	II.A	
RSc2252	RS01307								BETA-KETOADIPYL COA THIOLEASE	II.A			
RSc2253	RS01306					-0.70	0.01	-1.13	0.00	pcaJ	3-OXOADIPATE COA-TRANSFERASE SUBUNIT B	II.A	
RSc2254	RS01305					-0.53	0.00	-0.96	0.02	pcaI	3-OXOADIPATE COA-TRANSFERASE SUBUNIT A	II.A	
RSc2255	RS01304					-0.58	0.01	-0.69	0.04		TRANSCRIPTION REGULATOR	V.I.A	
RSc2256	RS01303					-1.00	0.00				SIGNAL PEPTIDE	V.I.C	
RSc2257	RS01302	-0.36	0.05			-0.90	0.00	-1.01	0.00		ABC TRANSPORTER AMINO-ACID-BINDING PERIPLASMIC PROTEIN	IV.D.2	
RSc2258	RS01301										ABC TRANSPORTER AMINO ACID TRANSMEMBRANE PROTEIN	IV.D.2	
RSc2259	RS01300			0.75	0.00			-1.06	0.02		ABC TRANSPORTER AMINO ACID TRANSMEMBRANE PROTEIN	IV.D.2	
RSc2260	RS01299					-0.60	0.00				ABC TRANSPORTER AMINO-ACID ATP-BINDING PROTEIN	IV.D.2	
RSc2261	RS01298					-0.48	0.00				ABC TRANSPORTER AMINO-ACID-BINDING PERIPLASMIC PROTEIN (PBP)	IV.D.2	
RSc2262	RS01297					-0.71	0.02				OXIDOREDUCTASE TRANSMEMBRANE D-AMINO ACID DEHYDROGENASE (SM)	II.3	
RSc2263	RS01296					-0.67	0.04				LIPOPROTEIN	V.I.C	
RSc2264	RS01295							-1.57	0.02		LIPOPROTEIN	V.I.D	
RSc2267	RS01292					-0.42	0.02	-0.68	0.02	SRso8	ISRS08-TRANSPOSASE ORFB	V.A	
RSc2268	RS01291									TISRS0_	ISRS08-TRANSPOSASE ORFA	V.A	
RSc2269	RS01290							1.19	0.02		SIGNAL PEPTIDE	V.I.D	
RSc2270	RS01289			0.43	0.04	-0.41	0.02			ragG	TRANSMEMBRANE POLYSACCHARIDE SYNTHASE	III.A.1	
RSc2271	RS01288			0.59	0.01	-0.61	0.00			ragF	GLYCOSYL-TRANSFERASE	III.A.1	
RSc2272	RS01287			0.32	0.01	-0.50	0.00	-0.65	0.01	ragE	TRANSMEMBRANE POLYSACCHARIDE TRANSPORT SYSTEM COMPONENT	III.A.1	
RSc2273	RS01286							-0.88	0.01	ragD	TRANSMEMBRANE POLYSACCHARIDE TRANSPORT SYSTEM COMPONENT	III.A.1	

RSc2274	RS01284			-0.59	0.04	-0.59	0.02		ragC	OUTER MEMBRANE LIPOPROTEIN	III.A.1		
RSc2275	RS01283		1.07	0.01	-0.52	0.02			ragB	SIGNAL PEPTIDE POLYSACCHARIDE TRANSPORT SYSTEM COMPONENT	III.A.1		
RSc2276	RS01282				-0.86	0.01			ragA	SIGNAL PEPTIDE POLYSACCHARIDE TRANSPORT SYSTEM COMPONENT	III.A.1		
RSc2277	RS01281		1.11	0.00	-0.62	0.01				TRANSMEMBRANE	V.I.C		
RSc2278	RS01280				-0.81	0.01				HYPOTHETICAL PROTEIN	V.I.D		
RSc2279	RS01279				-0.69	0.00				SIGNAL PEPTIDE	V.I.D		
RSc2280	RS01277				-0.98	0.01		1.11	0.01	SIGNAL PEPTIDE	V.I.C		
RSc2281	RS01276		0.81	0.00						TRANSMEMBRANE	V.I.D		
RSc2282	RS01275		-1.64	0.04	-0.25	0.04	2.29	0.02		HYPOTHETICAL PROTEIN	V.I.D		
RSc2283	RS01274				-0.30	0.05	0.54	0.01		HYPOTHETICAL PROTEIN	V.I.D		
RSc2284	RS01272		0.49	0.05			0.90	0.04		TRANSMEMBRANE COG3713, Outer membrane protein V - related protein	III.B.2		
RSc2285	RS01271		-3.43	0.00	-0.91	0.00	3.34	0.00		SIGNAL PEPTIDE	V.I.C		
RSc2286	RS01270		-3.06	0.00	-0.65	0.01	2.22	0.00		CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSc2287	RS01269									COG0526, Thiol-disulfide isomerase and thioredoxins	II.B.7		
RSc2288	RS01268				-0.72	0.00				CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSc2289	RS01267							1.42	0.01	CYTOCHROME C1 PRECURSOR	I.G.1		
RSc2290	RS01265									OXIDOREDUCTASE IRON OXIDASE PRECURSOR	I.G.1		
RSc2291	RS01264				-2.30	0.00	-0.93	0.01		TRANSGLYCOSYLASE	V.I.C		
RSc2292	RS01263						-0.66	0.01		TRANSMEMBRANE	V.I.C		
RSc2293	RS01262									CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSc2294	RS01261						-0.91	0.02		CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSc2295	RS01259						-0.84	0.02		SIGNAL PEPTIDE HYPOTHETICAL PROTEIN	V.I.C		
RSc2296	RS01258									TRANSMEMBRANE	V.I.C		
RSc2297	RS01257				-0.89	0.01	1.03	0.00		SIGNAL PEPTIDE	V.I.C		
RSc2298	RS01256									SIGNAL PEPTIDE COG2132, Multicopper oxidases	I		
RSc2299	RS01255									SIGNAL PEPTIDE COG2132, Multicopper oxidases	I		
RSc2300	RS01254		0.48	0.04						SIGNAL PEPTIDE COG165, Type II secretory pathway, pseudopilin PulG - related protein	III.A.2		
RSc2301	RS01252									COG165, Type II secretory pathway, pseudopilin PulG - related protein	III.A.2		
RSc2302	RS01251									SIGNAL PEPTIDE COG165, Type II secretory pathway, pseudopilin PulG - related protein	III.A.2		
RSc2303	RS01250									Type II secretory pathway, GSPD-RELATED PROTEIN	III.A.2		
RSc2304	RS01248				-0.80	0.04				TRANSMEMBRANE PROLINE RICH PROTEIN	V.I.C		
RSc2305	RS01247									TRANSMEMBRANE	V.I.C		
RSc2306	RS01246									TRANSMEMBRANE	V.I.C		
RSc2307	RS01245									SIGNAL PEPTIDE	V.I.C		
RSc2308	RS01244									Type II secretory pathway GSPE - RELATED PROTEIN	III.A.2		
RSc2309	RS01243									TRANSMEMBRANE Type II secretory pathway, GSPF-RELATED PROTEIN	III.A.2		
RSc2310	RS01241						-1.15	0.01		TRANSMEMBRANE Type II secretory pathway, pseudopilin PulG - related protein	III.A.2		
RSc2311	RS01240									TRANSCRIPTION REGULATOR TWO-COMPONENT SENSOR HISTIDINE KINASE	V.I.A		
RSc2312	RS01239									TRANSCRIPTION REGULATOR TWO-COMPONENT RESPONSE REGULATOR	V.I.A		
RSc2313	RS01237				-0.78	0.00				TRANSPPOSASE	V.A		
RSc2314	RS01236				-0.66	0.00			0.65	0.01	TRANSPPOSASE	V.A	
RSc2315	RS01234				-1.24	0.00	-1.00	0.00		1.13	0.00	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc2316	RS01233										TRANSMEMBRANE DRUG TRANSPORT PROTEIN	I.V.D	
RSc2317	RS01232				-0.96	0.01					COG3545, Esterase of the alpha/beta hydrolase fold	I	
RSc2318	RS01231						-0.75	0.05		0.59	0.00	TRANSCRIPTION REGULATOR	V.I.A
RSc2319	RS01230		0.49	0.04							COG2267, Lysophospholipase	I	
RSc2320	RS01229				-0.87	0.01	-1.63	0.00			CONSERVED HYPOTHETICAL PROTEIN	V.I.C	
RSc2321	RS01228				-0.53	0.02	-1.15	0.00			OXIDOREDUCTASE COG0300, Short-chain dehydrogenases of various substrate specificities	V.I.A	
RSc2322	RS01227				-0.94	0.00					TRANSCRIPTION REGULATOR	V.I.A	
RSc2323	RS01226				-0.51	0.01					TRANSMEMBRANE TRANSPORTER PROTEIN	I.V.D	
RSc2324	RS01224				-0.55	0.03	-1.07	0.04			TRANSMEMBRANE TRANSPORT PROTEIN	I.V.D	
RSc2325	RS01223				-1.17	0.05	-0.43	0.03			TRANSCRIPTION REGULATOR	V.I.A	
RSc2326	RS01222				-0.48	0.00					LIPOPROTEIN	V.I.B	
RSc2327	RS01221				0.14	0.02					TRANSCRIPTION REGULATOR	V.I.A	
RSc2328	RS01220		-2.78	0.00	0.57	0.01					SIGNAL PEPTIDE COG0596, Hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	V.I.C	
RSc2329	RS01219										COG2249, NADPH-quinone reductase (modulator of drug activity B)	V.I.C	
RSc2330	RS01218										HYPOTHETICAL PROTEIN	V.I.D	
RSc2331	RS01214				-0.45	0.00					REMNANT OF ISRs010-TRANSPPOSASE	V.A	
RSc2332	RS01210				-0.53	0.00					HYPOTHETICAL PROTEIN	V.I.D	
RSc2333	RS01209		0.64	0.02	-0.32	0.02			0.54	0.01	SERYL-TRNA SYNTHETASE	II.B.6	
RSc2334	RS01208		1.90	0.04							COG2256, ATPase related to the helicase subunit of the Holliday junction resolvase	II.B.8	
RSc2335	RS01207				-0.30	0.03			1.13	0.01	TRANSMEMBRANE LIPOPROTEIN	V.I.C	
RSc2336	RS01206				-0.67	0.00	-0.66	0.01		1.15	0.00	SIGNAL PEPTIDE PERIPLASMIC CARRIER PROTEIN	I.V.D
RSc2337	RS01205										TRANSMEMBRANE CELL DIVISION PROTEIN FTSK	I.V.A	
RSc2338	RS01204		0.38	0.01	-0.51	0.02					OXIDOREDUCTASE THIOREDOXIN REDUCTASE	I.F.2	
RSc2339	RS01203										CONSERVED HYPOTHETICAL PROTEIN	V.I.C	
RSc2340	RS01202						-0.86	0.03			TRANSMEMBRANE	V.I.C	
RSc2341	RS01201				-0.36	0.02					TRANSCRIPTION REGULATOR NITROGEN REGULATORY PROTEIN P-II	I.A.18	
RSc2342	RS01200		0.52	0.01					1.01	0.00	COG2226, Methylase involved in ubiquinone/menaquinone biosynthesis	V.I.B	
RSc2343	RS01199										SIGNAL PEPTIDE NH3-DEPENDENT NAD+ SYNTHETASE	I.B.9	
RSc2344	RS01198										CONSERVED HYPOTHETICAL PROTEIN	V.I.C	
RSc2345	RS01197										INORGANIC PYROPHOSPHATASE	I.F	
RSc2346	RS01196										OXIDOREDUCTASE ALDEHYDE DEHYDROGENASE	I.H	
RSc2347	RS01195		0.44	0.05					1.04	0.03	OXIDOREDUCTASE TOLUENESULFONATE ZINC-INDEPENDENT ALCOHOL DEHYDROGENASE	I.H.1	
RSc2348	RS01194						-0.72	0.01	-0.83	0.04		TRANSMEMBRANE PERMEASE	I.V.D
RSc2349	RS01193										SIGNAL PEPTIDE	V.I.C	
RSc2350	RS01192										OXIDOREDUCTASE CYTOCHROME B	I.G	
RSc2351	RS01191										PROTEIN PORPHYRIN BIOSYNTHESIS	I.B.4	
RSc2352	RS01190		0.46	0.02	-0.36	0.00	0.59	0.01	1.00	0.01	TRANSMEMBRANE BIFUNCTIONAL PROTEIN: UROPORPHYRIN-III C-METHYLTRANSFERASE	I.B.4	
RSc2353	RS01189		0.51	0.02							PORPHOBILINOGEN DEAMINASE	I.B.4	
RSc2354	RS01188										PHOSPHOENOLPYRUVATE CARBOXYLASE	I.H	
RSc2355	RS01187				-4.01	0.00	3.95	0.00	2.61	0.00		HYPOTHETICAL PROTEIN	V.I.D
RSc2356	RS01186										CONSERVED HYPOTHETICAL PROTEIN	V.I.C	
RSc2357	RS01185				-1.02	0.00	-0.75	0.00			TRANSCRIPTION REGULATOR RNA POLYMERASE SIGMA-E FACTOR SIGMA-24	I.E.1	
RSc2358	RS01184										TRANSMEMBRANE	V.I.C	
RSc2359	RS01183										ARGININOSUCCINATE LYASE	I.A.17	
RSc2360	RS01182										2H PHOSPHOESTERASE (2'-5' RNA LIGASE)	II.B.6	
RSc2361	RS01181		0.80	0.00							BIODEGRADATIVE ARGININE DECARBOXYLASE	I.I.3	
RSc2362	RS01180				-0.25	0.02	0.21	0.03			DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE	I.F.2	
RSc2363	RS01179										FDHD PROTEIN HOMOLOG	I.H.2	
RSc2364	RS01178										SUPEROXIDE DISMUTASE CU-ZN PRECURSOR	I.V.G.4	
RSc2365	RS01177										SIGNAL PEPTIDE	V.I.D	
RSc2366	RS01176										TRANSMEMBRANE COG2864, Cytochrome B subunit of formate dehydrogenase	I	
RSc2367	RS01175										lipoprotein	V.I.C	
RSc2368	RS01174		-0.34	0.03							OXIDOREDUCTASE FORMATE DEHYDROGENASE (IRON-SULFUR SUBUNIT)	I.H.2	
RSc2369	RS01173										OXIDOREDUCTASE FORMATE DEHYDROGENASE (LARGE SUBUNIT)	I.H.2	
RSc2370	RS01172		1.66	0.02	-2.69	0.00	-2.17	0.01	0.77	0.01	TRANSMEMBRANE	V.I.D	
RSc2371	RS01171				-0.68	0.02					CONSERVED HYPOTHETICAL PROTEIN	V.I.C	
RSc2372	RS01170				-2.94	0.00	2.65	0.00	4.70	0.00		FERREDOXIN	I
RSc2373	RS01168				-0.63	0.00					PROLINE RICH PROTEIN	V.I.C	
RSc2374	RS01167				-0.42	0.02					CONSERVED HYPOTHETICAL PROTEIN	V.I.C	
RSc2375	RS01166										MRP ATPase involved in chromosome partitioning	I.V.A	
RSc2376	RS01165				-0.43	0.00					TRANSMEMBRANE COG2885, Outer membrane protein and related peptidoglycan-associated lipoprotein	III.B.2	
RSc2377	RS01164		0.63	0.04	-0.42	0.00					METHIONYL-tRNA SYNTHETASE	III.D.1	
RSc2378	RS01163		0.41	0.05	-0.54	0.01					LIPOPROTEIN	V.I.C	
RSc2379	RS02766		0.55	0.03	-0.44	0.03					COG0729, Outer membrane protein	III.B.2	
RSc2380	RS02765										CONSERVED HYPOTHETICAL PROTEIN	V.I.C	
RSc2381	RS02764				-0.24	0.02	1.26	0.00	1.59	0.01	CONSERVED HYPOTHETICAL PROTEIN	V.I.C	
RSc2382	RS02763		0.57	0.05			0.46	0.04			PANTOATE-BETA-ALANINE LIGASE	I.B.11	
RSc2383	RS02761				-0.33	0.00					CONSERVED HYPOTHETICAL PROTEIN	V.I.C	
RSc2384	RS02760								1.12	0.00	PARTITION-RELATED PROTEIN	V.B	
RSc2385	RS02759								0.56	0.00	COBYRIC ACID SYNTHASE	I.B.3	

RSc2391	RS02758			-0.58	0.00				cobP	COBALAMIN BIOSYNTHESIS BIFUNCTIONAL PROTEIN: COBINAMIDE KINASE AII.B.3	
RSc2392	RS02743								cobD	TRANSMEMBRANE COBALAMIN BIOSYNTHESIS PROTEIN COBD	
RSc2393	RS02729		1.03	0.04					cobC	COBALAMIN BIOSYNTHESIS PROTEIN PYRIDOXAL-PHOSPHATE-DEPENDENT	
RSc2394	RS02728					-0.61	0.03			ABC TRANSPORTER ABC-TYPE TRANSPORTER, PERIPLASMIC COMPONENT	
RSc2395	RS02727								gpmB	COG0406, Fructose-2,6-bisphosphatase	
RSc2396	RS02726		0.90	0.00			0.87	0.04	cobS	TRANSMEMBRANE COBALAMIN 5'-PHOSPHATE SYNTHASE EC 2.---	
RSc2397	RS02725								cobU	TRANSMEMBRANE NICOTINATE-NUCLEOTIDE--DIMETHYLBENZIMIDAZOLE PHC	
RSc2398	RS02720				0.79	0.00	1.07	0.03		ABC TRANSPORTER ATP-BINDING PROTEIN	
RSc2399	RS02719									ABC TRANSPORTER TRANSMEMBRANE PROTEIN	
RSc2400	RS02718		1.23	0.05						TONB-DEPENDENT RECEPTOR PROTEIN	
RSc2401	RS02717		0.92	0.00		-0.31	0.02			CONSERVED HYPOTHETICAL PROTEIN	
RSc2402	RS02716					-0.46	0.03	0.86	0.01	CONSERVED HYPOTHETICAL PROTEIN	
RSc2403	RS02715					-0.53	0.01	0.83	0.00	CONSERVED HYPOTHETICAL PROTEIN	
RSc2404	RS05747		0.32	0.02		-0.33	0.02			CONSERVED HYPOTHETICAL PROTEIN	
RSc2406	RS02787					-1.60	0.00	-1.62	0.00	SIGNAL PEPTIDE HYPOTHETICAL	
RSc2407	RS05754					-0.60	0.00		ISRso14	ISRso14-TRANSPOSASE ORFA	
RSc2410	RS02708					-0.75	0.00			HYPOTHETICAL PROTEIN	
RSc2411	RS02707		0.27	0.04		-0.28	0.04	0.68	0.05	TRANSMEMBRANE PROLIPOPROTEIN DIACYLGLYCERYL TRANSFERASE	
RSc2412	RS02706					-0.60	0.00	-1.37	0.01	TRANSCRIPTION REGULATOR	
RSc2413	RS02702								ivd	DIHYDROXY-ACID DEHYDRATASE	
RSc2414	RS02701		0.45	0.02		-0.38	0.02	1.05	0.00	HYPOTHETICAL PROTEIN	
RSc2415	RS02700					-0.35	0.01	1.35	0.02	DNA POLYMERASE III (CHI SUBUNIT)	
RSc2416	RS02698		0.76	0.01		-0.37	0.02		pepA	CYTOSOL AMINOPEPTIDASE	
RSc2417	RS02697		0.76	0.05						TRANSMEMBRANE COG0795, Permease	
RSc2418	RS02695					-0.67	0.02			TRANSMEMBRANE COG0795, Permease	
RSc2419	RS02694									CONSERVED HYPOTHETICAL PROTEIN	
RSc2420	RS02693								hpaF	5-CARBOXYMETHYL-2-HYDROXYMUCONATE DELTA-ISOMERASE	
RSc2421	RS02692		0.89	0.02		0.58	0.03	0.60	0.00	UROPORPHYRINOGEN-III C-METHYLTRANSFERASE	
RSc2422	RS02690		0.92	0.00		0.68	0.00	-1.36	0.04	SULFATE ADENYLYLTRANSFERASE SUBUNIT 1	
RSc2423	RS02689							-0.78	0.00	SULFATE ADENYLYLTRANSFERASE SUBUNIT 2	
RSc2424	RS02687							0.88	0.00	5' ADENYLYLSULFATE APS REDUCTASE	
RSc2425	RS02684					1.07	0.00		cysH	CONSERVED HYPOTHETICAL PROTEIN	
RSc2426	RS02683		0.35	0.02				-1.50	0.00	OXIDOREDUCTASE SULFITE REDUCTASE	
RSc2427	RS02682					-0.35	0.01		cysI1	TRANSMEMBRANE COG0730, Permease	
RSc2428	RS02680					0.52	0.00	-0.46	0.05	TRANSCRIPTION REGULATOR CYS REGULON TRANSCRIPTIONAL ACTIVATOR	
RSc2429	RS02679		0.59	0.02		-0.46	0.00		cysB2	ABC TRANSPORTER AMINO ACID-BINDING PERIPLASMIC PROTEIN (PBP)	
RSc2430	RS02678									OXIDOREDUCTASE COG2084, 3-hydroxyisobutyrate dehydrogenase and related bet	
RSc2431	RS02676									TRANSCRIPTION REGULATOR	
RSc2432	RS02675					-0.60	0.00	-0.76	0.03	TRANSMEMBRANE COG0038, Chloride channel protein	
RSc2433	RS02671					-0.72	0.03	-0.98	0.02	TRANSMEMBRANE SIGNAL TRANSDUCTION PROTEIN GGDEF DOMAIN	
RSc2434	RS02670		0.55	0.00						COG0451, Nucleoside-diphosphate-sugar epimerase	
RSc2435	RS02668		0.75	0.00		-0.50	0.01		argM	OXIDOREDUCTASE REDUCTASE	
RSc2436	RS02667		1.40	0.00		-0.59	0.00	-0.60	0.00	SUCCINYLORNITHINE TRANSAMINASE AND ACETYLORNITHINE AMINOTRANS	
RSc2437	RS02666		0.92	0.00		-0.41	0.03			ACETYLTRANSFERASE	
RSc2438	RS02664		0.90	0.00		-0.44	0.04			ABC TRANSPORTER AMINO ACID ATP-BINDING PROTEIN	
RSc2439	RS02663		0.78	0.01						ABC TRANSPORTER AMINO ACID ATP-BINDING PROTEIN	
RSc2440	RS01355		0.72	0.00				-1.34	0.01	ABC TRANSPORTER AMINO-ACID TRANSMEMBRANE PROTEIN	
RSc2441	RS01353		0.88	0.01					livH2	ABC TRANSPORTER AMINO-ACID TRANSMEMBRANE PROTEIN	
RSc2442	RS01352		1.58	0.01						ABC TRANSPORTER AMINO ACID-BINDING PERIPLASMIC PROTEIN	
RSc2443	RS01351					-0.60	0.00		lytB	LYTB PROTEIN	
RSc2444	RS01350					-0.30	0.01		fkpB	FKBP-TYPE 16 KDA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE	
RSc2445	RS01349					-0.32	0.00	-0.35	0.00	DNA REPAIR PROTEIN RADC	
RSc2446	RS01348					-0.18	0.03	-0.24	0.01	50S RIBOSOMAL SUBUNIT PROTEIN L28	
RSc2447	RS01159		0.69	0.04				-0.72	0.01	50S RIBOSOMAL SUBUNIT PROTEIN L33	
RSc2448	RS01158								rpmG	OXIDOREDUCTASE L-ASPARTATE OXIDASE (QUINOLINATE SYNTHETASE B)	
RSc2449	RS01157					-0.35	0.00		nadB1	NICOTINATE-NUCLEOTIDE PYROPHOSPHORYLASE (CARBOXYLATING) QUINO	
RSc2450	RS01156					-0.58	0.01		nadA	QUINOLINATE SYNTHETASE A	
RSc2451	RS01155					-0.40	0.01			OXIDOREDUCTASE STEAROYL-COA DESATURASE	
RSc2452	RS01154					-0.33	0.00			TRANSMEMBRANE COG3264, Small-conductance mechanosensitive channel	
RSc2453	RS01153					-0.48	0.04			ENDONUCLEASE	
RSc2454	RS01151		0.48	0.04					purN	COG0144, tRNA and rRNA cytosine-C5-methylase	
RSc2455	RS01150					-0.61	0.00			PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE	
RSc2456	RS01149					-0.22	0.05		vsrC	TRANSCRIPTION REGULATOR RESPONSE REGULATOR VSRC	
RSc2457	RS01148					-0.34	0.00		vsrB	TRANSCRIPTION REGULATOR COMPOSITE TWO-COMPONENT REGULATORY	
RSc2458	RS01147								ribF	RIBOFLAVIN BIOSYNTHESIS PROTEIN	
RSc2459	RS01146								ileS	ISOLEUCYL-TRNA SYNTHETASE	
RSc2460	RS01145					-0.64	0.01		ispA	LIPOPROTEIN SIGNAL PEPTIDASE	
RSc2461	RS01144					-0.46	0.01			TRANSMEMBRANE	
RSc2462	RS01143					-0.52	0.00		dfp	DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN FLAVOPROTEIN	
RSc2463	RS01142									OXIDOREDUCTASE COG2141, Coenzyme F420-dependent N5,N10-methylene tetra	
RSc2464	RS01141								dut	DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE DUTPASE	
RSc2465	RS01140								ctpA	ATP-DEPENDENT PROTEASE (ATP-BINDING SPECIFICITY SUBUNIT)	
RSc2466	RS01139					-0.71	0.00	-0.74	0.00	CONSERVED HYPOTHETICAL PROTEIN	
RSc2467	RS01138					-1.43	0.00		cspD	TRANSCRIPTION REGULATOR COLD SHOCK-LIKE PROTEIN CSPD	
RSc2468	RS01137					-0.98	0.02	-1.11	0.02	TRANSMEMBRANE	
RSc2469	RS01136									TRANSMEMBRANE	
RSc2470	RS01135									HYPOTHETICAL PROTEIN	
RSc2471	RS01134									RHS-RELATED PROTEIN	
RSc2472	RS01133					-0.39	0.04			HYPOTHETICAL PROTEIN	
RSc2473	RS01132					-0.30	0.03	-0.66	0.02	TRANSMEMBRANE	
RSc2474	RS01131					-0.38	0.03			HYPOTHETICAL PROTEIN	
RSc2475	RS01130									HYPOTHETICAL PROTEIN	
RSc2476	RS01129									HYPOTHETICAL PROTEIN	
RSc2477	RS01127									BACTERIOPHAGE-RELATED PROTEIN	
RSc2478	RS01126					-0.36	0.00			PROPHAGE PROTEIN	
RSc2479	RS01124									TRANSMEMBRANE PROPHAGE PROTEIN	
RSc2480	RS01121					-0.29	0.01			BACTERIOPHAGE-RELATED PROTEIN	
RSc2481	RS01119					-0.22	0.00			CONSERVED HYPOTHETICAL PROTEIN	
RSc2482	RS01114		-0.18	0.02		-0.48	0.00			CONSERVED HYPOTHETICAL PROTEIN	
RSc2483	RS01112									CONSERVED HYPOTHETICAL PROTEIN	
RSc2484	RS01111									CONSERVED HYPOTHETICAL PROTEIN	
RSc2485	RS01110					-0.83	0.00			HYPOTHETICAL PROTEIN	
RSc2486	RS01109							-0.72	0.00	HYPOTHETICAL PROTEIN	
RSc2487	RS05745					-0.43	0.01	-1.13	0.02	CONSERVED HYPOTHETICAL PROTEIN	
RSc2488	RS05744					0.74	0.00			HYPOTHETICAL PROTEIN	
RSc2489	RS01107		0.53	0.02		-0.47	0.00			HYPOTHETICAL PROTEIN	
RSc2490	RS01106		0.33	0.01		-0.20	0.01	0.45	0.01	INTEGRASE	
RSc2491	RS01105							-0.77	0.01	OXIDOREDUCTASE ISOCITRATE DEHYDROGENASE [NADP]	
RSc2492	RS01104								icd	SIGNAL PEPTIDE	
RSc2493	RS01103									TRANSMEMBRANE	
RSc2494	RS01102		0.41	0.02		-0.41	0.01			SIGNAL PEPTIDE COG1858, Cytochrome c peroxidase	
RSc2495	RS01101		0.46	0.03		-0.61	0.01	0.12	0.02	SIGNAL PEPTIDE	
RSc2496	RS01100					-0.74	0.00			ARYLSULFATASE PRECURSOR (ARYL-SULFATE SULPHOHYDROLASE)	
RSc2497	RS01099					-0.34	0.00			SIGNAL PEPTIDE	
RSc2498	RS01098					-0.41	0.02			TRANSCRIPTION REGULATOR	
RSc2499	RS01097									TRANSCRIPTION REGULATOR	
RSc2500	RS01095					-0.88	0.00	-1.02	0.01	MULTIDRUG RESISTANCE PROTEIN	
RSc2501	RS01094								0.21	0.01	TRANSMEMBRANE
RSc2502	RS01093									PUTATIVE GAMMA-GLUTAMYLTRANSFERASE	
RSc2503	RS01092		1.02	0.00						TRANSMEMBRANE	
RSc2504	RS01091									TRANSMEMBRANE COG2321, Predicted metalloprotease	
RSc2505	RS05743					-0.54	0.05			OXIDOREDUCTASE COG1028, Dehydrogenases with different specificities (related t	
										TRANSCRIPTION REGULATOR	

RSc2506	RS01080						ogt	METHYLATED-DNA--PROTEIN-CYSTEINE METHYLTRANSFERASE	II.B.8
RSc2507	RS01075							TRANSMEMBRANE	VI.C
RSc2508	RS01074					0.44 0.05		CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2509	RS01073					-1.53 0.00		HYPOTHETICAL PROTEIN	VI.D
RSc2510	RS01072					-1.16 0.00		SIGNAL PEPTIDE COG1638, TRAP-type C4-dicarboxylate transport system, periplasmic	IV.D.3
RSc2511	RS01071					-0.81 0.03		SIGNAL PEPTIDE	VI.B
RSc2512	RS01070							SIGNAL PEPTIDE CYCLOHEXADIENYL DEHYDRATASE PRECURSOR	IA.8
RSc2513	RS01069							HYPOTHETICAL PROTEIN	VI.D
RSc2514	RS01068							SIGNAL PEPTIDE	VI.C
RSc2515	RS01067					-0.71 0.00		COG2206, HD-GYP domain	VI.A
RSc2516	RS01066					-0.99 0.00		TRANSMEMBRANE ABC TYPE TRANSPORTER : PERIPLASMIC GLYCINE BETAIN	IV.D
RSc2517	RS01065					-0.53 0.04		TRANSMEMBRANE CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2518	RS01064					-1.25 0.01		TRANSMEMBRANE COG2610, H ⁺ /gluconate symporter and related permeases	IV.D.3
RSc2519	RS01063					-1.45 0.00		HYPOTHETICAL PROTEIN	VI.D
RSc2520	RS01062							CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2521	RS01061							DNA-BINDING PROTEIN HU-BETA (NS1) (HU-1)	II.C.1
RSc2522	RS01060					0.90 0.00		CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2523	RS01059					-1.47 0.00		TRANSMEMBRANE	VI.C
RSc2524	RS01058					-0.62 0.00		TRANSMEMBRANE COG1994, Zn-dependent protease	II.A.4
RSc2525	RS01057					-0.70 0.01		HYPOTHETICAL PROTEIN	VI.B
RSc2526	RS01055					-1.79 0.00		SUPEROXIDE DISMUTASE [FE]	IV.G.4
RSc2527	RS01054					0.88 0.00		EXODEOXYRIBONUCLEASE VII LARGE SUBUNIT	II.A.1
RSc2528	RS01053					0.89 0.02		TRANSMEMBRANE BIOPOLYMER TRANSPORT EXBB-LIKE PROTEIN	IV.D
RSc2529	RS01052					-0.60 0.01		TRANSMEMBRANE BIOPOLYMER TRANSPORT EXBD-RELATED PROTEIN	IV.D
RSc2530	RS01051					-0.52 0.02		TETRAACYLDISACCHARIDE 4'-KINASE	II.B.2
RSc2531	RS05763					-0.41 0.00		CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2532	RS05764					-0.41 0.00		3-DEOXY-MANNO-OCTULOSONATE (CMP-KDO SYNTHETASE)(CKS)	III.A.1
RSc2533	RS05765					-0.45 0.00		ADENYLATE KINASE (ATP-AMP TRANSPHOSPHORYLASE)	ID.2
RSc2534	RS05766					-0.20 0.01		OXIDOREDUCTASE 3-HYDROXYACYL-CoA DEHYDROGENASE TYPE II	II.1
RSc2535	RS00706							TRANSCRIPTION REGULATOR	VI.A
RSc2536	RS00704					-1.71 0.00		OXIDOREDUCTASE TRANSMEMBRANE ALDEHYDE DEHYDROGENASE	II.4
RSc2537	RS00708					-0.61 0.00		TRANSCRIPTION REGULATOR TRANSCRIPTION REGULATOR	VI.A
RSc2538	RS00712							TRANSMEMBRANE COG0385, Na ⁺ -dependent transporter	IV.D
RSc2539	RS00715					-0.53 0.00		N-ACETYLMURAMOYL-L-ALANINE AMIDASE AMIC PRECURSOR	III.B.3
RSc2540	RS00716							COG0802, ATPase or kinase	VI.C
RSc2541	RS00718							COG1600, Uncharacterized Fe-S protein	I.H
RSc2542	RS00721					-0.50 0.01		TRANSMEMBRANE LIPOPROTEIN	VI.C
RSc2543	RS00722					-0.51 0.00		Methylated-DNA--protein-cysteine methyltransferase	II.B.8
RSc2544	RS00723					-0.41 0.05		INTEGRASE/RECOMBINASE	II.B.8
RSc2545	RS00724							CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2546	RS00725							TRANSMEMBRANE	VI.C
RSc2547	RS00726					-0.73 0.00		TRANSMEMBRANE ACYL-HOMOSERINE LACTONE ACYLASE	II
RSc2548	RS00727					0.38 0.01		TRANSMEMBRANE INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE I.F.12	IF.12
RSc2549	RS00728					-0.52 0.00		CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2550	RS00729					0.40 0.00		OXIDOREDUCTASE UDP-N-ACETYLENOLPYRUVOYLGLUCOSAMINE REDUCTASE	III.B.3
RSc2551	RS00730							COG1752, Predicted esterase of the alpha-beta hydrolase superfamily	I
RSc2552	RS00731					-0.30 0.05		CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2553	RS00732							ARGININOSUCCINATE SYNTHASE	IA.17
RSc2554	RS00733					0.57 0.02		ORNITHINE CARBAMOYLTRANSFERASE	IA.17
RSc2555	RS00734					-0.45 0.03		CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2556	RS00735					-0.44 0.00		30S RIBOSOMAL SUBUNIT PROTEIN S20	III.C.2
RSc2557	RS00736					-0.52 0.04		TRANSMEMBRANE	VI.C
RSc2558	RS00740							CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2559	RS00742							TRANSMEMBRANE DEDA PROTEIN	VI.C
RSc2560	RS00743					-0.70 0.02		TRANSCRIPTION REGULATOR	VI.A
RSc2561	RS00746					-1.31 0.01		LIPOPROTEIN	VI.C
RSc2562	RS00750							TRANSMEMBRANE	VI.C
RSc2563	RS00753					0.61 0.01		DNA MISMATCH REPAIR PROTEIN	II.B.8
RSc2564	RS00755							TRNA DELTA2-ISOPENTENYLPIRROPHOSPHATE TRANSFERASE	II.D.1
RSc2565	RS00758					0.22 0.02		ACETYLTRANSFERASE	I
RSc2566	RS00760							METHYLATED-DNA--PROTEIN-CYSTEINE METHYLTRANSFERASE	II.B.8
RSc2567	RS00763					-1.14 0.00		CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2568	RS00764					-0.42 0.00		ALKYLATED DNA REPAIR	II.B.8
RSc2569	RS00766					-0.56 0.01		DNA-3-METHYLADENINE GLYCOSYLASE	II.B.8
RSc2570	RS00768					0.83 0.03		TRANSCRIPTION REGULATOR ADA REGULATORY PROTEIN OF ADAPTATIVE R	II.B.8
RSc2571	RS00770							CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2572	RS00771							LIPOPROTEIN	VI.D
RSc2573	RS00774					-0.43 0.00		ISRs015-TRANSPOSASE	VI.A
RSc2574	RS00781							CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2575	RS00938							TRANSMEMBRANE CONJUGAL TRANSFER PROTEIN TRBI	VI.B
RSc2576	RS00782							CONJUGAL TRANSFER LIPOPROTEIN TRBG	VI.B
RSc2577	RS00783					-0.56 0.05		TRANSMEMBRANE CONJUGAL TRANSFER PROTEIN TRBF	VI.B
RSc2578	RS00784							TRANSMEMBRANE CONJUGAL TRANSFER PROTEIN TRBL	VI.B
RSc2579	RS00786							LIPOPROTEIN	VI.C
RSc2580	RS00788							SIGNAL PEPTIDE CONJUGAL TRANSFER PROTEIN TRBJ	VI.B
RSc2581	RS00789							CONJUGAL TRANSFER PROTEIN TRBE	VI.B
RSc2582	RS00791							TRANSMEMBRANE CONJUGAL TRANSFER PROTEIN TRBD	VI.B
RSc2583	RS00793							TRANSMEMBRANE CONJUGAL TRANSFER PROTEIN TRBC	VI.B
RSc2584	RS00795							CONJUGAL TRANSFER PROTEIN TRBB	VI.B
RSc2585	RS00797							HYPOTHETICAL/UNKNOWN	VI.C
RSc2586	RS00798					0.82 0.02		TRANSMEMBRANE Plasmid Conjugation protein TraG	VI.B
RSc2587	RS00835					-0.55 0.00		LIPOPROTEIN	VI.C
RSc2588	RS00836					-0.56 0.00		TRANSCRIPTION REGULATOR PLASMID REPLICATION REGULATORY PROTEIN V.B	VI.B
RSc2589	RS00837					-0.65 0.00		LIMONENE-1,2-EPOXIDE HYDROLASE	II.4
RSc2590	RS00838					-0.50 0.00		LIMONENE-1,2-EPOXIDE HYDROLASE	II.4
RSc2591	RS00839					-0.46 0.00		TRANSCRIPTION REGULATOR TRANSCRIPTIONAL REGULATOR	VI.A
RSc2592	RS00840							CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2593	RS00841							COG2272, Carboxylesterase type B	VI.C
RSc2594	RS00842							GLUTATHIONE-S-TRANSFERASE	II.B.7
RSc2595	RS00843							CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2596	RS00844					0.77 0.02		COG1335, Amidase related to nicotinamidase	I
RSc2597	RS00845					-0.29 0.01		OXIDOREDUCTASE COG1028, Dehydrogenases with different specificities (related to	VI.A
RSc2598	RS00846							TRANSCRIPTION REGULATOR	VI.A
RSc2599	RS00847					-1.02 0.03		HYPOTHETICAL PROTEIN	VI.B
RSc2600	RS00848					-0.48 0.00		HYPOTHETICAL PROTEIN	VI.B
RSc2601	RS00849							COG3843, Type IV secretory pathway VirD2 (relaxase) - related protein	VI.B
RSc2602	RS00850							TRANSMEMBRANE CONJUGAL TRANSFER PROTEIN TRAF	VI.B
RSc2603	RS00851							CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2604	RS00852							CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2605	RS00853					-0.69 0.05		PARTITION PROTEIN	VI.B
RSc2606	RS00854							REPLICATION INITIATION REPA - LIKE PROTEIN	VI.B
RSc2607	RS00855					-0.55 0.05		CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2608	RS00857					-0.28 0.03		CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2609	RS00858					-0.48 0.04		lipoprotein	VI.B
RSc2610	RS00859							TRANSCRIPTION REGULATOR	VI.A
RSc2611	RS00860					-0.49 0.01		CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2612	RS00912					-0.54 0.04		TRANSMEMBRANE	VI.C
RSc2613	RS00913							CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2614	RS00916							CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2615	RS00917					-0.56 0.03		CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2616	RS00918					-0.75 0.00		CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSc2617	RS00919					-1.29 0.01		CONSERVED HYPOTHETICAL PROTEIN	VI.C

RSc2842	RS00263	0,43	0,03	-0,52	0,00			-0,70	0,00	ddIB	D-ALANINE--D-ALANINE LIGASE B	III.B.3
RSc2843	RS00262									murC	UDP-N-ACETYLMURAMATE--ALANINE LIGASE	III.B.3
RSc2844	RS00261	0,32	0,05							murG	UDP-N-ACETYLMURAMATE--ALANINE LIGASE	III.B.3
RSc2845	RS00260			-0,47	0,00			-0,68	0,03	ftsW	TRANSMEMBRANE CELL DIVISION PROTEIN FTSW	IV.A
RSc2846	RS00259							-1,34	0,00	murD	UDP-N-ACETYLMURAMATE--D-GLUTAMATE LIGASE	III.B.3
RSc2847	RS00258	0,55	0,00	-0,35	0,00			-1,21	0,00	mraY	TRANSMEMBRANE HOSPHO-N-ACETYLMURAMATE--D-GLUTAMATE--D-AMINOPEPTIDE-TRANSFERASE	III.B.3
RSc2848	RS00257									murF	UDP-N-ACETYLMURAMATE--D-GLUTAMATE--D-AMINOPEPTIDE-TRANSFERASE	III.B.3
RSc2849	RS00256									murE	UDP-N-ACETYLMURAMATE--D-GLUTAMATE--D-AMINOPEPTIDE-TRANSFERASE	III.B.3
RSc2850	RS00255	0,48	0,04	-0,41	0,02			-1,21	0,00	ftsI	TRANSMEMBRANE PENICILLIN-BINDING PROTEIN 3 PRECURSOR PBP-3	IV.A
RSc2851	RS00254	0,34	0,04	-0,43	0,01			-0,75	0,03	ftsL	TRANSMEMBRANE CELL DIVISION PROTEIN FTSL	IV.A
RSc2852	RS00253									mraW	COG0275, S-adenosylmethionine-dependent methyltransferase involved in cell envelope	III.B
RSc2853	RS00252			-0,77	0,00						CONSERVED HYPOTHETICAL PROTEIN	VLC
RSc2854	RS00251			-0,46	0,01						COG2941, Ubiquinone biosynthesis protein	I.B.5
RSc2855	RS00250			1,26	0,00	1,80	0,00	0,60	0,05		SIGNAL PEPTIDE OUTER MEMBRANE PORIN PROTEIN	IV.D
RSc2856	RS00249			0,38	0,02	0,88	0,02				TRANSMEMBRANE METABOLITE TRANSPORT PROTEIN	IV.D
RSc2857	RS00248	0,96	0,01	-0,31	0,03					fadD1	LONG-CHAIN-FATTY-ACID--COA LIGASE	I.I.1
RSc2858	RS00247	1,78	0,00	-1,63	0,00			2,80	0,00		ZINC PROTEASE	II.A.4
RSc2859	RS00246	0,66	0,02								OXIDOREDUCTASE COG0243, Anaerobic dehydrogenase, typically selenocysteine-c	I
RSc2860	RS00245			-0,36	0,02					fruR	TRANSCRIPTION REGULATOR TRANSCRIPTION REGULATION REPRESSOR	I.H.8
RSc2861	RS00244					-2,28	0,02			fruB	MULTIPHOSPHORYL TRANSFER PROTEIN MTP	I.H.8
RSc2862	RS00243									fruK	1-PHOSPHOFRUCTOKINASE	I.H.8
RSc2863	RS00242									fruA	TRANSMEMBRANE PTS SYSTEM, FRUCTOSE-SPECIFIC IIBC COMPONENT (EIIIB IV.D.3	IV.D.3
RSc2864	RS00241	0,60	0,01	-0,52	0,00	0,57	0,04				ABC TRANSPORTER ABC-type branched-chain amino acid transport systems, peripl	IV.D.2
RSc2865	RS00240										HYPOTHETICAL PROTEIN	VI.D
RSc2866	RS00239			-0,36	0,00					dppF1	ABC TRANSPORTER OLIGOPEPTIDE ATP-BINDING PROTEIN	IV.D.7
RSc2867	RS00238	0,53	0,03	-0,38	0,02	0,52	0,02			dppD1	ABC TRANSPORTER OLIGOPEPTIDE ATP-BINDING PROTEIN	IV.D.7
RSc2868	RS00237			-0,23	0,03					dppC1	TRANSMEMBRANE DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN	IV.D.7
RSc2869	RS00236									dppB1	ABC TRANSPORTER TRANSMEMBRANE PROTEIN (DIPEPTIDE TRANSPORT SY	IV.D.7
RSc2870	RS00235			-0,52	0,00					dppA1	PERIPLASMIC DIPEPTIDE TRANSPORT PROTEIN	IV.D.7
RSc2871	RS00234									hipO	HIPPURATE HYDROLASE	I.I
RSc2872	RS00233									paaF	ENOYL-COA HYDRATASE	I.I.4
RSc2873	RS00232			-0,59	0,00					paaG1	ENOYL-COA HYDRATASE	I.I.4
RSc2874	RS00231			-0,31	0,03	-0,70	0,01			paal	PHENYLACETIC ACID DEGRADATION PROTEIN	I.I.4
RSc2875	RS00230	0,53	0,02	-0,36	0,00					paak	PHENYLACETYL-CoA-LIGASE	I.I.4
RSc2876	RS00229	0,51	0,04								TRANSMEMBRANE MEMBRANE-BOUND LYTIC MUREIN TRANSGLYCOSYLASE	III.B.3
RSc2877	RS00228										TRANSMEMBRANE	VLC
RSc2878	RS00227					0,59	0,04			apaG	CONSERVED HYPOTHETICAL PROTEIN	VLC
RSc2879	RS00226	0,57	0,01	-0,21	0,02					rpe	RIBULOSE-PHOSPHATE 3-EPIMERASE	I.F.19
RSc2880	RS00225			-0,47	0,01					gph	PHOSPHOGLYCOLATE PHOSPHATASE	I.I.4
RSc2881	RS00224			0,86	0,00	0,69	0,01			trpE	ANTHRANILATE SYNTHASE COMPONENT I	I.A.6
RSc2882	RS00223			1,19	0,00	0,96	0,01			trpG	PANTHRANILATE SYNTHASE COMPONENT II (GLUTAMINE AMIDO-TRANSFERASE	I.A.6
RSc2883	RS00222			1,17	0,00	0,96	0,00				SIGNAL PEPTIDE	VLC
RSc2884	RS00221	-0,78	0,00	1,13	0,00					trpD1	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE	I.A.6
RSc2885	RS00220			1,05	0,00	2,84	0,00			trpC1	INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE	I.A.6
RSc2886	RS00219			0,98	0,00	1,04	0,01				CONSERVED HYPOTHETICAL PROTEIN	VLC
RSc2887	RS00218	-1,09	0,05	0,31	0,03	0,85	0,00			ung	URACIL-DNA GLYCOSYLASE	II.B.8
RSc2888	RS00217					-1,11	0,00	-0,37	0,01		HYPOTHETICAL PROTEIN	VI.B
RSc2889	RS00216					-0,65	0,05				TRANSMEMBRANE	VLC
RSc2890	RS00215	0,64	0,00	-0,48	0,00						COG3975, Predicted protease with the C-terminal PDZ domain	II.A.4
RSc2891	RS00214	1,14	0,02							dsbC	OXIDOREDUCTASE COG0604, NADPH:quinone reductase and related Zn-dependen	I
RSc2892	RS00213	0,26	0,04	-0,55	0,00			-0,44	0,00		THIOL-DISULFIDE INTERCHANGE PROTEIN	II.B.7
RSc2893	RS00212	0,68	0,02			0,89	0,02				OXIDOREDUCTASE	I
RSc2894	RS00211	-0,62	0,05								TRANSMEMBRANE	VI.D
RSc2895	RS00210	-0,31	0,05	0,47	0,02						SIGNAL PEPTIDE	VI.D
RSc2896	RS00209										CONSERVED HYPOTHETICAL PROTEIN	VLC
RSc2897	RS00208	-3,14	0,01	-5,22	0,00	4,40	0,03	3,50	0,00		CONSERVED HYPOTHETICAL PROTEIN	VLC
RSc2898	RS00207	0,64	0,02					-0,27	0,00		COG0102, GTPase, probable translation factor	II.B.7
RSc2899	RS00206			1,01	0,00	1,50	0,00				TRANSMEMBRANE	VLC
RSc2900	RS00205			-0,45	0,02					hemA	OXIDOREDUCTASE GLUTAMYL-TRNA REDUCTASE	I.B.4
RSc2901	RS00204	0,79	0,02	-0,54	0,01			0,65	0,01	prfA	PEPTIDE CHAIN RELEASE FACTOR 1 RF-1	II.B.7
RSc2902	RS00203			-0,54	0,01						LIPOPROTEIN	VLC
RSc2903	RS00202	0,87	0,01	-0,54	0,00					hemK	Methylase of polypeptide chain release factors	II.B.7
RSc2904	RS00201	0,56	0,01			0,53	0,05				CONSERVED HYPOTHETICAL PROTEIN	VLC
RSc2905	RS00200	0,64	0,04							ubiX	3-OCTAPRENYL-4-HYDROXYBENZOATE CARBOXY-LYASE	I
RSc2906	RS00199			-0,89	0,00	0,99	0,00	2,10	0,00		TRANSMEMBRANE	VLD
RSc2907	RS00198			-0,53	0,01						SIGNAL PEPTIDE	VLC
RSc2908	RS00197			-0,53	0,01					mdoG	SIGNAL PEPTIDE PERIPLASMIC GLUCANS BIOSYNTHESIS	IV.F.2
RSc2909	RS00196			1,13	0,00					mdoH	TRANSMEMBRANE PERIPLASMIC GLUCANS BIOSYNTHESIS PROTEIN	IV.F.2
RSc2910	RS00195			-0,78	0,00	0,49	0,02	2,50	0,00		SIGNAL PEPTIDE	VLC
RSc2911	RS00194			-0,58	0,00	0,80	0,01				CONSERVED HYPOTHETICAL PROTEIN	VLC
RSc2912	RS00193			-0,58	0,01						CONSERVED HYPOTHETICAL PROTEIN	VLC
RSc2913	RS00192	0,57	0,04	-0,51	0,00						ABC TRANSPORTER ATP-BINDING PROTEIN	IV.D
RSc2914	RS00191	0,77	0,00	-0,83	0,00					cyoD1	OXIDOREDUCTASE TRANSMEMBRANE CYTOCHROME O UBIQUINOL OXIDASE	I.H.3
RSc2915	RS00190	0,91	0,00	-0,80	0,00	0,72	0,00	0,68	0,01	cyoC1	OXIDOREDUCTASE TRANSMEMBRANE CYTOCHROME O UBIQUINOL OXIDASE	I.H.3
RSc2916	RS00189	1,20	0,00	-0,71	0,00	2,11	0,00			cyoB1	OXIDOREDUCTASE TRANSMEMBRANE CYTOCHROME O UBIQUINOL OXIDASE	I.H.3
RSc2917	RS00188	0,84	0,02	-0,94	0,01			-0,95	0,00	cyoA1	OXIDOREDUCTASE TRANSMEMBRANE CYTOCHROME O UBIQUINOL OXIDASE	I.H.3
RSc2918	RS00187			-1,38	0,00			-1,08	0,01		TRANSCRIPTION REGULATOR EXTRACYTOPLASMIC FUNCTION SIGMA FACTO	I.E.1
RSc2919	RS00186	0,61	0,01	-1,10	0,00	-1,08	0,01	-3,16	0,01		TRANSMEMBRANE IRON TRANSPORT - SENSORY TRANSDUCTION PROTEIN	IV.D.5
RSc2920	RS00185										SIGNAL PEPTIDE HYDROXAMATE-TYPE FERRISIDEROPHORE RECEPTOR	IV.D.5
RSc2921	RS00184	0,74	0,02	-0,92	0,01					ggI2	GAMMA-GLUTAMYLTRANSEPTIDASE PRECURSOR	I.B.6
RSc2922	RS00183			-0,52	0,05						SIGNAL PEPTIDE OUTER MEMBRANE RECEPTOR	III.B.2
RSc2923	RS00182	1,08	0,00	-0,40	0,02						TRANSCRIPTION REGULATOR TRANSMEMBRANE SENSOR HISTIDINE KINASE	VI.A
RSc2924	RS00181										COG0456, Acetyltransferase	I
RSc2925	RS00180	0,88	0,00					-0,79	0,00	sspB	STRINGENT STARVATION PROTEIN B	I.E.1
RSc2926	RS00179	0,82	0,00							sspA	TRANSCRIPTION MODULATOR PROTEIN	I.E.1
RSc2927	RS00178	0,91	0,03							petC	TRANSMEMBRANE CYTOCHROME C1 PRECURSOR	I.G.1
RSc2928	RS00177									petB	TRANSMEMBRANE CYTOCHROME B SUBUNIT	I.G.1
RSc2929	RS00176									petA	OXIDOREDUCTASE TRANSMEMBRANE UBIQUINOL-CYTOCHROME C REDUCTA	I.G.1
RSc2930	RS00175			-0,60	0,00					mscL	TRANSMEMBRANE LARGE-CONDUCTANCE MECHANOSENSITIVE CHANNEL	IV.D
RSc2931	RS00174										CONSERVED HYPOTHETICAL PROTEIN	VLC
RSc2932	RS00173	0,59	0,00								SIGNAL PEPTIDE HTRA-LIKE SERINE PROTEASE	II.A.4
RSc2933	RS00172			-0,44	0,01						SIGNAL PEPTIDE PORIN	IV.D
RSc2934	RS00171			-0,39	0,00						ABC TRANSPORTER COG1840, ABC-type Fe3+ transport system, periplasmic comp	IV.D.5
RSc2935	RS00170										TRANSCRIPTION REGULATOR RESPONSE REGULATOR	VI.A
RSc2936	RS00169										TRANSCRIPTION REGULATOR TRANSMEMBRANE SENSOR KINASE	VI.A
RSc2937	RS00168										SIGNAL PEPTIDE PERIPLASMIC IRON-BINDING PROTEIN	IV.D.5
RSc2938	RS00167	0,37	0,03								ABC TRANSPORTER TRANSMEMBRANE PROTEIN	IV.D
RSc2939	RS00166			-0,47	0,00						ABC TRANSPORTER ATP-BINDING PROTEIN	IV.D
RSc2940	RS00165	0,47	0,00							tatC	TRANSMEMBRANE SEC-INDEPENDENT PROTEIN TRANSLOCASE PROTEIN TATIV.E.2	IV.E.2
RSc2941	RS00164			-0,57	0,00	-0,56	0,03			tatB	SEC-INDEPENDENT PROTEIN TRANSLOCASE PROTEIN TATB	IV.E.2
RSc2942	RS00163			0,38	0,00					tatA	SIGNAL PEPTIDE SEC-INDEPENDENT PROTEIN TRANSLOCASE PROTEIN TATA	IV.E.2
RSc2943	RS00162	0,40	0,04	-0,47	0,01			-0,25	0,05		TRANSMEMBRANE	VLC
RSc2944	RS00161			-0,45	0,03			-0,88	0,01	hisE	PHOSPHORIBOSYL-ATP PYROPHOSPHATASE	I.A.4
RSc2945	RS00160	0,76	0,01			0,82	0,01	-0,77	0,00	hisI	PHOSPHORIBOSYL-AMP CYCLOHYDROLASE	I.A.4
RSc2946	RS00159	0,65	0,02					-0,66	0,00	hisF	CYCLASE (IMIDAZOLE GLYCEROL PHOSPHATE SYNTHASE - SUBUNIT WITH HIS	I.A.4
RSc2947	RS00158	0,50	0,04							hisA	PHOSPHORIBOSYLFORMIMINO-5-AMINOIMIDAZOLE CARBOXAMIDE RIBOTIDE	I.A.4
RSc2948	RS00157			-0,53	0,03			0,99	0,03	hisH	AMIDOTRANSFERASE (GLUTAMINE AMIDOTRANSFERASE - SUBUNIT WITH HIS	I.A.4
RSc2949	RS00156										TRANSMEMBRANE COG2095, Multiple antibiotic transporter	IV.D
RSc2950	RS00155	0,38	0,01	-0,36	0,04					hisB	OXIDOREDUCTASE IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE	I.A.4
RSc2951	RS00154			0,23	0,03					hisC1	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE	I.A.4
RSc2952	RS00153	0,43	0,00	-0,28	0,05					hisD	OXIDOREDUCTASE HISTIDINOL DEHYDROGENASE	I.A.4
RSc2953	RS04753	0,95	0,00	-0,41	0,00	1,05	0,03	-0,33	0,04	murA	UDP-N-ACETYLMURAMATE--D-GLUCOSAMINE 1-CARBOXYVINYLT	III.B.3

RSc3067	RS00511			-1.04	0.00			-2.05	0.00	TRANSMEMBRANE	V.I.C
RSc3068	RS00512			-0.39	0.01					TRANSMEMBRANE COG0668, Small-conductance mechanosensitive channel	V.I.C
RSc3069	RS00513			-0.70	0.00					TRANSMEMBRANE TRANSPORTER PROTEIN	I.V.D
RSc3070	RS00514			-1.14	0.00					GLUTATHIONE S-TRANSFERASE	I.I.B.7
RSc3071	RS00520					1.11	0.03	1.27	0.00	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc3072	RS00521							2.35	0.00	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc3073	RS00522									HYPOTHETICAL PROTEIN	V.I.D
RSc3074	RS00523									HYPOTHETICAL PROTEIN	V.I.D
RSc3075	RS00524		0.79	0.01		-0.66	0.00			SIGNAL PEPTIDE	V.I.D
RSc3076	RS00525	1.13	0.04			-0.96	0.00			HYPOTHETICAL PROTEIN	V.I.D
RSc3077	RS00528									TRANSMEMBRANE COG0053, Co/Zn/Cd cation transporters	I.V.D.4
RSc3078	RS00529					-0.99	0.01	-1.18	0.02	TRANSCRIPTION REGULATOR RESPONSE REGULATOR	V.I.A
RSc3079	RS00530									TRANSCRIPTION REGULATOR COMPOSITE TWO COMPONENT REGULATORY	V.I.A
RSc3080	RS00531									TRANSCRIPTION REGULATOR	V.I.A
RSc3081	RS00532					-0.32	0.03			LIPOPROTEIN	V.I.D
RSc3082	RS00533									PSEUDOGENE (C-TERMINAL FRAGMENT)	V.I.D
RSc3083	RS00535									SIGNAL PEPTIDE	V.I.D
RSc3084	RS00536		0.70	0.01		-0.22	0.04	1.25	0.00	TRANSMEMBRANE	V.I.C
RSc3085	RS00537					-0.35	0.02			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc3086	RS00538					0.35	0.01			SIGNAL PEPTIDE HIGH POTENTIAL IRON-SULFUR PROTEIN (HIPIP)	I.H
RSc3087	RS00539					-0.65	0.00			TRANSCRIPTION REGULATOR RESPONSE REGULATOR	V.I.A
RSc3088	RS00540		0.54	0.02		0.19	0.04	0.45	0.01	SIGNAL PEPTIDE	V.I.C
RSc3089	RS00541					-0.90	0.00	-0.89	0.00	ISRsso11	V.A
RSc3090	RS00542					-0.57	0.00			ISRsso11	V.A
RSc3091	RS00544		0.55	0.00		-0.38	0.01	0.75	0.00	ISRsso11	V.A
RSc3092	RS00545					-2.61	0.00	-1.70	0.00	SIGNAL PEPTIDE OUTER MEMBRANE PORIN	I.II.B.2
RSc3093	RS00546							-1.15	0.00	SIGNAL PEPTIDE	V.I.C
RSc3094	RS00547					-0.64	0.00			TRANSMEMBRANE CARBOXYPEPTIDASE G2 PRECURSOR (FOLATE HYDROLASE)	V.I.C
RSc3095	RS00548					-0.70	0.02			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc3096	RS00549									SERINE-RICH PROTEIN	V.I.D
RSc3097	RS00550									TRANSMEMBRANE GLUTATHIONE-REGULATED POTASSIUM-EFFLUX SYSTEM	I.V.D.4
RSc3098	RS00551					-0.80	0.00	-1.21	0.04	OXIDOREDUCTASE COG2249, NADPH-quinone reductase	V.I.C
RSc3099	RS00552					0.44	0.01	2.25	0.00	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc3100	RS00553									SIGNAL PEPTIDE	V.I.C
RSc3101	RS00554	-5.08	0.00		0.79	0.04		-1.47	0.00	COG4319, Ketosteroid isomerase homolog	V.I.C
RSc3102	RS00555				1.07	0.05		-0.61	0.00	SERINE PROTEASE	I.I.A.4
RSc3103	RS00556							-1.04	0.04	TRANSCRIPTION REGULATOR	V.I.C
RSc3104	RS00557									OXIDOREDUCTASE 4-HYDROXYPHENYLPIRUVATE DIOXYGENASE	I
RSc3105	RS00558							0.55	0.03	SIGNAL PEPTIDE CALCIUM-BINDING PROTEIN	V.I.C
RSc3106	RS00559									TRANSMEMBRANE GENERAL SECRETION PATHWAY RELATED PROTEIN	I.V.E.2
RSc3107	RS00560							0.79	0.01	TRANSMEMBRANE GENERAL SECRETION PATHWAY PROTEIN G	I.V.E.2
RSc3108	RS00561									TRANSMEMBRANE GENERAL SECRETORY PATHWAY PROTEIN H	I.V.E.2
RSc3109	RS00562									TRANSMEMBRANE GENERAL SECRETORY PATHWAY PROTEIN I	I.V.E.2
RSc3110	RS00563									TRANSMEMBRANE GENERAL SECRETORY PATHWAY PROTEIN J	I.V.E.2
RSc3111	RS00564									TRANSMEMBRANE GENERAL SECRETORY PATHWAY PROTEIN K	I.V.E.2
RSc3112	RS00565									TRANSMEMBRANE GENERAL SECRETORY PATHWAY PROTEIN L	I.V.E.2
RSc3113	RS00566									TRANSMEMBRANE GENERAL SECRETORY PATHWAY PROTEIN M	I.V.E.2
RSc3114	RS00567									TRANSMEMBRANE GENERAL SECRETORY PATHWAY PROTEIN N	I.V.E.2
RSc3115	RS00568									TRANSMEMBRANE GENERAL SECRETORY PATHWAY PROTEIN D	I.V.E.2
RSc3116	RS00569									GENERAL SECRETION PATHWAY PROTEIN E	I.V.E.2
RSc3117	RS00571									TRANSMEMBRANE GENERAL SECRETORY PATHWAY PROTEIN F	I.V.E.2
RSc3118	RS00572									TRANSMEMBRANE	V.I.C
RSc3119	RS00574									TRANSMEMBRANE	V.I.C
RSc3120	RS00575									TRANSCRIPTION REGULATOR	V.I.A
RSc3121	RS00576									COG3467, Flavir-nucleotide-binding protein	V.I.C
RSc3122	RS00577									HYPOTHETICAL PROTEIN	V.I.D
RSc3124	RS00480									OXIDOREDUCTASE COG4231, Indolepyruvate ferredoxin oxidoreductase, alpha and I	V.I.D
RSc3125	RS00478	0.92	0.01							HYPOTHETICAL PROTEIN	V.I.D
RSc3126	RS00477	1.34	0.00							EXODEOXYRIBONUCLEASE I	I.I.A.1
RSc3127	RS00476	0.93	0.01							ETHANOLAMINE AMMONIA-LYASE SMALL SUBUNIT	I.I.2
RSc3128	RS00475	0.98	0.02							ETHANOLAMINE AMMONIA-LYASE HEAVY CHAIN	I.I.2
RSc3129	RS00474									OXIDOREDUCTASE NAD+ DEPENDENT ACETALDEHYDE DEHYDROGENASE	I.I
RSc3130	RS00473	0.93	0.00							TRANSCRIPTION REGULATOR ACETOIN CATABOLISM REGULATORY PROTEIN I	I
RSc3131	RS00472	1.15	0.01							OXIDOREDUCTASE PROPANOL-PREFERRING ALCOHOL DEHYDROGENASE	I.H.2
RSc3132	RS00471	1.07	0.01							OXIDOREDUCTASE D-LACTATE DEHYDROGENASE (D-LDH)	I.F
RSc3133	RS00470									TRANSCRIPTION REGULATOR	V.I.A
RSc3134	RS00469									ANTIBIOTIC RESISTANCE (ACETYLTTRANSFERASE)	I.V.G.4
RSc3135	RS00468									TRANSMEMBRANE MSF TRANSPORTER	I.V.D
RSc3136	RS00467									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc3137	RS00466									TRANSMEMBRANE METHYL-ACCEPTING CHEMOTAXIS PROTEIN	I.V.C
RSc3138	RS00465									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc3139	RS00464									OXIDOREDUCTASE	I.I
RSc3140	RS00463	0.84	0.05							TRANSCRIPTION REGULATOR	V.I.A
RSc3141	RS00462	1.30	0.02							SERINE PROTEASE	I.I.A.4
RSc3142	RS00461	1.07	0.04							TRANSMEMBRANE LIPOPROTEIN	V.I.D
RSc3143	RS00460									TRANSMEMBRANE TRANSPORT PROTEIN	I.V.D
RSc3144	RS00459									TRANSMEMBRANE SIGNAL TRANSDUCTION PROTEIN GGDEF DOMAIN	V.I.A
RSc3145	RS00458									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc3146	RS00457	1.81	0.00							ISRsso9-TRANSPOSASE	V.A
RSc3147	RS00456									HYPOTHETICAL PROTEIN	V.I.D
RSc3148	RS00455									ABC TRANSPORTER COG0683, ABC-type branched-chain amino acid transport syst	I.V.D
RSc3149	RS00451									TRANSMEMBRANE	V.I.B
RSc3150	RS00450									TRANSCRIPTION REGULATOR	V.I.A
RSc3151	RS00448									TRANSMEMBRANE	V.I.C
RSc3152	RS00447									OXIDOREDUCTASE TRYPTOPHAN 2-MONOXYGENASE	V.I.C
RSc3153	RS00446									OXIDOREDUCTASE COG1091, dTDP-4-dehydrohamnose reductase	I.II.B
RSc3154	RS00444	0.59	0.01							HYPOTHETICAL PROTEIN	V.I.D
RSc3155	RS00443									SIGNAL PEPTIDE	V.I.C
RSc3156	RS00442									SIGNAL PEPTIDE HYDROLASE	I.I
RSc3157	RS00441									TRANSCRIPTION REGULATOR COLD SHOCK-LIKE PROTEIN CSPC	V.I.A
RSc3158	RS00440									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc3159	RS00439									TRANSMEMBRANE COG2081, Flavoprotein	V.I.C
RSc3160	RS00438									COG2890, Methylase of polypeptide chain release factors	I.II.B.7
RSc3161	RS00437									TRANSCRIPTION REGULATOR TWO COMPONENT SENSOR HISTIDINE KINASE	V.I.A
RSc3162	RS00436									TRANSCRIPTION REGULATOR TWO COMPONENT RESPONSE REGULATOR	V.I.A
RSc3163	RS00435									HEMAGGLUTININ-RELATED AUTOTRANSFER PROTEIN	I.II.A
RSc3164	RS00434									TPR DOMAIN PROTEIN	V.I.C
RSc3165	RS00433									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc3166	RS00432									TRANSMEMBRANE	V.I.C
RSc3167	RS00430									ADENYLYLSULFATE KINASE (APS KINASE)	I.F.3
RSc3168	RS00429									TPR DOMAIN PROTEIN	V.I.B
RSc3169	RS01160									ISRsso13-TRANSPOSASE	V.A
RSc3170	RS00428									TRANSMEMBRANE PSEUDOGENE (TRANSPORT PROTEIN, FRAGMENT)	V.I.C
RSc3171	RS00427									BACTERIOPHAGE-RELATED PROTEIN	V.I.D
RSc3172	RS00426									SITE-SPECIFIC INTEGRASE/Resolvase	V
RSc3173	RS00425									BACTERIOPHAGE-RELATED PROTEIN	V.D
RSc3174	RS04746	0.47	0.04							BACTERIOPHAGE-RELATED PROTEIN	V.D
RSc3175	RS01339									HYPOTHETICAL PROTEIN	V.I.B
RSc3176	RS05984									TRANSMEMBRANE	V.I.D
RSc3177	RS00423									ACETYLTTRANSFERASE	I
RSc3178	RS05983									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc3179	RS00422									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
										Transposase	V.A

RSc3295	RS02524	1.27	0.01	-0.75	0.01	-0.79	0.00	gcvP	OXIDOREDUCTASE TRANSMEMBRANE GLYCINE DEHYDROGENASE [DECARBONYLATION]	I.18
RSc3296	RS02527	1.81	0.03	-0.83	0.01	2.20	0.00	sdaA2	L-SERINE AMONYA-LYASE, L-SERINE DEHYDRATASE 2 (L-SERINE DEAMINASE)	I.1.3
RSc3297	RS02525			-0.57	0.00				TRANSMEMBRANE	V.I.C
RSc3298	RS02526			-0.51	0.01				CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc3299	RS02528	0.66	0.03			1.20	0.01		TRANSMEMBRANE	V.I.C
RSc3300	RS02529	0.76	0.00	-0.99	0.00	0.98	0.04	putA	SIGNAL PEPTIDE AMINO-ACID TRANSPORT PROTEIN	IV.D.2
RSc3301	RS02530			-1.08	0.00	0.88	0.04	priA	OXIDOREDUCTASE BIFUNCTIONAL PROTEIN: PROLINE DEHYDROGENASE AND	I.1.3
RSc3302	RS02531	0.45	0.01	-0.55	0.00	-0.93	0.03	hemE	PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y)	II.B.8
RSc3303	RS02532	0.59	0.01						UROPORPHYRINOGEN DECARBOXYLASE	I.B.4
RSc3304	RS02533			-0.52	0.00				SIGNAL PEPTIDE	V.I.C
RSc3305	RS02534			-1.14	0.00	0.89	0.02		CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc3306	RS02535			-1.21	0.00				HYPOTHETICAL PROTEIN	V.I.D
RSc3307	RS02536	0.35	0.02	-0.61	0.00				TRANSMEMBRANE METHYL-ACCEPTING CHEMOTAXIS PROTEIN	IV.C
RSc3308	RS02537	0.99	0.01	-0.73	0.04			gstM	TRANSCRIPTION REGULATOR	V.I.A
RSc3309	RS02538							gstM	GLUTATHIONE S-TRANSFERASE	II.B.7
RSc3310	RS02539							pstS2	ABC TRANSPORTER PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR	I.F.20
RSc3311	RS02540			-1.29	0.00	0.98	0.01		HYPOTHETICAL PROTEIN	V.I.D
RSc3312	RS02542	0.54	0.01						ESTERASE / LIPASE	I.I.1
RSc3313	RS02543			-0.69	0.00	-0.79	0.03		CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc3314	RS02544			-1.16	0.00				SIGNAL PEPTIDE	V.I.D
RSc3315	RS02545					2.74	0.00		TRANSMEMBRANE	V.I.C
RSc3316	RS02546	0.83	0.01			-0.60	0.04	atpC1	ATP SYNTHASE EPSILON CHAIN	I.E.2
RSc3317	RS02547	0.90	0.00			1.51	0.00	atpD	ATP SYNTHASE BETA CHAIN	I.E.2
RSc3318	RS02548	0.72	0.00			0.97	0.00	atpG	ATP SYNTHASE GAMMA CHAIN	I.E.2
RSc3319	RS02549	-0.27	0.04	0.89	0.00	-0.22	0.02	atpA	ATP SYNTHASE ALPHA CHAIN	I.E.2
RSc3320	RS02550					1.00	0.00	atpH	ATP SYNTHASE DELTA CHAIN	I.E.2
RSc3321	RS02551	0.61	0.02			0.81	0.00	atpF	TRANSMEMBRANE ATP SYNTHASE B CHAIN	I.E.2
RSc3322	RS02552	0.60	0.00			0.88	0.00	atpE	TRANSMEMBRANE ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN)	I.E.2
RSc3323	RS02553	0.87	0.01			1.01	0.00	atpB	TRANSMEMBRANE ATP SYNTHASE A CHAIN	I.E.2
RSc3324	RS02554			-0.32	0.02			atpI	TRANSMEMBRANE FOF1-type ATP synthase, subunit I	I.E.2
RSc3325	RS02555	0.67	0.01	-0.34	0.03			parB2	CHROMOSOME PARTITIONING PROTEIN PARB	IV.A
RSc3326	RS02560	0.60	0.02	-0.27	0.04			parA2	CHROMOSOME PARTITIONING PROTEIN PARA	IV.A
RSc3327	RS02561			-0.36	0.04			gidB	GLUCOSE INHIBITED DIVISION PROTEIN B	IV.A
RSc3328	RS02562	0.89	0.03			0.52	0.04	gidA	GLUCOSE INHIBITED DIVISION PROTEIN A	IV.A
RSc3329	RS02563			-0.83	0.00				ABC TRANSPORTER AMINO-ACID-BINDING PERIPLASMIC PROTEIN (BPB)	IV.D.2
RSc3330	RS02564			-0.56	0.00	-0.64	0.01		SIGNAL PEPTIDE	V.I.D
RSc3331	RS02565			-0.45	0.05				COG1028, Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenase)	I
RSc3332	RS02566			0.67	0.00	-0.92	0.01		TRANSCRIPTION REGULATOR	V.I.A
RSc3333	RS02567								CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc3334	RS02568					1.33	0.03		TRANSCRIPTION REGULATOR	V.I.A
RSc3335	RS02569			-1.24	0.01	1.94	0.00		COG451, Nucleoside-diphosphate-sugar epimerase	I
RSc3336	RS02570	-0.75	0.02	-0.73	0.00				CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc3337	RS02571	1.49	0.04	-0.52	0.05				TRANSMEMBRANE COG0730, Permease	IV.D
RSc3338	RS02572			-0.40	0.00				TRANSMEMBRANE	V.I.D
RSc3339	RS02574			-1.37	0.00	-0.39	0.04		HYPOTHETICAL PROTEIN	V.I.B
RSc3340	RS02575								ABC TRANSPORTER TRANSMEMBRANE PROTEIN	IV.D
RSc3341	RS02576								ABC TRANSPORTER TRANSMEMBRANE PROTEIN	IV.D
RSc3342	RS02578			-0.58	0.00				ABC TRANSPORTER SUBSTRATE-BINDING PERIPLASMIC PROTEIN (BPB)	IV.D
RSc3343	RS02579			-0.70	0.06				ABC TRANSPORTER ATP-BINDING PROTEIN	IV.D
RSc3344	RS02581			-0.74	0.00				ABC TRANSPORTER ATP-BINDING PROTEIN	IV.D
RSc3345	RS02583	0.47	0.04					betA	OXIDOREDUCTASE CHOLINE DEHYDROGENASE LIPOPROTEIN	I.F
RSc3346	RS02584	0.34	0.04	-0.71	0.01				LYSOPHOSPHOLIPASE	I.I.1
RSc3347	RS02622			-1.71	0.00				TRANSCRIPTION REGULATOR	V.I.A
RSc3348	RS02623			-1.53	0.00				TRANSMEMBRANE CATION-TRANSPORTING ATPASE	IV.D.4
RSc3349	RS02624			-1.63	0.00	-2.04	0.00	copZ	COG2608, Copper chaperone	IV.G.4
RSc3350	RS02625			-0.71	0.00			ompW	SIGNAL PEPTIDE OUTER MEMBRANE PROTEIN W	III.B.2
RSc3352	RS02627			-0.68	0.00				COG2423, Ornithine cyclodeaminase	I
RSc3353	RS02628	0.55	0.01	-0.60	0.00				TRANSMEMBRANE	V.I.C
RSc3354	RS02629			-0.56	0.00	-0.89	0.00		TRANSCRIPTION REGULATOR	V.I.C
RSc3355	RS02630			-0.56	0.05			phhA	OXIDOREDUCTASE PHENYLALANINE 4-HYDROXYLASE	I.I.3
RSc3356	RS02631							phhB	PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE	I
RSc3357	RS02632			-0.66	0.00	-0.50	0.02		HYPOTHETICAL PROTEIN	V.I.D
RSc3358	RS02633								SET DOMAIN PROTEIN	V.I.C
RSc3359	RS02634					-0.33	0.05	dbhB	HISTONE-LIKE DNA-BINDING PROTEIN HU-BETA (NS1)	II.C.1
RSc3360	RS02635			-0.67	0.01	-0.32	0.05		TRANSMEMBRANE	V.I.C
RSc3361	RS02636			-0.73	0.00				OXIDOREDUCTASE COG1893, Ketopantoate reductase	I
RSc3362	RS02637					0.74	0.01		CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc3363	RS02638			-0.36	0.05			cpdB	TRANSMEMBRANE 2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE PRECURSOR	I.F.1
RSc3364	RS02639							minC	CELL DIVISION INHIBITOR	IV.A
RSc3365	RS02640			-0.38	0.00	0.32	0.04	minD	SEPTUM SITE-DETERMINING PROTEIN MIND	IV.A
RSc3366	RS02641	0.49	0.00	-0.37	0.00	-1.15	0.00	minE	CELL DIVISION TOPOLOGICAL SPECIFICITY FACTOR	IV.A
RSc3367	RS02642			-0.84	0.00				COG1804, CaIb, Predicted acyl-CoA transferases/carnitine dehydratase	I
RSc3368	RS02643			-2.28	0.00	2.63	0.00	comJ	COG2961, Protein involved in catabolism of external DNA	II
RSc3369	RS02644			-0.57	0.02	-0.45	0.03		AVRPPHE AVIRULENCE PROTEIN-HOMOLOG	V.I.B
RSc3370	RS02645					0.97	0.04		COG1254, ACYLPHOSPHATASE	I.H
RSc3371	RS02646	0.71	0.00						ABC TRANSPORTER TRANSMEMBRANE PROTEIN	IV.D
RSc3372	RS02647	0.72	0.00	-0.51	0.03				ABC TRANSPORTER COMPOSITE ATP-BINDING TRANSMEMBRANE PROTEIN	IV.D
RSc3373	RS02648								TRANSCRIPTION REGULATOR	V.I.A
RSc3374	RS02649			-0.54	0.00	-0.56	0.01	pfs	BIFUNCTIONAL PROTEIN (MTA/SAH NUCLEOSIDASE) (P46); 5'-METHYLTHIOADENOSINE	I.F.9
RSc3375	RS02660			-1.07	0.00	1.26	0.00		CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc3376	RS02650	0.60	0.04	-1.68	0.00	2.67	0.00		SIGNAL PEPTIDE	V.I.C
RSc3377	RS02651	1.53	0.01	-1.80	0.00	1.30	0.00		CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc3378	RS02652			-2.03	0.00	1.10	0.00		COG1502, Phosphatidylserine/phosphatidylglycerophosphate/cardiopolin synthases and	I
RSc3379	RS02653			-0.37	0.00				SIGNAL PEPTIDE	V.I.C
RSc3380	RS02654			-0.80	0.00	-0.33	0.04		SIGNAL PEPTIDE	V.I.D
RSc3381	RS02655			-1.16	0.00				TRANSMEMBRANE	V.I.D
RSc3382	RS02656							kdpA	TRANSMEMBRANE POTASSIUM-TRANSPORTING ATPASE A CHAIN	IV.D.4
RSc3383	RS02657							kdpB	TRANSMEMBRANE POTASSIUM-TRANSPORTING ATPASE (B CHAIN)	IV.D.4
RSc3384	RS02658							kdpC	TRANSMEMBRANE POTASSIUM-TRANSPORTING ATPASE C CHAIN	IV.D.4
RSc3385	RS02659							kdpD	TRANSCRIPTION REGULATOR TWO-COMPONENT SENSOR KINASE PROTEIN KIV.D	I
RSc3386	RS05666					-2.30	0.02		ABC TRANSPORTER COG1464, ABC-type metal ion transport system, periplasmic component	IV.D.5
RSc3387	RS05667			-0.78	0.00	0.48	0.03		TRANSCRIPTION REGULATOR TWO-COMPONENT RESPONSE REGULATOR WITH	V.I.A
RSc3388	RS05668								TRANSCRIPTION REGULATOR TWO-COMPONENT RESPONSE REGULATOR WITH	V.I.A
RSc3389	RS05670								HYPOTHETICAL PROTEIN	V.I.B
RSc3390	RS05671								SIGNAL PEPTIDE PORIN	IV
RSc3391	RS05672								ABC TRANSPORTER COG0715, ABC-type nitrate/sulfonate/bicarbonate transport system	IV.D
RSc3392	RS05673								TRANSCRIPTION REGULATOR RESPONSE REGULATOR	V.I.A
RSc3393	RS05676			-0.60	0.00			tISRsof	ISRso5-TRANSPOSASE	V.A
RSc3394	RS05675								RESTRICTION MODIFICATION ENZYME R SUBUNIT	II.B.8
RSc3395	RS01703								CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSc3396	RS01704								TYPE I RESTRICTION ENZYME M PROTEIN	II.B.8
RSc3397	RS01705			-0.83	0.00	-0.78	0.04		TRANSCRIPTION REGULATOR COG1959	V.I.A
RSc3398	RS01706	-0.76	0.03						TRANSMEMBRANE FLAVOHEMOPROTEIN (HEMOGLOBIN-LIKE PROTEIN)	I.G.1
RSc3399	RS01707								TRANSMEMBRANE	V.I.C
RSc3400	RS01708	0.75	0.03						TRANSMEMBRANE TRANSPORTER	IV.D
RSc3401	RS01709								SKWP PROTEIN 1	V.I.C
RSc3402	RS01711	-0.82	0.00	1.07	0.02				TRANSMEMBRANE	V.I.B
RSc3403	RS01712			-0.72	0.03				TRANSCRIPTION REGULATOR TWO-COMPONENT SENSOR KINASE	V.I.A
RSc3404	RS01713			-0.53	0.01				TRANSCRIPTION REGULATOR RESPONSE REGULATOR	V.I.A
RSc3405	RS01714	-0.37	0.03						TRANSMEMBRANE	V.I.C
RSc3406	RS01715								COG0596, Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	I
RSc3407	RS01716								OXIDOREDUCTASE COG0665, Glycine/D-amino acid oxidase (deaminating)	I.I.3

RSp0081	RS05540		0,60	0,03	-2,21	0,00	-1,11	0,00	1,98	0,00	CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSp0082	RS05556										HYPOTHETICAL PROTEIN	V.I.D		
RSp0083	RS05555				-0,83	0,00					HYPOTHETICAL PROTEIN	V.I.D		
RSp0084	RS05553				-0,70	0,04					HYPOTHETICAL PROTEIN	V.I.D		
RSp0085	RS05538		0,92	0,01	-0,85	0,01					RHS-RELATED PROTEIN	V.I.B		
RSp0086	RS05537								1,76	0,00	RHS-RELATED PROTEIN	V.I.C		
RSp0087	RS05535				1,17	0,01	-0,68	0,01			CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSp0088	RS05533										HYPOTHETICAL PROTEIN	V.I.D		
RSp0089	RS05532				-0,63	0,02					HYPOTHETICAL PROTEIN	V.I.D		
RSp0090	RS05531										INTEGRASE/RECOMBINASE	V		
RSp0091	RS05552							-0,93	0,00		HYPOTHETICAL PROTEIN	V.I.D		
RSp0092	RS05551							-1,00	0,05		HYPOTHETICAL PROTEIN	V.I.D		
RSp0093	RS05871				-2,62	0,01	3,45	0,00			TIS1421 TIS1421-transposase ORFB	V.A		
RSp0094	RS05870						-0,75	0,00			TIS1421 TIS1421-transposase ORFA	V.A		
RSp0095	RS06004				-0,54	0,00					HYPOTHETICAL PROTEIN	V.I.D		
RSp0096	RS05526										RHS-RELATED PROTEIN	V.I.C		
RSp0097	RS05527						1,40	0,00	-0,62	0,04	ANKYRIN-REPEAT HARBORING PROTEIN	V.I.B		
RSp0098	RS05528				-2,97	0,00	-5,01	0,00	2,88	0,00	HYPOTHETICAL PROTEIN	V.I.D		
RSp0099	RS03024				-2,65	0,00	-4,53	0,00	3,08	0,00	3,05	0,00	ripA TYPE III EFFECTOR PROTEIN AWR1	V.I.E
RSp0100	RS03023				-1,01	0,01	0,80	0,03	-2,38	0,00		FERRISIDEROPHORE RECEPTOR PROTEIN	IV.D.5	
RSp0101	RS03022						0,30	0,03	1,04	0,00		CONSERVED HYPOTHETICAL PROTEIN	V.I.C	
RSp0102	RS03021						-0,59	0,00			COG3293, Transposase and inactivated derivatives	V.A		
RSp0103	RS03020						-0,84	0,00			VGR-RELATED PROTEIN	V.I.C		
RSp0104	RS03019						-0,90	0,00			TRANSMEMBRANE	V.I.C		
RSp0105	RS03018						-1,09	0,00			CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSp0106	RS03016										SIGNAL PEPTIDE MOLYBDATE-BINDING PERIPLASMIC PROTEIN	IV.D.1		
RSp0107	RS03015						-0,80	0,00	1,32	0,01	TRANSMEMBRANE TRANSPORT PROTEIN	V.I.C		
RSp0108	RS03014						-0,72	0,00			TRANSCRIPTION REGULATOR	V.I.A		
RSp0109	RS03013						-0,69	0,03			COG0714, MoxR-like ATPases	V.I.C		
RSp0110	RS03012				0,70	0,01	-0,49	0,00			TRANSMEMBRANE	V.I.C		
RSp0111	RS03011										TRANSMEMBRANE	V.I.C		
RSp0112	RS03010										CARBONIC ANHYDRASE	I.F.18		
RSp0113	RS03009				0,46	0,02	-0,39	0,01			TRANSMEMBRANE COG0659, Sulfate permease and related transporters	IV.D		
RSp0114	RS03008				0,57	0,04					TRANSMEMBRANE	V.I.C		
RSp0115	RS03007				0,76	0,04					SIGNAL PEPTIDE	V.I.B		
RSp0116	RS03006						-1,21	0,01			CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSp0117	RS03005						-1,44	0,05	-0,99	0,04	HYPOTHETICAL PROTEIN	V.I.D		
RSp0118	RS03004						-0,49	0,00			HYPOTHETICAL PROTEIN	V.I.D		
RSp0119	RS03003								-0,54	0,04	TRANSMEMBRANE	V.I.C		
RSp0120	RS03002										TRANSMEMBRANE ACONITATE HYDRATASE 1	I.H.6		
RSp0121	RS03001						-0,16	0,05			METHYLCITRATE SYNTHASE (CITRATE SYNTHASE 2)	I		
RSp0122	RS03000										prpC CARBOXYVINYL-CARBOXYPHOSPHONATE PHOSPHORYLMUTASE	I.I.4		
RSp0123	RS02999										prpB2 TRANSCRIPTION REGULATOR PROPIONATE CATABOLISM OPERON REGULAT(I	V.I.C		
RSp0124	RS02998				0,66	0,00	-0,43	0,00			TRANSMEMBRANE LIPOPROTEIN	V.I.C		
RSp0125	RS02997						-0,52	0,00			TRANSMEMBRANE PROLIN RICH PROTEIN	V.I.D		
RSp0127	RS02994						-0,63	0,01			ISRso1 ISRso1 TRANSPOSASE	V.A		
RSp0128	RS02993						-0,79	0,05	1,19	0,00	COG0210, Superfamily I DNA and RNA helicases	II.B.8		
RSp0129	RS02991										HYPOTHETICAL PROTEIN	V.I.D		
RSp0130	RS02992						-0,66	0,00			0,98	0,00	HYPOTHETICAL PROTEIN	V.I.B
RSp0131	RS02990										HYPOTHETICAL PROTEIN	V.I.D		
RSp0132	RS02988				-0,71	0,00					TRANSMEMBRANE SIGNAL TRANSDUCTION PROTEIN GGDEF DOMAIN	V.I.A		
RSp0133	RS02987						-0,43	0,03			TRANSMEMBRANE	V.I.C		
RSp0134	RS02986										TRANSMEMBRANE	V.I.C		
RSp0135	RS02985				-0,66	0,04	-0,88	0,02			TRANSMEMBRANE COG4257 STREPTOGRAMIN LYASE	IV.F		
RSp0136	RS02984										OXIDOREDUCTASE COG1902, NADH:flavin oxidoreductases	I		
RSp0137	RS02983						-1,10	0,01	-1,59	0,00	TRANSCRIPTION REGULATOR	V.I.A		
RSp0138	RS02982				0,44	0,03	-0,36	0,01	1,43	0,01	TRANSMEMBRANE PECTINESTERASE (PECTIN METHYLESTERASE)	II.A.3		
RSp0139	RS02981						-0,46	0,00			COG1246, N-acetylglutamate synthase and related acetyltransferases	I		
RSp0140	RS02980										TRANSMEMBRANE COG2165, Type II secretory pathway, pseudopilin	IV.E.2		
RSp0141	RS02979										TRANSMEMBRANE GENERAL SECRETION PATHWAY GSPG RELATED PROTEIN IV.E.2	IV.E.2		
RSp0142	RS02978										TRANSMEMBRANE GENERAL SECRETION PATHWAY GSPG RELATED PROTEIN IV.E.2	IV.E.2		
RSp0143	RS02977										GSPD-RELATED PROTEIN	IV.E.2		
RSp0144	RS02976										TRANSMEMBRANE PROLIN-RICH PROTEIN	V.I.C		
RSp0145	RS02975										TRANSMEMBRANE	V.I.C		
RSp0146	RS02974				0,46	0,05					TRANSMEMBRANE	V.I.C		
RSp0147	RS02973								-2,02	0,00	HYPOTHETICAL PROTEIN	V.I.D		
RSp0148	RS02972				1,22	0,01	-0,45	0,04			GENERAL SECRETION PATHWAY GSPG-RELATED PROTEIN	IV.E.2		
RSp0149	RS02971				0,88	0,02					TRANSMEMBRANE GENERAL SECRETION PATHWAY GSPF-RELATED PROTEIN IV.E.2	IV.E.2		
RSp0150	RS02970								-2,05	0,01	TRANSMEMBRANE GENERAL SECRETION PATHWAY GSPG-RELATED PROTEIN IV.E.2	IV.E.2		
RSp0151	RS02969										RHS-RELATED PROTEIN	V.I.B		
RSp0152	RS02967										HYPOTHETICAL PROTEIN	V.I.D		
RSp0153	RS06008										HYPOTHETICAL PROTEIN	V.I.D		
RSp0154	RS06009										TRANSMEMBRANE	V.I.D		
RSp0157	RS05520										HYPOTHETICAL PROTEIN	V.I.B		
RSp0158	RS06026				-1,08	0,00	1,45	0,00			HYPOTHETICAL PROTEIN	V.I.D		
RSp0159	RS06025				-3,70	0,00	4,47	0,00	1,39	0,04	HYPOTHETICAL PROTEIN	V.I.D		
RSp0160	RS05518				-3,62	0,00	4,13	0,00	4,62	0,00	CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSp0161	RS05517										TRANSMEMBRANE	V.I.C		
RSp0162	RS05516						0,63	0,00	2,59	0,01	egl ENDOGLUCANASE PRECURSOR (ENDO-1,4-BETA-GLUCANASE)	II.A.3		
RSp0163	RS05515						0,64	0,01			PHOSPHOPANTHETHEINYL TRANSFERASE	I		
RSp0164	RS05514				-1,66	0,03	1,26	0,01			TRANSMEMBRANE COG0534, Na ⁺ -driven multidrug efflux pump	IV.G		
RSp0165	RS05513										CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSp0166	RS05511										cysC2 ADENYLYLSULFATE KINASE	I.F.3		
RSp0167	RS04679										SULFOTRANSFERASE	I		
RSp0168	RS04680						-0,44	0,04			HYPOTHETICAL PROTEIN	V.I.D		
RSp0169	RS04681										TRANSMEMBRANE	V.I.D		
RSp0170	RS04682						-1,53	0,03			HYPOTHETICAL PROTEIN	V.I.D		
RSp0171	RS04683								0,59	0,00	HYPOTHETICAL PROTEIN	V.I.B		
RSp0172	RS04684						0,50	0,00	0,63	0,01	CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSp0173	RS04685								0,74	0,03	CYSTEINE DESULFURASE (tRNA sulfurtransferase)	II.B.6		
RSp0174	RS04686						0,38	0,01	1,09	0,01	COG0500, SAM-dependent methyltransferases	I		
RSp0175	RS04687				0,44	0,04	-0,89	0,00	-1,55	0,00	VGR-RELATED PROTEIN	V.I.C		
RSp0176	RS04688				0,56	0,00	-1,39	0,00	-2,34	0,00	CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSp0177	RS04689				-1,17	0,00	1,94	0,00	-0,55	0,03	HYPOTHETICAL PROTEIN	V.I.B		
RSp0178	RS04690				0,62	0,02	-0,92	0,00	-1,16	0,02	HYPOTHETICAL PROTEIN	V.I.D		
RSp0179	RS04691						-0,72	0,00	-0,93	0,04	-0,92	0,01	CONJUGAL TRANSFERT TRBI-RELATED PROTEIN	V.I.B
RSp0180	RS04692										CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSp0181	RS04693										CONSERVED HYPOTHETICAL PROTEIN	V.I.C		
RSp0182	RS04694										TRANSMEMBRANE TRANSPORTER	IV.D		
RSp0183	RS04695										3-CARBOXYMUONATE CYCLASE	I		
RSp0184	RS04696						-0,25	0,00			HYPOTHETICAL PROTEIN	V.I.D		
RSp0185	RS04697						-0,60	0,04			TRANSCRIPTION REGULATOR	V.I.A		
RSp0186	RS04698										ABC TRANSPORTER COG0834: ABC-type amino acid transport/signal transduction s	IV.D		
RSp0187	RS04699										HYPOTHETICAL PROTEIN	V.I.D		
RSp0188	RS04700								-0,42	0,02	PSEUDOGENE, OXYDOREDUCTASE (FRAGMENT)	V.I.B		
RSp0189	RS04701										TRANSMEMBRANE TYPE IV PILUS ASSEMBLY FimV-RELATED PROTEIN	III.A.2		
RSp0190	RS04702						-0,55	0,05			TRANSMEMBRANE COG0730: Predicted permeases	IV.D		
RSp0191	RS04703						-0,54	0,01			HYPOTHETICAL PROTEIN	V.I.D		
RSp0192	RS04705										TRANSMEMBRANE	V.I.C		
RSp0193	RS04706						2,25	0,00	3,30	0,00	PPR REPEATS CONTAINING PROTEIN	V.I.B		
RSp0194	RS04707						-0,53	0,02			COG0332, 3-oxoacyl-[acyl-carrier-protein]	I		
RSp0195	RS04708										HYPOTHETICAL PROTEIN	V.I.D		

RSp0311	RS05459					oprM	OUTER MEMBRANE CHANEL LIPOPROTEIN	IV.D
RSp0312	RS05457					mexD	TRANSMEMBRANE MULTIDRUG EFFLUX SYSTEM PROTEIN	IV.D
RSp0313	RS05456					mexC	MULTIDRUG EFFLUX SYSTEM PROTEIN	IV.G.2
RSp0314	RS05454			-0.64	0.01		TRANSCRIPTION REGULATOR TWO COMPONENT RESPONSE REGULATOR	VIA
RSp0315	RS05453			-0.66	0.02		TRANSCRIPTION REGULATOR TRANSMEMBRANE SENSOR KINASE	VIA
RSp0316	RS05452						OXIDOREDUCTASE COG2070, Dioxygenase related to 2-nitropropane dioxygenase	I
RSp0317	RS05451						CONSERVED HYPOTHETICAL PROTEIN	VIC
RSp0318	RS05449			-0.47	0.00		COG0589, Universal stress protein UspA and related nucleotide-binding proteins	VIC
RSp0319	RS05448						TRANSMEMBRANE METAL-TRANSPORTING P-TYPE ATPASE	IV.F.1
RSp0320	RS05447						TRANSCRIPTION REGULATOR	VIA
RSp0321	RS05446						CYSTEINE-RICH PROTEIN	VIC
RSp0322	RS05445			0.68	0.00		2-ISOPROPYLMALATE SYNTHASE	IA.1
RSp0323	RS05444					leuA2	CONSERVED HYPOTHETICAL PROTEIN	VIC
RSp0324	RS05442			-2.47	0.00		OXIDOREDUCTASE DEHYDROGENASE, SMALL CHAIN	II
RSp0325	RS05441						OXIDOREDUCTASE DEHYDROGENASE, LARGE CHAIN	II
RSp0326	RS05440						ORGANIC HYDROPEROXIDE RESISTANCE PROTEIN	IV.G.4
RSp0327	RS05439						CONSERVED HYPOTHETICAL PROTEIN	VIC
RSp0328	RS05438						TRANSCRIPTION REGULATOR	VIA
RSp0329	RS05429			0.37	0.02		OXIDOREDUCTASE 3-ISOPROPYLMALATE DEHYDROGENASE	IA.1
RSp0330	RS00703					leuB2	ACONITATE HYDRATASE 1	I.H.6
RSp0331	RS00705					acnA3	TRANSCRIPTION REGULATOR	VIA
RSp0332	RS00707					acnB	TRANSMEMBRANE ACONITATE HYDRATASE 2	I.H.6
RSp0333	RS00709					osmB2	TRANSMEMBRANE OSMOTICALLY INDUCIBLE LIPOPROTEIN B2	IV.F.2
RSp0334	RS00710						SIGNAL TRANSDUCTION PROTEIN EAL - GGDEF DOMAINS	VIA
RSp0335	RS00711						TRANSCRIPTION REGULATOR HNS-LIKE PROTEIN	VIA
RSp0336	RS00713			0.59	0.01		TRANSCRIPTION REGULATOR	VIA
RSp0337	RS00714			0.55	0.04		TRANSMEMBRANE PORIN PRECURSOR	IV
RSp0338	RS00717			0.27	0.04		TRANSCRIPTION REGULATOR NEGATIVE REGULATOR OF EXOPOLYSACCHAR	III.A.1
RSp0339	RS00719					epsR	FLAGELLA SYNTHESIS PROTEIN FLGN	IV.C
RSp0340	RS00833					figN	NEGATIVE REGULATOR OF FLAGELLIN SYNTHESIS (ANTI-SIGMA-28 FACTOR)	IV.C
RSp0341	RS00720					figM	FLAGELLA BASAL BODY P-RING FORMATION PROTEIN	IV.C
RSp0342	RS00738					figB	FLAGELLAR BASAL-BODY ROD PROTEIN FLGB	IV.C
RSp0343	RS00739					figC	FLAGELLAR BASAL-BODY ROD PROTEIN FLGC	IV.C
RSp0344	RS00744					figD	BASAL-BODY ROD MODIFICATION PROTEIN FLGD	IV.C
RSp0345	RS00745					figE	FLAGELLAR HOOK PROTEIN FLGE	IV.C
RSp0346	RS00747					figF	FLAGELLAR BASAL-BODY ROD PROTEIN FLGF	IV.C
RSp0347	RS00748					figG	FLAGELLAR BASAL-BODY ROD PROTEIN FLGG (DISTAL ROD PROTEIN)	IV.C
RSp0348	RS00749					figH	FLAGELLAR L-RING PROTEIN PRECURSOR	IV.C
RSp0349	RS00751					figI	SIGNAL PEPTIDE FLAGELLAR P-RING PROTEIN PRECURSOR	IV.C
RSp0350	RS00752					figJ	FLAGELLAR PROTEIN FLGJ	IV.C
RSp0351	RS00754					figK	FLAGELLAR HOOK-ASSOCIATED PROTEIN 1	IV.C
RSp0352	RS00756					figL	FLAGELLAR HOOK-ASSOCIATED PROTEIN 3	IV.C
RSp0353	RS00757						TRANSMEMBRANE	VIC
RSp0354	RS00759						OXIDOREDUCTASE COG0644, Dehydrogenase (flavoproteins)	I
RSp0355	RS00761			0.63	0.00		METHYLASE	VIC
RSp0356	RS00762						SIGNAL PEPTIDE	VIC
RSp0357	RS00765						3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I	I.B.1
RSp0358	RS00767					fabB	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE II	I.B.1
RSp0359	RS00769					fabF2	OXIDOREDUCTASE 3-OXOACYL-[ACYL-CARRIER-PROTEIN] REDUCTASE	I.B.1
RSp0360	RS00772					fabG2	OXIDOREDUCTASE COG4706, 3-hydroxyacyl-(acyl carrier protein) dehydratase	I
RSp0361	RS00773						3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE	I.B.1
RSp0362	RS00775						TRANSMEMBRANE COG4258, Predicted exporter	IV.D
RSp0363	RS00776						SIGNAL PEPTIDE	VIC
RSp0364	RS00778						COG0824, Thioesterase	I
RSp0365	RS00779					hutH2	HISTIDINE AMMONIA-LYASE	I.I.3
RSp0366	RS00785						TRANSMEMBRANE COG0463, Glycosyltransferase AND COG4261, Predicted acyltr	I
RSp0367	RS00787						COG0365, Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases AND COG0764, 3-	I
RSp0368	RS00790						TRANSMEMBRANE	VIC
RSp0369	RS00792						ACYL-CARRIER PROTEIN	I
RSp0370	RS00794						ACYL-CARRIER PROTEIN	I
RSp0371	RS00796						TRANSMEMBRANE 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE	II.B.1
RSp0372	RS00799						CONSERVED HYPOTHETICAL PROTEIN	VIC
RSp0373	RS00800					fljR	TRANSMEMBRANE FLAGELLAR BIOSYNTHETIC PROTEIN FLJR	IV.C
RSp0374	RS00802					fljQ	TRANSMEMBRANE FLAGELLAR BIOSYNTHETIC PROTEIN FLJQ	IV.C
RSp0375	RS00803					fljP	TRANSMEMBRANE FLAGELLAR BIOSYNTHETIC PROTEIN FLJP	IV.C
RSp0376	RS00804					fljO	TRANSMEMBRANE FLAGELLAR PROTEIN FLJO	IV.C
RSp0377	RS00805					fljN	FLAGELLAR MOTOR SWITCH PROTEIN FLJN	IV.C
RSp0378	RS00806					fljM	FLAGELLAR MOTOR SWITCH PROTEIN FLJM	IV.C
RSp0379	RS00807					fljL	TRANSMEMBRANE FLAGELLAR FLJL PROTEIN	IV.C
RSp0380	RS00808						SIGNAL TRANSDUCTION PROTEIN EAL - GGDEF DOMAINS	VIA
RSp0381	RS00809						TRANSCRIPTION REGULATOR	VIA
RSp0382	RS00810						FLAGELLIN	IV.C
RSp0383	RS00811					fljC	FLAGELLAR HOOK-ASSOCIATED PROTEIN 2 (FILAMENT CAP PROTEIN)	IV.C
RSp0384	RS00812					fljD	FLAGELLAR PROTEIN FLJD	IV.C
RSp0385	RS00813					fljS	FLAGELLAR PROTEIN FLJS	IV.C
RSp0386	RS00814					fljT	TRANSCRIPTION REGULATOR	VIA
RSp0387	RS00815						CONSERVED HYPOTHETICAL PROTEIN	VIC
RSp0388	RS00816						TRANSMEMBRANE COG3774, Mannosyltransferase OCH1 and related enzymes	II.B
RSp0389	RS00817					fljE	FLAGELLAR HOOK-BASAL BODY COMPLEX PROTEIN FLJE	IV.C
RSp0390	RS00818					fljF	TRANSMEMBRANE FLAGELLAR M-RING PROTEIN	IV.C
RSp0391	RS00819					fljG	FLAGELLAR MOTOR SWITCH PROTEIN FLJG	IV.C
RSp0392	RS00820					fljH	FLAGELLAR ASSEMBLY PROTEIN FLJH	IV.C
RSp0393	RS00821					fljI	FLAGELLUM-SPECIFIC ATP SYNTHASE	IV.C
RSp0394	RS00822					fljJ	FLAGELLAR PROTEIN	IV.C
RSp0395	RS00823					fljK	FLAGELLAR HOOK-LENGTH CONTROL PROTEIN	IV.C
RSp0396	RS00824						TRANSMEMBRANE	VIC
RSp0397	RS00825					pat	PHOSPHOTHIOIC ACETYLTRANSFERASE	IV.G.4
RSp0398	RS00826						TRANSMEMBRANE SIGNAL TRANSDUCTION PROTEIN GGDEF DOMAIN	VIA
RSp0399	RS00827						HYPOTHETICAL PROTEIN	VLD
RSp0400	RS00828						TRANSMEMBRANE SIGNAL TRANSDUCTION PROTEIN GGDEF DOMAIN	VIA
RSp0401	RS00829						LIPOPROTEIN	VLD
RSp0402	RS00830						TRANSMEMBRANE	VIC
RSp0403	RS00831						SIGNAL PEPTIDE	VIC
RSp0404	RS00861						TRANSMEMBRANE	VLB
RSp0405	RS00862						HYPOTHETICAL PROTEIN	VLD
RSp0406	RS00863						HYPOTHETICAL PROTEIN	VLD
RSp0407	RS00864						TRANSMEMBRANE	VLD
RSp0408	RS00865						HYPOTHETICAL PROTEIN	VLD
RSp0409	RS00866						TRANSMEMBRANE	VLD
RSp0410	RS00867						TRANSMEMBRANE	VIC
RSp0411	RS00868						TRANSMEMBRANE COG0628, Permease	IV.D
RSp0412	RS00869						TRANSMEMBRANE COG0477, Permeases of the major facilitator superfamily	IV.D
RSp0413	RS00870						CONSERVED HYPOTHETICAL PROTEIN	VIC
RSp0414	RS00871						FERRIC SIDEROPHORE RECEPTOR	IV.D.5
RSp0415	RS00872						TRANSCRIPTION REGULATOR EXTRACYTOPLASMIC FUNCTION SIGMA FACTO	I.E.1
RSp0416	RS00873						SIGNAL PEPTIDE FERRIC SIDEROPHORE RECEPTOR OUTER MEMBRANE PRO	IV.D.5
RSp0417	RS00874						CYSTEINE SYNTHASE	IV.D.5
RSp0418	RS00875						ORNITHINE CYCLODEAMINASE	IV.D.5
RSp0419	RS00876						Siderophore synthetase component	IV.D.5
RSp0420	RS00877						TRANSMEMBRANE EFFLUX PROTEIN	IV.D.5
RSp0421	RS00878						Siderophore synthetase component	IV.D.5
RSp0422	RS00879						Siderophore synthetase component	IV.D.5

RSp0542	RS05800			0.61	0.01					CONSERVED HYPOTHETICAL PROTEIN	VI.C			
RSp0543	RS05799			-0.52	0.00		-1.09	0.02		HYPOTHETICAL PROTEIN	VI.D			
RSp0544	RS03936									HYPOTHETICAL PROTEIN	VI.B			
RSp0546	RS03935			-0.36	0.00			-2.17	0.00	HYPOTHETICAL PROTEIN	VI.C			
RSp0547	RS03933			-0.34	0.05					ISRs08: ISRS08-TRANSPOSASE ORFA	VI.D			
RSp0549	RS03931			-0.75	0.04					TRANSMEMBRANE	VI.D			
RSp0550	RS03929			-0.71	0.01					SIGNAL PEPTIDE ACTIVATION/SECRETION PROTEIN	IV.E.2			
RSp0551	RS03928									TRANSMEMBRANE COG0402, Cytosine deaminase and related metal-dependent hyl				
RSp0552	RS03927		0.43	0.04		-0.61	0.00			TRANSMEMBRANE	VI.C			
RSp0553	RS03926									CONSERVED HYPOTHETICAL PROTEIN	VI.C			
RSp0554	RS03925					-1.83	0.00		-1.70	0.00	SIGNAL PEPTIDE CHROMATE RESISTANCE PROTEIN	IV.D.1		
RSp0555	RS03924					-0.65	0.01			TRANSMEMBRANE CHROMATE TRANSPORT PROTEIN	IV.D.1			
RSp0556	RS03923					-0.48	0.00			CONSERVED HYPOTHETICAL PROTEIN	VI.C			
RSp0557	RS03922		0.43	0.02					-0.47	0.01	ISRs01f: ISRS016-TRANSPOSASE ORFA	VA		
RSp0559	RS03920		-0.41	0.02						TRANSMEMBRANE	VA			
RSp0560	RS03918					-0.29	0.05		-1.03	0.03	HYPOTHETICAL PROTEIN	VI.D		
RSp0561	RS03917					-1.13	0.02				PSEUDOGENE (TRANSCRIPTION REGULATOR C-terminal fragment)	VI.C		
RSp0562	RS03916									PSEUDOGENE (TRANSCRIPTION REGULATOR N-terminal fragment)	VI.C			
RSp0563	RS03915									COG0526, Thiol-disulfide isomerase and thioredoxins	II.B.7			
RSp0564	RS03914									LIPOPROTEIN	VI.C			
RSp0565	RS03913					-0.45	0.02			SIGNAL PEPTIDE	VI.C			
RSp0567	RS03911									ISRs0t: ISRS010-TRANSPOSASE ORFB	VA			
RSp0568	RS03910							0.78	0.01	CONSERVED HYPOTHETICAL PROTEIN	VI.C			
RSp0569	RS03909								1.54	0.00	HYPOTHETICAL PROTEIN	VI.D		
RSp0570	RS06032									COG1475, Predicted transcriptional regulators	VI.A			
RSp0571	RS06031					-0.68	0.04			CONSERVED HYPOTHETICAL PROTEIN	VI.C			
RSp0572	RS03907		-1.73	0.00	-4.10	0.00	0.72	0.05	2.68	0.00	CONSERVED HYPOTHETICAL PROTEIN	VI.C		
RSp0573	RS03906								-0.95	0.03	HYPOTHETICAL PROTEIN	VI.B		
RSp0574	RS03905										CONSERVED HYPOTHETICAL PROTEIN	VI.C		
RSp0575	RS03904					1.22	0.00				CONSERVED HYPOTHETICAL PROTEIN	VI.C		
RSp0576	RS03903					-0.90	0.00				CONSERVED HYPOTHETICAL PROTEIN	VI.C		
RSp0577	RS03902					-0.68	0.01			1.66	0.00	CONSERVED HYPOTHETICAL PROTEIN	VI.C	
RSp0578	RS03901										HYPOTHETICAL PROTEIN	VI.D		
RSp0579	RS03900					0.84	0.05				BACTERIOPHAGE-RELATED PROTEIN	VI.D		
RSp0580	RS03899										PRODUCT OF A TRUNCATED BACTERIOPHAGE GENE	VI.D		
RSp0583	RS03897			0.61	0.00				0.77	0.04	EXOGLUCANASE A (1,4-BETA-CELLOBIOSIDASE)	II.A.3		
RSp0585	RS03895										REMNANT OF IS1421-TRANSPOSASE ORFA	VA		
RSp0586	RS03894					-0.89	0.02				HYPOTHETICAL PROTEIN	VI.D		
RSp0587	RS03893					-2.52	0.04		3.95	0.00	SIGNAL PEPTIDE	VI.B		
RSp0588	RS03892										TRANSPOSASE FRAGMENT	VA		
RSp0589	RS03890					-0.30	0.05				OXIDOREDUCTASE DEHYDROGENASE/REDUCTASE	II		
RSp0590	RS03889										TRANSCRIPTION REGULATOR	VI.A		
RSp0591	RS03891					-0.41	0.05		-1.13	0.04	HYPOTHETICAL PROTEIN	VI.D		
RSp0592	RS03888										HYPOTHETICAL PROTEIN	VI.D		
RSp0593	RS03887					-1.26	0.00		1.16	0.00	HYPOTHETICAL PROTEIN	VI.D		
RSp0594	RS03886										HYPOTHETICAL PROTEIN	VI.D		
RSp0595	RS03884					-0.67	0.00		-0.47	0.02	CONSERVED HYPOTHETICAL PROTEIN	VI.C		
RSp0596	RS03883								1.91	0.00	TRANSMEMBRANE	VI.B		
RSp0597	RS03882										CONSERVED HYPOTHETICAL PROTEIN	VI.C		
RSp0598	RS03881								-0.93	0.02	TRANSCRIPTION REGULATOR RESPONSE REGULATOR	VI.A		
RSp0599	RS03880					-1.67	0.01				TRANSCRIPTION REGULATOR	VI.A		
RSp0600	RS03879										COG4319, Ketosteroid isomerase homolog	VI.C		
RSp0601	RS03878										CONSERVED HYPOTHETICAL PROTEIN	VI.C		
RSp0602	RS03877		-0.65	0.02		-0.73	0.01		0.50	0.02	phnB: SIGNAL PEPTIDE	VI.D		
RSp0603	RS03876		-2.65	0.00	0.53	0.02	-1.60	0.00	2.34	0.00	3.13	0.00	SERINE PROTEASE	II.A.4
RSp0604	RS03875								-1.55	0.03			PHENYLACETIC ACID DEGRADATION PROTEIN	II.A
RSp0605	RS03874					-0.43	0.04						PHENYLACETIC ACID DEGRADATION PROTEIN	II.A
RSp0606	RS03873												PHENYLACETIC ACID DEGRADATION PROTEIN	II.A
RSp0607	RS03872					-0.44	0.03						PHENYLACETIC ACID DEGRADATION PROTEIN	II.A
RSp0608	RS03871					-0.58	0.03						FERREDOXIN REDUCTASE	I.G.1
RSp0609	RS03758					-1.38	0.02						HYPOTHETICAL PROTEIN	VI.D
RSp0610	RS03757												CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSp0611	RS03756								-0.65	0.00			TRANSMEMBRANE	VI.C
RSp0612	RS03755												TRANSMEMBRANE	VI.C
RSp0613	RS03754												TRANSCRIPTION REGULATOR	VI.A
RSp0614	RS03753												OXIDOREDUCTASE COG0778, Nitroreductase	I
RSp0615	RS03752					0.54	0.03						COBYRINIC ACID A,C-DIAMIDE SYNTHASE	II.B.3
RSp0616	RS03751					0.71	0.02						COB(II)ALAMIN ADENOSYLTRANSFERASE	II.B.3
RSp0617	RS03750					1.60	0.03						COBALAMIN BIOSYNTHESIS PROTEIN	II.B.3
RSp0618	RS03749					0.94	0.01						OXIDOREDUCTASE BIFUNCTIONAL PROTEIN: PRECORRIN-3 METHYLTRANSFERASE	II.B.3
RSp0619	RS03748												PRECORRIN METHYLASE	II.B.3
RSp0620	RS03747								0.81	0.04			PRECORRIN-4 C11-METHYLTRANSFERASE	II.B.3
RSp0621	RS03746												PRECORRIN-2 C20-METHYLTRANSFERASE	II.B.3
RSp0622	RS03745								1.02	0.05			TRANSMEMBRANE COBALAMIN BIOSYNTHESIS PROTEIN D	II.B.3
RSp0623	RS03744					0.73	0.00						TRANSMEMBRANE PRECORRIN ISOMERASE	II.B.3
RSp0624	RS03743					0.65	0.00		2.29	0.00			PRECORRIN-6B METHYLASE METHYLTRANSFERASE	II.B.3
RSp0625	RS03742					0.70	0.00		-1.09	0.00			MAGNESIUM CHELATASE (SUBUNITS D/I)	I
RSp0626	RS03741					0.50	0.03						COBALAMIN BIOSYNTHESIS PROTEIN	II.B.3
RSp0627	RS03740					0.89	0.00		-0.45	0.00			FERREDOXIN	I.G.1
RSp0628	RS03739					0.91	0.00		-0.42	0.01			TRANSMEMBRANE HIGH AFFINITY NICKEL TRANSPORTER	IV.D.1
RSp0629	RS03738		0.84	0.03	0.60	0.03	-0.83	0.00		-1.99	0.00		VGR-RELATED PROTEIN	VI.C
RSp0630	RS03737					0.63	0.00						PHOSPHOLIPASE	VI.C
RSp0631	RS03736					0.66	0.00		-0.91	0.00			LIPOPROTEIN WITH COG0790, FOG: TPR repeat, SEL1 subfamily	VI.C
RSp0632	RS03735					0.76	0.04		-0.78	0.00			CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSp0633	RS03734		1.52	0.03	0.85	0.00	-0.86	0.00		-1.26	0.05		HYPOTHETICAL PROTEIN	VI.D
RSp0634	RS03733					-0.39	0.02						LIPOPOLYSACCHARIDE HEPTOSYLTRANSFERASE	II.B.2
RSp0635	RS03732												TRANSMEMBRANE ACYLTRANSFERASE	VI.C
RSp0636	RS03731					1.36	0.01		-0.36	0.05			TRANSCRIPTION REGULATOR COG4941, Predicted RNA polymerase sigma factor	VI.A
RSp0637	RS03730								-1.69	0.01			CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSp0638	RS03729												ABC TRANSPORTER COG4615, ABC-type siderophore export system, fused ATPase	IV.F
RSp0639	RS03728					0.63	0.01		-0.27	0.03			COG2220, Predicted Zn-dependent hydrolases of the beta-lactamase fold	I
RSp0640	RS03727					0.47	0.02		-0.31	0.04			CONSERVED HYPOTHETICAL PROTEIN	VI.C
RSp0641	RS05860					0.75	0.01						PEPTIDE SYNTHETASE	IV.G
RSp0642	RS05859					0.39	0.02						PEPTIDE SYNTHETASE	IV.G.3
RSp0643	RS05579					-0.77	0.00		1.12	0.00			HYPOTHETICAL PROTEIN	VI.D
RSp0644	RS05578												SIGNAL PEPTIDE	VI.D
RSp0645	RS05577												TRANSCRIPTION REGULATOR	VI.A
RSp0646	RS05576					0.68	0.01						1-AMINOCYCLOPROPANE-1-CARBOXYLATE DEAMINASE (ACC DEAMINASE)	I
RSp0647	RS05575												ENOYL-COENZYME A HYDRATASE	I
RSp0648	RS05574												ENOYL-COA HYDRATASE	I
RSp0649	RS05573												OXIDOREDUCTASE 3-HYDROXYISOBUTYRATE DEHYDROGENASE	II.A.2
RSp0650	RS05572												OXIDOREDUCTASE METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE	II.A.2
RSp0651	RS05571												ACETYL-COENZYME A SYNTHETASE (ACETATE--COA LIGASE)	I.C
RSp0652	RS05570												OXIDOREDUCTASE ACYL-COA DEHYDROGENASE	I
RSp0653	RS05569												TRANSCRIPTION REGULATOR	VI.A
RSp0654	RS05568								-1.16	0.00			TRANSCRIPTION REGULATOR TWO COMPONENT SENSOR HISTIDINE KINASE	IV.G
RSp0655	RS05567												TRANSCRIPTION REGULATOR TWO COMPONENT RESPONSE REGULATOR	IV.G
RSp0656	RS05566					-0.58	0.03						TRANSMEMBRANE COPPER RESISTANCE PROTEIN	IV.G
RSp0657	RS01792					0.98	0.00						COPPER RESISTANCE PROTEIN B	IV.G.4
RSp0658	RS01791					-0.38	0.03						SIGNAL PEPTIDE COPPER RESISTANCE PROTEIN C	IV.G.4
RSp0659	RS01790					0.40	0.02						TRANSMEMBRANE COPPER RESISTANCE PROTEIN D	IV.G.4
RSp0660	RS01789					-0.24	0.01						PORIN	IV.D

RSp0661	RS01788			-0.46	0.01				COG1335 Amidase related to nicotinamidase	I
RSp0662	RS01787								TRANSCRIPTION REGULATOR	V.I.A
RSp0663	RS01786					-0.78	0.03		TRANSMEMBRANE TRANSPORT PROTEIN	IV.D
RSp0664	RS01785			-0.44	0.01			0.63	TRANSCRIPTION REGULATOR	V.I.A
RSp0665	RS01784			-0.30	0.00				TRANSMEMBRANE MAGNESIUM AND COBALT TRANSPORT PROTEIN	IV.D.7
RSp0666	RS01783								DNA-3-METHYLADENINE GLYCOSYLASE I	II.B.8
RSp0667	RS01782			-0.39	0.02			-1.21	TRANSMEMBRANE CYNX-RELATED TRANSPORT PROTEIN	IV
RSp0668	RS01781								CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0669	RS01780								OUTER MEMBRANE CHANNEL LIPOPROTEIN	IV.D
RSp0670	RS01779					0.21	0.05		TRANSMEMBRANE TRANSPORTER LIPOPROTEIN	IV.D.7
RSp0671	RS01778					-0.73	0.00		ENOYL COA-HYDRATASE	I.I.4
RSp0672	RS01777			-3.50	0.00	-1.12	0.00	3.55	LRR-GALA FAMILY TYPE III EFFECTOR PROTEIN (GALA 2)	V.I.C
RSp0673	RS01776							-0.44	LIPOPROTEIN	V.I.C
RSp0674	RS01775	1.47	0.02			-0.77	0.00	-1.69	LIPOPROTEIN	V.I.C
RSp0675	RS01774					-0.62	0.01	-1.59	LIPOPROTEIN	V.I.C
RSp0676	RS01773	-2.02	0.00			-0.76	0.00	3.92	LIPOPROTEIN	V.I.C
RSp0677	RS01772							1.74	5-METHYL-TETRAHYDROPTEROYL-TRIGLUTAMATE--HOMOCYSTEINE METHYL-T	I.A.12
RSp0678	RS01771					-0.90	0.01		TRANSCRIPTION REGULATOR TRANSCRIPTIONAL ACTIVATOR PROTEIN METR	I.A.12
RSp0679	RS01770	3.40	0.00	0.83	0.00	-0.90	0.01	2.65	OXIDOREDUCTASE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (PNP/PMP OXIDA	I.A.10
RSp0680	RS01769	4.24	0.00	1.04	0.00	-0.96	0.00	2.12	DIAMINOPIMELATE DECARBOXYLASE	I.A.13
RSp0681	RS01768	3.26	0.00	0.76	0.00	-0.77	0.00	2.18	INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE	I.A.6
RSp0682	RS01767	1.47	0.00	0.87	0.03	-0.40	0.00	0.75	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE (GLYCOSYLTRANSFERASE	I.A.6
RSp0683	RS01766	4.94	0.00	0.87	0.00	-0.47	0.03	0.83	OXIDOREDUCTASE TRIMETHYLAMINE DEHYDROGENASE	II
RSp0684	RS01765	4.26	0.00	0.87	0.00	-0.65	0.00	1.01	COG0325, Predicted enzyme with a TIM-barrel fold	V.I.C
RSp0685	RS01764	4.35	0.00	0.82	0.00	-0.59	0.00	0.63	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0686	RS01763	3.93	0.00	0.58	0.00			0.60	TRANSMEMBRANE	V.I.C
RSp0687	RS01762	-0.99	0.01			0.58	0.04		TRANSCRIPTION REGULATOR	V.I.A
RSp0688	RS01761					-0.45	0.04		OXIDOREDUCTASE ACYL-CoA DEHYDROGENASE	I.I.1
RSp0689	RS01760					-0.12	0.04	0.91	TRANSMEMBRANE COG5472, Predicted small integral membrane protein	V.I.C
RSp0690	RS01759								TRANSCRIPTION REGULATOR COG2808, Transcriptional regulator	V.I.A
RSp0691	RS01758								FUMARYLACETOACETASE (FUMARYLACETOACETATE HYDROLASE)	I.I.3
RSp0692	RS01757								OXIDOREDUCTASE HOMOGENTISATE 1,2-DIOXYGENASE DIOXYGENASE	I.I.3
RSp0693	RS01756								TRANSCRIPTION REGULATOR TRANSCRIPTION REGULATOR	V.I.A
RSp0694	RS01755			-7.88	0.00	7.44	0.00	2.38	COG0346, Lactoylglutathione lyase and related lyases	I
RSp0695	RS01754			-6.81	0.00	6.90	0.00	3.04	OXIDOREDUCTASE TRYPTOPHAN-2,3-DIOXYGENASE	I.A.6
RSp0696	RS01753			-6.37	0.00	5.69	0.00	2.50	SIGNAL PEPTIDE COG0644, Dehydrogenases (flavoproteins)	I
RSp0697	RS01752			-7.32	0.00	6.34	0.00	0.97	COG0520, Selenocysteine lyase	I
RSp0698	RS01751			-6.97	0.00	7.20	0.00	3.15	OXIDOREDUCTASE DEHYDROGENASE/REDUCTASE	I
RSp0699	RS01750			-5.62	0.00	6.25	0.00	1.27	AMINOTRANSFERASE	I
RSp0700	RS01749			0.51	0.03				PEPTIDE CHAIN RELEASE FACTOR HOMOLOG	II.B.7
RSp0701	RS01748			0.47	0.03	-0.52	0.00	-0.71	RTCB-LIKE PROTEIN	V.I.C
RSp0702	RS01747			-1.97	0.01				CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0703	RS01746								OXIDOREDUCTASE COG0654, 2-polyphenyl-6-methoxyphenol hydroxylase and relat	I
RSp0704	RS01745					-0.73	0.02		COG0491, Zn-dependent hydrolases, including glyoxylases	V.I.A
RSp0705	RS01744			0.68	0.03				TRANSCRIPTION REGULATOR	V.I.A
RSp0706	RS01743					-0.34	0.02		ABC TRANSPORTER AMINO-ACID TRANSMEMBRANE PROTEIN	IV.D.2
RSp0707	RS01742								ABC TRANSPORTER AMINO-ACID COMPOSITE ATP-BINDING TRANSMEMBRANE	IV.D.2
RSp0708	RS01741							0.83	ABC TRANSPORTER AMINO-ACID COMPOSITE ATP-BINDING TRANSMEMBRANE	IV.D.2
RSp0709	RS01740					0.26	0.00	1.41	SIGNAL PEPTIDE	V.I.C
RSp0710	RS01739							1.21	OXIDOREDUCTASE CYTOCHROME P-450-LIKE MONOOXYGENASE	I.G.1
RSp0711	RS01738					-0.42	0.01		TRANSMEMBRANE	V.I.C
RSp0712	RS01737							-0.65	TRANSMEMBRANE COG5486, Predicted metal-binding integral membrane protein	III.B.1
RSp0713	RS01736					-0.50	0.04	-0.45	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0714	RS01735			0.73	0.02	-0.30	0.01		CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0715	RS01734								D-ALANINE AMINOTRANSFERASE (D-ASPARTATE AMINOTRANSFERASE)	I.F.14
RSp0716	RS01733					-1.69	0.00		SIGNAL PEPTIDE	V.I.B
RSp0717	RS01732					-0.64	0.03		HYPOTHETICAL PROTEIN	V.I.D
RSp0718	RS01731					-1.18	0.00		HYPOTHETICAL PROTEIN	V.I.D
RSp0719	RS01730			0.70	0.00	-1.09	0.00		COG1858, Cytochrome c peroxidase	I
RSp0720	RS01729					-1.02	0.03		SIGNAL PEPTIDE	V.I.C
RSp0721	RS01728					-0.44	0.05		SIGNAL PEPTIDE	V.I.C
RSp0722	RS01727					-0.31	0.01	1.11	TRANSMEMBRANE	V.I.C
RSp0723	RS01726								COG1712, Predicted dinucleotide-utilizing enzyme	V.I.C
RSp0724	RS01725								TRANSMEMBRANE	V.I.D
RSp0725	RS01724							-1.32	HYPOTHETICAL PROTEIN	V.I.D
RSp0726	RS01723								OXIDOREDUCTASE COG0535, Predicted Fe-S oxidoreductases	V.I.C
RSp0727	RS01722					-0.40	0.04		TRANSMEMBRANE MFS TRANSPORTER	IV.D
RSp0728	RS01721					-0.34	0.01		CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0729	RS01720					-1.00	0.00		CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0730	RS01719					0.32	0.01		HYPOTHETICAL PROTEIN	V.I.D
RSp0731	RS01718								CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0732	RS01717					0.77	0.01		TRANSMEMBRANE COG3000, Sterol desaturase	I
RSp0733	RS01716					2.35	0.00		TREHALOSE-6-PHOSPHATE SYNTHASE (ALPHA,ALPHA-TREHALOSE-PHOSPHAT	IV.F.2
RSp0734	RS01715					-5.90	0.00	5.74	TRANSMEMBRANE	V.I.D
RSp0735	RS01714							4.07	HYPOTHETICAL PROTEIN	V.I.D
RSp0736	RS01713					0.45	0.04		CONSERVED HYPOTHETICAL PROTEIN	V.I.B
RSp0737	RS01712								CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0738	RS01711							-1.31	TRANSMEMBRANE	V.I.C
RSp0739	RS01710							-2.39	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0740	RS01968								HYPOTHETICAL PROTEIN	V.I.D
RSp0741	RS01967								VGR-RELATED PROTEIN	V.I.C
RSp0742	RS01966					-0.97	0.00		TRANSMEMBRANE	V.I.C
RSp0743	RS01965					-0.94	0.00		CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0744	RS01964			0.43	0.03	-0.92	0.00		CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0745	RS01963					-0.98	0.00	-2.64	LIPOPROTEIN	V.I.C
RSp0746	RS01962					-1.01	0.00	-1.32	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0747	RS01961			0.33	0.03	-1.14	0.00	-1.58	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0748	RS01960					-1.19	0.00	-0.60	LIPOPROTEIN	V.I.C
RSp0749	RS01959					-1.24	0.00	-0.95	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0750	RS01958					-1.24	0.00	-0.95	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0751	RS01957					-0.24	0.01	0.59	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0752	RS01956					0.54	0.01	-0.93	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0753	RS01955					0.45	0.02	-0.83	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0754	RS01954					0.78	0.01	-0.97	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0755	RS01953								CLPAB-TYPE CHAPERONE	I.A.4
RSp0756	RS01952								VGR-RELATED PROTEIN	V.I.C
RSp0757	RS01951					0.70	0.00	-0.88	HYPOTHETICAL PROTEIN	V.I.D
RSp0758	RS01950					0.54	0.04	-0.94	TRANSMEMBRANE	V.I.B
RSp0759	RS01949					0.78	0.02	-1.12	TRANSMEMBRANE	V.I.D
RSp0760	RS01948					0.66	0.01	-0.83	HYPOTHETICAL PROTEIN	V.I.D
RSp0761	RS01947							-0.41	TRANSMEMBRANE	V.I.D
RSp0762	RS01946					0.82	0.00	-0.52	HYPOTHETICAL PROTEIN	V.I.D
RSp0763	RS01945							-0.59	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0764	RS01944							-0.71	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0765	RS01943					0.56	0.04	-0.28	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0766	RS01942					0.65	0.00	-0.58	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0767	RS01941							0.92	TRANSMEMBRANE	V.I.D
RSp0768	RS01940					0.90	0.00	-0.55	COG2885, Outer membrane protein and related peptidoglycan-associated (lipo)prote	V.I.B
RSp0769	RS01939					0.68	0.01		HYPOTHETICAL PROTEIN	V.I.B
RSp0770	RS01938					0.37	0.00	-0.64	TRANSMEMBRANE	V.I.C
RSp0771	RS01937					0.42	0.02	-0.69	TRANSMEMBRANE	V.I.B
RSp0772	RS01936							-0.79	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
								-0.97	TRANSMEMBRANE	V.I.B
									TRANSMEMBRANE	V.I.D
								-0.90	TRANSMEMBRANE	V.I.C
								-0.76	VGR-RELATED PROTEIN	V.I.C
								-0.47	TRANSMEMBRANE	V.I.C
								-0.32	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
								-0.94	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
								-0.93	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
								0.81	SIGNAL PEPTIDE	V.I.C

RSp0773	RS01935	0.63	0.01	-0.88	0.00	-3.33	0.00	-2.57	0.00	SIGNAL PEPTIDE	V.I.D
RSp0774	RS01934									HYPOTHETICAL PROTEIN	V.I.D
RSp0775	RS01933									HYPOTHETICAL PROTEIN	V.I.D
RSp0776	RS01932									HYPOTHETICAL PROTEIN	V.I.D
RSp0777	RS01931									TRANSMEMBRANE	V.I.D
RSp0778	RS01929			-0.81	0.01					TRANSCRIPTION REGULATOR TRANSCRIPTIONAL ACTIVATOR PROTEIN OF QUINONE	I.E.1
RSp0779	RS01928	2.23	0.01	-2.10	0.00					AUTONUCLEIC ACID SYNTHASE (ACYL HOMOSERINE LACTONE SYNTHASE)	I.E.1
RSp0780	RS01927	2.21	0.00	1.80	0.02	-2.29	0.00			Abyhdrolase	I.D.1
RSp0781	RS01926			2.42	0.03	-1.92	0.00			COG0266, Cystathionine beta-lyases/cystathionine gamma-synthases	I
RSp0782	RS01925	1.35	0.05	2.65	0.02	-2.19	0.00			tRNA synthetase - related protein	I
RSp0783	RS01924			2.09	0.05	-1.81	0.00	-1.06	0.04	COG0236, Acyl carrier protein	I.D
RSp0784	RS01923			2.58	0.02	-2.36	0.00			TRANSMEMBRANE FATTY ACID DESATURASE	I.I.1
RSp0785	RS01922			2.09	0.01	-1.66	0.00	-1.00	0.03	HYPOTHETICAL PROTEIN	V.I.D
RSp0786	RS01921			2.26	0.02	-2.02	0.00	-1.87	0.00	COG0332, 3-oxoacyl-[acyl-carrier-protein]	I.B.16
RSp0787	RS01920			2.51	0.02	-2.24	0.00	-1.30	0.02	TRANSMEMBRANE COG0318, Acyl-CoA synthetases (AMP-forming)/AMP-acid ligase	I
RSp0788	RS01919			2.44	0.02	-2.42	0.00			COG2192, Predicted carbamoyl transferase	I
RSp0789	RS01918			2.25	0.02	-1.27	0.00	-0.98	0.01	HYPOTHETICAL PROTEIN	V.I.B
RSp0790	RS01917			2.00	0.04	-2.27	0.00			COG0596, Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	I
RSp0791	RS01916			1.91	0.04			-0.90	0.00	COG0236, Acyl carrier protein	I
RSp0792	RS01915			2.69	0.03	-2.49	0.00			TRANSMEMBRANE FATTY ACID DESATURASE	I.I.1
RSp0793	RS01914					-1.55	0.00	-3.76	0.03	HYPOTHETICAL PROTEIN	V.I.D
RSp0794	RS01913			1.13	0.01	0.26	0.03			AMINOTRANSFERASE	I.F.14
RSp0795	RS01912			0.41	0.01	-0.81	0.00			COG4757, Predicted alpha/beta hydrolase	I.I
RSp0796	RS01911									TRANSCRIPTION REGULATOR	V.I.A
RSp0797	RS01910									TRANSMEMBRANE TRANSPORT PROTEIN	I.V.D
RSp0798	RS01909									HYPOTHETICAL PROTEIN	V.I.B
RSp0799	RS01908			0.83	0.01					COG0389, Nucleotidyltransferase/DNA polymerase involved in DNA repair	I.I.B.8
RSp0800	RS01907									DNA POLYMERASE III (ALPHA CHAIN)	I.I.B.8
RSp0801	RS01906					-0.48	0.03	-0.47	0.00	TRANSCRIPTION REGULATOR	V.I.A
RSp0802	RS01905							-0.26	0.05	TRANSMEMBRANE COG0471, Di- and tricarboxylate transporters	I.V.D
RSp0803	RS01904					0.91	0.00	-0.57	0.04	SIGNAL PEPTIDE HEMAGGLUTININ-RELATED PROTEIN	V.I.B
RSp0804	RS01903			0.57	0.00			-1.32	0.00	ELONGATION FACTOR G (EF-G PROTEIN)	I.I.B.7
RSp0805	RS01902									TRANSCRIPTION REGULATOR	V.I.A
RSp0806	RS01901					-0.63	0.00			TRANSMEMBRANE	V.I.C
RSp0807	RS01900					1.53	0.00			FERREDOXIN	I.G.1
RSp0808	RS01899									TRANSMEMBRANE	V.I.C
RSp0809	RS01898									HYPOTHETICAL PROTEIN	V.I.B
RSp0810	RS01897					-0.79	0.01	-0.91	0.05	ATP SYNTHASE EPSILON CHAIN	I.E.2
RSp0811	RS01896									SIGNAL PEPTIDE TONB-DEPENDENT RECEPTOR PROTEIN	I.II.B.2
RSp0812	RS01895							-0.53	0.04	TRANSMEMBRANE	V.I.C
RSp0813	RS01894			-1.97	0.01	0.60	0.05	-3.62	0.01	TRANSMEMBRANE SIGNAL TRANSDUCTION PROTEIN EAL - GGDEF DOMAINS	V.I.A
RSp0814	RS01893									OXIDOREDUCTASE MALATE-QUINONE OXIDOREDUCTASE	I.H.6
RSp0815	RS01892							-1.38	0.03	TRANSCRIPTION REGULATOR	V.I.A
RSp0816	RS01891									TRANSCRIPTION REGULATOR	V.I.A
RSp0817	RS01890									OUTER MEMBRANE DRUG EFFLUX LIPOPROTEIN	I.V.E
RSp0818	RS01889									TRANSMEMBRANE DRUG EFFLUX PROTEIN	I.V.D
RSp0819	RS01888									DRUG EFFLUX LIPOPROTEIN	I.V.E
RSp0820	RS01887							-0.39	0.01	COG2706, 3-carboxymuconate cyclase	I
RSp0821	RS01886									TRANSMEMBRANE	V.I.C
RSp0822	RS05373			-2.15	0.01	3.61	0.00	3.75	0.00	AvrPphF-RELATED PROTEIN	V.I.B
RSp0823	RS05372					1.03	0.01			TRANSCRIPTION REGULATOR TRANSCRIPTIONAL REGULATOR	V.I.A
RSp0824	RS05371			-0.83	0.01	0.89	0.00	0.70	0.02	GLUCONOLACTONASE (D-GLUCONO-DELTA-LACTONE LACTONOHYDROLASE)	I
RSp0825	RS05370			-2.77	0.00	-5.99	0.00	5.76	0.03	COG0421, Spermidine synthase	I.F.15
RSp0826	RS05369									5-DEHYDRO-4-DEOXYGLUCARATE DEHYDRATASE	I.F
RSp0827	RS05368									COG1012, NAD-dependent aldehyde dehydrogenases	I
RSp0828	RS05367									TRANSMEMBRANE GLUCARATE TRANSPORTER (D-GLUCARATE PERMEASE)	I.V.D
RSp0829	RS05366									GLUCARATE DEHYDRATASE	I.I.4
RSp0830	RS05365									D-GALACTARATE DEHYDRATASE (D-GALACTARATE DEHYDROGENASE)	I
RSp0831	RS05364									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0832	RS05363									COG3386, Gluconolactonase	I
RSp0833	RS05362			-0.64	0.00	1.78	0.00	2.20	0.03	TRANSMEMBRANE POLYGALACTURONASE	I.IA.3
RSp0834	RS05361					2.04	0.00	1.27	0.01	TRANSMEMBRANE HEXURONATE TRANSPORTER	I.V.D
RSp0835	RS05360			0.80	0.04					BIFUNCTIONAL NMN ADENYLYLTRANSFERASE/NUDIX HYDROLASE : NICOTINAMIDE	I.B.9
RSp0836	RS05359					0.44	0.00			NICOTINATE PHOSPHORIBOSYLTRANSFERASE-RELATED PROTEIN	I
RSp0837	RS05358			-2.70	0.00	1.00	0.00	3.65	0.00	HYPOTHETICAL PROTEIN	V.I.D
RSp0838	RS05357									HYPOTHETICAL PROTEIN	V.I.D
RSp0839	RS05356			-4.87	0.00	5.74	0.00	3.89	0.00	HYPOTHETICAL PROTEIN	V.I.B
RSp0840	RS05355			-1.35	0.02	2.20	0.00	2.58	0.00	TRANSMEMBRANE METHYL-ACCEPTING CHEMOTAXIS TRANSDUCER	I.V.C
RSp0841	RS05354			-4.14	0.00	-7.08	0.00	7.19	0.00	LIPOPROTEIN	V.I.B
RSp0842	RS05353			-1.82	0.00	-3.98	0.00	4.11	0.00	LEUCINE-RICH-REPEAT PROTEIN	V.I.B
RSp0843	RS05352							3.77	0.00	TRANSCRIPTION REGULATOR	V.I.A
RSp0844	RS05351			-1.35	0.03	1.40	0.00	2.22	0.00	COG0702, PREDICTED NUCLEOSIDE-DIPHOSPHATE-SUGAR EPIMERASE	I
RSp0845	RS05350			-3.07	0.00	3.39	0.00	2.68	0.01	HYPOTHETICAL PROTEIN	V.I.D
RSp0846	RS05349			-1.15	0.03	0.49	0.00			AWR TYPE III EFFECTOR FAMILY PROTEIN	V.I.C
RSp0847	RS05348									AWR TYPE III EFFECTOR FAMILY PROTEIN	V.I.C
RSp0848	RS01619			-4.65	0.00	5.62	0.00	3.99	0.00	HYPOTHETICAL PROTEIN	V.I.D
RSp0849	RS01620							-1.20	0.02	TRANSCRIPTION REGULATOR 3-COMPARTMENT SIGNAL TRANSDUCTION SYSTEM, COMF	I.E.1
RSp0850	RS01621					-0.46	0.03			TRANSMEMBRANE 3-COMPARTMENT SIGNAL TRANSDUCTION SYSTEM, COMF	I.E.1
RSp0851	RS01622									TRANSCRIPTION REGULATOR TRANSCRIPTIONAL REGULATOR PRHJ	I.E.1
RSp0852	RS01623			-1.19	0.01	2.26	0.00	1.37	0.02	TRANSCRIPTION REGULATOR RESPONSE REGULATOR	I.E.1
RSp0853	RS01624			-5.53	0.01	6.91	0.00			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp0854	RS01625			-7.19	0.00	7.85	0.00	3.38	0.00	HRP-RELATED PROTEIN	V.I.B
RSp0855	RS01626			-3.65	0.00	-7.68	0.03	7.21	0.00	HRP PILUS SUBUNIT HRPY	I.V.E.2
RSp0856	RS01627			-4.56	0.00	-6.67	0.00	6.34	0.00	HRPX	I.V.E.2
RSp0857	RS01628			-1.96	0.01	-4.34	0.00	5.71	0.00	TRANSMEMBRANE HRPW	I.V.E.2
RSp0858	RS01629					-4.45	0.00	4.08	0.00	HRPV	V.I.C
RSp0859	RS01630			-3.91	0.00	-7.07	0.00	7.62	0.00	TRANSMEMBRANE HRP CONSERVED PROTEIN HRCS	I.V.E.2
RSp0860	RS01631					7.89	0.00	5.12	0.00	TRANSMEMBRANE HRP CONSERVED PROTEIN HRCS	I.V.E.2
RSp0861	RS01632			-5.74	0.00	7.23	0.01	5.73	0.00	HRP CONSERVED PROTEIN HRCQ	I.V.E.2
RSp0862	RS01633			-5.45	0.00	5.58	0.00	2.68	0.01	HRP ASSOCIATED PROTEIN HpaP	V.I.C
RSp0863	RS01634			-2.55	0.00	3.43	0.00	1.91	0.00	TRANSMEMBRANE HRP CONSERVED PROTEIN HRCV	I.V.E.2
RSp0864	RS01635					1.01	0.00			TRANSMEMBRANE HRP CONSERVED PROTEIN HRCU	I.V.E.2
RSp0865	RS01636			-3.36	0.00	-6.96	0.00	6.35	0.00	HRPK	I.V.E.2
RSp0866	RS01637					-7.61	0.00	8.00	0.00	HRPJ PROTEIN	V.I.C
RSp0867	RS01638			-1.77	0.01	-4.76	0.00	6.09	0.00	TRANSMEMBRANE HRP CONSERVED LIPOPROTEIN HRCJ	I.V.E.2
RSp0868	RS01639					-6.64	0.00	7.37	0.00	HRPH	V.I.C
RSp0869	RS01640					-5.43	0.00	6.28	0.00	HRPF	I.V.E.2
RSp0870	RS01641					-3.98	0.00	4.60	0.00	HRP CONSERVED PROTEIN HRCN	I.V.E.2
RSp0871	RS01642					-5.71	0.00	6.03	0.00	HRPD	V.I.C
RSp0872	RS01643					-4.02	0.00	5.88	0.00	TRANSMEMBRANE HRP CONSERVED PROTEIN HRCT	I.V.E.2
RSp0873	RS01644			-3.09	0.00	-5.10	0.00	7.69	0.00	TRANSCRIPTION REGULATOR REGULATORY PROTEIN HRPB	I.E.1
RSp0874	RS01645			-0.85	0.00	-1.33	0.00	1.08	0.00	TRANSMEMBRANE HRP CONSERVED PROTEIN HRCC	I.V.E.2
RSp0875	RS01646					-5.69	0.00	5.99	0.00	POPC PROTEIN	V.I.E
RSp0876	RS01647			-3.94	0.00	-8.93	0.00	8.89	0.00	POPB PROTEIN	V.I.E
RSp0877	RS01648			-5.80	0.00	-8.95	0.00	9.14	0.00	POPA PROTEIN	V.I.E
RSp0878	RS01649							0.63	0.00	SIGNAL PEPTIDE OUTER MEMBRANE RECEPTOR PROTEIN PRHA	I.E.1
RSp0879	RS01650			-1.79	0.03	3.20	0.00	2.72	0.00	HYPOTHETICAL PROTEIN	V.I.D
RSp0880	RS01651					1.35	0.00			SIGNAL PEPTIDE POLYGALACTURONASE PRECURSOR (PECTINASE)	I.IA.3
RSp0881	RS01652					-0.42	0.02	2.81	0.00	TRANSMEMBRANE GLYCOSYL HYDROLASE	V.I.B
RSp0882	RS01653			-5.23	0.00	6.16	0.00	4.61	0.00	HYPOTHETICAL PROTEIN	V.I.D
RSp0883	RS01654			-4.56	0.02	-1.36	0.00	1.30	0.00	HYPOTHETICAL PROTEIN	V.I.B
RSp0884	RS01655			-0.45	0.02	0.48	0.01	0.60	0.01	TRANSMEMBRANE	V.I.B

RSp1001	RSO2334				0,96	0,01				SIGNAL PEPTIDE	VI.D	
RSp1002	RSO2335				0,76	0,04				SIGNAL PEPTIDE TEK PROTEIN	VI.C	
RSp1003	RSO2336			0,42	0,05					TRANSCRIPTION REGULATOR TRANSCRIPTION REGULATOR XPSR	III.A.1	
RSp1004	RSO2337					-0,62	0,01			TRANSMEMBRANE DTDp-GLUCOSE 4,6-DEHYDRATASE	II.B.2	
RSp1005	RSO2338				0,43	0,03		-1,37	0,00	TRANSMEMBRANE	VI.B	
RSp1006	RSO2340	0,20	0,05						-0,41	0,00	EPS AMINOTRANSFERASE	III.A.1
RSp1007	RSO2341									ACETYL TRANSFERASE	III.A.1	
RSp1008	RSO2342			0,37	0,00					TRANSMEMBRANE GLYCOSYL TRANSFERASE	III.A.1	
RSp1009	RSO2343			0,42	0,01				-0,38	0,03	GLYCOSYLTRANSFERASE	III.A.1
RSp1010	RSO2344									CONSERVED HYPOTHETICAL PROTEIN	VI.C	
RSp1011	RSO2345			0,31	0,01					OXIDOREDUCTASE COG1063, Threonine dehydrogenase and related Zn-dependent	VI.C	
RSp1012	RSO2346			0,40	0,03			-0,50	0,00	COG0110, Acetyltransferase	VI.C	
RSp1013	RSO2347	-0,46	0,00	0,26	0,01	-0,61	0,01	-0,92	0,03	COG0438, Glycosyltransferase	VI.C	
RSp1014	RSO2348			0,32	0,05					TRANSMEMBRANE EPS I POLYSACCHARIDE EXPORT INNER MEMBRANE PRO	III.A.1	
RSp1015	RSO2349									TRANSMEMBRANE EPS I POLYSACCHARIDE EXPORT INNER MEMBRANE PRO	III.A.1	
RSp1016	RSO2350									OXIDOREDUCTASE NDP-N-ACETYL-D-GALACTOSAMINURONIC ACID DEHYDR	II.B	
RSp1017	RSO2355			0,52	0,00			-0,63	0,02	UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE	III.A.1	
RSp1018	RSO2356	0,27	0,00					-0,63	0,01	TRANSMEMBRANE EPS I POLYSACCHARIDE EXPORT PROTEIN	III.A.1	
RSp1019	RSO2353	0,34	0,02	0,43	0,01			-0,81	0,00	LOW MOLECULAR WEIGHT PROTEIN-TYROSINE-PHOSPHATASE	III.A.1	
RSp1020	RSO2354	0,30	0,02					-0,38	0,02	TRANSMEMBRANE EPS I POLYSACCHARIDE EXPORT OUTER MEMBRANE PRO	III.A.1	
RSp1021	RSO2358							-0,71	0,01	HYPOTHETICAL PROTEIN	VI.D	
RSp1022	RSO2359							2,87	0,04	HYPOTHETICAL PROTEIN	VI.D	
RSp1023	RSO2360			0,34	0,02	-0,43	0,01	0,99	0,02	TRANSCRIPTION REGULATOR RESPONSE REGULATOR	VI.A	
RSp1024	RSO2361					1,86	0,00			AWR TYPE III EFFECTOR FAMILY PROTEIN	VI.C	
RSp1025	RSO2362			-1,07	0,00	0,99	0,00	1,16	0,00	TRANSMEMBRANE AMINO-ACID EFFLUX PROTEIN	IV.D.2	
RSp1026	RSO2363							1,02	0,05	SIGNAL PEPTIDE	VI.C	
RSp1027	RSO2364					-0,45	0,00			TRANSMEMBRANE METHYL-ACCEPTING CHEMOTAXIS TRANSDUCER	VI.C	
RSp1028	RSO2365					-0,54	0,03	-1,72	0,02	HYPOTHETICAL PROTEIN	VI.D	
RSp1029	RSO2366									OXIDOREDUCTASE TRANSMEMBRANE ACYL-CoA DESATURASE (FATTY ACID [I	I.1	
RSp1030	RSO2367					-0,33	0,04			COG3687, PREDICTED METAL- DEPENDENT HYDROLASE	VI.C	
RSp1031	RSO2368					-1,94	0,01	3,50	0,00	HYPOTHETICAL PROTEIN	VI.D	
RSp1032	RSO2369					-1,07	0,00	1,68	0,00	CONSERVED HYPOTHETICAL PROTEIN	VI.C	
RSp1033	RSO2370							-0,58	0,01	COG2916, DNA-binding protein H-NS - related protein	VI.A	
RSp1034	RSO2371					-0,71	0,00			SIGNAL PEPTIDE	VI.C	
RSp1035	RSO2372					-0,60	0,01	-1,05	0,00	CONSERVED HYPOTHETICAL PROTEIN	VI.C	
RSp1036	RSO2373					-0,52	0,00	-0,51	0,04	CONSERVED HYPOTHETICAL PROTEIN	VI.C	
RSp1037	RSO2374					-1,69	0,04			TRANSMEMBRANE	VI.C	
RSp1038	RSO2375					-0,56	0,00			TRANSMEMBRANE LIPOPROTEIN	VI.D	
RSp1039	RSO2376			0,51	0,04					TRANSMEMBRANE OUTER MEMBRANE CHANNEL LIPOPROTEIN	IV.D	
RSp1040	RSO2377					-0,38	0,01			TRANSMEMBRANE CATION EFFLUX SYSTEM PROTEIN	IV.D.4	
RSp1041	RSO2378					-0,61	0,01			TRANSMEMBRANE CATION TRANSPORTER PROTEIN	IV.D.4	
RSp1042	RSO2379					-0,37	0,03	-0,56	0,05	TRANSCRIPTION REGULATOR TWO-COMPONENT RESPONSE REGULATOR	VI.A	
RSp1043	RSO2380					-0,46	0,02	-0,72	0,03	TRANSCRIPTION REGULATOR TWO-COMPONENT SENSOR HISTIDINE KINASE	VI.A	
RSp1044	RSO2381					-0,40	0,02			TRANSMEMBRANE COBALT-NICKEL-RESISTANCE SYSTEM PROTEIN	IV.G	
RSp1045	RSO2382									HYPOTHETICAL PROTEIN	VI.B	
RSp1046	RSO2383							-0,97	0,03	TRANSMEMBRANE AMINO ACID TRANSPORTER PROTEIN	IV.D.2	
RSp1047	RSO2384					1,17	0,00			TRANSMEMBRANE TRANSPORTER PROTEIN	IV.D	
RSp1048	RSO2385					0,56	0,00			OXIDOREDUCTASE FORMATE DEHYDROGENASE	I.H.2	
RSp1049	RSO2386					0,49	0,00			HYPOTHETICAL PROTEIN	VI.D	
RSp1050	RSO2387									FORMATE DEHYDROGENASE ASSOCIATED PROTEIN (FDHD PROTEIN)	I.H.2	
RSp1051	RSO2388									SIGNAL TRANSDUCTION PROTEIN EAL DOMAIN	VI.A	
RSp1052	RSO2389							-0,82	0,01	TRANSMEMBRANE POTASSIUM UPTAKE PROTEIN	IV.D.4	
RSp1053	RSO2390					0,63	0,00	-0,82	0,01	TRANSCRIPTION REGULATOR COLD SHOCK PROTEIN ACTIVATOR	VI.A	
RSp1054	RSO2391	0,24	0,03					-0,50	0,03	TRANSCRIPTION REGULATOR COLD SHOCK PROTEIN ACTIVATOR	VI.A	
RSp1055	RSO2392					0,36	0,03	-1,06	0,02	OXIDOREDUCTASE TRANSMEMBRANE ALDEHYDE DEHYDROGENASE	I.I.4	
RSp1056	RSO2393					-0,44	0,00			BETA-ALANINE-PYRUVATE AMINOTRANSFERASE (OMEGA-AMINO ACID-PYR	I.F.14	
RSp1057	RSO2394									TRANSCRIPTION REGULATOR	VI.A	
RSp1058	RSO2395					-0,48	0,00			ACETOACETATE DECARBOXYLASE	I	
RSp1059	RSO2396					-0,44	0,00	0,97	0,04	OXIDOREDUCTASE DEHYDROGENASE/REDUCTASE	I	
RSp1060	RSO2397							0,56	0,03	TRANSMEMBRANE COG1752, Predicted esterase of the alpha-beta hydrolase super	I	
RSp1061	RSO2398									OXIDOREDUCTASE COG0673, Predicted dehydrogenases and related proteins	I	
RSp1062	RSO2469					-1,81	0,03	-0,94	0,00	FERRISDEROPHORE RECEPTOR	IV.D.5	
RSp1063	RSO2470			0,61	0,01	-0,40	0,02			SIGNAL PEPTIDE	VI.D	
RSp1064	RSO2472									TRANSMEMBRANE	VI.C	
RSp1065	RSO2471									SIGNAL PEPTIDE	VI.B	
RSp1066	RSO3027	0,62	0,01							CONSERVED HYPOTHETICAL PROTEIN	VI.C	
RSp1067	RSO6033									CONSERVED HYPOTHETICAL PROTEIN	VI.C	
RSp1068	RSO2476									CONSERVED HYPOTHETICAL PROTEIN	VI.C	
RSp1069	RSO2556							-0,72	0,05	TRANSMEMBRANE	VI.D	
RSp1070	RSO2559			0,60	0,04					TRANSMEMBRANE	VI.E	
RSp1071	RSO2473									HEMAGGLUTININ-RELATED PROTEIN	VI.B	
RSp1072	RSO2541					-0,36	0,01	-1,77	0,03	CONSERVED HYPOTHETICAL PROTEIN	VI.C	
RSp1073	RSO2477							-0,51	0,03	HEMAGGLUTININ-RELATED PROTEIN	VI.C	
RSp1074	RSO2573									HEMOLYSIN ACTIVATING-LIKE PROTEIN	IV.E.2	
RSp1075	RSO2577			0,65	0,00			-0,99	0,02	ACTIVATION/SECRETION PROTEIN	IV.E.2	
RSp1076	RSO2580					0,99	0,02			OXIDOREDUCTASE GLUCOSE-FRUCTOSE OXIDOREDUCTASE	I.F	
RSp1077	RSO2582					-0,78	0,00	-0,58	0,01	TRANSMEMBRANE	VI.D	
RSp1078	RSO2585					-0,78	0,00			LIPOPROTEIN	VI.B	
RSp1079	RSO2586					-0,22	0,03			TRANSCRIPTION REGULATOR SIGMA-54 INTERACTING PROTEIN	VI.A	
RSp1080	RSO2587									TRANSMEMBRANE	VI.C	
RSp1081	RSO2588							-0,37	0,01	SIGNAL PEPTIDE	VI.D	
RSp1082	RSO2589					-0,49	0,03			TRANSMEMBRANE PILUS ASSEMBLY PROTEIN TADD	III.A.2	
RSp1083	RSO2590									TRANSMEMBRANE PILUS ASSEMBLY PROTEIN TADC	III.A.2	
RSp1084	RSO2591									TRANSMEMBRANE PILUS ASSEMBLY PROTEIN TADB	III.A.2	
RSp1085	RSO2592					-0,46	0,00			SECRETION ATPase	III.A.2	
RSp1086	RSO2593									PILUS ASSEMBLY PROTEIN	III.A.2	
RSp1087	RSO2594	0,41	0,05			-0,27	0,02			SIGNAL PEPTIDE PILUS ASSEMBLY PROTEIN, SECRETIN CPAC	III.A.2	
RSp1088	RSO2597									CONSERVED HYPOTHETICAL PROTEIN	VI.C	
RSp1089	RSO2596									SIGNAL PEPTIDE COG3745, Flp pilus assembly protein	III.A.2	
RSp1090	RSO2595									TRANSMEMBRANE COG4961, FLP PILUS ASSEMBLY PROTEIN	III.A.2	
RSp1091	RSO2612							0,91	0,00	TRANSMEMBRANE PREPILIN PEPTIDASE	III.A.2	
RSp1092	RSO2598									PILIN	III.A.2	
RSp1093	RSO2599									TRANSMEMBRANE	VI.C	
RSp1094	RSO2600					1,38	0,00			TRANSMEMBRANE	VI.C	
RSp1095	RSO2601					-0,53	0,00	0,90	0,00	SIGNAL PEPTIDE ACTIVATION/SECRETION PROTEIN	IV.E.2	
RSp1096	RSO2602					-0,61	0,00	-0,80	0,01	TRANSCRIPTION REGULATOR	VI.A	
RSp1097	RSO2603					-0,37	0,01	-1,20	0,00	TRANSMEMBRANE SIGNAL TRANSDUCTION PROTEIN EAL - GGDEF DOMAINS	VI.A	
RSp1098	RSO2604					-0,51	0,01	-1,64	0,00	TRANSCRIPTION REGULATOR HNS-LIKE PROTEIN	VI.A	
RSp1099	RSO2605							-2,13	0,01	TRANSMEMBRANE METHYL-ACCEPTING CHEMOTAXIS TRANSDUCER	IV.C	
RSp1100	RSO2606									TRANSMEMBRANE LIPOPROTEIN	VI.B	
RSp1101	RSO2607			0,35	0,01	-0,44	0,00			UDP-GLUCOSE 4-EPIMERASE	I.I.4	
RSp1102	RSO2608					-0,68	0,00			INTEGRASE/RECOMBINASE	VI.A	
RSp1103	RSO2609									HYPOTHETICAL PROTEIN	VI.D	
RSp1104	RSO2610							1,71	0,04	TREHALOSE-PHOSPHATASE	IV.F.2	
RSp1105	RSO2613									ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE	IV.F.2	
RSp1106	RSO2614					-1,64	0,00	-0,53	0,04	TRANSCRIPTION REGULATOR	VI.A	
RSp1107	RSO2615	0,23	0,05			-1,66	0,00			ORGANIC HYDROPEROXIDE RESISTANCE PROTEIN	IV.G.4	
RSp1108	RSO2616					-1,43	0,01			SIGNAL PEPTIDE LIPASE	I.I.1	
RSp1109	RSO2617					-0,74	0,00			CONSERVED HYPOTHETICAL PROTEIN	VI.C	
RSp1110	RSO2618					-0,89	0,01	-0,58	0,05	TRANSCRIPTION REGULATOR	VI.A	
RSp1111	RSO2619							-1,02	0,00	LIPASE	I.I.1	
RSp1112	RSO2620					-2,47	0,03	0,74	0,03	TRANSMEMBRANE TRANSMEMBRANE MULTIDRUG EFFLUX SYSTEM PROTEIN I	IV.G.2	

RSp113	RS02621				1.07	0.04			TRANSMEMBRANE TRANSMEMBRANE MULTIDRUG-EFFLUX SYSTEM LIPOPRO	IV.D	
RSp114	RS05506	0.94	0.05		0.88	0.02			OUTER-MEMBRANE DRUG EFFLUX PROTEIN	IV.D	
RSp115	RS05505								TRANSCRIPTION REGULATOR	V.IA	
RSp116	RS05504								LOW SPECIFICITY L-THREONINE ALDOLASE	I.I.3	
RSp117	RS05502								TRANSMEMBRANE	V.I.D	
RSp118	RS05501			-0.40	0.05		-1.27	0.01	CONSERVED HYPOTHETICAL PROTEIN	V.I.C	
RSp119	RS05500			-0.54	0.04		-0.73	0.04	TRANSCRIPTION REGULATOR	V.IA	
RSp120	RS05499			-0.75	0.00				COG2030, Acyl dehydratase	I	
RSp121	RS05498								TRANSCRIPTION REGULATOR	V.IA	
RSp122	RS05497					0.89	0.01		COG2220, Predicted Zn-dependent hydrolases of the beta-lactamase fold	I.I	
RSp123	RS05496					3.04	0.00		OXIDOREDUCTASE KOG1208, Dehydrogenases with different specificities (related t	I	
RSp124	RS05494	-2.66	0.00	-1.14	0.00	3.95	0.00	2.61	OXIDOREDUCTASE NADP-DEPENDENT ZINC-TYPE ALCOHOL DEHYDROGENASE	I	
RSp125	RS05495	-3.26	0.00	-1.25	0.00	1.86	0.00	1.96	HYPOTHETICAL PROTEIN	V.I.D	
RSp126	RS05493			-0.43	0.02				TRANSCRIPTION REGULATOR	V.IA	
RSp127	RS05492		0.50	0.02	-0.41	0.01			ABC TRANSPORTER TRANSMEMBRANE PROTEIN	IV.D	
RSp128	RS05491			-0.52	0.00				ARSENATE REDUCTASE (ARSENICAL PUMP MODIFIER)	IV.G	
RSp129	RS05489	-0.92	0.03	-0.52	0.00	1.00	0.00	1.10	TRANSCRIPTION REGULATOR ARSENICAL RESISTANCE OPERON REPRESSOR	IV.G	
RSp130	RS05488								HYPOTHETICAL PROTEIN	V.I.D	
RSp131	RS05485								HYPOTHETICAL PROTEIN	V.I.D	
RSp132	RS05487								CONSERVED HYPOTHETICAL PROTEIN	V.I.C	
RSp133	RS05510								HYPOTHETICAL PROTEIN	V.I.D	
RSp134	RS05509			-0.29	0.02	-0.87	0.03		HYPOTHETICAL PROTEIN	V.I.D	
RSp137	RS05482								TRANSMEMBRANE RHS-RELATED PROTEIN	V.I.C	
RSp138	RS05481		1.02	0.00	-0.57	0.03			CONSERVED HYPOTHETICAL PROTEIN	V.I.C	
RSp139	RS05480		0.82	0.01					VGR-RELATED PROTEIN	V.I.C	
RSp140	RS05478		0.61	0.05			-0.60	0.00	ABC TRANSPORTER SUBSTRATE-BINDING PERIPLASMIC PROTEIN (BBP)	IV.D	
RSp141	RS05474				-1.26	0.00	-0.73	0.04	TRANSCRIPTION REGULATOR	V.IA	
RSp142	RS05470				-0.49	0.01			TRANSCRIPTION REGULATOR	V.IA	
RSp143	RS05469				-0.42	0.03			GLUTAMINASE A	I.A.19	
RSp144	RS05467						-0.65	0.05	ABC TRANSPORTER COG4149, ABC-type molybdate transport system, permease co	IV.D	
RSp145	RS05462				-0.50	0.01			ABC TRANSPORTER ATP-BINDING PROTEIN	IV.D	
RSp146	RS05458								TRANSCRIPTION REGULATOR	V.IA	
RSp147	RS05455		0.78	0.01	-0.30	0.01		-2.32	OXIDOREDUCTASE COG2085, Predicted dinucleotide-binding enzymes	I	
RSp148	RS05450								SIGNAL PEPTIDE COG0596, Predicted hydrolases or acyltransferases (alpha/beta hyl	I	
RSp150	RS05437				2.41	0.00	2.62	0.04	HYPOTHETICAL PROTEIN	V.I.D	
RSp151	RS05436								COG1942, Uncharacterized protein, 4-oxalocrotonate tautomerase homolog	V.I.C	
RSp153	RS05434			-0.21	0.05				TRANSCRIPTION REGULATOR	V.IA	
RSp154	RS05433								TRANSMEMBRANE	V.I.C	
RSp155	RS05432								SIGNAL TRANSDUCTION PROTEIN EAL - GGDEF DOMAINS	V.IA	
RSp156	RS05430								SIGNAL PEPTIDE	V.I.D	
RSp157	RS05428		0.69	0.03					TRANSCRIPTION REGULATOR	V.IA	
RSp158	RS05427								COG3813, Uncharacterized protein conserved in bacteria	V.I.C	
RSp159	RS05426								COG0589, Universal stress protein UspA and related nucleotide-binding proteins	IV.G	
RSp160	RS05425		0.33	0.00	-0.37	0.02	-0.57	0.05	SIGNAL PEPTIDE COG3678, P pilus assembly/Cpx signaling pathway, periplasmic inl	V.IA	
RSp161	RS05646				-0.23	0.01			TRANSCRIPTION REGULATOR TWO-COMPONENT RESPONSE REGULATOR	V.IA	
RSp162	RS05645						-0.37	0.04	TRANSCRIPTION REGULATOR TWO-COMPONENT SENSOR HISTIDINE KINASE	V.IA	
RSp163	RS05644				-0.58	0.02	-1.92	0.01	HYPOTHETICAL PROTEIN	V.I.D	
RSp164	RS05643				-0.46	0.04			TRANSCRIPTION REGULATOR	V.IA	
RSp165	RS05642				-0.57	0.02			SIGNAL PEPTIDE	V.I.B	
RSp166	RS05641								SIGNAL PEPTIDE COG4727, Uncharacterized protein conserved in bacteria	V.I.C	
RSp167	RS05823				1.08	0.00			COG2303, BetA, Choline dehydrogenase and related flavoproteins AND KOG2624, T	I	
RSp168	RS05639				0.51	0.05			TRANSMEMBRANE	V.I.C	
RSp169	RS05059				0.54	0.00			CONSERVED HYPOTHETICAL PROTEIN	V.I.C	
RSp170	RS05060						-0.59	0.04	SIGNAL PEPTIDE	V.I.C	
RSp171	RS05061				-0.47	0.04			TRANSMEMBRANE	V.I.C	
RSp172	RS05062						-0.44	0.04	TRANSMEMBRANE	V.I.C	
RSp173	RS05063				-0.26	0.04	-0.46	0.03	TRANSMEMBRANE COG1858, Cytochrome c peroxidase	I	
RSp174	RS05064		0.68	0.01					ACID PHOSPHATASE	I.F	
RSp175	RS05065				-0.46	0.00			CONSERVED HYPOTHETICAL PROTEIN	V.I.C	
RSp176	RS05066	0.04	0.04				2.45	0.01	HYPOTHETICAL PROTEIN	V.I.D	
RSp177	RS05067								TRANSMEMBRANE	V.I.C	
RSp178	RS05068				-0.78	0.02			TRANSCRIPTION REGULATOR COMPOSITE TWO-COMPONENT TRANSCRIPTION	V.IA	
RSp179	RS05069				-0.58	0.01		1.51	TIS1021-TRANSPOSASE	V.A	
RSp180	RS05070		0.91	0.03	-1.47	0.00	1.85	0.00	HEMAGGLUTININ/HEMOLYSIN-RELATED PROTEIN	V.I.C	
RSp181	RS05071		1.33	0.02	-1.90	0.00			TRANSMEMBRANE TYPE I SECRETION SYSTEM OUTER MEMBRANE EFFLUX P	IV.E.2	
RSp182	RS05072		1.76	0.04	-1.24	0.00	-3.02	0.04	ABC TRANSPORTER TYPE I SECRETION SYSTEM, ATP-BINDING TRANSMEMBR	IV.E.2	
RSp183	RS05073		1.31	0.01	-1.47	0.00	-3.58	0.00	TRANSMEMBRANE TYPE I SECRETION SYSTEM PROTEIN	IV.E.2	
RSp184	RS05074								FRUCTOKINASE-LIKE PROTEIN (SUGAR KINASE)	I	
RSp185	RS03129				-0.53	0.00		-0.22	D-SERINE DEAMINASE (D-SERINE DEHYDRATASE)	I.A.10	
RSp186	RS03130				-0.86	0.00			TRANSCRIPTION REGULATOR	V.IA	
RSp187	RS03131				-0.48	0.01			N-ACYL-D-GLUTAMATE DEACYLASE	I	
RSp188	RS03132		-0.59	0.05	-0.72	0.00			COG0251, Translation initiation inhibitor	I.B.7	
RSp189	RS03133		-0.21	0.04	-0.26	0.01			TRANSMEMBRANE HIGH-AFFINITY GLUCONATE TRANSPORTER (GNT-III SYST	IV.D.3	
RSp190	RS03134		0.41	0.02	-0.51	0.00			BIFUNCTIONAL ALKH PROTEIN (KHG/KDPG ALDOLASE); 4-HYDROXY-2-OXOGL I.F.	1.B	
RSp191	RS04751								3,4-DIHYDROXY-2-BUTANONE 4-PHOSPHATE SYNTHASE	I.B.7	
RSp192	RS03136								TRANSCRIPTION REGULATOR	V.IA	
RSp193	RS03137		0.97	0.03					TRANSMEMBRANE COG1807, 4-amino-4-deoxy-L-arabinose transferase and related	I	
RSp194	RS03138								TRANSMEMBRANE	V.I.B	
RSp195	RS03139				-0.39	0.02	-0.80	0.03	TRANSCRIPTION REGULATOR TWO COMPONENT TRANSMEMBRANE SENSOR	V.IA	
RSp196	RS03140				-0.50	0.03			TRANSCRIPTION REGULATOR TWO COMPONENT RESPONSE REGULATOR	V.IA	
RSp197	RS03141				-0.82	0.00			MEMBRANE FUSION PROTEIN	III.B.2	
RSp198	RS03142		0.73	0.03					TRANSMEMBRANE DRUG EFFLUX PUMP	IV.D	
RSp199	RS03143								TRANSMEMBRANE DRUG EFFLUX PROTEIN	IV.D	
RSp200	RS03144				-0.92	0.02	0.92	0.04	TRANSMEMBRANE OUTER MEMBRANE CHANNEL LIPOPROTEIN	IV.D	
RSp201	RS03145								SIGNAL PEPTIDE	V.I.C	
RSp202	RS03146						0.91	0.02	TRANSMEMBRANE O-ANTIGEN POLYMERASE	I.B.2	
RSp203	RS03147								SIGNAL TRANSDUCTION PROTEIN GGDEF DOMAIN	V.IA	
RSp204	RS03148				-0.66	0.03			HYPOTHETICAL PROTEIN	V.I.D	
RSp205	RS03149				-0.33	0.02			CONSERVED HYPOTHETICAL PROTEIN	V.I.C	
RSp206	RS03150								OXIDOREDUCTASE TRANSMEMBRANE CYTOCHROME BD-II OXIDASE (SUBUN I.G.1	I	
RSp207	RS03151								OXIDOREDUCTASE TRANSMEMBRANE CYTOCHROME BD-II OXIDASE (SUBUN I.G.1	I	
RSp208	RS03152		0.37	0.05	-0.41	0.02			SIGNAL TRANSDUCTION PROTEIN EAL - GGDEF DOMAINS	V.IA	
RSp209	RS03153		-0.66	0.02					TRANSMEMBRANE METHYL-ACCEPTING CHEMOTAXIS TRANSDUCER PROTEIN	V.I.C	
RSp210	RS03154				-0.58	0.03	-1.81	0.00	TRANSMEMBRANE LIPOPROTEIN	V.I.C	
RSp211	RS03155		1.03	0.02					TRANSMEMBRANE CARDIOLIPIN SYNTHETASE	I.B.1	
RSp212	RS03156				-0.43	0.02	3.92	0.01	HYPOTHETICAL PROTEIN	V.I.D	
RSp213	RS03157		0.81	0.01					TRANSMEMBRANE COG0534, Na+-driven multidrug efflux pump	IV.G	
RSp214	RS03158				-0.59	0.03	-1.07	0.00	COG3644, Uncharacterized protein conserved in bacteria	V.I.C	
RSp215	RS03159				0.93	0.00			PSEUDOGENE (TRUNCATED ANKYRIN REPEAT HARBORING PROTEIN)	V.I.B	
RSp216	RS03160				-0.64	0.00	-0.96	0.01	ISRs014-TRANSPOSASE ORFB	V.A	
RSp218	RS03162						1.91	0.00	1.19	PSEUDOGENE (N-TERMINAL FRAGMENT)	V.I.D
RSp219	RS03163								OXIDOREDUCTASE NITRATE REDUCTASE LARGE SUBUNIT	I.H.2	
RSp220	RS03164								OXIDOREDUCTASE FLAVOPROTEIN FAD	I.H.2	
RSp221	RS03165								OXIDOREDUCTASE NITRITE REDUCTASE NADPH (SMALL SUBUNIT)	I.H.2	
RSp222	RS03166								OXIDOREDUCTASE NITRITE REDUCTASE NADPH (LARGE SUBUNIT)	I.H.2	
RSp223	RS03167								TRANSMEMBRANE HIGH AFFINITY NITRATE TRANSPORTER	I.H.2	
RSp224	RS03168				-0.41	0.02	-0.76	0.05	TRANSMEMBRANE AEROTAXIS SENSOR RECEPTOR (CHEMOTAXIS TRANSDUC	IV.C	
RSp225	RS03169								ISOPENTENYL TRANSFERASE	I	
RSp226	RS03170								HYPOTHETICAL PROTEIN	V.I.D	
RSp227	RS03171				-0.80	0.04			OXIDOREDUCTASE COG2141, Coenzyme F420-dependent N5,N10-methylene tetra	I	
RSp228	RS03172						3.51	0.02	SIGNAL PEPTIDE	V.I.C	
RSp229	RS03173				-0.37	0.05			COG0596, Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfam	I	

RSp1349	RS04778								TRANSCRIPTION REGULATOR	V.I.A					
RSp1350	RS04779			-0.39	0.02				COG3832, Uncharacterized conserved protein	V.I.C					
RSp1351	RS04780			-0.44	0.00				TRANSCRIPTION REGULATOR	V.I.A					
RSp1352	RS04781								TRANSMEMBRANE COG1280, Threonine efflux protein	I.V.D.2					
RSp1353	RS04783			-0.79	0.00	-1.16	0.02	-2.72	0.00	COG0251, Translation initiation inhibitor	I.I.B.7				
RSp1354	RS04818			-0.40	0.01	-0.67	0.01	-2.09	0.01	HYPOTHETICAL PROTEIN	V.I.D				
RSp1355	RS04819								TRANSMEMBRANE LIPOPROTEIN	V.I.D					
RSp1356	RS04820								TRANSMEMBRANE	V.I.D					
RSp1357	RS04822			-0.31	0.01				TRANSCRIPTION REGULATOR	V.I.A					
RSp1358	RS04784	-0.75	0.03						BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE	I.A.2					
RSp1359	RS04823								TRANSMEMBRANE EFFLUX PUMP ANTIBIOTIC RESISTANCE PROTEIN	I.V.D					
RSp1360	RS04825			-0.45	0.01	-1.07	0.00	-1.37	0.00	TRANSMEMBRANE	V.I.D				
RSp1361	RS04826								HYPOTHETICAL PROTEIN	V.I.B					
RSp1363	RS04782								TRANSMEMBRANE METHYL-ACCEPTING CHEMOTAXIS TRANSDUCER	I.V.C					
RSp1365	RS02094	-4.71	0.02						OXIDOREDUCTASE 2-OXOGLUTARATE DEHYDROGENASE E1 DECARBOXYLASE	I.I.6					
RSp1365	RS02093			0.68	0.00	-0.32	0.00		TRANSMEMBRANE COG0204, 1-acyl-sn-glycerol-3-phosphate acyltransferase	I					
RSp1366	RS02092					0.94	0.00	1.09	0.03	TRANSMEMBRANE THIAMINE BIOSYNTHESIS PROTEIN APBE	I.B.8				
RSp1367	RS02091					0.62	0.05		COG3245, Cytochrome c5	I.G.1					
RSp1368	RS02090								OXIDOREDUCTASE NITROUS-OXIDE REDUCTASE	I.F.5					
RSp1369	RS02089								TRANSCRIPTION REGULATOR TRANSMEMBRANE REGULATORY PROTEIN NOS1	I.F.5					
RSp1370	RS02088								SIGNAL PEPTIDE PERIPLASMIC COPPER-BINDING PROTEIN NOSD	I.F.5					
RSp1371	RS02087								ABC TRANSPORTER ABC-TYPE COPPER TRANSPORT SYSTEM, ATPase compo	I.F.5					
RSp1372	RS02086								TRANSMEMBRANE PROTEIN NOSY	I.F.5					
RSp1373	RS02085							-2.64	0.03	NOSL LIPOPROTEIN	I.F.5				
RSp1374	RS02084								SKWP PROTEIN 2	V.I.C					
RSp1375	RS02083			1.05	0.00				TRANSMEMBRANE	V.I.C					
RSp1376	RS02082					-0.80	0.00		TRANSMEMBRANE COG1296, Predicted branched-chain amino acid permease (azal	I.V.D					
RSp1377	RS02081					-2.23	0.00	-1.94	0.03	TRANSCRIPTION REGULATOR	V.I.A				
RSp1378	RS02080					-2.33	0.00	-3.58	0.00	COG2963: Transposase and inactivated derivatives	V.A				
RSp1379	RS02079							0.73	0.03	SIGNAL PEPTIDE	V.I.D				
RSp1380	RS02078			0.42	0.05				OXIDOREDUCTASE COG1249, Pyruvate/2-oxoglutarate dehydrogenase complex, dif	I					
RSp1381	RS02077			0.54	0.04				PHNA PROTEIN ALKYLPHOSPHONATE UPTAKE	V.I.C					
RSp1382	RS02076			-0.60	0.05	-0.54	0.01	-1.68	0.02	SIGNAL PEPTIDE	V.I.C				
RSp1383	RS02075								ALKANESULFONATES BINDING PROTEIN PRECURSOR	I.F.20					
RSp1384	RS02074					1.09	0.02	2.45	0.03	TRANSMEMBRANE	V.I.D				
RSp1385	RS02073								TRANSMEMBRANE	V.I.C					
RSp1386	RS02072			-2.39	0.00	2.47	0.00	0.95	0.01	LIPOPROTEIN	V.I.C				
RSp1387	RS02071								TRANSCRIPTION REGULATOR	V.I.A					
RSp1388	RS02070			-1.65	0.04	1.90	0.00	-3.77	0.00	HYPOTHETICAL PROTEIN	V.I.D				
RSp1389	RS02069					0.45	0.02		COG2220, PREDICTED ZINC-DEPENDENT HYDROLASE	I.I					
RSp1390	RS02068								TRANSCRIPTION REGULATOR RNA POLYMERASE SIGMA FACTOR FOR FLAGE	I.V.C					
RSp1391	RS02067					2.61	0.00		FLAGELLAR SYNTHESIS REGULATOR FieN	I.V.C					
RSp1392	RS02066								FLAGELLAR BIOSYNTHETIC PROTEIN FLHF	I.V.C					
RSp1393	RS02065								TRANSMEMBRANE FLAGELLAR BIOSYNTHESIS PROTEIN FLHA	I.V.C					
RSp1394	RS02064								TRANSMEMBRANE FLAGELLAR BIOSYNTHETIC PROTEIN FLHB	I.V.C					
RSp1395	RS02063							0.71	0.02	TRANSCRIPTION REGULATOR TRANSCRIPTION REGULATOR	V.I.A				
RSp1396	RS02062								TRANSMEMBRANE TRANSPORTER	I.V.D					
RSp1397	RS02061								3-DEHYDROQUINATE DEHYDRATASE (3-DEHYDROQUINASE) (TYPE II DHQASE)	I.A.5					
RSp1398	RS02060								OXIDOREDUCTASE SHIKIMATE 5-DEHYDROGENASE	I.A.5					
RSp1399	RS02059							0.62	0.02	SIGNAL PEPTIDE PORIN	I.V.D				
RSp1400	RS02058					-0.86	0.01		COG3185, 4-hydroxyphenylpyruvate dioxygenase AND COG1082, Sugar phosphate	I.I					
RSp1401	RS02057					-1.24	0.01		CHEMOTAXIS PROTEIN CHEZ	I.V.C					
RSp1402	RS02056					-0.74	0.02	-0.79	0.02	TRANSCRIPTION REGULATOR CHEMOTAXIS RESPONSE REGULATOR PROTEI	I.V.C				
RSp1403	RS02055								PROTEIN-GLUTAMATE METHYLESTERASE	I.V.C					
RSp1404	RS02054								CHEMOTAXIS PROTEIN	I.V.C					
RSp1405	RS02053					-0.60	0.02		CHEMOTAXIS PROTEIN METHYLTRANSFERASE	I.V.C					
RSp1406	RS02052							-1.08	0.02	TRANSMEMBRANE METHYL-ACCEPTING CHEMOTAXIS PROTEIN I (SERINE CH	I.V.C				
RSp1407	RS02051								CHEMOTAXIS PROTEIN CHEW	I.V.C					
RSp1408	RS05777								TRANSCRIPTION REGULATOR CHEMOTAXIS SENSOR HISTIDINE KINASE PROT	I.V.C					
RSp1409	RS05776					-0.64	0.00		TRANSCRIPTION REGULATOR CHEMOTAXIS RESPONSE REGULATOR PROTEI	I.V.C					
RSp1410	RS05775								TRANSMEMBRANE CHEMOTAXIS PROTEIN (MOTILITY PROTEIN B)	I.V.C					
RSp1411	RS05774					-0.91	0.00	-0.95	0.02	TRANSMEMBRANE CHEMOTAXIS PROTEIN (MOTILITY PROTEIN A)	I.V.C				
RSp1412	RS05773					-0.94	0.00		TRANSCRIPTION REGULATOR FLAGELLAR TRANSCRIPTIONAL ACTIVATOR	I.V.C					
RSp1413	RS03127					-1.29	0.01	-2.23	0.04	TRANSCRIPTION REGULATOR FLAGELLAR TRANSCRIPTIONAL ACTIVATOR	I.V.C				
RSp1414	RS05841					-0.38	0.05		HYPOTHETICAL PROTEIN	V.I.D					
RSp1415	RS03126								HYPOTHETICAL PROTEIN	V.I.D					
RSp1416	RS03125								TRANSMEMBRANE	V.I.B					
RSp1417	RS03124			-1.10	0.00	1.10	0.02	-0.38	0.04	0.95	0.02	2.21	0.00	TRANSMEMBRANE TRANSMEMBRANE EFFLUX PROTEIN	I.V.D
RSp1418	RS03123			-3.43	0.00	1.05	0.00			3.13	0.00	3.02	0.00	HYDROLASE	I.I
RSp1419	RS03122			-3.09	0.00	1.23	0.00	-0.22	0.01	2.48	0.00	2.80	0.00	PEPTIDE SYNTHASE	I.I.B.7
RSp1420	RS06015													HYPOTHETICAL PROTEIN	V.I.D
RSp1421	RS03121					-0.67	0.00					1.86	0.00	COG1804, Predicted acyl-CoA transferases/carnitine dehydratase	I
RSp1422	RS03120													PEPTIDE SYNTHETASE	I.I.B.7
RSp1423	RS03119													OXIDOREDUCTASE COG0644, Dehydrogenases (flavoproteins)	I
RSp1424	RS03118					0.79	0.01							DIAMINOBUTYRATE-PYRUVATE AMINOTRANSFERASE	I.V.F.2
RSp1425	RS03117					0.58	0.02					1.77	0.00	OXIDOREDUCTASE L-ORNITHINE 5-MONOXYGENASE	I.V.D.5
RSp1426	RS03116					0.66	0.00					1.44	0.00	HYPOTHETICAL PROTEIN	V.I.D
RSp1427	RS03115							0.43	0.01					SIGNAL PEPTIDE	V.I.D
RSp1428	RS03114					0.89	0.00					2.98	0.02	COG0607, Rhodanese-related sulfurtransferase	I
RSp1429	RS03113					0.48	0.04							COG0657, Esterase/lipase	I
RSp1430	RS03112					0.65	0.01							CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1431	RS03111													OXIDOREDUCTASE COG0665, Glycine/D-amino acid oxidases (deaminating)	I
RSp1432	RS03110					1.04	0.00							COG2140, Thermophilic glucose-6-phosphate isomerase and related metalloenzymes	I
RSp1433	RS03109					0.67	0.02	-0.38	0.04					HYPOTHETICAL PROTEIN	V.I.D
RSp1434	RS03108							-0.24	0.03					COG0318, Acyl-CoA synthetases (AMP-forming) / AMP-acid ligases II	I
RSp1435	RS03107					0.58	0.04							TRANSMEMBRANE COG0596, Predicted hydrolases or acyltransferases (alpha/beta	I
RSp1436	RS03106													Acetyltransferase	I
RSp1437	RS03105					0.60	0.05					1.78	0.00	HYPOTHETICAL PROTEIN	V.I.B
RSp1438	RS03104					-0.82	0.01					0.96	0.01	TRNA SYNTHETASE	I.I.D.1
RSp1439	RS03103													SERINE ACETYLTRANSFERASE	I.A.9
RSp1440	RS06034					2.84	0.00							HYPOTHETICAL PROTEIN	V.I.D
RSp1441	RS03102											-1.01	0.03	TRANSCRIPTION REGULATOR TWO-COMPONENT SENSOR KINASE	V.I.A
RSp1442	RS03101											0.47	0.01	TRANSCRIPTION REGULATOR TWO-COMPONENT RESPONSE REGULATOR	V.I.A
RSp1443	RS03100													SIGNAL PEPTIDE	V.I.B
RSp1444	RS03099							-0.48	0.05					HEMAGGLUTININ-RELATED PROTEIN	V.I.C
RSp1445	RS03098											-0.95	0.01	SIGNAL PEPTIDE ACTIVATION/SECRETION PROTEIN	I.V.E.2
RSp1446	RS03097													CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE	I.C
RSp1447	RS03096											1.10	0.01	ABC TRANSPORTER ABC-type branched-chain amino acid transport systems, peripl	I.V.D.2
RSp1448	RS03095													PYRUVATE KINASE II	I.H.8
RSp1449	RS03094													OXIDOREDUCTASE HYDROXYPYRUVATE REDUCTASE	I.I.4
RSp1450	RS03093											-0.80	0.01	TRANSCRIPTION REGULATOR	V.I.A
RSp1451	RS03092											-1.06	0.05	HYPOTHETICAL PROTEIN	V.I.D
RSp1452	RS03091											-0.66	0.01	HYPOTHETICAL PROTEIN	V.I.D
RSp1453	RS03090							-0.50	0.01					SIGNAL PEPTIDE COG3258, CYTOCHROME C	I.H
RSp1454	RS03089							-0.71	0.04					TRANSCRIPTION REGULATOR TWO-COMPONENT TRANSMEMBRANE SENSOR	V.I.A
RSp1455	RS03088													TRANSCRIPTION REGULATOR TWO-COMPONENT RESPONSE REGULATOR	V.I.A
RSp1456	RS05806													OUTER MEMBRANE LIPOPROTEIN	I.II.B.2
RSp1457	RS03087													SIGNAL PEPTIDE CATION-EFFLUX SYSTEM PROTEIN	I.V.D.4
RSp1458	RS03086													TRANSMEMBRANE TRANSPORTER PROTEIN	I.V.D
RSp1459	RS03085					0.46	0.00							SIGNAL PEPTIDE COG1574, Predicted metal-dependent hydrolase with the TIM-barr	I.I
RSp1460	RS03084							-2.71	0.01	4.14	0.03	4.03	0.03	HYPOTHETICAL PROTEIN	V.I.B
RSp1461	RS03083					-3.58	0.00	-3.74	0.00	5.07	0.03	3.21	0.00	SIGNAL PEPTIDE	V.I.C

RSp1462	RS03082	-1.66	0.00	2.30	0.00	2.78	0.00	3.96	0.00	Outer membrane efflux protein	IV.D
RSp1463	RS03081	-2.06	0.00	2.88	0.00	3.82	0.00	3.88	0.00	ABC TRANSPORTER HlyD family secretion protein	IV.D
RSp1464	RS03080	-0.89	0.00	1.52	0.01	3.76	0.01	3.23	0.00	ABC TRANSPORTER ABC-type transport system, ATPase component	IV.D
RSp1465	RS03079					1.41	0.02			ABC TRANSPORTER ABC-type transport system, permease component	IV.D
RSp1466	RS03078	-4.91	0.00	5.32	0.00	4.29	0.00	4.56	0.00	SIGNAL PEPTIDE	V.I.C
RSp1467	RS03077	-4.32	0.00	5.05	0.00	4.81	0.00	2.99	0.00	SIGNAL PEPTIDE	V.I.C
RSp1468	RS03076									SIGNAL PEPTIDE COG4313, Protein involved in meta-pathway of phenol degradation	IV.F.1
RSp1469	RS03075									TYROSINE PHOSPHATASE	V.I.B
RSp1470	RS03074			-0.41	0.05					TRANSCRIPTION REGULATOR	V.I.A
RSp1471	RS03073			-0.54	0.01					TRANSCRIPTION REGULATOR	V.I.A
RSp1472	RS03072	1.26	0.01	-0.46	0.01					4-CARBOXYMUCONOLACTONE DECARBOXYLASE	I
RSp1473	RS03071			-0.37	0.03					OXIDOREDUCTASE COG0667, Oxidoreductase (related to aryl-alcohol dehydrogenase)	V.I.B
RSp1474	RS06014	-4.48	0.00	3.88	0.00	3.42	0.00			HYPOTHETICAL PROTEIN	V.I.B
RSp1475	RS03068	-3.83	0.00	5.09	0.00	3.03	0.00			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1476	RS03067									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1477	RS03066									SIGNAL PEPTIDE	V.I.D
RSp1478	RS03065	0.95	0.01							TRANSCRIPTION REGULATOR	V.I.A
RSp1479	RS03064			-0.29	0.00	-0.57	0.05			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1480	RS03063			-0.30	0.04					CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1481	RS03062	1.77	0.00	-0.30	0.04					CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1482	RS03061	0.96	0.01	0.52	0.03					TRANSMEMBRANE	V.I.C
RSp1483	RS03060	1.69	0.02							TRANSMEMBRANE COG2885, Outer membrane protein	V.I.C
RSp1484	RS03059	1.26	0.00							CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1485	RS03058	1.13	0.00							OXIDOREDUCTASE COG0596, Hydrolase or acyltransferase (alpha/beta hydrolase s	V.I.C
RSp1486	RS03057	1.13	0.00							TRANSMEMBRANE	V.I.C
RSp1487	RS03056	1.44	0.00							COG0439, Biotin carboxylase	I
RSp1488	RS03055	0.73	0.01					1.26	0.02	3'-HYDROXYMETHYLCEPHEM-O-CARBAMOYLTRANSFERASE	II.B
RSp1489	RS03054	1.24	0.00			-1.98	0.02			HYPOTHETICAL PROTEIN	V.I.D
RSp1490	RS03053	0.69	0.01					1.10	0.00	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1491	RS03052	1.02	0.00							TRANSMEMBRANE	V.I.D
RSp1492	RS03051	0.92	0.00			0.33	0.00			COG2192, Carbamoyl transferase	I
RSp1493	RS05842	-1.23	0.02	0.62	0.01	-0.78	0.05			HYPOTHETICAL PROTEIN	V.I.B
RSp1494	RS03050			-0.35	0.01					HYPOTHETICAL PROTEIN	V.I.D
RSp1495	RS03046	0.39	0.01	-0.25	0.02					COG0431, Flavoprotein	V.I.C
RSp1496	RS03045									TRANSMEMBRANE CATION-EFFLUX SYSTEM PROTEIN	IV.D.4
RSp1497	RS03044									SIGNAL PEPTIDE LIPOPROTEIN	V.I.C
RSp1498	RS03043									SIGNAL PEPTIDE OUTER MEMBRANE USHER PROTEIN	III.B.2
RSp1499	RS03042									TRANSMEMBRANE PILI ASSEMBLY CHAPERONE	IV.B
RSp1500	RS03041					-1.25	0.05			SIGNAL PEPTIDE	V.I.C
RSp1501	RS03040	-0.99	0.01							SIGNAL PEPTIDE	V.I.C
RSp1502	RS03039									SIGNAL PEPTIDE	V.I.C
RSp1503	RS03038									TRANSMEMBRANE MAJOR ANAEROBICALLY INDUCED OUTER MEMBRANE PROTEIN	II.H.2
RSp1504	RS03037									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1505	RS03036									TRANSMEMBRANE NITRIC OXIDE REDUCTASE (SUBUNIT B)	I.H.2
RSp1506	RS03035									TRANSCRIPTION REGULATOR	V.I.A
RSp1507	RS03034									ABC TRANSPORTER ATP-BINDING PROTEIN	IV.D
RSp1508	RS03033	-0.48	0.05	0.93	0.00					ABC TRANSPORTER TRANSMEMBRANE PROTEIN	IV.D
RSp1509	RS03032			-0.30	0.04					TRANSMEMBRANE PERIPLASMIC SUBSTRATE-BINDING PROTEIN	IV.D
RSp1510	RS03031	0.48	0.01	-0.62	0.00	0.86	0.01	1.27	0.02	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1511	RS04788							1.19	0.05	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1512	RS04789									TRANSCRIPTION REGULATOR	V.I.A
RSp1513	RS04790									TRANSMEMBRANE COG4125, Predicted membrane protein	V.I.C
RSp1514	RS04791					-0.68	0.03			TRANSCRIPTION REGULATOR	V.I.A
RSp1515	RS04792					-1.31	0.01			COG0251, TdcF, Putative translation initiation inhibitor	II.B.7
RSp1516	RS04793									AMINO-ACID DEHYDRATASE	I.I.3
RSp1517	RS04794									COG2964: Uncharacterized protein conserved in bacteria	V.I.C
RSp1518	RS04795			-1.06	0.00	1.08	0.00	1.44	0.00	SIGNAL PEPTIDE	V.I.C
RSp1519	RS04796			-0.45	0.01					TRANSMEMBRANE SULFATE TRANSPORTER	IV.D
RSp1520	RS04797									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1521	RS04798	0.38	0.01	-0.35	0.03					COG3946, Type IV secretory pathway VirJ component - related protein	V.I.C
RSp1522	RS04799			-0.44	0.00					TRANSMEMBRANE	V.I.C
RSp1523	RS04800			-0.77	0.00	-1.48	0.05	-0.48	0.00	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1524	RS04801									TRANSMEMBRANE SIGNAL TRANSDUCTION PROTEIN GGDEF DOMAIN	V.I.A
RSp1525	RS04802	0.66	0.05							TRANSMEMBRANE COG0705, Uncharacterized membrane protein	V.I.C
RSp1526	RS04803	0.38	0.02	0.35	0.01	1.02	0.01	1.60	0.00	HYPOTHETICAL PROTEIN	V.I.B
RSp1527	RS04804			0.39	0.00					SIGNAL PEPTIDE	V.I.C
RSp1528	RS04805									HYPOTHETICAL PROTEIN	V.I.B
RSp1529	RS04806	-1.23	0.01					4.00	0.00	OXIDOREDUCTASE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC)	I.F
RSp1530	RS04807			-0.72	0.00					OXIDOREDUCTASE L-ASCORBATE OXIDASE (ASCORBASE)	I.F
RSp1531	RS06038									SIGNAL PEPTIDE HYPOTHETICAL PROTEIN	V.I.D
RSp1532	RS04809			-0.40	0.00	-0.23	0.01	-0.50	0.00	LIPOPROTEIN	V.I.C
RSp1533	RS04810			-0.38	0.05					LIPOPROTEIN	V.I.D
RSp1534	RS04811			-0.47	0.01			-0.88	0.02	SIGNAL PEPTIDE COG0760, Peptidyl-prolyl isomerase	II.B.7
RSp1535	RS04812			0.39	0.00			-1.47	0.00	SIGNAL PEPTIDE ACTIVATION/SECRETION PROTEIN	IV.E.2
RSp1536	RS04813	-1.21	0.02	-3.06	0.00	2.34	0.00	3.89	0.00	SIGNAL PEPTIDE HEMAGGLUTININ-RELATED PROTEIN	V.I.C
RSp1537	RS04814									TRANSMEMBRANE	V.I.C
RSp1538	RS06035									LIPOPROTEIN	V.I.D
RSp1539	RS05770			-0.53	0.02					HEMAGGLUTININ-RELATED PROTEIN	V.I.C
RSp1540	RS02096									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1541	RS02097					-1.15	0.02	1.23	0.02	HYPOTHETICAL PROTEIN	V.I.D
RSp1542	RS02098			-0.39	0.02					HYPOTHETICAL PROTEIN	V.I.D
RSp1543	RS02099									CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1544	RS02100					-1.80	0.01			HYPOTHETICAL PROTEIN	V.I.D
RSp1545	RS02101									HEMAGGLUTININ-RELATED PROTEIN	V.I.B
RSp1546	RS02102			-0.64	0.00					CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1547	RS02103					0.61	0.02			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1548	RS02104					-1.29	0.03			HYPOTHETICAL PROTEIN	V.I.D
RSp1549	RS02105	-0.49	0.02	-0.47	0.04	-1.11	0.00	-2.31	0.00	HYPOTHETICAL PROTEIN	V.I.D
RSp1550	RS02106			-0.56	0.00	-1.11	0.00			CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1551	RS02107			-0.59	0.01	-1.32	0.00	-1.00	0.00	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1552	RS02108									SIGNAL PEPTIDE PROTEASE	II.A.4
RSp1553	RS02109			0.73	0.03	-0.45	0.01			TRANSCRIPTION REGULATOR TRANSMEMBRANE TWO-COMPONENT SENSOR	V.I.A
RSp1554	RS02110									TRANSCRIPTION REGULATOR TWO-COMPONENT RESPONSE REGULATOR	V.I.A
RSp1555	RS02111	-3.10	0.00	-6.74	0.00	7.61	0.00	5.11	0.00	SECRETED PROTEIN PopF1	IV.E.2
RSp1556	RS02112			1.01	0.00					TRANSCRIPTION REGULATOR TRANSCRIPTION REGULATION REPRESSOR HE	I.F
RSp1557	RS02113	0.29	0.01	-0.29	0.03					glk GLUCOKINASE	I.H.8
RSp1558	RS02114									OXIDOREDUCTASE 6-PHOSPHOGLUCONOLACTONASE	I.F.19
RSp1559	RS02115			-0.45	0.00					OXIDOREDUCTASE GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE	I.F.19
RSp1560	RS02116			0.24	0.01					OXIDOREDUCTASE PHOSPHOGLUCONATE DEHYDRATASE	I.F.16
RSp1561	RS02117									COG0589, Universal stress protein UspA and related nucleotide-binding proteins	IV.G
RSp1562	RS02118			-0.41	0.00					CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1563	RS02119	-0.50	0.04	-0.58	0.00	-0.69	0.01	0.88	0.03	TRANSMEMBRANE	V.I.C
RSp1564	RS02120			-1.73	0.00	-1.14	0.00			TRANSMEMBRANE CYTOCHROME C OXIDASE POLYPEPTIDE II (CYTOCHROME I.G.1	I.G.1
RSp1565	RS02121									OXIDOREDUCTASE CYTOCHROME C OXIDASE POLYPEPTIDE I (CYTOCHROME I.G.1	I.G.1
RSp1566	RS02122			-0.38	0.01					OXIDOREDUCTASE GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE	I.G.19
RSp1567	RS02123									OXIDOREDUCTASE CYTOCHROME-C OXIDASE	I.G.1
RSp1568	RS02124			-0.51	0.05					TRANSMEMBRANE COG5605, Predicted small integral membrane protein	III.B.1
RSp1569	RS02125	0.95	0.00	-0.86	0.01					TRANSMEMBRANE LIPOPROTEIN	V.I.B
RSp1570	RS02126			-0.38	0.04					HYPOTHETICAL PROTEIN	V.I.D
RSp1571	RS02127	-0.65	0.01	0.82	0.01	-1.31	0.00	-0.57	0.00	TRANSCRIPTION REGULATOR TRANSCRIPTIONAL REGULATOR	IV.A
RSp1572	RS02128			0.74	0.01	-1.38	0.00	-1.35	0.02	TRANSMEMBRANE TRANSPORT PROTEIN	IV.D
RSp1573	RS02129			-0.52	0.01	-0.57	0.02	-0.70	0.05	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1574	RS02130			-0.41	0.00			-0.58	0.01	TRANSCRIPTION REGULATOR TRANSCRIPTIONAL REGULATOR	V.I.A

RSp1575	RS02131		0,75	0,01	-0,48	0,00				ABC TRANSPORTER AMINO-ACID-BINDING PERIPLASMIC PROTEIN (BBP)	IV.D.2		
RSp1576	RS02132		0,90	0,01	-0,49	0,02	-0,41	0,02		ABC TRANSPORTER AMINO-ACID TRANSMEMBRANE PROTEIN	IV.D.2		
RSp1577	RS02133									ABC TRANSPORTER AMINO-ACID TRANSMEMBRANE PROTEIN	IV.D.2		
RSp1578	RS02134		0,86	0,01			0,66	0,05	speB	AGMATINASE	I.F.15		
RSp1579	RS02135		0,90	0,02	-0,39	0,00		0,82	0,00	TRANSCRIPTION REGULATOR	V.I.A		
RSp1580	RS02136				-0,65	0,00		1,23	0,04	TRANSMEMBRANE	V.I.C		
RSp1581	RS02137	-1,97	0,00		2,27	0,00	2,03	0,00	2,67	0,00	katE	OXIDOREDUCTASE CATALASE hydroperoxidase HPII	IV.G.4
RSp1582	RS02138		-4,16	0,00	-0,23	0,00						HYPOTHETICAL PROTEIN	V.I.D
RSp1583	RS02139		1,11	0,02	-0,34	0,01						TRANSMEMBRANE O-acetylhomoserine sulfhydrylase	I
RSp1584	RS02143				-0,52	0,02						HYPOTHETICAL PROTEIN	V.I.D
RSp1585	RS02144											TRANSMEMBRANE RHS-RELATED PROTEIN	V.I.C
RSp1586	RS02145											HYPOTHETICAL PROTEIN	V.I.D
RSp1587	RS02141				-0,32	0,02						REMNANT OF A TRANSPOSASE	V.A
RSp1588	RS02142				-0,45	0,01						REMNANT OF A TRANSPOSASE GENE	V.A
RSp1589	RS02146											HYPOTHETICAL PROTEIN	V.I.D
RSp1590	RS02147											OXIDOREDUCTASE COG0665, Glycine/D-amino acid oxidases (deaminating)	I.I.3
RSp1591	RS02148				-0,47	0,01						OXIDOREDUCTASE ALDEHYDE DEHYDROGENASE	I
RSp1592	RS02149				-0,18	0,03						ABC TRANSPORTER ABC-type branched-chain amino acid transport systems, peripl	IV.D.2
RSp1593	RS02150		0,70	0,05	-0,33	0,04						TRANSCRIPTION REGULATOR TRANSCRIPTION REGULATOR	V.I.A
RSp1594	RS02151											SIGNAL PEPTIDE PORIN	IV.D
RSp1595	RS02152				-0,44	0,02						TRANSMEMBRANE METABOLITE TRANSPORT PROTEIN	IV.D
RSp1596	RS02153				-0,49	0,01						HYPOTHETICAL PROTEIN	V.I.D
RSp1597	RS02154											TRANSMEMBRANE TRANSPORT PROTEIN	IV.D
RSp1598	RS02155											TRANSMEMBRANE TRANSPORT PROTEIN	IV.G.2
RSp1599	RS02156						-0,77	0,05				OUTER MEMBRANE DRUG EFFLUX LIPOPROTEIN	IV.G.2
RSp1600	RS02157		0,77	0,00	-0,90	0,00						TRANSMEMBRANE	V.I.D
RSp1601	RS02158		-1,74	0,05	1,99	0,00	2,62	0,00				CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1602	RS02159		-0,53	0,00	-0,42	0,05			0,99	0,02		HYPOTHETICAL PROTEIN	V.I.D
RSp1603	RS02160						1,39	0,00	1,21	0,00		HYPOTHETICAL PROTEIN	V.I.B
RSp1604	RS02161				0,34	0,02	2,21	0,00	1,49	0,00		TRANSMEMBRANE	V.I.D
RSp1605	RS02162				0,60	0,03	1,63	0,00				HYPOTHETICAL PROTEIN	V.I.D
RSp1606	RS02163				0,21	0,01	1,56	0,00	1,27	0,04		TRANSMEMBRANE	V.I.D
RSp1607	RS02164						2,50	0,00				HYPOTHETICAL PROTEIN	V.I.D
RSp1608	RS02165						1,45	0,00				HYPOTHETICAL PROTEIN	V.I.D
RSp1609	RS02166						1,68	0,03				TRANSMEMBRANE ACID SPHINGOMYELINASE-LIKE PHOSPHODIESTERASE	V.I.C
RSp1610	RS02167	-4,43	0,00		-0,44	0,00	1,99	0,00	2,68	0,00		HYPOTHETICAL PROTEIN	V.I.D
RSp1611	RS02168										gabD2	OXIDOREDUCTASE SUCCINATE-SEMIALDEHYDE DEHYDROGENASE	I.F.18
RSp1612	RS02169				-0,42	0,01					ttuC	OXIDOREDUCTASE TARTRATE DEHYDROGENASE	I.I.4
RSp1613	RS02170				-0,42	0,02					hpaI2	2,4-DIHYDROXYHEPT-2-ENE-1,7-DIOIC ACID ALDOLASE	I.I.4
RSp1614	RS02171											TRANSMEMBRANE TRANSPORT PROTEIN	IV.D
RSp1615	RS02172										uxaA	ALTRONATE HYDROLASE (ALTRONIC ACID HYDRATASE)	I.I.4
RSp1616	RS02173											TRANSCRIPTION REGULATOR TRANSCRIPTION REGULATOR	V.I.A
RSp1617	RS02174											TRANSCRIPTION REGULATOR COG1475 TRANSCRIPTION REGULATOR	V.I.A
RSp1618	RS02175						-1,09	0,01				HYPOTHETICAL PROTEIN	V.I.D
RSp1619	RS02176											PHOSPHOADENOSINE PHOSPHOSULFATE SULFOTRANSFERASE	I
RSp1620	RS02177											SURFACE-EXPOSED ADHESIN PROTEIN	I.II.A
RSp1621	RS02178				-0,83	0,00					rcsB	TRANSCRIPTION REGULATOR CAPSULAR SYNTHESIS RESPONSE REGULATO	III.A.1
RSp1622	RS02179										rcsC	TRANSCRIPTION REGULATOR CAPSULAR SYNTHESIS REGULATORY PROTEIN	III.A.1
RSp1623	RS02180				-0,66	0,05	-0,37	0,05				RESPONSE REGULATOR WITH EAL DOMAIN	V.I.A
RSp1624	RS02182						-1,72	0,01			tISRso1	REMNANT OF A ISRso16-TRANSPOSASE ORFA	V.A
RSp1626	RS02184						0,29	0,05	-0,84	0,00		CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1627	RS02185								-0,40	0,01		CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1628	RS02186				-0,51	0,00	-1,01	0,02	1,10	0,04	SRso1f	ISRso16-TRANSPOSASE ORFB	V.A
RSp1629	RS02187						-1,98	0,01			tISRso1f	C-TERMINUS OF tISRso16 ORFA TRANSPOSASE	V.A
RSp1630	RS02188											REMNANT OF CYANATE LYASE	V.I.C
RSp1632	RS02190										oprB	TRANSMEMBRANE PORIN B PRECURSOR OUTER (GLUCOSE PORIN)	IV.D.3
RSp1633	RS02191						0,74	0,00			xyI	ABC TRANSPORTER D-XYLOSE-BINDING PERIPLASMIC PROTEIN	IV.D.3
RSp1634	RS02192										xyI	ABC TRANSPORTER D-XYLOSE ATP-BINDING PROTEIN	IV.D.3
RSp1635	RS02193				-0,37	0,05					xyI	ABC TRANSPORTER XYLOSE TRANSMEMBRANE PROTEIN	IV.D.3
RSp1636	RS02194											OXIDOREDUCTASE COG0451, Nucleoside-diphosphate-sugar epimerase	I
RSp1637	RS02195				-0,39	0,02						TRANSCRIPTION REGULATOR TRANSCRIPTION REGULATOR	V.I.D
RSp1638	RS02196						1,42	0,03				TRANSMEMBRANE COG0697, Permeases of the drug/metabolite transporter (DMT)	IV.A
RSp1639	RS02197											TRANSCRIPTION REGULATOR TRANSCRIPTIONAL REGULATOR	V.I.A
RSp1640	RS02198				-1,25	0,00			-1,35	0,00		TRANSMEMBRANE LIPOPROTEIN	V.I.C
RSp1641	RS02199				-1,33	0,00	-0,39	0,01	-1,30	0,00		TRANSMEMBRANE	V.I.C
RSp1642	RS02200				-1,14	0,00	-1,12	0,00	-2,29	0,00		TRANSMEMBRANE	V.I.C
RSp1643	RS02202				-1,79	0,00	-1,18	0,00	-1,34	0,01		HYPOTHETICAL PROTEIN	V.I.D
RSp1644	RS02203				0,61	0,03						TRANSCRIPTION REGULATOR TRANSCRIPTION REGULATOR	V.I.A
RSp1645	RS02204				-0,67	0,00						CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1646	RS02205				-0,40	0,01			-0,52	0,01		SIGNAL PEPTIDE	V.I.C
RSp1647	RS02206		0,50	0,00								COG1352, Methylase of chemotaxis methyl-accepting proteins	IV.C
RSp1649	RS02208											TRANSMEMBRANE	V.I.D
RSp1650	RS02209				-0,51	0,00						TRANSCRIPTION REGULATOR COG5662, Predicted transmembrane transcriptional	V.I.A
RSp1651	RS02210				-0,59	0,01						TRANSCRIPTION REGULATOR RNA POLYMERASE SIGMA FACTOR	I.E.1
RSp1652	RS02211				-1,16	0,00						COG1409, Phosphohydrolase	I
RSp1653	RS02212											OXIDOREDUCTASE Cytochrome C oxidase subunit II	I.G.1
RSp1654	RS02213	0,37	0,03	0,43	0,00	-1,47	0,00	1,22	0,00	1,68	0,00	SIGNAL PEPTIDE	V.I.D
RSp1655	RS02214				-0,43	0,00			0,99	0,00		HYPOTHETICAL PROTEIN	V.I.D
RSp1656	RS02215				0,63	0,00	-0,64	0,00		0,75	0,04	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1657	RS02216						-0,51	0,00				CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE	I.C
RSp1658	RS02217				0,80	0,05	-0,51	0,00	-0,92	0,05		COG0824, Thioesterase	I
RSp1659	RS02218				0,42	0,04		0,34	0,02			ACYL-CARRIER-PROTEIN	I.B.1
RSp1660	RS02219				0,82	0,02	-0,38	0,01				TRANSMEMBRANE	V.I.D
RSp1661	RS02220				0,45	0,04						CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1662	RS02221											PEPTIDE CHAIN RELEASE FACTOR RF-3	II.B.7
RSp1663	RS02222				-1,06	0,00	-0,52	0,00	-0,93	0,00	prfC	CONSERVED HYPOTHETICAL PROTEIN	V.I.C
RSp1664	RS02223											TRANSMEMBRANE RIBONUCLEASE RNASE BN (RBN)	II.A.2
RSp1665	RS02224											TRANSMEMBRANE	V.I.D
RSp1666	RS02225						0,85	0,04	1,66	0,00		SIGNAL PEPTIDE	V.I.B
RSp1667	RS02226	-0,59	0,04									TRANSCRIPTION REGULATOR SIGMA-54 INTERACTING RESPONSE REGULATC	V.I.A
RSp1668	RS02227						0,96	0,00				TRANSCRIPTION REGULATOR SIGMA-54 INTERACTING PROTEIN	V.I.A
RSp1669	RS02228								1,10	0,00		HYPOTHETICAL PROTEIN	V.I.D
RSp1670	RS02229				-1,11	0,04			2,43	0,00		SIGNAL PEPTIDE	V.I.D
RSp1671	RS02230										rhoN2	TRANSCRIPTION REGULATOR RNA POLYMERASE SIGMA N (SIGMA 54) FACTO	I.E.1
RSp1672	RS02231								0,92	0,00		COG3233, Deacetylase	I
RSp1673	RS02232				-0,30	0,02						TRANSMEMBRANE LIPOPROTEIN	V.I.D
RSp1674	RS02233											HYPOTHETICAL PROTEIN	V.I.D
RSp1676	RS02235											TRANSCRIPTION REGULATOR COMPOSITE TWO-COMPONENT REGULATORY	V.I.A
RSp1677	RS02236											INTEGRASE / RECOMBINASE	V.A
RSp1678	RS02237		0,70	0,00	-0,45	0,00						TRANSMEMBRANE COG2252, Permease	IV.D