

UBABSL4_8849G0011	245 ATP synthase F0, A subunit			0.0648		UBAL3_94530092	86
UBABSL4_8849G0012	76 Conserved hypothetical protein			0.038		UBAL3_94530093	74
UBABSL4_8849G0013	242 Conserved hypothetical protein			0.006			
UBABSL4_8849G0014	102 Conserved hypothetical protein					UBAL3_95530023	63
UBABSL4_8849G0015	259 Conserved hypothetical protein			0.0111		UBAL3_95530022	71
UBABSL4_8849G0016	227 transposase						
UBABSL4_8849G0017	131 transposase						
UBABSL4_8849G0018	165 Phosphoglycolate phosphatase (EC 3.1.3.18)					UBAL3_94530097	62
UBABSL4_8849G0019	171 Probable membrane protein					UBAL3_94530096	63
UBABSL4_13011G0001	92 radical SAM family protein					UBAL3_95950042	77
UBABSL4_13011G0002	106 Conserved hypothetical protein					UBAL3_95950043	71
UBABSL4_13011G0003	329 Chemotaxis protein (CheV)	0.10386	0.0957	0.0438		UBAL3_95950044	86
UBABSL4_13011G0004	214 methyl-accepting chemotaxis sensory transducer			0.027		UBAL3_96120012	82
UBABSL4_13011G0005	250 metallo-beta-lactamase family protein		0.04316	0.05212	0.0462	UBAL3_96120013	92
UBABSL4_13011G0006	392 methyl-accepting chemotaxis sensory transducer	0.39708	0.25692	0.18557	0.0221	UBAL3_95950046	74
UBABSL4_13011G0007	266 glycogen debranching enzyme GlgX					UBAL3_94530062	68
UBABSL4_13011G0008	460 glycogen debranching enzyme GlgX					UBAL3_94530062	
UBABSL4_13011G0009	89 Conserved hypothetical protein					UBAL3_95680133	47
UBABSL4_13011G0010	265 Putative catalytic LigB subunit of aromatic ring-opening dioxygenase			0.0163		UBAL3_95950049	66
UBABSL4_13011G0011	376 Methyltransferase			0.0038		UBAL3_95950050	50
UBABSL4_13011G0012	427 histidyl-tRNA synthetase	0.00842	0.08645	0.0203		UBAL3_95950051	58
UBABSL4_13011G0013	443 Iron-sulfur protein			0.0554		UBAL3_95950052	76
UBABSL4_13011G0014	91 Conserved hypothetical protein			0.1268		UBAL3_95950053	69
UBABSL4_13011G0015	197 Probable cytochrome C oxidase			0.0439		UBAL3_95950054	89
UBABSL4_13011G0016	374 Conserved protein of unknown function			0.0347		UBAL3_95950055	82
UBABSL4_13011G0017	135 Probable cytochrome-c oxidase			0.0855		UBAL3_95950056	85
UBABSL4_13011G0018	147 Conserved protein of unknown function					UBAL3_95950057	73
UBABSL4_13011G0019	71 Conserved protein of unknown function					UBAL3_95950058a	82
UBABSL4_13011G0020	50 Conserved protein of unknown function					UBAL3_95950059	88
UBABSL4_8997G0001	280 ABC-2 type transporter			0.0155		UBAL3_94170028	76
UBABSL4_8997G0002	164 Conserved protein of unknown function		0.10593	0.0088		UBAL3_94170029	83
UBABSL4_8997G0003	355 signal peptide peptidase SppA, 36K type			0.0122		UBAL3_94170030	71
UBABSL4_8997G0004	222 Putative hydroxypyruvate reductase/glycerate kinase			0.0065		UBAL3_94170032	46
UBABSL4_8997G0005	371 Conserved protein of unknown function			0.0078		UBAL3_94170034	60
UBABSL4_8997G0006	115 Conserved protein of unknown function			0.0125		UBAL3_94170035	58
UBABSL4_8997G0007	223 Conserved protein of unknown function			0.0518		UBAL3_94170036	42
UBABSL4_8997G0008	121 Conserved protein of unknown function					UBAL3_94170037	46
UBABSL4_8997G0009	128 Conserved hypothetical protein					UBAL3_94170038	84
UBABSL4_8997G0010	410 major facilitator superfamily transporter					UBAL3_94170039	42
UBABSL4_8997G0011	157 CBS domain containing protein		0.24205	0.0368		UBAL3_94170040	69
UBABSL4_8997G0012	185 Conserved protein of unknown function			0.0702		UBAL3_94170041	48
UBABSL4_8997G0013	125 histidine triad (HIT) protein					UBAL3_94170042	80
UBABSL4_8997G0013a	165 Conserved protein of unknown function			0.2186		UBAL3_94170043	96
UBABSL4_8997G0014	88 Conserved protein of unknown function			0.1475		UBAL3_94170043	96
UBABSL4_8997G0015	194 Uracil phosphoribosyltransferase	0.01854		0.0521		UBAL3_94170044	73
UBABSL4_8997G0016	333 aspartate carbamoyltransferase		0.01956	0.0087		UBAL3_94170045	79
UBABSL4_8997G0017	228 dihydroorotase	0.01578	0.02381	0.0063		UBAL3_94170046	72
UBABSL4_8997G0018	127 carbamoyl-phosphate synthase, small subunit			0.1363		UBAL3_94170047	61
UBABSL4_7601G0001	169 Conserved protein of unknown function			0.0085		UBAL3_24060060	68
UBABSL4_7601G0003	451 Putative TPR-domain containing protein	0.00798	0.00481	0.0352		UBAL3_24060058	
UBABSL4_7601G0004	145 Putative TPR-domain containing protein			0.0298		UBAL3_24060058	69
UBABSL4_7601G0005	363 Putative DegT/DnrJ/EryC1/StrS aminotransferase			0.0119		UBAL3_24060057	70
UBABSL4_7601G0006	218 Probable dethiobiotin synthase					UBAL3_24060056	58
UBABSL4_7601G0007	257 Exodeoxyribonuclease III (EC 3.1.1.12)			0.0225		UBAL3_24060055	71
UBABSL4_7601G0008	172 Probable cation transport protein		0.03787	0.0335		UBAL3_24060054	67
UBABSL4_7601G0009	233 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)			0.0062		UBAL3_24060053	60
UBABSL4_7601G0010	124 Putative methylenetetrahydrofolate reductase	0.05802	0.01751	0.0349		UBAL3_24060052	81
UBABSL4_7601G0011	193 Putative methylenetetrahydrofolate reductase		0.05063	0.0523		UBAL3_24060052	85
UBABSL4_7601G0012	184 Methylenetetrahydrofolate cyclohydrolase (EC 3.5.4.9)	0.0391	0.25964	0.0549		UBAL3_24060051	85
UBABSL4_7601G0013	383 Conserved hypothetical protein			0.0038		UBAL3_24060049	75
UBABSL4_7601G0016	183 Conserved hypothetical protein						

UBABSL4_7601G0017	91 GTP cyclohydrolase I (EC 3.5.4.16)			0.0476		UBAL3_24060046	98	
UBABSL4_7601G0018	99 GTP cyclohydrolase I (EC 3.5.4.16)			0.0146		UBAL3_24060046	82	
UBABSL4_7601G0019	210 5-formyltetrahydrofolate cyclo-ligase					UBAL3_24060045	58	
UBABSL4_7601G0020	279 N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)			0.0103		UBAL3_24060044	75	
UBABSL4_8072G0001	168 Conserved protein of unknown function					UBAL3_90980012	48	
UBABSL4_8072G0002	241 glutamyl-tRNA synthetase		0.06758		0.012	UBAL3_90980011		
UBABSL4_8072G0003	194 glutamyl-tRNA synthetase		0.02239			UBAL3_90980011	60	
UBABSL4_8072G0004	167 Conserved hypothetical protein				0.0086	UBAL3_90980010	89	
UBABSL4_8072G0005	260 Conserved protein of unknown function					UBAL3_90980009	55	
UBABSL4_8072G0006	71 Probable pyruvate:ferredoxin oxidoreductase epsilon subunit		0.03058		0.1219	UBAL3_90980006a	90	
UBABSL4_8072G0007	223 Pyruvate:ferredoxin oxidoreductase gamma subunit	0.8194	1.5162	1.17826	0.2264	UBAL3_90980006	91	
UBABSL4_8072G0008	298 Putative pyruvate:ferredoxin oxidoreductase beta sul	0.29523	0.83285	0.45179	0.6632	UBAL3_90980005	96	
UBABSL4_8072G0009	282 Pyruvate:ferredoxin oxidoreductase alpha subunit (E	0.95995	0.86735	0.72383	0.3274	UBAL3_90980004	95	
UBABSL4_8072G0010	128 hypothetical protein				0.1578			
UBABSL4_8072G0011	135 Conserved protein of unknown function		0.02664	0.08043		UBAL3_90980003	71	
UBABSL4_8072G0012	95 Conserved protein of unknown function				0.0456	UBAL3_90980002	90	
UBABSL4_8072G0013	212 heat shock protein DnaJ domain protein				0.0204	UBAL3_90980001	65	
UBABSL4_8072G0014	109 Conserved protein of unknown function				0.0132	UBAL3_79520072	58	
UBABSL4_8072G0015	114 Conserved protein of unknown function		0.0631	0.01905	0.0506	UBAL3_79520072	76	
UBABSL4_8072G0016	74 hypothetical protein						0.0424	
UBABSL4_11757G0001	119 Conserved hypothetical protein							
UBABSL4_11757G0002	157 Conserved hypothetical protein				0.0368			
UBABSL4_11757G0003	196 O-methyltransferase family protein				0.0074			
UBABSL4_11757G0004	205 GCN5-related N-acetyltransferase				0.0141			
UBABSL4_11757G0005	119 glyoxalase family protein							
UBABSL4_11757G0006	59 Glyoxalase/bleomycin resistance					UBAL3_48660039	53	
UBABSL4_11757G0007	150 flavin-nucleotide-binding protein-like					UBAL3_48660038	67	
UBABSL4_11757G0008	93 hypothetical protein							
UBABSL4_11757G0009	125 metallo-beta-lactamase family protein							
UBABSL4_11757G0010	52 Conserved hypothetical protein				0.0277			
UBABSL4_11757G0011	73 hypothetical protein				0.079			
UBABSL4_11757G0012	94 addiction module toxin, RelE/StbE family				0.046			
UBABSL4_11757G0013	68 hypothetical protein				0.0212			
UBABSL4_11757G0014	119 transcriptional regulator-like				0.0242	UBAL3_95680030	45	
UBABSL4_11757G0015	144 transposase				1.0219			
UBABSL4_11757G0016	85 hypothetical protein							
UBABSL4_1871G0001	193 hypothetical protein				0.0374			
UBABSL4_1871G0002	184 metallophosphoesterase					UBAL3_95660013	87	
UBABSL4_1871G0002a	123 Conserved hypothetical protein				0.0704			
UBABSL4_1871G0003	88 nucleotidyltransferase substrate binding					UBAL3_82700041	69	
UBABSL4_1871G0004	105 DNA polymerase, beta domain protein region				0.0137	2.3056	UBAL3_95660006	82
UBABSL4_1871G0005	169 Putative uracil-DNA glycosylase							
UBABSL4_1871G0006	380 glycine oxidase ThiO				0.0532	UBAL3_95450101	69	
UBABSL4_1871G0006a	85 UDP-glucose 6-dehydrogenase				0.0679	UBAL3_95450100	77	
UBABSL4_1871G0007a	76 UDP-glucose 6-dehydrogenase				0.0569	UBAL3_95450100	77	
UBABSL4_1871G0007	132 Conserved protein of unknown function				0.0328	UBAL3_95450099	42	
UBABSL4_1871G0008	241 sugar fermentation stimulation protein				0.0299	UBAL3_95450098	68	
UBABSL4_1871G0009	275 HipA toxin/antitoxin							
UBABSL4_1871G0010	113 hypothetical protein				0.0128			
UBABSL4_1871G0011	83 hypothetical protein				0.0695			
UBABSL4_1871G0012	351 Conserved protein of unknown function					UBAL3_96120037	33	
UBABSL4_3175G0001	202 cobalamin biosynthesis CbiG		0.0215			UBAL3_79520030	72	
UBABSL4_3175G0002	87 Precorrin-6y C5,15-methyltransferase, CbiT				0.0166	UBAL3_79520029	63	
UBABSL4_3175G0003	227 Precorrin-6y C5,15-methyltransferase, CbiE					UBAL3_79520028	49	
UBABSL4_3175G0004	279 cobalamin biosynthesis protein CbiD	0.04851	0.04512	0.19847	0.0052	UBAL3_79520027	66	
UBABSL4_3175G0005	77 cobalamin biosynthesis protein CbiD				0.056	UBAL3_79520027		
UBABSL4_3175G0006	105 Ribosomal protein L9		0.08564	0.18613		UBAL3_79520026	65	
UBABSL4_3175G0007	45 Ribosomal protein L34					UBAL3_79520025	91	
UBABSL4_3175G0008	108 Conserved protein of unknown function				0.1069	UBAL3_79520024a	63	
UBABSL4_3175G0009	415 Putative inner-membrane protein		0.02878			UBAL3_79520024	63	

UBABSL4_3175G0010	445 tRNA modification GTPase TrmE		0.0097		UBAL3_79520023	54
UBABSL4_3175G0011	611 glucose inhibited division protein A		0.0047		UBAL3_79520022	71
UBABSL4_3175G0012	199 glucose inhibited division protein B				UBAL3_79520021	48
UBABSL4_3175G0013	188 Cobyriinic acid a,c-diamide synthase, CbiA				UBAL3_79520020	78
UBABSL4_3175G0014	288 parB-like partition protein				UBAL3_79520019	61
UBABSL4_3175G0015	41 Conserved protein of unknown function	0.43865	0.68852		UBAL3_79520018	88
UBABSL4_3522G0001	120 Putative diguanylate phosphodiesterase				UBAL3_44810024	73
UBABSL4_3522G0002	150 DNA topoisomerase III (EC 5.99.1.2)				UBAL3_44810025	
UBABSL4_3522G0003	512 DNA topoisomerase III (EC 5.99.1.2)			0.0123 0.0334 0.0085	UBAL3_44810025	84
UBABSL4_3522G0004	143 Conserved hypothetical protein				UBAL3_44810026	89
UBABSL4_3522G0005	133 Single-strand DNA-binding protein				UBAL3_44810028	78
UBABSL4_3522G0006	78 Conserved hypothetical protein				UBAL3_44810029	80
UBABSL4_3522G0007	64 hypothetical protein					
UBABSL4_3522G0008	370 DNA repair protein RadC				UBAL3_44810030	74
UBABSL4_3522G0009	71 hypothetical protein					
UBABSL4_3522G0010	410 Conserved protein of unknown function			0.025	UBAL3_44810031	88
UBABSL4_3522G0011	322 Conserved hypothetical protein					
UBABSL4_3522G0012	57 hypothetical protein					
UBABSL4_3522G0013	155 Conserved hypothetical protein				UBAL3_44810033	82
UBABSL4_3522G0014	84 Putative conjugal transfer protein (TrbI)				UBAL3_44810034	96
UBABSL4_3522G0015	188 Putative conjugal transfer protein (TrbI)			0.0169	UBAL3_44810034	97
UBABSL4_3918G0001	291 integral membrane protein MviN		0.0198		UBAL3_96270003	74
UBABSL4_3918G0002	35 Ribosomal protein S20		0.1225		UBAL3_78920001	89
UBABSL4_3918G0004	214 Probable DNA polymerase III, delta subunit		0.0067		UBAL3_78920002	60
UBABSL4_3918G0005	76 Conserved protein of unknown function				UBAL3_78920003	76
UBABSL4_3918G0006	118 Conserved protein of unknown function				UBAL3_78920003	77
UBABSL4_3918G0007	262 Leucyl-tRNA synthetase (EC 6.1.1.4)		0.033		UBAL3_78920004	65
UBABSL4_3918G0008	578 Leucyl-tRNA synthetase (EC 6.1.1.4)		0.0549		UBAL3_78920004	70
tRNA-Arg-ACG		tRNA Arg ACG				
UBABSL4_3918G0009	200 Conserved hypothetical protein					
UBABSL4_3918G0010	135 hypothetical protein					
UBABSL4_3918G0011	103 hypothetical protein					
UBABSL4_3918G0012	50 hypothetical protein					
UBABSL4_3918G0013	142 hypothetical protein			0.0121		
UBABSL4_3918G0014	322 Conserved hypothetical protein					
UBABSL4_3918G0015	85 Conserved hypothetical protein					
UBABSL4_11208G0001	201 Probable transposase				UBAL3_80630090	47
UBABSL4_11208G0002	252 IstB domain protein ATP-binding protein				UBAL3_95530028	85
UBABSL4_11208G0003	214 Conserved hypothetical protein		0.0067		UBAL3_95530029	82
UBABSL4_11208G0004	105 Resolvase helix-turn-helix domain protein				UBAL3_95530030	59
UBABSL4_11208G0005	63 hypothetical protein					
UBABSL4_11208G0006	377 Putative potassium channel protein				UBAL3_78920114	66
UBABSL4_11208G0007	71 Conserved hypothetical protein				UBAL3_78920115	74
UBABSL4_11208G0008	229 Probable cyclic nucleotide-binding protein		0.0378		UBAL3_78920116	74
UBABSL4_11208G0009	520 Putative competence protein (ComEC)				UBAL3_78920117	
UBABSL4_11208G0010	403 Phosphoglucosamine mutase (EC 5.4.2.10)	0.01616			UBAL3_78920118	81
UBABSL4_11208G0011	231 Conserved protein of unknown function				UBAL3_78920119	51
UBABSL4_11208G0012	208 Conserved protein of unknown function				UBAL3_78920120	75
UBABSL4_11208G0013	54 hypothetical protein					
UBABSL4_11208G0014	284 Dihydropteroate synthase (EC 2.5.1.15)		0.0152		UBAL3_78920121	61
UBABSL4_11208G0015	23 hypothetical protein					
UBABSL4_12514G0001	185 Diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s)				UBAL3_44810003	45
UBABSL4_12514G0002	346 diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s)				UBAL3_94530058	36
UBABSL4_12514G0003	579 Conserved hypothetical protein					
UBABSL4_12514G0004	93 hypothetical protein					
UBABSL4_12514G0005	69 hypothetical protein					
UBABSL4_12514G0006	43 transposase					
UBABSL4_12514G0007	99 hypothetical protein		0.6819			
UBABSL4_12514G0008	536 outer membrane efflux protein		0.0296		UBAL3_80420067	65
UBABSL4_12514G0009	302 Secretion protein (HlyD)		0.0048		UBAL3_80420066	80

UBABSL4_12514G0010	128 ABC transporter ATP-binding protein									UBAL3_80420065	69	
UBABSL4_12514G0011	297 ABC transporter ATP-binding protein									UBAL3_80420065	69	
UBABSL4_12514G0012	99 ABC transporter ATP-binding protein									UBAL3_80420065	69	
UBABSL4_12514G0013	381 Putative ABC transporter permease protein					0.0076				UBAL3_80420064	84	
UBABSL4_12514G0014	335 Putative ABC transporter permease protein									UBAL3_80420063	82	
UBABSL4_12514G0015	42 hypothetical protein											
UBABSL4_12854G0001	52 Cytochrome 572					2.9408		0.3984	0.1811		UBAL3_96270029	87
UBABSL4_12854G0002	80 hypothetical protein											
UBABSL4_12854G0003	122 hypothetical protein								0.0257	0.014	0.009	
UBABSL4_12854G0004	68 hypothetical protein											
UBABSL4_12854G0005	270 hypothetical protein					0.0267			0.0349	0.0697	0.0162	
UBABSL4_12854G0006	153 hypothetical protein					0.0283		0.1015	0.0205	0.0447	0.0286	
UBABSL4_12854G0007	167 hypothetical protein								0.0564			
UBABSL4_12854G0008	224 Conserved hypothetical protein							0.0142		0.0306	0.0098	
UBABSL4_12854G0009	220 Conserved protein of unknown function					0.0131		0.0432	0.0235	0.0143	0.005	
UBABSL4_12854G0010	201 hypothetical protein					0.0215			0.0773	0.0781	0.0255	
UBABSL4_12854G0011	741 Probable conjugal transfer protein (TraD)	0.0206				0.0175		0.0385	0.014	0.0424	0.0808	
UBABSL4_12854G0012	467 Putative conjugal transfer protein (TraA)					0.0711		0.2376	0.3549	0.1344	0.0183	
UBABSL4_12854G0013	81 IstB domain protein ATP-binding protein					5.0771	0.4956	0.9249	0.7478	1.6669	1.9784	
UBABSL4_12854G0014	470 Putative conjugal transfer protein (TraA)					2.1729		5.48	7.6722	4.1468	5.4309	
UBABSL4_12854G0015	22 hypothetical protein					0.0153		0.054		0.02	0.0219	
										0.0279	UBAL3_69480059	
UBABSL4_11026G0001	143 phosphoribosylformylglycinamide cyclo-ligase					0.0807					UBAL3_92050044	
UBABSL4_11026G0002	340 Conserved hypothetical protein					0.0212					UBAL3_92050043	
UBABSL4_11026G0004	382 Conserved hypothetical protein					0.102					UBAL3_92050042	
UBABSL4_11026G0005	170 Ribonuclease III					0.0339					UBAL3_92050041	
UBABSL4_11026G0006	229 3-oxoacyl-(Acyl-carrier-protein) synthase II (EC 2.3.1.41)	0.02371				0.0189					UBAL3_92050040	
UBABSL4_11026G0007	166 3-oxoacyl-(Acyl-carrier-protein) synthase II (EC 2.3.1.41)					0.1043					UBAL3_92050040	
UBABSL4_11026G0008	77 acyl carrier protein	0.14014	0.35252			0.1124					UBAL3_92050039	
UBABSL4_11026G0009	255 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100)	0.00852				0.0735					UBAL3_92050038	
UBABSL4_11026G0010	312 malonyl CoA-acyl carrier protein transacylase	0.03132				0.0046					UBAL3_92050037	
UBABSL4_11026G0011	331 3-oxoacyl-(acyl-carrier-protein) synthase III	0.01087	0.0164			0.0305					UBAL3_92050036	
UBABSL4_11026G0012	336 fatty acid/phospholipid synthesis protein PlsX	0.00646				0.0215					UBAL3_92050035	
UBABSL4_11026G0013	61 Ribosomal protein S32					0.0236					UBAL3_92050034	
UBABSL4_11026G0014	162 Conserved protein of unknown function	0.14745				0.0445					UBAL3_92050034	
UBABSL4_11026G0015	165 poly(rRNA) synthetase					0.0175					UBAL3_92050033	
UBABSL4_11196G0001	81 Conserved protein of unknown function					0.0178					UBAL3_80630032	
UBABSL4_11196G0002	287 flagellin domain protein	0.80174	0.08146	0.10971		0.0503					UBAL3_80630031	
UBABSL4_11196G0003	115 Probable anti-sigma-28 factor, FlgM					0.2133					UBAL3_80630030	
UBABSL4_11196G0004	154 Conserved hypothetical protein					0.0562					UBAL3_80630029	
UBABSL4_11196G0005	309 flagellar hook-associated protein FlgK	0.13141	0.03492	0.00703		0.056					UBAL3_80630028	
UBABSL4_11196G0006	209 flagellar hook-associated protein FlgK					0.0414					UBAL3_80630028	
UBABSL4_11196G0007	313 Probable flagellar hook-associated protein, FlgL	0.45406	0.02873	0.03122		0.0876					UBAL3_80630027	
UBABSL4_11196G0008	50 hypothetical protein											
UBABSL4_11196G0009	95 Conserved protein of unknown function										UBAL3_80630026	
UBABSL4_11196G0010	199 flagellin domain protein	20.9831	1.93403	1.37492		0.7599					UBAL3_80630025	
UBABSL4_11196G0012	485 Putative flagellar hook-associated protein, FlID			0.00448		0.0327					UBAL3_80630024	
UBABSL4_11196G0013	87 flagellar protein Flis					0.0497					UBAL3_80630023	
UBABSL4_11196G0014	129 Conserved hypothetical protein										UBAL3_80630022	
UBABSL4_11196G0015	119 Conserved protein of unknown function					0.0485					UBAL3_80630021	
UBABSL4_11888G0001	25 hypothetical protein											
UBABSL4_11888G0002	146 Conserved hypothetical protein											
UBABSL4_11888G0003	329 ABC transporter, periplasmic component	0.09293	0.0495			0.0526					UBAL3_48660049	
UBABSL4_11888G0004	201 Conserved protein of unknown function					0.0144					UBAL3_80630096	
UBABSL4_11888G0005	153 Putative flavohemoprotein	0.39966	1.09994			0.2546					UBAL3_80630095	
UBABSL4_11888G0005a	71 Conserved protein of unknown function					0.1016					UBAL3_80630085	
UBABSL4_11888G0006	116 Conserved protein of unknown function			0.02808		0.0497					UBAL3_80630085	
UBABSL4_11888G0007	368 glycine cleavage system T protein			0.03836		0.0118					UBAL3_80630084	
UBABSL4_11888G0008	133 glycine cleavage H-protein	0.10177	0.51385	1.46943		0.0542					UBAL3_80630083	
UBABSL4_11888G0009	418 Glycine dehydrogenase (decarboxylating)					0.0173					UBAL3_80630082	
UBABSL4_11888G0010	105 transposase					0.055						

UBABSL4_11888G0011	266 transposase								0.0271				
UBABSL4_11888G0012	221 thioredoxin reductase		0.02456						0.0065			UBAL3_94530070	82
UBABSL4_11888G0013	69 Conserved protein of unknown function								0.0209			UBAL3_94530069	77
UBABSL4_7945G0001	55 Conserved hypothetical protein												
UBABSL4_7945G0002	41 hypothetical protein												
UBABSL4_7945G0003	110 hypothetical protein												
UBABSL4_7945G0005	138 Ketosteroidisomerase-related protein											UBAL3_80150042	85
UBABSL4_7945G0006	255 Conserved hypothetical protein							0.2514	0.0057			0.0086 UBAL3_80150043	84
UBABSL4_7945G0007	160 hypothetical protein												
UBABSL4_7945G0008	67 Conserved hypothetical protein (TN)												
UBABSL4_7945G0009	58 hypothetical protein												
UBABSL4_7945G0010	64 hypothetical protein												
UBABSL4_7945G0011	325 Putative conjugal transfer protein (TraA)											UBAL3_69480059	47
UBABSL4_7945G0012	371 Ti-type conjugative transfer relaxase TraA												
UBABSL4_7945G0013	223 Conserved hypothetical protein												
UBABSL4_7945G0014	126 Conserved hypothetical protein											UBAL3_96270025	32
UBABSL4_10737G0001	112 hypothetical protein		1.6319	5.7351	6.3549	10.817	9.6445	0.2862	0.1932	9.7269			0.0925
UBABSL4_10737G0002	192 transposase		2.0626	4.391	15.023	12.935	13.362	0.5842	0.3757	16.707			0.0539
UBABSL4_10737G0003	50 transposase									1.2105			
tRNA-Leu-TAG	tRNA Leu TAG												
UBABSL4_10737G0004	286 Conserved hypothetical protein											UBAL3_92050183	45
UBABSL4_10737G0005	933 Probable ATP-dependent Clp protease								0.0093			UBAL3_92050184	71
UBABSL4_10737G0006	217 excinuclease ABC, C subunit								0.0332			UBAL3_92050185	73
UBABSL4_10737G0007	317 excinuclease ABC, C subunit											UBAL3_92050185	
UBABSL4_10737G0008	84 Conserved hypothetical protein											UBAL3_92050186	71
UBABSL4_10737G0009	147 Cell division protein (FtsY)								0.01477			UBAL3_92050187	77
UBABSL4_10737G0010	145 Conserved protein of unknown function									0.0098		UBAL3_92050188	57
UBABSL4_10737G0011	205 Putative phosphate starvation-inducible protein (PhoH)		0.12282	0.10593					0.0141			UBAL3_92050189	83
UBABSL4_10737G0012	196 Cytochrome 579		9.32276	1.5966	0.15511				0.8685			UBAL3_94240192a	78
UBABSL4_11503G0001	375 Osmosensitive K ⁺ channel His kinase sensor											UBAL3_95450016	72
UBABSL4_11503G0002	495 Probable transporter											UBAL3_78920073	54
UBABSL4_11503G0003	177 Conserved hypothetical protein											UBAL3_95450063	48
UBABSL4_11503G0005	281 Nitrogenase iron protein (NifH) (EC 1.18.6.1)											UBAL3_78920077	90
UBABSL4_11503G0006	447 Nitrogenase, molybdenum-iron protein alpha chain (NifD) (EC 1.18.6.1)								0.0032			UBAL3_78920078	97
UBABSL4_11503G0007	405 Nitrogenase, molybdenum-iron protein beta chain (NifK) (EC 1.18.6.1)											UBAL3_78920079	91
UBABSL4_11503G0009	467 Nitrogenase MoFe cofactor biosynthesis protein (NifE) (EC 1.18.6.1)											UBAL3_78920080	90
UBABSL4_11503G0010	478 Nitrogenase molybdenum-iron cofactor biosynthesis protein (NifN) (EC 1.18.6.1)											UBAL3_78920081	80
UBABSL4_11503G0011	133 Nitrogenase molybdenum-iron protein (NifX)											UBAL3_78920082	86
UBABSL4_11503G0012	154 NifX-associated protein											UBAL3_78920083	92
UBABSL4_11503G0013	522 Nitrogenase cofactor biosynthesis protein (NifB)											UBAL3_78920085	88
UBABSL4_11503G0014	86 Putative ferredoxin											UBAL3_78920086	86
UBABSL4_11503G0015	23 hypothetical protein												
UBABSL4_11887G0001	288 Signal transduction histidine kinase									0.0801			
UBABSL4_11887G0002	371 Conserved hypothetical protein									0.1167			
UBABSL4_11887G0003	60 hypothetical protein												
UBABSL4_11887G0004	93 HNH endonuclease											UBAL3_48660076	69
UBABSL4_11887G0005	449 Probable transport protein											UBAL3_80290078	82
UBABSL4_11887G0006	169 DNA-3-methyladenine glycosylase (EC 3.2.2.21)											UBAL3_80290080	63
UBABSL4_11887G0007	441 Phosphoketolase (EC 4.1.2.9)		0.04486	0.03939		0.1374	0.1531	0.0363	0.0949	0.2085	0.3053	0.2136	0.1358
UBABSL4_11887G0008	232 Phosphoketolase (EC 4.1.2.9)											UBAL3_80290081	87
UBABSL4_11887G0010	201 hypothetical protein												
UBABSL4_11887G0011	467 Multi-sensor signal transduction histidine kinase								0.01395			UBAL3_80290082	68
UBABSL4_11887G0012	395 Diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s)								0.0183			UBAL3_80290084	60
UBABSL4_11887G0013	85 Glycogen synthase (EC 2.4.1.21)											UBAL3_80290085	60
UBABSL4_11887G0014	96 Glycogen synthase (EC 2.4.1.21)											UBAL3_80290085	73
UBABSL4_12165G0001	114 Conserved hypothetical protein											UBAL3_92050124	77
UBABSL4_12165G0002	219 ferredoxin								0.0395			UBAL3_92050125	86
UBABSL4_12165G0003	544 Putative fumarate reductase/succinate dehydrogenase		0.03732	0.24464	0.39518				0.0451			UBAL3_92050126	79
UBABSL4_12165G0004	396 succinyl-CoA synthetase, beta subunit		0.5127	1.04457	0.72109				0.0364			UBAL3_92050127	89

UBABSL4_12165G0005	307 succinyl-CoA synthetase, alpha subunit	0.11022	0.48037	0.31122	0.1034	UBAL3_92050128	94
UBABSL4_12165G0006	157 thiol-specific antioxidant protein	0.43106	0.80187	0.57399	0.1195	UBAL3_92050129	93
UBABSL4_12165G0007	65 hypothetical protein						
UBABSL4_12165G0008	79 Conserved hypothetical protein						
UBABSL4_12165G0009	336 NADH dehydrogenase (Quinone)				0.0301	UBAL3_94240063	73
UBABSL4_12165G0010	155 Conserved hypothetical protein				0.0093		
UBABSL4_12165G0011	523 Conserved hypothetical protein		0.01038		0.0221		
UBABSL4_12165G0012	74 hypothetical protein						
UBABSL4_12165G0013	285 Conserved protein of unknown function				0.0101	UBAL3_94240065	64
UBABSL4_1756G0001	140 Peptidoglycan glycosyltransferase (EC 2.4.1.129)				0.0206	UBAL3_94530108	83
UBABSL4_1756G0002	73 Conserved hypothetical protein					UBAL3_94530109	69
UBABSL4_1756G0003	108 orotate phosphoribosyltransferase				0.0534	UBAL3_94530110	82
UBABSL4_1756G0004	213 Probable major facilitator superfamily protein				0.0068	UBAL3_96270001	59
UBABSL4_1756G0005	105 Glucan 1,4-alpha-glucosidase					UBAL3_96270002	58
UBABSL4_1756G0006	651 Glucan 1,4-alpha-glucosidase				0.0089	UBAL3_96270002	80
UBABSL4_1756G0007	218 amino acid permease-associated region				0.0066	UBAL3_94240001	67
UBABSL4_1756G0008	363 phosphate ABC transporter, periplasmic				0.0119	UBAL3_94240002	51
UBABSL4_1756G0009	396 DNA uptake lipoprotein				0.0291	UBAL3_94240004	92
UBABSL4_1756G0010	134 hypothetical protein				0.0646		
UBABSL4_1756G0011	74 hypothetical protein						
UBABSL4_1756G0012	172 two component, sigma54 specific, transcriptional regulator, Fis family				0.0252	UBAL3_94240006	59
UBABSL4_3335G0001	198 acriflavin resistance protein				0.0073	UBAL3_92050088	91
UBABSL4_3335G0002	73 Conserved protein of unknown function				0.0198	UBAL3_92050089	72
UBABSL4_3335G0003	64 Alcohol dehydrogenase, zinc-binding type 2					UBAL3_92050090	76
UBABSL4_3335G0004	208 Alcohol dehydrogenase, zinc-binding type 2				0.0208	UBAL3_92050090	82
UBABSL4_3335G0005	130 Conserved protein of unknown function				0.7768	UBAL3_92050091	64
UBABSL4_3335G0006	248 Conserved hypothetical protein					UBAL3_92050092	70
UBABSL4_3335G0007	143 Conserved hypothetical protein					UBAL3_92050092	84
UBABSL4_3335G0008	93 hypothetical protein		0.23206		1.2565		
UBABSL4_3335G0009	83 transposase						
UBABSL4_3335G0011	134 Conserved protein of unknown function				0.0108	UBAL3_92050093	56
UBABSL4_3335G0012	291 band 7 family protein	1.30236	0.41408	0.22013	0.0545	UBAL3_92050094	90
UBABSL4_3335G0013	85 XRE family plasmid maintenance system antidote protein						
UBABSL4_3478G0001	111 8-amino-7-oxononanoate synthase					UBAL3_80420040	36
UBABSL4_3478G0002	245 Amylo-alpha-1,6-glucosidase				0.0059	UBAL3_80420039	42
UBABSL4_3478G0003	422 Amylo-alpha-1,6-glucosidase					UBAL3_80420039	62
UBABSL4_3478G0003a	262 penicillin-binding protein, transpeptidase				0.0496	UBAL3_80420038	78
UBABSL4_3478G0004	147 Conserved protein of unknown function					UBAL3_80420036	80
UBABSL4_3478G0004a	138 Ribosomal protein L17	1.22602	2.46312	2.87959	0.0627	UBAL3_80420035	91
UBABSL4_3478G0005	331 DNA-directed RNA polymerase, alpha subunit		0.1793	0.46579		UBAL3_80420034	75
UBABSL4_3478G0006	210 Ribosomal protein S4	0.3545	0.36826	0.37743		UBAL3_80420033	85
UBABSL4_3478G0006a	129 Ribosomal protein S11		0.27883	0.12625		UBAL3_80420032	95
UBABSL4_3478G0007a	125 Ribosomal protein S13		0.05755	0.15635		UBAL3_80420031	83
UBABSL4_3478G0007	38 translation initiation factor IF-1					UBAL3_80420029	100
UBABSL4_3478G0008	225 methionine aminopeptidase, type I			0.00965	0.0064	UBAL3_80420028	71
UBABSL4_5705G0001	247 Glucosamine-1-phosphate n-acetyltransferase (EC 2.3.1.157)				0.0526	UBAL3_74420044	57
UBABSL4_5705G0002	41 Conserved protein of unknown function				0.0352	UBAL3_74420045	78
UBABSL4_5705G0003	122 Conserved protein of unknown function	0.11094		0.0178	0.0828	UBAL3_74420046	47
UBABSL4_5705G0004	227 Conserved protein of unknown function				0.0254	UBAL3_74420047	
UBABSL4_5705G0005	153 Conserved protein of unknown function				0.0566	UBAL3_74420047	74
UBABSL4_5705G0006	122 Putative LD-carboxypeptidase family protein					UBAL3_74420048	60
UBABSL4_5705G0006a	147 Putative LD-carboxypeptidase family protein					UBAL3_74420048	60
UBABSL4_5705G0007	81 Conserved hypothetical protein					UBAL3_74420049	54
UBABSL4_5705G0008	185 Cobyrinic acid a,c-diamide synthase				0.0078	UBAL3_74420050	82
UBABSL4_5705G0008a	136 Creatininase				0.0849	UBAL3_74420051	81
UBABSL4_5705G0009	121 diguanylate cyclase/phosphodiesterase				0.0119	UBAL3_95450144	69
UBABSL4_5705G0010	40 Putative CO dehydrogenase beta subunit/acetyl-CoA synthase epsilon subunit				0.7574	UBAL3_74420055	90
UBABSL4_11740G0001	22 hypothetical protein						
UBABSL4_11740G0002	164 phosphoribosylaminoimidazole carboxylase, catalytic subunit		0.02193			UBAL3_95680017	75

UBABSL4_11740G0003	214 Conserved protein of unknown function			0.0472		UBAL3_95680018	63
UBABSL4_11740G0004	166 Conserved hypothetical protein					UBAL3_95680019	42
UBABSL4_11740G0005	457 putative adenylate/guanylate cyclase					UBAL3_95680020	53
UBABSL4_11740G0006	486 Conserved hypothetical protein			0.0119		UBAL3_95680021	49
UBABSL4_11740G0007	309 Conserved protein of unknown function			0.0187		UBAL3_95680022	44
UBABSL4_11740G0008	80 Putative ABC transporter					UBAL3_95680023	59
UBABSL4_11740G0009	228 Putative ABC transporter					UBAL3_95680023	82
UBABSL4_11740G0010	226 ABC transporter			0.0192		UBAL3_95680024	53
UBABSL4_11740G0011	212 Probable ABC transporter, permease protein			0.0068		UBAL3_95680025	81
UBABSL4_11740G0012	89 Cytochrome-c peroxidase					UBAL3_95680026	70
UBABSL4_11853G0001	402 UDP-N-acetylglucosamine 1-carboxyvinyltransferase	0.00895	0.0108	0.0072		UBAL3_94240186	77
UBABSL4_11853G0002	217 ATP phosphoribosyltransferase		0.01501	0.0133		UBAL3_94240185	71
UBABSL4_11853G0003	436 Histidinol dehydrogenase	0.04657	0.0825	0.0066	0.005	UBAL3_94240184	69
UBABSL4_11853G0004	362 Histidinol-phosphate aminotransferase (EC 2.6.1.9)			0.0199		UBAL3_94240183	49
UBABSL4_11853G0005	209 Imidazoleglycerol-phosphate dehydratase					UBAL3_94240182	75
UBABSL4_11853G0006	69 imidazole glycerol phosphate synthase, glutamine			0.0209		UBAL3_94240181	71
UBABSL4_11853G0007	120 imidazole glycerol phosphate synthase, glutamine			0.0361		UBAL3_94240181	74
UBABSL4_11853G0008	250 phosphoribosylformimino-5-aminoimidazole		0.02606	0.0231		UBAL3_94240180	68
UBABSL4_11853G0009	176 Histidine biosynthesis protein (HisF) (EC 5.3.1.16)		0.19741	0.0164		UBAL3_94240179	89
UBABSL4_11853G0010	101 Histidine biosynthesis bifunctional protein (HisE)			0.0286		UBAL3_94240178	69
UBABSL4_11853G0011	124 histidine triad (HIT) protein					UBAL3_94240177	66
UBABSL4_11853G0012	31 Ribosomal protein S21		0.07005	0.2327		UBAL3_94240176	100
UBABSL4_11894G0001	245 Putative methyltransferase			0.0177		UBAL3_80630020	65
UBABSL4_11894G0002	526 Putative heptosyltransferase family protein			0.0027		UBAL3_80630019	51
UBABSL4_11894G0003	223 Conserved protein of unknown function			0.0194		UBAL3_80630018	63
UBABSL4_11894G0004	296 Conserved protein of unknown function			0.0341		UBAL3_80630018	71
UBABSL4_11894G0005	449 Probable heptosyltransferase family protein			0.0096		UBAL3_80630017	71
UBABSL4_11894G0006	174 Probable heptosyltransferase family protein					UBAL3_80630017	55
UBABSL4_11894G0007	228 Conserved protein of unknown function					UBAL3_80630016	57
UBABSL4_11894G0008	70 hypothetical protein						
UBABSL4_11894G0008a	174 Conserved protein of unknown function			0.0497		UBAL3_80630014	58
UBABSL4_11894G0009	269 Putative ABC transporter, permease protein			0.0215		UBAL3_80630012	81
UBABSL4_11894G0009a	111 Inorganic diphosphatase			0.143		UBAL3_80630010	86
UBABSL4_11894G0010	134 hypothetical protein						
UBABSL4_4178G0002	119 oxidoreductase FAD/NAD(P)-binding domain			0.0485		UBAL3_69480044	36
UBABSL4_4178G0003	95 oxidoreductase FAD/NAD(P)-binding domain					UBAL3_69480044	
UBABSL4_4178G0004	552 diguanylate cyclase/phosphodiesterase with GAF			0.0052		UBAL3_69480045	32
UBABSL4_4178G0005	117 hypothetical protein						
UBABSL4_4178G0006	142 hypothetical protein						
UBABSL4_4178G0007	145 radical SAM domain protein			0.0099			
UBABSL4_4178G0008	357 radical SAM domain protein			0.004			
UBABSL4_4178G0009	221 Conserved hypothetical protein		0.00983	0.0326			
UBABSL4_4178G0010	262 membrane protein-like			0.0055		UBAL3_69480043	65
UBABSL4_4178G0011	572 Putative Cl-channel, voltage gated			0.0025		UBAL3_69480042	86
UBABSL4_4178G0012	299 monooxygenase, FAD-binding					UBAL3_69480041	60
UBABSL4_7770G0001	341 Nitrite/sulfite reductase			0.0465		UBAL3_95680100	57
UBABSL4_7770G0003	136 Conserved protein of unknown function					UBAL3_95680099	46
UBABSL4_7770G0004	94 hypothetical protein						
UBABSL4_7770G0005	795 hypothetical protein		0.00956	0.0036	0.0014		
UBABSL4_7770G0007	98 chaperone protein DnaJ			0.0294		UBAL3_80420059	
UBABSL4_7770G0007a	178 Putative GrpE protein					UBAL3_80420057	
UBABSL4_7770G0008	216 Glutamate dehydrogenase			0.0401		UBAL3_80420056	32
UBABSL4_7770G0008a	296 chaperone protein DnaK		0.11738	0.0439		UBAL3_80420058	
UBABSL4_7770G0009	264 Putative heat shock protein Hsp70		0.07403	0.0164		UBAL3_79320011	41
UBABSL4_7770G0010	153 hypothetical protein						
UBABSL4_7770G0011	245 filamentation induced by cAMP protein Fic						
UBABSL4_9876G0001	349 flagellar M-ring protein FlIF			0.0289		UBAL3_80630068	82
UBABSL4_9876G0001a	134 flagellar motor switch protein FlIG			0.0108		UBAL3_80630067	98
UBABSL4_9876G0002	106 Flagellar hook-basal body complex subunit FlIE			0.0408		UBAL3_80630069	91

UBABSL4_9876G0003	146 flagellar basal-body rod protein FigC			0.0692		UBAL3_80630070	87
UBABSL4_9876G0004	125 flagellar basal-body rod protein FigB			0.0115		UBAL3_80630071	90
UBABSL4_9876G0005	460 Putative two component, sigma54 specific, transcriptional regulator, Fis family			0.0314		UBAL3_80630072	79
UBABSL4_9876G0006	251 Putative PAS/PAC sensor signal transduction histidine kinase			0.0287		UBAL3_80630073	60
UBABSL4_9876G0007	77 Putative PAS/PAC sensor signal transduction histidine kinase			0.0187		UBAL3_80630073	50
UBABSL4_9876G0008	544 Putative TPR-domain containing protein			0.0186		UBAL3_80630074	55
UBABSL4_9876G0009	280 sigma54 specific transcriptional regulator, Fis family	0.00776		0.0361		UBAL3_80630076	66
UBABSL4_9876G0010	77 sigma54 specific transcriptional regulator, Fis family			0.0375		UBAL3_80630076	70
UBABSL4_10765G0001	420 Alpha, alpha-trehalose-phosphate synthase			0.0481		UBAL3_95450128	60
UBABSL4_10765G0002	272 Trehalose-6-phosphate phosphatase			0.0106		UBAL3_95450127	54
UBABSL4_10765G0003	302 dTDP-4-dehydrorhamnose reductase			0.0382		UBAL3_95450126	60
UBABSL4_10765G0004	225 ADP-L-glycero-D-manno-heptose-6-epimerase	0.0193		0.109		UBAL3_95450123	77
UBABSL4_10765G0005	613 Conserved protein of unknown function			0.0094		UBAL3_95450122	64
UBABSL4_10765G0006	117 cytochrome c, class I			0.0123		UBAL3_95450121	47
UBABSL4_10765G0007	90 Conserved hypothetical protein						
UBABSL4_10765G0008	125 Conserved hypothetical protein						
UBABSL4_10765G0009	121 Conserved hypothetical protein						
UBABSL4_10765G0010	586 transposase	0.00741					
UBABSL4_10765G0011	110 Conserved hypothetical protein			0.0131			
UBABSL4_11442G0001	94 Putative pirin domain protein			0.0614		UBAL3_80290032	85
UBABSL4_11442G0002	69 Conserved protein of unknown function			0.1254		UBAL3_80290033	66
UBABSL4_11442G0003	71 Conserved protein of unknown function			0.1422		UBAL3_80290033	58
UBABSL4_11442G0004	376 Putative sulfide-quinone reductase			0.0192		UBAL3_80290034	67
UBABSL4_11442G0005	63 hypothetical protein						
UBABSL4_11442G0006	392 Conserved hypothetical protein					UBAL3_80290036	37
UBABSL4_11442G0007	146 Conserved hypothetical protein						
UBABSL4_11442G0008	60 hypothetical protein			0.024			
UBABSL4_11442G0009	639 Probable citrate transporter			0.0113		UBAL3_80290038	64
UBABSL4_11442G0010	275 Conserved protein of unknown function			0.0052		UBAL3_80290039	53
UBABSL4_11442G0011	148 Putative transcriptional regulator, MarR family			0.0097		UBAL3_80290040	78
UBABSL4_11480G0001	274 Putative glycosyl hydrolase, BNR repeat	0.01313	0.21398	0.2211	0.0189	UBAL3_92050057	83
UBABSL4_11480G0002	215 Conserved protein of unknown function		0.03535	0.1275		UBAL3_92050058	75
UBABSL4_11480G0003	119 Conserved protein of unknown function					UBAL3_92050059	52
UBABSL4_11480G0004	86 Conserved protein of unknown function					UBAL3_92050060	56
UBABSL4_11480G0005	89 Conserved hypothetical protein					UBAL3_92050061	58
UBABSL4_11480G0006	308 Putative oligopeptide ABC transporter					UBAL3_92050062	85
UBABSL4_11480G0007	96 Putative oligopeptide ABC transporter					UBAL3_92050063	88
UBABSL4_11480G0008	85 Putative oligopeptide ABC transporter			0.0509		UBAL3_92050063	88
UBABSL4_11480G0009	326 Conserved protein of unknown function	0.06661		0.0266		UBAL3_92050064	52
UBABSL4_11480G0010	609 Conserved hypothetical protein			0.0024		UBAL3_94530006a	67
UBABSL4_11480G0011	111 transposase			0.156			
UBABSL4_12275G0001	86 hypothetical protein						
UBABSL4_12275G0002	503 RNA-directed DNA polymerase			0.0029		UBAL3_93670015	65
UBABSL4_12275G0005	460 Putative endonuclease			0.0697	0.0533	UBAL3_94530056	76
UBABSL4_12275G0007	204 Arsenical resistance operon trans-acting	0.06387				UBAL3_95450074	53
UBABSL4_12275G0008	173 arsenite-activated ATPase ArsA					UBAL3_95450073	62
UBABSL4_12275G0009	318 arsenite-activated ATPase ArsA					UBAL3_95450073	62
UBABSL4_12275G0010	129 regulatory protein, ArsR			0.0335		UBAL3_94320016	68
UBABSL4_12275G0011	511 Glucose-6-phosphate isomerase	0.0085		0.0423		UBAL3_94320015	77
UBABSL4_12275G0012	204 Phosphoglycerate mutase			0.0707		UBAL3_94320014	64
UBABSL4_12275G0013	224 Glucan 1,4-alpha-glucosidase					UBAL3_94530076	70
UBABSL4_12275G0014	434 Glucan 1,4-alpha-glucosidase					UBAL3_94530076	70
UBABSL4_12515G0001	225 Formate--tetrahydrofolate ligase			0.0449		UBAL3_92050026	64
UBABSL4_12515G0002	332 Formate--tetrahydrofolate ligase	0.00654		0.0043		UBAL3_92050026	80
UBABSL4_12515G0003	252 Sec-independent protein translocase, TatC			0.0343		UBAL3_92050025	75
UBABSL4_12515G0004	97 Conserved protein of unknown function			0.1339		UBAL3_92050024	64
UBABSL4_12515G0005	71 Conserved protein of unknown function			0.1626		UBAL3_92050023	60
UBABSL4_12515G0006	176 Ribosomal-protein-alanine acetyltransferase			0.1148		UBAL3_92050022	67
UBABSL4_12515G0007	228 Probable glycoprotein endopeptidase					UBAL3_92050021	55

UBABSL4_12515G0008	473 DNA repair protein RadA		0.00459														UBAL3_92050020	85	
UBABSL4_12515G0009	289 pantoate-beta-alanine ligase																	UBAL3_92050019	61
UBABSL4_12515G0010	281 Putative tetrapyrrole methylase family protein																	UBAL3_92050018	62
UBABSL4_12515G0011	67 Probable SirA family protein																	UBAL3_92050017	86
UBABSL4_12832G0001	43 hypothetical protein			0.3542												0.438		0.0254	
UBABSL4_12832G0002	192 Conserved hypothetical protein			3.6492	1.0455	0.7804	1.8929	3.5162	1.2519	2.9078			1.3046	1.8611	1.4551	2.3357	3.0231	UBAL3_96120003	99
UBABSL4_12832G0003	155 DNA (cytosine-5-)-methyltransferase			1.474		0.2417		2.1778	0.2068	0.3444			0.3887	0.7685	0.1215	1.1264	1.1636	UBAL3_93200035	84
UBABSL4_12832G0004	247 DNA (cytosine-5-)-methyltransferase			1.3566		0.3033		1.0933	0.0649	0.6483			0.7959	0.5032	0.3431	1.5661	1.7436	UBAL3_93200035	79
UBABSL4_12832G0005	180 hypothetical protein								0.1781	0.0401			0.1585	0.0575	0.1395	0.0285	0.0243		
UBABSL4_12832G0006	91 hypothetical protein								0.7044	0.0951			0.0348		0.1035	0.0376			
UBABSL4_12832G0007	144 putative transcriptional regulator, MerR family								0.779	0.01			0.022		0.1308		0.0304	UBAL3_93200020	52
UBABSL4_12832G0008	131 Mercury transporter MerC								0.734	0.0551			0.1452		0.024				
UBABSL4_12832G0009	551 mercuric reductase		0.00394	0.0829					0.4653	0.0314			0.1093		0.1538	0.0342	0.0278	UBAL3_93200019	49
UBABSL4_12832G0010	380 transposase, IS204/IS1001/IS1096/IS1165 family			0.0401			0.1594		0.4639	0.0987			0.1252		0.1487	0.0676	0.0173	UBAL3_95450062	78
UBABSL4_12832G0011	176 Conserved protein of unknown function			0.1731					0.1821	0.041			0.0901		0.2675	0.107	0.0311	UBAL3_95530042	60
UBABSL4_8928G0001	109 glucose-1-phosphate thymidyltransferase		0.1485	0.01992	0.2795			0.6194	0.147	0.1324			0.3781	0.2376	0.1152	0.267	0.1504	UBAL3_94170082	96
UBABSL4_8928G0002	181 dTDP-4-dehydrorhamnose 3,5-epimerase			0.06598	0.5891			0.3347	0.746	0.1771	0.2391		0.6306	0.6008	0.3989	0.4918	0.3261	UBAL3_94170083	100
UBABSL4_8928G0003	61 hypothetical protein				0.2497				0.2627				0.9876	0.3396	0.6175	0.0561	0.1254		
UBABSL4_8928G0004	200 Conserved hypothetical protein				0.4569				0.3376		0.1226		0.4756	0.5179	0.5023	0.3423	0.2842	UBAL3_94170085	
UBABSL4_8928G0005	146 transposase				2.5038	0.8249	0.5132	1.6595	0.9248	3.8416	0.4348		6.8841	5.4625	8.1275	3.5406	2.2311		
UBABSL4_8928G0006	455 hypothetical protein				3.4145	0.6176	0.4117	1.1982	1.7805	4.0502	0.4122	0.133	6.7175	5.1446	7.2236	4.2961	2.597		
UBABSL4_8928G0007	338 cation diffusion facilitator family transporter				0.3154	0.2375	0.2217		0.1997	0.4741	0.0939		1.8667	1.3789	1.5603	1.109	0.9928	UBAL3_93200002	
UBABSL4_8928G0008	44 Conserved hypothetical protein				0.3462				0.3642	0.5574			1.8015	1.177	1.4982	0.778	0.4472	UBAL3_93200003a	
UBABSL4_8928G0009	213 hypothetical protein				3.3609	0.7539	1.407	1.1375	1.9017	1.3542	0.7721	0.5683	2.1435	2.2611	3.1244	3.1341	2.0168		
UBABSL4_8928G0010	172 diguanylate cyclase with PAS/PAC sensor				0.1771				0.3925	0.0932	0.0503		0.8664	1.0538	1.1863	0.4279	0.3495	UBAL3_93200004	95
UBABSL4_11581G0001	90 Conserved hypothetical protein																		
UBABSL4_11581G0002	81 Conserved hypothetical protein																		
UBABSL4_11581G0003	200 Conserved hypothetical protein																		
UBABSL4_11581G0004	216 TonB family protein																	UBAL3_93200026	48
UBABSL4_11581G0005	139 Biopolymer transport protein ExbD/TolR																	UBAL3_93200025	56
UBABSL4_11581G0006	140 MotA/TolQ/ExbB proton channel																	UBAL3_93200024	63
UBABSL4_11581G0007	248 TonB-dependent receptor																	UBAL3_93200033	75
UBABSL4_11581G0009	373 TonB-dependent receptor																	UBAL3_93200033	87
UBABSL4_11581G0010	150 TonB-dependent receptor																	UBAL3_93200033	53
UBABSL4_11581G0011	216 two component transcriptional regulator, winged																	UBAL3_93200028	43
UBABSL4_11758G0001	36 hypothetical protein																		
UBABSL4_11758G0002	309 Putative helicase																	UBAL3_92050009	48
UBABSL4_11758G0003	679 Putative helicase			0.01759														UBAL3_92050009	70
UBABSL4_11758G0004	557 Putative helicase				0.0273				0.3452	0.0207			0.0057	0.0558		0.0061	0.0078	UBAL3_92050009	64
UBABSL4_11758G0006	99 hypothetical protein																		
UBABSL4_11758G0007	253 Conserved protein of unknown function																	UBAL3_96270019	28
UBABSL4_11758G0008	86 hypothetical protein																		
UBABSL4_11758G0009	94 Single-stranded DNA-binding protein													0.0551				UBAL3_92050173	66
UBABSL4_11758G0010	65 hypothetical protein																		
UBABSL4_11758G0011	143 Conserved hypothetical protein																	UBAL3_95450088	38
UBABSL4_12302G0001	174 HNH endonuclease							0.6962										UBAL3_48660076	75
UBABSL4_12302G0002	110 Conserved hypothetical protein			0.01974															
UBABSL4_12302G0003	46 hypothetical protein																		
UBABSL4_12302G0004	189 Conserved hypothetical protein			0.06319															
UBABSL4_12302G0005	508 sigma54 specific transcriptional regulator, Fis family											0.0085						UBAL3_94240097	68
UBABSL4_12302G0006	367 UDP-galactopyranose mutase			0.00592														UBAL3_94240099	88
UBABSL4_12302G0007	73 hypothetical protein																		
UBABSL4_12302G0008	337 glycosyl transferase, family 2											0.0342						UBAL3_94240100	81
UBABSL4_12302G0009	587 periplasmic sensor signal transduction histidine kinase											0.0074						UBAL3_94240101	75
UBABSL4_12302G0010	197 glycosyl transferase, family 2																	UBAL3_94240102	68
UBABSL4_12310G0001	82 Glycine dehydrogenase (decarboxylating)											0.0176						UBAL3_80630081	70
UBABSL4_12310G0002	266 transposase											0.0163							
UBABSL4_12310G0003	231 Conserved protein of unknown function																	UBAL3_94240165	54

UBABSL4_12310G0004	124	Conserved protein of unknown function				0.01751			0.0116	UBAL3_94240164	67	
UBABSL4_12310G0005	418	seryl-tRNA synthetase				0.01558			0.0656	UBAL3_94240163	73	
UBABSL4_12310G0006	149	Conserved protein of unknown function				0.01457				UBAL3_44810095	75	
UBABSL4_12310G0007	119	phosphoribosyltransferase								UBAL3_44810094	63	
UBABSL4_12310G0008	36	hypothetical protein										
UBABSL4_12310G0009	362	Radical SAM domain protein							0.0598	UBAL3_74420056	70	
UBABSL4_12310G0010	223	Conserved protein of unknown function							0.0388	UBAL3_74420057	60	
UBABSL4_17878G0001	206	RNA-directed DNA polymerase								UBAL3_93670015	60	
UBABSL4_17878G0002	227	Conserved hypothetical protein							0.0191	UBAL3_95950035	40	
UBABSL4_17878G0003	80	hypothetical protein										
UBABSL4_17878G0004	85	putative GAF sensor protein										
UBABSL4_17878G0005	193	hypothetical protein							0.0075			
UBABSL4_17878G0006	92	hypothetical protein										
UBABSL4_17878G0007	316	Conserved hypothetical protein							0.0091			
UBABSL4_17878G0008	131	transposase										
UBABSL4_17878G0009	143	transposase										
UBABSL4_17878G0010	53	hypothetical protein										
UBABSL4_17883G0001	179	3-deoxy-manno-octulosonate-8-phosphatase				0.01213			0.0161	UBAL3_95950028	59	
UBABSL4_17883G0002	182	CDP-diacylglycerol-glycerol-3-phosphate								UBAL3_95950029	79	
UBABSL4_17883G0003	206	Conserved hypothetical protein								UBAL3_95950030	64	
UBABSL4_17883G0004	332	peptidase M23B							0.4867	UBAL3_95950031	79	
UBABSL4_17883G0005	497	periplasmic sensor signal transduction histidine kinase				0.00437			0.0145	UBAL3_95950032	75	
UBABSL4_17883G0006	338	Conserved hypothetical protein										
UBABSL4_17883G0007	243	Conserved hypothetical protein								UBAL3_95950037	59	
UBABSL4_17883G0009	153	Conserved hypothetical protein								UBAL3_95950038	55	
UBABSL4_17883G0010	107	Conserved hypothetical protein								UBAL3_95950038	55	
UBABSL4_17883G0011	277	sodium/hydrogen exchanger								UBAL3_95950039	57	
UBABSL4_3895G0001	281	methyl-accepting chemotaxis sensory transducer							0.0565	UBAL3_96120012	73	
UBABSL4_3895G0002	203	metallo-beta-lactamase family protein							0.0711	UBAL3_96120013	91	
UBABSL4_3895G0004	327	methyl-accepting chemotaxis sensory transducer	0.43462	0.2695	0.14277				0.1191	UBAL3_95950046	74	
UBABSL4_3895G0005	334	methyl-accepting chemotaxis sensory transducer							0.0734	UBAL3_96120017	70	
UBABSL4_3895G0006	409	putative diguanylate cyclase							0.1376			
UBABSL4_3895G0007	133	Conserved hypothetical protein							0.2495			
UBABSL4_3895G0008	274	hypothetical protein				0.0556	0.2464		0.0053			
UBABSL4_3895G0009	346	phage integrase family protein				0.088			0.0042	0.0092	UBAL3_95660014	29
UBABSL4_3895G0010	673	FOG; Transposase-like									UBAL3_94240161	46
UBABSL4_4347G0001	200	glycoside hydrolase, family 57								UBAL3_94530082	37	
UBABSL4_4347G0002	117	glycoside hydrolase, family 57				0.01856			0.0617	UBAL3_94530082	60	
UBABSL4_4347G0003	179	4-alpha-glucanotransferase								UBAL3_94530081	80	
UBABSL4_4347G0004	226	4-alpha-glucanotransferase							0.0447	UBAL3_94530081	53	
UBABSL4_4347G0005	335	galactose-1-phosphate uridylyltransferase				0.20401	0.20094		0.0732	UBAL3_94530080	94	
UBABSL4_4347G0006	452	Probable aldolase	0.26951	0.39391	0.35551				0.0128	UBAL3_94530079	79	
UBABSL4_4347G0007	310	Putative glycoside hydrolase, family 57							0.0605	UBAL3_94530078	84	
UBABSL4_4347G0008	50	Conserved protein of unknown function				0.14388	0.54287		0.1443	UBAL3_94530077	61	
UBABSL4_4347G0009	65	hypothetical protein										
UBABSL4_4646G0001	186	Putative ATP-dependent Clp protease, ATPase subunit				0.2514	0.32689		0.3645	UBAL3_80420043	88	
UBABSL4_4646G0001a	104	O-sialoglycoprotein endopeptidase (EC 3.4.24.57)								UBAL3_80420044	73	
UBABSL4_4646G0002a	139	O-sialoglycoprotein endopeptidase (EC 3.4.24.57)								UBAL3_80420044	73	
UBABSL4_4646G0002	246	arginyl-tRNA synthetase							0.0469	UBAL3_80420045	61	
UBABSL4_4646G0003	179	arginyl-tRNA synthetase				0.02426			0.0161	UBAL3_80420045	80	
UBABSL4_4646G0004	190	queuine tRNA-ribosyltransferase								UBAL3_80420046	75	
UBABSL4_4646G0005	55	preprotein translocase, YajC subunit							0.0262	UBAL3_80420047	67	
UBABSL4_4646G0006	211	SecD export membrane protein								UBAL3_80420048	68	
UBABSL4_4646G0007	285	SecF export membrane protein							0.0962	UBAL3_80420049	84	
UBABSL4_4714G0001	77	chaperone protein DnaK				0.09343			0.2061	UBAL3_80420058	88	
UBABSL4_4714G0002	255	chaperone protein DnaK	1.43315	1.76321	1.30716				0.3394	UBAL3_80420058	96	
UBABSL4_4714G0003	227	heat-inducible transcription repressor HrcA							0.0064	UBAL3_80420055	66	
UBABSL4_4714G0004	96	Conserved hypothetical protein								UBAL3_80420054	79	

UBABSL4_10676G0009	151 Ppx/GppA phosphatase									0.0764						UBAL3_94530005	69
UBABSL4_10718G0001	239 Conserved hypothetical protein									0.006							
UBABSL4_10718G0002	325 Putative transposase									0.0222						UBAL3_24060025	70
UBABSL4_10718G0003	134 Putative transposase															UBAL3_24060024	66
UBABSL4_10718G0004	188 Conserved hypothetical protein																
UBABSL4_10718G0005	39 hypothetical protein																
UBABSL4_10718G0006	296 Probable sodium/calcium exchanger membrane region															UBAL3_92050106	66
UBABSL4_10718G0007	415 Probable transporter protein															UBAL3_92050105	59
UBABSL4_10718G0008	96 hypothetical protein																
UBABSL4_10718G0009	243 transposase																
UBABSL4_10954G0001	305 Putative A/G-specific DNA glycosylase															UBAL3_82700015	57
UBABSL4_10954G0002	264 Conserved hypothetical protein															UBAL3_82700014	63
UBABSL4_10954G0003	153 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphokinase															UBAL3_82700013	59
UBABSL4_10954G0004	394 Aspartate aminotransferase (EC 2.6.1.1)	0.08588	0.27844	0.54012						0.0256						UBAL3_82700012	86
UBABSL4_10954G0005	127 5-carboxymethyl-2-hydroxymuconate															UBAL3_82700011	63
UBABSL4_10954G0006	177 Dihydrodipicolinate reductase			0.05521						0.0571						UBAL3_82700010	84
UBABSL4_10954G0007	95 Dihydrodipicolinate reductase			0.09143						0.0607						UBAL3_82700010	55
UBABSL4_10954G0008	224 dihydrodipicolinate synthase			0.02424						0.0322						UBAL3_82700009	78
UBABSL4_10954G0009	299 diaminopimelate decarboxylase		0.13233	0.19246						0.0531						UBAL3_82700007	86
UBABSL4_11165G0001	96 transcriptional regulator, LysR family		0.07494	0.05655						0.0301						UBAL3_95320053	88
UBABSL4_11165G0002	261 outer membrane efflux protein		0.06891	0.03328						0.0111						UBAL3_95320055	87
UBABSL4_11165G0003	270 outer membrane efflux protein	0.05013	0.01998	0.02413						0.0053						UBAL3_95320055	
UBABSL4_11165G0004	253 Conserved protein of unknown function		0.01422	0.01717						0.0057						UBAL3_95320056	62
UBABSL4_11165G0005	161 Conserved protein of unknown function									0.0269						UBAL3_95320057	67
UBABSL4_11165G0006	195 ABC transporter, ATPase subunit															UBAL3_95320058	71
UBABSL4_11165G0007	274 ABC-2 type transporter															UBAL3_95320059	82
UBABSL4_11165G0008	245 oxidoreductase FAD/NAD(P)-binding domain		0.00886							0.0471						UBAL3_95320060	64
UBABSL4_11165G0009	210 Conserved protein of unknown function									0.0069						UBAL3_95320060a	45
UBABSL4_11484G0001	117 hypothetical protein									0.0863							
UBABSL4_11484G0002	461 transposase									0.0751							
UBABSL4_11484G0003	81 hypothetical protein																
UBABSL4_11484G0004	216 Conserved hypothetical protein									0.0267							
UBABSL4_11484G0005	142 phosphoribosyltransferase									0.0406						UBAL3_44810094	57
UBABSL4_11484G0006	153 heat shock protein Hsp20									0.0189						UBAL3_74420024	56
UBABSL4_11484G0007	241 Conserved hypothetical protein															UBAL3_92050050	52
UBABSL4_11484G0008	64 hypothetical protein																
UBABSL4_11484G0009	419 Conserved hypothetical protein																
UBABSL4_11784G0001	177 Conserved protein of unknown function									0.0082						UBAL3_69480040	42
UBABSL4_11784G0002	518 glucose-6-phosphate 1-dehydrogenase		0.01042	0.09223						0.0306						UBAL3_69480039	81
UBABSL4_11784G0003	393 bifunctional transaldolase/phosphoglucose isomerase	0.06888	0.15102	0.21273						0.0477						UBAL3_69480038	70
UBABSL4_11784G0004	257 transketolase		0.04899	0.24503						0.0281						UBAL3_69480037	78
UBABSL4_11784G0005	400 transketolase			0.00543						0.1118						UBAL3_69480037	78
UBABSL4_11784G0006	136 squalene-hopene cyclase															UBAL3_69480035	79
UBABSL4_11784G0007	511 squalene-hopene cyclase									0.0367						UBAL3_69480035	79
UBABSL4_11784G0008	237 Conserved protein of unknown function															UBAL3_69480034	41
UBABSL4_11784G0009	392 Conserved protein of unknown function		0.01385							0.0074						UBAL3_69480033	86
UBABSL4_15692G0001	144 Conserved hypothetical protein	2.49087	0.49958	0.39962	7.1926	32.061	0.2601	0.4206	1.8753	5.0077	3.3762	3.8311	0.7552	1.0246	2.9241	1.9509	
UBABSL4_15692G0002	64 Conserved hypothetical protein				1.9039	7.5274	0.5853			3.255	2.9755	4.31	0.8901	0.7357	0.8023	0.8881	
UBABSL4_15692G0003	72 hypothetical protein									0.4451	0.0601	0.0881	0.0719	0.3488	0.0951	0.0607	
UBABSL4_15692G0004	72 hypothetical protein									0.4451	0.1202	0.1321	0.218	0.0951	0.0759		
UBABSL4_15692G0005	291 Conserved hypothetical protein				0.1047					0.8811	0.1041	0.7082	0.5502	0.1588	0.0601	UBAL3_92050097	50
UBABSL4_15692G0006	41 hypothetical protein				0.3715					0.0352		0.1547	0.2526	0.2297	0.0835	0.0533	
UBABSL4_15692G0007	587 putative type IV secretory pathway VirD4 components				0.0519					0.9828	0.0098	0.5077	0.1059	0.5401	0.0991	0.0652	
UBABSL4_15692G0008	282 hypothetical protein				0.108					1.2502		0.3823	0.1469	0.4119	0.091	0.0388	
UBABSL4_15692G0009	69 hypothetical protein				0.2207					1.3935		0.1379	0.273	0.0744	0.0317		
UBABSL4_1894G0001	54 hypothetical protein																
UBABSL4_1894G0002	163 6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (Riboflavin synthase)		0.27976							0.0531						UBAL3_96150011	65

UBABSL4_1894G0003	51	GTP cyclohydrolase II	0.07053	0.12774																UBAL3_96150010	88
UBABSL4_1894G0004	195	GTP cyclohydrolase II		0.08352																UBAL3_96150010	97
UBABSL4_1894G0005	272	NAD+ synthase		0.03992					0.0212											UBAL3_96150009	80
UBABSL4_1894G0006	261	NAD+ synthase							0.0829											UBAL3_96150009	80
UBABSL4_1894G0007	173	Putative thioredoxin family protein							0.0167											UBAL3_96150008	69
UBABSL4_1894G0008	306	Alcohol dehydrogenase, zinc-binding domain							0.0236											UBAL3_96150007	67
UBABSL4_2345G0001	36	hypothetical protein																			
UBABSL4_2345G0003	331	Conserved protein of unknown function		0.00656																UBAL3_57480017	69
UBABSL4_2345G0004	384	lysine 2,3-aminomutase YodO family protein							0.0488											UBAL3_57480016	81
UBABSL4_2345G0004a	206	Conserved protein of unknown function		0.01746	0.01054															UBAL3_57480017	88
UBABSL4_2345G0005	210	Putative 2-deoxycytidine 5-triphosphate deaminase	0.09668	0.15415	0.1034															UBAL3_57480014	91
IRNA-Asn-GTT		IRNA Asn GTT																			
UBABSL4_2345G0006	165	Conserved protein of unknown function							0.0525											UBAL3_48660006	37
UBABSL4_2345G0007	117	Conserved protein of unknown function							0.0123											UBAL3_48660006	42
UBABSL4_2429G0001	204	hypothetical protein							0.0424												
UBABSL4_2429G0002	181	hypothetical protein							0.0319												
UBABSL4_2429G0003	962	malto-oligosyltrehalose synthase		0.01016					0.009											UBAL3_94530061	73
UBABSL4_2429G0004	556	Trehalose synthase (EC 5.4.99.16)		0.00391					0.0467											UBAL3_93200070	81
UBABSL4_2429G0005	328	Trehalose synthase (EC 5.4.99.16)							4.739	0.0308	1.8452	0.0097	0.0474	0.0287	0.0104	0.0033				UBAL3_93200071	
UBABSL4_2429G0006	157	Trehalose synthase (EC 5.4.99.16)																		UBAL3_93200071	76
UBABSL4_2429G0007	155	glycogen debranching enzyme GlgX							0.0372											UBAL3_94530062	
UBABSL4_2429G0008	411	glycogen debranching enzyme GlgX	0.07439	0.07133	0.2592	0.0911	0.1641	0.4675	0.2455		1.056	0.7302	0.6258	0.799	0.6803					UBAL3_94530062	96
UBABSL4_7963G0001	140	Conserved hypothetical protein																		UBAL3_94240134	54
UBABSL4_7963G0002	52	hypothetical protein							0.0555												
UBABSL4_7963G0003	166	hypothetical protein																			
UBABSL4_7963G0004	67	hypothetical protein							0.0861												
UBABSL4_7963G0005	90	Conserved hypothetical protein																			
UBABSL4_7963G0006	376	Conserved hypothetical protein							0.0345											UBAL3_94240136	93
UBABSL4_7963G0007	228	ABC transporter related	0.01578	0.01429					0.0253											UBAL3_94240137	85
UBABSL4_7963G0008	163	efflux transporter, RND family, MFP subunit																		UBAL3_94240138	75
UBABSL4_9214G0001	233	Putative P-loop ATPase protein family							0.0186											UBAL3_44810086	72
UBABSL4_9214G0002	46	sigma 54 modulation protein/ribosomal protein																		UBAL3_44810087	93
UBABSL4_9214G0003	139	sigma 54 modulation protein/ribosomal protein	0.73032	1.29386	0.71081				0.1038											UBAL3_44810087	86
UBABSL4_9214G0004	297	RNA polymerase, sigma 54 subunit, RpoN		0.01211					0.0534											UBAL3_44810088	76
UBABSL4_9214G0005	249	ABC transporter, ATP-binding protein		0.0939	0.16134				0.0116											UBAL3_44810089	90
UBABSL4_9214G0006	220	Putative OstA family protein							0.0459											UBAL3_44810090	80
UBABSL4_9214G0007	123	Conserved protein of unknown function							0.0235											UBAL3_44810091	72
UBABSL4_9214G0008	296	malate dehydrogenase	0.16005	0.40101	0.66392				0.2242											UBAL3_44810092	98
UBABSL4_10878G0001	175	alanyl-tRNA synthetase							0.0082											UBAL3_44810104	58
UBABSL4_10878G0002	167	Holliday junction resolvase YagF							0.0173											UBAL3_44810103	51
UBABSL4_10878G0003	346	aminodeoxychorismate lyase							0.0042											UBAL3_44810102	69
UBABSL4_10878G0004	361	valyl-tRNA synthetase																		UBAL3_44810101	77
UBABSL4_10878G0005	441	valyl-tRNA synthetase							0.0196											UBAL3_44810101	71
UBABSL4_10878G0006	122	nicotinate-nucleotide pyrophosphorylase							0.0236											UBAL3_44810100	69
UBABSL4_10878G0007	60	nicotinate-nucleotide pyrophosphorylase																		UBAL3_44810100	69
UBABSL4_10878G0008	241	biotin--acetyl-CoA--carboxylase ligase																		UBAL3_44810099	45
UBABSL4_10992G0001	151	Formyltetrahydrofolate deformylase							0.0191												
UBABSL4_10992G0002	137	1-acyl-sn-glycerol-3-phosphate acyltransferase							0.0105												
UBABSL4_10992G0003	281	1-acyl-sn-glycerol-3-phosphate acyltransferase							0.0051											UBAL3_94240089	70
UBABSL4_10992G0004	134	Conserved hypothetical protein							0.0215											UBAL3_94240080	78
UBABSL4_10992G0005	142	Conserved hypothetical protein							0.0305											UBAL3_94240082	62
UBABSL4_10992G0006	108	histidinol-phosphate aminotransferase							0.0267												
UBABSL4_10992G0007	178	histidinol-phosphate aminotransferase							0.0081												
UBABSL4_10992G0008	65	sigma54 specific transcriptional regulator, Fis family																		UBAL3_94240091	52
UBABSL4_11318G0001	410	Conserved hypothetical protein							0.0106												
UBABSL4_11318G0003	139	hypothetical protein							0.0104												
UBABSL4_11318G0004	414	major facilitator superfamily transporter							0.0035											UBAL3_95450027	60

UBABSL4_11318G0005	241 glycosyl transferase, family 9				0.012		UBAL3_95450026	59
UBABSL4_11318G0006	215 two component transcriptional regulator, LuxR				0.0201		UBAL3_95450025	77
UBABSL4_11318G0007	101 periplasmic sensor signal transduction histidine kinase						UBAL3_95450024	80
UBABSL4_11318G0008	222 periplasmic sensor signal transduction histidine kinase						UBAL3_95450024	80
UBABSL4_11318G0009	217 amino acid permease						UBAL3_95450023	79
UBABSL4_11388G0001	450 tRNA-[6]A37 modification enzyme (MiaB)				0.0289		UBAL3_95320041	75
UBABSL4_11388G0002	117 Conserved protein of unknown function				0.0123		UBAL3_95320040	51
UBABSL4_11388G0003	193 Putative SAM-dependent methyltransferases		0.01125		0.0299		UBAL3_95320039	67
UBABSL4_11388G0004	101 hypothetical protein				0.0143			
UBABSL4_11388G0005	608 permease YjgP/YjgQ family protein						UBAL3_95320037	80
UBABSL4_11388G0006	284 Ferrochelatase						UBAL3_95320036	63
UBABSL4_11388G0007	182 Conserved protein of unknown function	1.26428	0.4348	0.60253	0.8957		UBAL3_95320030	82
UBABSL4_11388G0008	164 Conserved protein of unknown function	1.65064	0.59218	0.60908	1.513		UBAL3_95320030	88
UBABSL4_11553G0001	63 Rod shape-determining protein MreC				0.0687		UBAL3_94530044	63
UBABSL4_11553G0002	172 Conserved hypothetical protein				0.0084		UBAL3_94530043	42
UBABSL4_11553G0003	615 Peptidoglycan glycosyltransferase						UBAL3_94530042	71
UBABSL4_11553G0004	364 Putative rod shape-determining protein (RodA)						UBAL3_94530041	56
UBABSL4_11553G0005	522 Ribonucleases G and E	0.31116	0.44789	0.57823	0.0193		UBAL3_94530040	87
UBABSL4_11553G0006	280 Conserved hypothetical protein				0.0052		UBAL3_94530037	76
UBABSL4_11553G0007	95 dihydroneopterin aldolase			0.03429			UBAL3_94530038	55
UBABSL4_11553G0008	301 Putative cobalamin B12-binding/Radical SAM family protein		0.2151	0.19118	0.3643		UBAL3_94530035	93
UBABSL4_11778G0001	46 hypothetical protein							
UBABSL4_11778G0002	192 Conserved protein of unknown function				0.0301		UBAL3_94240071	81
UBABSL4_11778G0003	302 transposase				0.1003			
UBABSL4_11778G0004	318 hypothetical protein		0.01024		0.0408	0.2123		
UBABSL4_11778G0005	72 transposase							
UBABSL4_11778G0006	268 peptidase U62, modulator of DNA gyrase		0.13369		0.0161		UBAL3_74420073	75
UBABSL4_11778G0007	116 peptidase U62, modulator of DNA gyrase						UBAL3_74420073	68
UBABSL4_11778G0008	237 peptidase U62, modulator of DNA gyrase		0.01518	0.05956	0.0183		UBAL3_74420072	94
UBABSL4_11796G0001	168 GCN5-related N-acetyltransferase				0.0172			
UBABSL4_11796G0002	93 hypothetical protein							
UBABSL4_11796G0003	60 hypothetical protein							
UBABSL4_11796G0004	55 hypothetical protein							
UBABSL4_11796G0005	115 hypothetical protein					0.0276		
UBABSL4_11796G0006	59 hypothetical protein							
UBABSL4_11796G0007	209 histidinol-phosphate phosphatase family protein						UBAL3_95680059	58
UBABSL4_11796G0008	42 hypothetical protein							
UBABSL4_11938G0001	166 Conserved protein of unknown function						UBAL3_44810050	69
UBABSL4_11938G0002	204 Conserved protein of unknown function						UBAL3_44810049	67
UBABSL4_11938G0003	425 Conserved hypothetical protein						UBAL3_44810048	71
UBABSL4_11938G0004	335 Putative twitching motility protein (Pit)						UBAL3_44810047	81
UBABSL4_11938G0005	142 Conserved hypothetical protein						UBAL3_44810046	72
UBABSL4_11938G0006	58 hypothetical protein							
UBABSL4_11938G0007	136 Conserved hypothetical protein						UBAL3_44810045	79
UBABSL4_11938G0008	171 transposase				0.4134			
UBABSL4_12002G0001	243 Conserved hypothetical protein				0.0178		UBAL3_78220010	40
UBABSL4_12002G0002	214 Ribonuclease HII						UBAL3_78220009	59
UBABSL4_12002G0003	116 Ribosomal protein L19	0.75844	1.65893	2.40549			UBAL3_78220008	89
UBABSL4_12002G0004	243 tRNA (guanine-N1)-methyltransferase				0.0059		UBAL3_78220007	71
UBABSL4_12002G0005	187 Probable 16S rRNA processing protein RimM						UBAL3_78220006	61
UBABSL4_12002G0006	69 Ribosomal protein S16			0.03147			UBAL3_78220005	78
UBABSL4_12002G0007	492 signal recognition particle protein		0.01828	0.07503	0.0674		UBAL3_78220004	77
UBABSL4_12002G0008	75 histone family protein DNA-binding protein		0.21582	1.10022			UBAL3_78220003	83
UBABSL4_12137G0001	38 hypothetical protein							
tRNA-Glu-CTC	tRNA Glu CTC							
UBABSL4_12137G0002	226 HAD-superfamily hydrolase, subfamily IA						UBAL3_94320043	63
UBABSL4_12137G0003	184 Conserved protein of unknown function				0.0627		UBAL3_94320044	68

UBABSL4_12137G0004	68 Conserved hypothetical protein				0.0849		UBAL3_94320045	83
UBABSL4_12137G0005	405 Conserved protein of unknown function				0.0214		UBAL3_94320046	64
UBABSL4_12137G0006	131 Conserved protein of unknown function				0.0551		UBAL3_94320047	81
UBABSL4_12137G0007	648 ribonuclease R		0.0067		0.0646		UBAL3_94320048	83
UBABSL4_13030G0001	60 hypothetical protein							
UBABSL4_13030G0002	152 hypothetical protein							
UBABSL4_13030G0003	63 Transposase						UBAL3_95390014	75
UBABSL4_13030G0004	331 Transposase						UBAL3_95390014	78
UBABSL4_13030G0005	520 Resolvase helix-turn-helix domain protein				0.0028		UBAL3_95530030	63
UBABSL4_13030G0006	64 Conserved hypothetical protein							
UBABSL4_13030G0007	214 Conserved hypothetical protein						UBAL3_49470014	66
UBABSL4_13030G0008	252 IstB domain protein ATP-binding protein				0.0057		UBAL3_95530028	86
UBABSL4_440G0001	258 Conserved hypothetical protein					0.0246	UBAL3_95390007	90
UBABSL4_440G0002	121 Conserved hypothetical protein				0.0119	0.0856	UBAL3_95390005	98
UBABSL4_440G0003	369 Conserved hypothetical protein				0.0039	0.0421 0.017	UBAL3_95390004	95
UBABSL4_440G0004	99 hypothetical protein							
UBABSL4_440G0005	85 Conserved hypothetical protein						UBAL3_95390003	60
UBABSL4_440G0006	519 transposase							
UBABSL4_440G0007	261 hypothetical protein							
UBABSL4_774G0001	132 Homoserine dehydrogenase				0.0546		UBAL3_95450115	62
UBABSL4_774G0002	153 Conserved protein of unknown function				0.066		UBAL3_95450116	81
UBABSL4_774G0003	253 Aspartate aminotransferase (EC 2.6.1.17)				0.114		UBAL3_95450117	80
UBABSL4_774G0004	168 ProbableDeoR family transcriptional regulator							
UBABSL4_774G0005	105 Antibiotic biosynthesis monooxygenase						UBAL3_48660032	74
UBABSL4_774G0006	146 Conserved hypothetical protein				0.0692			
UBABSL4_774G0007	53 Conserved hypothetical protein							
UBABSL4_1519G0001	44 hypothetical protein				0.0328		UBAL3_95680064	
UBABSL4_1519G0002	165 3-deoxy-D-manno-octulosonic-acid transferase				0.0175		UBAL3_95680065	54
UBABSL4_1519G0002a	142 3-deoxy-D-manno-octulosonic-acid transferase						UBAL3_95680065	72
UBABSL4_1519G0003	399 lipid-A-disaccharide synthase		0.00544		0.0036		UBAL3_95680067	63
UBABSL4_1519G0004	320 oxidoreductase domain protein	0.05058	0.01357		0.009		UBAL3_95680068	81
UBABSL4_1519G0005	114 Conserved protein of unknown function						UBAL3_95680069	80
UBABSL4_1519G0006	195 UDP-N-acetylglucosamine acyltransferase		0.05011		0.0074		UBAL3_95680070	85
UBABSL4_1807G0001	247 Conserved protein of unknown function	0.1096	0.21844	0.16704	0.0584		UBAL3_94240030	93
UBABSL4_1807G0003	211 Conserved protein of unknown function		0.05114	0.14923	0.0137		UBAL3_94240030	
UBABSL4_1807G0004	167 Conserved protein of unknown function		0.11846	0.0195	0.1296		UBAL3_94240031	86
UBABSL4_1807G0005	333 transcriptional activator domain				0.0043		UBAL3_94240033	65
UBABSL4_1807G0006	421 transcriptional activator domain				0.0034		UBAL3_94240033	
UBABSL4_1807G0007	83 hypothetical protein							
UBABSL4_1807G0008	88 hypothetical protein							
UBABSL4_2023G0002	168 Conserved protein of unknown function				0.0172		UBAL3_79320021	93
UBABSL4_2023G0003	41 hypothetical protein							
UBABSL4_2023G0004	46 hypothetical protein				0.0314			
UBABSL4_2023G0005	145 phosphoglycerate mutase 1 family		0.11232		0.0597		UBAL3_79320020	79
UBABSL4_2023G0006	62 transposase							
UBABSL4_2023G0007	108 Conserved protein of unknown function						UBAL3_79320019	66
UBABSL4_2023G0008	350 Glycerol-3-phosphate dehydrogenase (NAD(P)(+))		0.0062		0.0289		UBAL3_79320018	80
UBABSL4_2518G0001	119 Sel1 domain protein repeat-containing protein						UBAL3_95450104	68
UBABSL4_2518G0002	46 hypothetical protein				0.0314			
UBABSL4_2518G0002a	152 probable cation diffusion facilitator family transporter				0.0285			
UBABSL4_2518G0003	242 tRNA/rRNA methyltransferase (SpoU)				0.006		UBAL3_95450105	68
UBABSL4_2518G0004	456 cysteinyl-tRNA synthetase		0.00476		0.019		UBAL3_95450106	76
UBABSL4_2518G0005	217 Survival protein SurE				0.0133		UBAL3_95450107	78
IRNA-Pro-GGG	IRNA Pro GGG							
UBABSL4_3692G0001	273 Probable binding-protein-dependent transport systems inner membrane component						UBAL3_82700020	69
UBABSL4_3692G0002	89 Probable binding-protein-dependent transport systems inner membrane component						UBAL3_82700020	86

UBABSL4_3692G0003	255 ABC transporter, ATP-binding protein				0.0057		UBAL3_82700021	88
UBABSL4_3692G0004	161 Probable ABC transporter ATP-binding protein						UBAL3_82700022	77
UBABSL4_3692G0005	81 Conserved protein of unknown function				0.0356		UBAL3_82700022a	73
UBABSL4_3692G0006	286 Putative DNA processing protein DprA				0.0202		UBAL3_82700023	63
UBABSL4_3692G0007	455 DNA topoisomerase I	0.01976	0.04773		0.0095		UBAL3_82700024	78
UBABSL4_6051G0001	274 Probable ABC transporter permease protein						UBAL3_93670007	65
UBABSL4_6051G0002	460 HNH endonuclease domain protein				0.0031			
UBABSL4_6051G0003	40 hypothetical protein							
UBABSL4_6051G0004	265 Undecaprenyl-phosphate galactosephosphotransferase (EC 2.7.8.6)						UBAL3_24060027	62
UBABSL4_6051G0005	142 Undecaprenyl-phosphate galactosephosphotransferase (EC 2.7.8.6)						UBAL3_24060027	64
UBABSL4_6051G0006	406 Putative glycosyl transferase, group 1						UBAL3_24060028	68
UBABSL4_6051G0007	508 Putative glycosyl transferase				0.0227			
UBABSL4_9270G0001	44 hypothetical protein							
UBABSL4_9270G0002	130 hypothetical protein							
UBABSL4_9270G0003	224 hypothetical protein							
UBABSL4_9270G0004	259 type IV pilus assembly PilZ						UBAL3_95680084	49
UBABSL4_9270G0005	112 metal dependent phosphohydrolase				0.0129		UBAL3_95680083	84
UBABSL4_9270G0006	193 D-lactate dehydrogenase (Cytochrome)				0.0224		UBAL3_95680082	67
UBABSL4_9270G0008	357 D-lactate dehydrogenase (Cytochrome)		0.00608		0.0162		UBAL3_95680082	76
UBABSL4_10021G0001	173 hypothetical protein (TN)							
UBABSL4_10021G0002	59 hypothetical protein					0.029		
UBABSL4_10021G0003	404 glutamate-1-semialdehyde-2,1-aminomutase	0.0335	0.34723	0.38162	0.0321		UBAL3_79520070	85
UBABSL4_10021G0004	174 Cytidylyltransferase family protein				0.0083		UBAL3_79520068	71
UBABSL4_10021G0005	241 transcription-repair coupling factor		0.01493	0.01802			UBAL3_79520067	68
UBABSL4_10021G0006	321 transcription-repair coupling factor				0.0045		UBAL3_79520067	59
UBABSL4_10021G0007	214 transcription-repair coupling factor						UBAL3_79520067	
UBABSL4_10815G0001	89 Conserved hypothetical protein				0.0324		UBAL3_94240108	61
UBABSL4_10815G0002	263 Conserved protein of unknown function				0.0165		UBAL3_94240107	83
UBABSL4_10815G0003	306 Conserved protein of unknown function						UBAL3_94240107	66
UBABSL4_10815G0004	432 hypothetical protein							
UBABSL4_10815G0005	370 glycosyl transferase, family 2						UBAL3_94240102	36
UBABSL4_10815G0006	218 Putative methyltransferase						UBAL3_80630020	34
UBABSL4_10815G0007	277 glycosyl transferase, family 2				0.0052		UBAL3_94240103	57
UBABSL4_10926G0001	119 Conserved protein of unknown function						UBAL3_93200075	44
UBABSL4_10926G0002	98 peptidase M24						UBAL3_93200076	84
UBABSL4_10926G0003	296 peptidase M24	0.09145	0.01823	0.05135	0.039		UBAL3_93200076	75
UBABSL4_10926G0004	210 O-methyltransferase family protein	0.16113	0.55667	1.01853	0.1305		UBAL3_93200077	78
UBABSL4_10926G0005	100 Putative rieske iron-sulfur family protein			0.46687	0.1587		UBAL3_93200080	75
UBABSL4_10926G0006	304 beta-lactamase domain protein						UBAL3_93200081	57
UBABSL4_10926G0007	40 hypothetical protein							
UBABSL4_11175G0001	71 Diaminopimelate epimerase			0.03058			UBAL3_80630101	79
UBABSL4_11175G0002	225 Conserved protein of unknown function						UBAL3_80630102	47
UBABSL4_11175G0003	349 Alcohol dehydrogenase GroES domain protein						UBAL3_80630103	71
UBABSL4_11175G0004	129 short-chain dehydrogenase/reductase SDR						UBAL3_80630104	58
UBABSL4_11175G0005	117 transcriptional regulator, TraR/DksA family						UBAL3_80630105	80
rRNA-Ser-CGA	rRNA Ser CGA							
UBABSL4_11175G0006	112 Putative sigma-54 specific transcriptional regulator, Fis family				0.0129		UBAL3_80630105a	48
UBABSL4_11217G0001	245 phosphoribosylaminoimidazolecarboxamide formyltransferase			0.07977	0.0236		UBAL3_95680037	71
UBABSL4_11217G0002	138 hypothetical protein							
UBABSL4_11217G0003	73 probable transcriptional regulator				0.0593			
UBABSL4_11217G0004	633 glycosyl transferase, family 39				0.0068		UBAL3_95680038	57
UBABSL4_11217G0005	408 Probable glycosyl transferase, family 9				0.0177		UBAL3_95680041	82
UBABSL4_11217G0006	197 Conserved protein of unknown function				0.0439		UBAL3_95680042	70
UBABSL4_11217G0007	279 Conserved protein of unknown function						UBAL3_95680042	70
UBABSL4_11218G0001	137 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (EC 1.1	0.02626	0.11095		0.0105		UBAL3_92050032	93
UBABSL4_11218G0002	345 Peptidase M50, putative membrane-associated zinc metallopeptidase				0.0084		UBAL3_92050031	79

UBABSL4_4700G0001	288 Conserved protein of unknown function				0.01				UBAL3_92050166	69			
UBABSL4_4700G0002	254 Conserved protein of unknown function								UBAL3_92050164	51			
UBABSL4_4700G0003	87 Conserved protein of unknown function				0.0332				UBAL3_92050163	70			
UBABSL4_4700G0004	436 ATP-dependent Clp protease, ATP-binding subunit	0.12418	0.30937	0.63501					UBAL3_92050162	88			
UBABSL4_4700G0005	202 ATP-dependent Clp protease, proteolytic subunit		0.2582	0.11287					UBAL3_92050161	94			
UBABSL4_4700G0006	363 trigger factor, N-terminal domain		0.00991	0.33799					UBAL3_92050160	56			
UBABSL4_8602G0001a	161 Conserved protein of unknown function				0.009			0.0425	UBAL3_92050009a	56			
UBABSL4_8602G0001	225 Conserved hypothetical protein				0.0128	0.269		0.0279	0.0228	0.0049	UBAL3_95660001a	59	
UBABSL4_8602G0002	81 Conserved hypothetical protein										UBAL3_95390015	86	
UBABSL4_8602G0003	178 Cobyrinic acid a,c-diamide synthase						0.0178	0.0291	0.0096	0.0061	UBAL3_95390016	87	
UBABSL4_8602G0003a	215 metallophosphoesterase								0.0146		UBAL3_95390018	74	
UBABSL4_8602G0004	192 metallophosphoesterase								0.0163	0.0089	0.0114	UBAL3_95390020	80
UBABSL4_9595G0001	307 Putative filamentous haemagglutinin family protein				0.6391	0.2685		0.0511	0.591	0.1923	UBAL3_78920045	79	
UBABSL4_9595G0002	58 Conserved protein of unknown function				0.4975	0.328			0.2361	0.0754	UBAL3_78920044	84	
UBABSL4_9595G0003	114 transposase				0.1012	0.1112		0.0275	0.045				
UBABSL4_9595G0004	353 Conserved protein of unknown function				0.6784	0.1168	0.0147	0.0356	0.3249	0.1115	UBAL3_78920048	82	
UBABSL4_9595G0005	174 Conserved hypothetical protein				0.4228	0.2551			0.3148	0.088	UBAL3_70870001	60	
UBABSL4_9595G0006	491 Conserved hypothetical protein				0.0911	0.0452		0.0511	0.0314	0.0022	UBAL3_70870002	71	
UBABSL4_9900G0001	500 Conserved protein of unknown function				0.0115						UBAL3_44810076	57	
UBABSL4_9900G0002	161 Conserved protein of unknown function										UBAL3_44810076	65	
UBABSL4_9900G0003	146 Conserved protein of unknown function										UBAL3_44810075	75	
UBABSL4_9900G0004	701 Conserved protein of unknown function										UBAL3_44810073	47	
UBABSL4_9900G0005	343 Conserved hypothetical protein										UBAL3_44810072	51	
UBABSL4_9900G0006	395 glycosyl transferase, group 1										UBAL3_44810071	66	
UBABSL4_10015G0001	74 Radical SAM domain protein										UBAL3_94530003	64	
UBABSL4_10015G0002	347 ubiquinone/menaquinone biosynthesis methyltransferase				0.0624						UBAL3_94530004	85	
UBABSL4_10015G0003	126 hypothetical protein	0.11419	0.06032		0.5725								
UBABSL4_10015G0004	350 diguanylate cyclase				0.0124		0.107				UBAL3_93200104	71	
UBABSL4_10015G0006	1613 diguanylate cyclase/phosphodiesterase with				0.0018						UBAL3_93200103	42	
UBABSL4_10015G0007	154 phenylalanyl-tRNA synthetase, beta subunit		0.0564		0.0281						UBAL3_93200102	67	
UBABSL4_10425G0001	155 hypothetical protein												
UBABSL4_10425G0002	62 Conserved hypothetical protein										UBAL3_94320031	79	
UBABSL4_10425G0003	321 GTP-binding protein (EngA)				0.018						UBAL3_94320032	82	
UBABSL4_10425G0004	152 GTP-binding protein (EngA)				0.038						UBAL3_94320032	78	
UBABSL4_10425G0005	116 ATPase										UBAL3_95450079	36	
UBABSL4_10425G0006	49 ATPase										UBAL3_95450079	61	
UBABSL4_10505G0001	28 hypothetical protein	6.76764	1.79847										
UBABSL4_10505G0002	191 Conserved protein of unknown function										UBAL3_95680002	62	
UBABSL4_10505G0003	164 Phosphopantetheine adenylyltransferase				0.0616						UBAL3_95680003	84	
UBABSL4_10505G0004	115 Aspartate aminotransferase				0.0125						UBAL3_95680004	81	
UBABSL4_10505G0005	235 Aspartate aminotransferase	0.05357	0.00924								UBAL3_95680004	81	
UBABSL4_10505G0006	53 putative regulatory protein, FmdB family		0.3054								UBAL3_95680005	87	
UBABSL4_10993G0001	79 NUDIX hydrolase										UBAL3_94170006	59	
UBABSL4_10993G0002	103 Probable ferredoxin										UBAL3_94170007	55	
UBABSL4_10993G0003	477 sigma54 specific transcriptional regulator, Fis family				0.006						UBAL3_94170008	76	
UBABSL4_10993G0004	179 Anthranilate synthase component I				0.0161						UBAL3_94170009	57	
UBABSL4_10993G0005	342 Anthranilate synthase component I	0.08414	0.05397		0.038						UBAL3_94170009		
UBABSL4_10993G0006	131 Anthranilate synthase component I				0.011						UBAL3_94170010	77	
UBABSL4_11152G0001	136 Conserved protein of unknown function				0.0106						UBAL3_94530062a	59	
UBABSL4_11152G0002	415 major facilitator superfamily transporter				0.0278						UBAL3_94530063	84	
UBABSL4_11152G0003	386 Probable threulose biosynthesis protein										UBAL3_94530064	68	
UBABSL4_11152G0004	271 alpha amylase, catalytic region				0.0053						UBAL3_94530065	72	
UBABSL4_11152G0005	211 alpha amylase, catalytic region										UBAL3_94530065		
UBABSL4_11152G0007	194 glutamate decarboxylase	0.01854	0.02239		0.0595						UBAL3_94530067	72	

UBABSL4_11187G0001	62 type II secretion system protein E																			UBAL3_44810057	94
UBABSL4_11187G0002	218 Conserved protein of unknown function																			UBAL3_44810058	70
UBABSL4_11187G0003	128 conserved hypothetical protein																			UBAL3_44810060	84
UBABSL4_11187G0004	343 Conserved hypothetical protein																				
UBABSL4_11187G0005	272 hypothetical protein																				
UBABSL4_11187G0006	315 Putative type II secretion system protein F																				
UBABSL4_11204G0001	244 geranylgeranyl reductase																			UBAL3_94530015	63
UBABSL4_11204G0002	354 Probable protease family protein																			UBAL3_94530014	53
UBABSL4_11204G0003	391 primosomal protein N'																			UBAL3_94530013	62
UBABSL4_11204G0004	56 hypothetical protein																				
UBABSL4_11204G0005	157 Regulatory protein					0.01383														UBAL3_94530012	81
UBABSL4_11204G0006	171 Glycine hydroxymethyltransferase					0.1788	0.30477					0.0253								UBAL3_94530011	78
UBABSL4_11396G0001	235 S-adenosyl-methyltransferase MraW											0.043								UBAL3_92050132	74
UBABSL4_11396G0002	96 Conserved hypothetical protein											0.1503								UBAL3_92050133	64
UBABSL4_11396G0003	567 Peptidoglycan glycosyltransferase																			UBAL3_92050134	72
UBABSL4_11396G0004	330 UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase (EC 6.3.2.13)											0.0087								UBAL3_92050136	71
UBABSL4_11396G0005	52 UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase (EC 6.3.2.13)																			UBAL3_92050136	71
UBABSL4_11396G0006	298 UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase (EC 6.3.2.10)											0.0097								UBAL3_92050137	60
UBABSL4_11410G0001	942 type III restriction enzyme, res subunit					0.097				0.1433	0.0851	0.0352	0.0642	0.2188	0.5608	0.8165	0.2562	0.311	UBAL3_95450048	76	
UBABSL4_11410G0002	271 Conserved hypothetical protein						0.2963				0.1183	0.0692		0.234	0.3058	0.7066	0.2526	0.3872	UBAL3_95450049	96	
UBABSL4_11410G0002a	186 CRISPR-associated protein, NE0113 family					0.2457				0.363	0.2585	0.1396		0.4262	0.5568	0.7426	0.1472	0.1234	UBAL3_95450050	98	
UBABSL4_11410G0003	156 Ankyrin	0.43382	0.18446	0.0696		0.1953				0.4328	0.2054	0.0925		0.5691	0.8631	0.6439	0.3511	0.2803	UBAL3_95450052	96	
UBABSL4_11410G0004	212 Conserved hypothetical protein					0.0718					0.2268	0.0136		0.3739	0.2687	0.8292	0.1373	0.098	UBAL3_95450053	88	
UBABSL4_11410G0005	159 Conserved hypothetical protein									0.4246	0.1008	0.0272		0.658	0.3908	0.9872	0.2261	0.1787	UBAL3_95450054	98	
UBABSL4_11422G0001	590 Glycyl-tRNA synthetase, beta subunit					0.00552						0.044								UBAL3_95450156	64
UBABSL4_11422G0002	290 Glycyl-tRNA synthetase alpha subunit					0.0337						0.0448								UBAL3_95450157	76
UBABSL4_11422G0003	62 Conserved protein of unknown function											0.3956								UBAL3_80420077	82
UBABSL4_11422G0004	111 transcriptional regulator, XRE family											0.013								UBAL3_80420074	79
UBABSL4_11422G0005	31 hypothetical protein																				
UBABSL4_11422G0006	218 ATPase, P-type (transporting), HAD superfamily,																			UBAL3_74420008	59
UBABSL4_11513G0001	286 Conserved hypothetical protein									6.3538		0.0101								UBAL3_96120025	60
UBABSL4_11513G0002	595 DNA topoisomerase III									5.9046										UBAL3_96120026	70
UBABSL4_11513G0003	124 DNA topoisomerase III									2.4425										UBAL3_96120026	82
UBABSL4_11513G0004	319 hypothetical protein									2.8483											
UBABSL4_11513G0005	238 icmL/dotI									4.0721		0.1347									
UBABSL4_11513G0006	43 hypothetical protein									1.4087											
UBABSL4_11589G0001	496 ATPase AAA-2 domain protein					0.04351						0.0262								UBAL3_94240025	90
UBABSL4_11589G0002	293 Conserved hypothetical protein											0.0049								UBAL3_94240026	81
UBABSL4_11589G0003	492 Conserved hypothetical protein											0.0117								UBAL3_94240027	78
UBABSL4_11589G0004	138 Conserved hypothetical protein											0.0209								UBAL3_94240027	78
UBABSL4_11589G0006	139 GPW/gp25 family protein											0.0311								UBAL3_94240028	88
UBABSL4_11589G0007	149 Conserved protein of unknown function	0.4542	1.08632	1.20963								0.4454								UBAL3_94240029	95
UBABSL4_11671G0001	397 Pyruvate:ferredoxin oxidoreductase alpha subunit (E)	0.15342	0.67499	0.12033								0.1526								UBAL3_79520040	96
UBABSL4_11671G0002	48 hypothetical protein																				
UBABSL4_11671G0003	204 Conserved protein of unknown function					0.03726						0.1556								UBAL3_79520041	47
UBABSL4_11671G0004	165 Putative hydrogenase-3 subunit (HycG)																			UBAL3_79520042	59
UBABSL4_11671G0005	448 Putative hydrogenase-3 subunit (HycE)																			UBAL3_79520043	63
UBABSL4_11671G0006	456 Putative hydrogenase-4 subunit (HyfF)											0.0064								UBAL3_79520044	75
tRNA-Pro-CGG tRNA Pro CGG																					
UBABSL4_11675G0001	104 acylphosphatase																			UBAL3_95450135	44
UBABSL4_11675G0002	315 RNA polymerase, sigma 70 subunit, RpoD family					0.03426	0.03792					0.0458								UBAL3_95450134	69
UBABSL4_11675G0003	173 adenine phosphoribosyltransferase					0.09356	0.39539					0.0334								UBAL3_95450133	70
UBABSL4_11675G0004	104 Conserved protein of unknown function											0.0277								UBAL3_95450132	59
UBABSL4_11675G0005	389 major facilitator superfamily protein											0.0074								UBAL3_95450131	62
UBABSL4_11713G0001	99 aspartyl-tRNA synthetase											0.0146								UBAL3_94170058	72

UBABSL4_11713G0002	69 Conserved protein of unknown function				UBAL3_94170059	60	
UBABSL4_11713G0003	74 Conserved protein of unknown function				UBAL3_80150041	67	
UBABSL4_11713G0004	643 Pseudouridine synthase, Rsu		0.01013		UBAL3_94170060	53	
UBABSL4_11713G0005	514 GMP synthase [glutamine-hydrolyzing]		0.00845	0.0056	UBAL3_94170061	81	
UBABSL4_11713G0006	159 inosine-5'-monophosphate dehydrogenase	0.1018	0.01366	0.0181	UBAL3_94170062	92	
UBABSL4_11756G0001	60 hypothetical protein						
UBABSL4_11756G0002	345 phage integrase		0.02085				
IRNA-Leu-CAG	IRNA Leu CAG						
UBABSL4_11756G0003	460 Fumarate hydratase, class II (EC 4.2.1.2)		0.04301	0.11802	0.1066	UBAL3_78920008	88
UBABSL4_11756G0004	109 Probable ferredoxin	1.73848	0.77549	3.05802	0.4235	UBAL3_78920007	94
UBABSL4_11756G0005	472 cation transport ATPas				0.0092		
UBABSL4_11866G0001	32 hypothetical protein			0.61073			
UBABSL4_11866G0002	236 uridylyate kinase		0.50296	0.34045	0.1039	UBAL3_94530026	92
UBABSL4_11866G0003	185 ribosome recycling factor	0.07316	0.22359	0.21715	0.0234	UBAL3_94530025	83
UBABSL4_11866G0004	408 alanine racemase				0.0035	UBAL3_94530024	53
UBABSL4_11866G0005	258 Putative integral membrane protein				0.0056	UBAL3_94530023	82
UBABSL4_11866G0006	262 ABC transporter ATP-binding protein				0.011	UBAL3_94530022	75
UBABSL4_12078G0001	133 Histidyl-tRNA lygase (EC 6.1.1.21)		0.02704		0.0217	UBAL3_95320027	83
UBABSL4_12078G0002	545 D-3-phosphoglycerate dehydrogenase	0.22352	0.55109	0.79289	0.0847	UBAL3_95320026	85
UBABSL4_12078G0003	220 aminotransferase, class V		0.18802	0.54287	0.1836	UBAL3_95320025	88
UBABSL4_12078G0004	126 aminotransferase, class V	0.26856	0.22838	0.16372	0.1145	UBAL3_95320025	86
UBABSL4_12078G0005	285 Ankyrin				0.0051	UBAL3_44810062	43
UBABSL4_12078G0006	266 Phosphate butyryltransferase				0.0108	UBAL3_80420068	65
UBABSL4_12508G0001	219 two component, sigma54 specific, transcriptional regulator, Fis family				0.0132	UBAL3_94240128	79
UBABSL4_12508G0002	474 Probable TPR-domain containing protein					UBAL3_94240129	73
UBABSL4_12508G0003	625 Probable TPR-domain containing protein					UBAL3_94240129	63
UBABSL4_12508G0004	264 Conserved protein of unknown function		0.01362	0.01645		UBAL3_94240130	67
UBABSL4_12508G0005	291 UBA/THIF-type NAD/FAD binding protein		0.05562	0.04104		UBAL3_94240131	73
UBABSL4_12508G0006	184 transposase						
UBABSL4_13826G0001	85 Conserved hypothetical protein					UBAL3_96270022	69
UBABSL4_13826G0002	198 Conserved hypothetical protein						
UBABSL4_13826G0004	176 hypothetical protein						
UBABSL4_13826G0005	97 Conserved hypothetical protein					UBAL3_80290018	81
UBABSL4_13826G0006	55 hypothetical protein						
UBABSL4_13826G0007	163 Conserved hypothetical protein						
UBABSL4_435G0001	222 Probable antirepressor protein (Ant)					UBAL3_44810010	79
UBABSL4_435G0002	98 Putative cobyrinic acid a,c-diamide synthase					UBAL3_44810013	85
UBABSL4_435G0002a	161 probable filamentation induced by cAMP protein Fic						
UBABSL4_435G0003	321 ParB-like partition protein					UBAL3_44810015	78
UBABSL4_435G0004	383 Probable DNA helicase					UBAL3_44810017	85
UBABSL4_731G0001	193 Conserved protein of unknown function				0.0224	UBAL3_24060066	57
UBABSL4_731G0002	125 Probable general secretion pathway protein I					UBAL3_24060065	71
UBABSL4_731G0002a	81 Probable general secretion pathway protein J					UBAL3_24060064	69
UBABSL4_731G0003	60 hypothetical protein			1.5148			
UBABSL4_731G0004	34 hypothetical protein						
UBABSL4_849G0001	93 hypothetical protein						
UBABSL4_849G0002	250 flagellar biosynthetic protein FliP					UBAL3_80630056	51
UBABSL4_849G0003	91 flagellar biosynthetic protein FliQ					UBAL3_80630055	46
UBABSL4_849G0004	95 Flagellar biosynthesis protein FliR					UBAL3_80630054	
UBABSL4_849G0005	285 flagellar biosynthetic protein FliB					UBAL3_80630053	27
UBABSL4_1259G0001	103 riboflavin synthase, alpha subunit				0.028	UBAL3_95450154	75
UBABSL4_1259G0002	76 Conserved hypothetical protein					UBAL3_95450153	66
UBABSL4_1259G0003	127 Conserved hypothetical protein				0.0341	UBAL3_95450151a	67
UBABSL4_1259G0004	271 precorrin-4 C11-methyltransferase		0.17628		0.0106	UBAL3_95450151	73
UBABSL4_1259G0005	254 Conserved hypothetical protein				0.0227	UBAL3_95450146	84

UBABSL4_9415G0004	295 NAD(+) kinase [EC 2.7.1.23]				0.0049				UBAL3_94170020	75		
UBABSL4_9415G0005	55 hypothetical protein											
UBABSL4_9462G0001	149 geranylgeranyl reductase								UBAL3_94530015	64		
UBABSL4_9462G0002	250 cytochrome c biogenesis protein				0.0231				UBAL3_94530016	91		
UBABSL4_9462G0003	185 Redoxin domain protein				0.0312				UBAL3_94530017	52		
UBABSL4_9462G0004	284 cytochrome c assembly protein				0.0711				UBAL3_94530019	98		
UBABSL4_9462G0005	330 ResB family protein				0.0656				UBAL3_94530020	81		
UBABSL4_9480G0001	463 Glutamate dehydrogenase				0.0312				UBAL3_80420056	38		
UBABSL4_9480G0002	112 ferredoxin								UBAL3_79320012	84		
UBABSL4_9480G0003	68 FeS assembly protein IscX								UBAL3_79320013	91		
UBABSL4_9480G0004	137 Conserved hypothetical protein								UBAL3_79320014	45		
UBABSL4_9480G0005	364 Putative ATP binding protein, Mrp like	0.03718	0.19763	0.23266				0.1149	UBAL3_79320015	87		
UBABSL4_9921G0001	128 Conserved protein of unknown function			0.04241					UBAL3_79520056	79		
UBABSL4_9921G0002	55 hypothetical protein											
UBABSL4_9921G0003	45 hypothetical protein											
UBABSL4_9921G0004	336 Ribonuclease III		0.08564	0.12926				0.0043	UBAL3_79520057	74		
UBABSL4_9921G0005	155 hypothetical protein							0.0093				
UBABSL4_9941G0001	168 Periplasmic phosphate binding protein			0.13572				0.0687	UBAL3_93200013	80		
UBABSL4_9941G0002	377 Phosphate ABC transporter, permease protein (PstC)							0.0191	UBAL3_93200014	89		
UBABSL4_9941G0003	221 Phosphate transport system permease protein 2								UBAL3_93200015			
UBABSL4_9941G0004	200 Phosphate import ATP-binding protein (PstB)		0.03597	0.20086					UBAL3_93200016	88		
UBABSL4_9941G0005	84 phosphate uptake regulator, PhoU		0.06423	0.16803					UBAL3_93200017	82		
UBABSL4_10095G0001	337 Isocitrate dehydrogenase (NAD(+))	6.50657	9.93695	4.54274			1.6781	0.4892	0.169	0.0279	UBAL3_48660056	96
UBABSL4_10095G0002	116 Probable isocitrate dehydrogenase (NADP)	0.75844	2.51166	2.73309			1.1317				UBAL3_48660057	97
UBABSL4_10095G0003	223 two component, sigma54 specific, transcriptional regulator, Fis		0.1371	0.11685			0.0194				UBAL3_48660058	75
UBABSL4_10095G0004	74 two component, sigma54 specific, transcriptional regulator, Fis family			0.20541			0.039				UBAL3_48660058	75
UBABSL4_10095G0005	211 multi-sensor signal transduction histidine		0.03409	0.04117			0.0342				UBAL3_48660059	76
UBABSL4_10484G0001	87 Acetylornithine and succinylornithine aminotransferase [EC 2.6.1.11]								UBAL3_82700003	81		
UBABSL4_10484G0002	226 Acetylornithine and succinylornithine aminotransferase (EC 2.6.1.11)			0.1201			0.0064		UBAL3_82700003			
UBABSL4_10484G0002a	208 Acetylornithine and succinylornithine aminotransferase (EC 2.6.1.11)			0.03654					UBAL3_82700003			
UBABSL4_10484G0004	81 ornithine carbamoyltransferase		0.04441						UBAL3_82700004	80		
UBABSL4_10484G0005	323 Argininosuccinate synthase		0.02784	0.1042			0.0402		UBAL3_82700005	86		
UBABSL4_10723G0001	347 Conserved hypothetical protein								UBAL3_94240141	53		
UBABSL4_10723G0002	267 hypothetical protein											
UBABSL4_10723G0003	120 transcriptional regulator, XRE family											
UBABSL4_10723G0004	156 hypothetical protein											
UBABSL4_10723G0005	255 DNA polymerase III [EC 2.7.7.7]								UBAL3_94240085	59		
UBABSL4_10730G0001	254 Probable flavoprotein reductase	0.05329	0.48148	0.5044			0.1534		UBAL3_80290070	94		
UBABSL4_10730G0003	251 Conserved protein of unknown function		0.02866	0.25954			0.1839		UBAL3_80290071	75		
UBABSL4_10730G0005	296 Dihydrolipoamide dehydrogenase						0.0097					
UBABSL4_10730G0006	56 Dihydrolipoamide dehydrogenase [EC 1.8.1.4]								UBAL3_80290072	67		
UBABSL4_10730G0007	363 Conserved hypothetical protein						0.0119					
UBABSL4_10797G0001	57 FOG: Transposase-like								UBAL3_48660010	66		
UBABSL4_10797G0002	40 hypothetical protein											
UBABSL4_10797G0003	479 Conserved protein of unknown function								UBAL3_48660052	88		
UBABSL4_10797G0004	298 Conserved hypothetical protein								UBAL3_48660053	88		
UBABSL4_10797G0005	203 Conserved protein of unknown function		0.02658				0.0355		UBAL3_48660054	94		
UBABSL4_11008G0001	214 Conserved protein of unknown function			0.14206			0.2157		UBAL3_96270005	71		
UBABSL4_11008G0002	174 Conserved hypothetical protein						0.0249		UBAL3_96270005a	49		
UBABSL4_11008G0003	83 Conserved protein of unknown function								UBAL3_96270006	72		
UBABSL4_11008G0004	203 Probable ATPase, PP-loop superfamily protein						0.0497		UBAL3_96270007	79		
UBABSL4_11008G0005	157 transposase						0.0184					
UBABSL4_11387G0001	296 CRISPR-associated protein, Cas1		0.0515	0.2531					UBAL3_78920056	24		

UBABSL4_11387G0002	186 CRISPR-associated protein, Cas2		0.3276	0.6475	1.2084		0.0862	UBAL3_78920057	37	
UBABSL4_11387G0003	227 CRISPR-associated protein, Cas3		0.3355	0.1769	1.8153		0.4942	UBAL3_78920058	36	
UBABSL4_11387G0004	389 CRISPR-associated protein, Cas4		0.6265	0.7224	1.1556		0.0824	UBAL3_78920059	48	
UBABSL4_11387G0005	228 CRISPR-associated protein, Cas5		0.334	0.7043	1.4787		0.492	UBAL3_78920060	45	
UBABSL4_11485G0001	108 Conserved protein of unknown function						0.0267	UBAL3_93200122	73	
UBABSL4_11485G0002	461 Conserved protein of unknown function	0.00471					0.025	UBAL3_93200123	76	
UBABSL4_11485G0003	248 Conserved hypothetical protein							UBAL3_93200124	53	
UBABSL4_11485G0004	55 hypothetical protein									
UBABSL4_11485G0005	117 transcriptional regulator, LysR family						0.0493	UBAL3_93200125	59	
UBABSL4_11494G0001	486 ABC1 family transporter						0.0059	UBAL3_94320009	74	
UBABSL4_11494G0002	524 Conserved protein of unknown function	0.02694					0.0165	UBAL3_94320008	76	
UBABSL4_11494G0003	369 ATPase (AAA+ superfamily)-like						0.0117	UBAL3_95680032	33	
UBABSL4_11494G0004	235 Cytochrome c oxidase cbb3 type, subunit I (EC 1.9.3.1)							UBAL3_24060032	95	
UBABSL4_11494G0005	50 Cytochrome-c oxidase, subunit I							UBAL3_80290001	94	
UBABSL4_11500G0001	134 cytochrome c, class I							UBAL3_95450121	38	
UBABSL4_11500G0002	457 amino-acid N-acetyltransferase	0.0095					0.0063	UBAL3_94170079	61	
UBABSL4_11500G0003	367 dTDP-glucose 4,6-dehydratase	0.0355					0.0236	UBAL3_94170081	76	
UBABSL4_11500G0004	294 glucose-1-phosphate thymidyltransferase	0.00739					0.0343	UBAL3_94170082	77	
UBABSL4_11500G0005	59 dTDP-4-dehydrothamnose 3,5-epimerase						0.0245	UBAL3_94170083	81	
UBABSL4_11608G0001	351 ATPase (AAA+ superfamily)-like							UBAL3_95680032	33	
UBABSL4_11608G0002	560 apolipoprotein N-acyltransferase	0.01357					0.0026	UBAL3_94170068	53	
UBABSL4_11608G0003	179 Conserved protein of unknown function	0.09043	0.06066				0.0484	UBAL3_94170069	57	
UBABSL4_11608G0004	153 Conserved protein of unknown function						0.1697	UBAL3_94170070	67	
UBABSL4_11608G0005	258 DNA ligase I, ATP-dependent DnlI						0.0112	0.0201	UBAL3_94170071	61
UBABSL4_11676G0001	125 Resolvase helix-turn-helix domain protein							UBAL3_95530030	60	
UBABSL4_11676G0002	51 hypothetical protein									
UBABSL4_11676G0003	272 transposase						0.0233			
UBABSL4_11676G0004	108 Conserved hypothetical protein							UBAL3_48660031	83	
UBABSL4_11676G0005	147 Conserved hypothetical protein							UBAL3_48660029	76	
UBABSL4_11696G0001	88 Conserved hypothetical protein									
UBABSL4_11696G0002	382 hypothetical protein						0.0113			
UBABSL4_11696G0003	113 transposase									
UBABSL4_11696G0004	208 Putative transposase							0.0151	UBAL3_80290055	35
UBABSL4_11696G0005	139 hypothetical protein									
UBABSL4_11993G0001	72 Conserved hypothetical protein									
UBABSL4_11993G0002	255 cytochrome B561							UBAL3_92050072	68	
UBABSL4_11993G0003	297 Conserved protein of unknown function	0.36459	0.42388	0.39482			0.0437	UBAL3_92050073	57	
UBABSL4_11993G0004	315 Conserved protein of unknown function							UBAL3_92050074	61	
UBABSL4_11993G0005	254 Conserved hypothetical protein							UBAL3_92050075	68	
UBABSL4_12142G0001	71 aldo/keto reductase						0.0406	UBAL3_93670006	85	
UBABSL4_12142G0002	215 Phosphoglycerate mutase						0.0201	UBAL3_93670005	73	
UBABSL4_12142G0003	476 Cobyrinic acid a,c-diamide synthase (CbiA)						0.003	UBAL3_93670004	45	
UBABSL4_12142G0004	326 Precorin-8X methylmutase CbiC/CobH	0.04413	0.21315				0.0177	UBAL3_93670003	74	
UBABSL4_12142G0005	399 Fusaric acid resistance protein conserved						0.0036	UBAL3_95320006	54	
UBABSL4_12176G0001	358 Conserved hypothetical protein						0.0121	UBAL3_79160029	79	
UBABSL4_12176G0002	400 Conserved hypothetical protein						0.0974	UBAL3_79160027	62	
IRNA-Met-CAT	IRNA Met CAT									
UBABSL4_12176G0003	59 hypothetical protein									
UBABSL4_12176G0004	91 hypothetical protein									
UBABSL4_12229G0001	252 Riboflavin kinase / FAD synthase (RibC) (EC 2.7.7.2)							UBAL3_57480023	64	
UBABSL4_12229G0002	138 Porphobilinogen synthase	0.18883					0.0732	UBAL3_57480022	85	
UBABSL4_12229G0003	549 Uroporphyrin-III C-methyltransferase / synthase	0.03164						UBAL3_57480021	66	
UBABSL4_12229G0004	316 porphobilinogen deaminase						0.0091	UBAL3_57480020	72	
UBABSL4_12229G0005	459 Glutamyl-IRNA reductase						0.0157	UBAL3_57480019	77	

UBABSL4_4516G0001	185 polysaccharide deacetylase								UBAL3_94240117	61				
UBABSL4_4516G0001a	119 Conserved protein of unknown function								UBAL3_94240118	78				
UBABSL4_4516G0002	132 Conserved protein of unknown function								UBAL3_94240118	47				
UBABSL4_4516G0003	120 polysaccharide export protein					0.1443			UBAL3_94240119	69				
UBABSL4_5063G0001	190 diguanylate cyclase phosphodiesterase								UBAL3_79800008	62				
UBABSL4_5063G0002	82 Conserved protein of unknown function					0.088			UBAL3_79800010	78				
UBABSL4_5063G0003	128 Conserved protein of unknown function					0.0564			UBAL3_79800010	76				
UBABSL4_5063G0004	322 Conserved protein of unknown function					0.0045			UBAL3_79800011	64				
UBABSL4_6017G0001	50 NADH dehydrogenase (quinone)					0.0289			UBAL3_95680012	59				
UBABSL4_6017G0002	105 Probable ferredoxin					0.055			UBAL3_95680011	62				
UBABSL4_6017G0003	107 Conserved protein of unknown function								UBAL3_95680010	58				
UBABSL4_6017G0004	334 Translation initiation factor, aIF-2B1/5-methylthioribose-1- phosphate ison	0.09752				0.0043			UBAL3_95680009	78				
UBABSL4_6067G0001	263 Conserved hypothetical protein								UBAL3_74420016	39				
UBABSL4_6067G0002	206 hypothetical protein					0.021								
UBABSL4_6067G0003	208 Putative non-canonical purine NTP pyrophosphatase, rdgB/HAM1 family	0.01044				0.0347			UBAL3_74420018	59				
UBABSL4_6067G0004	49 hypothetical protein													
UBABSL4_6142G0001	231 Conserved hypothetical protein					0.0062	0.0686	0.0224	0.0951	0.037	0.0142	UBAL3_95390007	44	
UBABSL4_6142G0002	67 hypothetical protein													
UBABSL4_6142G0003	44 hypothetical protein													
UBABSL4_6142G0004	416 FOG: transposase-like	0.0732				0.3852	0.059	0.0721		0.0389				
								0.1829	0.0373	0.0906	0.037	0.0053	UBAL3_48660010	57
UBABSL4_6593G0001	52 Conserved hypothetical protein												UBAL3_95680117	69
UBABSL4_6593G0002	303 3-hydroxyisobutyrate dehydrogenase					0.0714							UBAL3_95680118	64
UBABSL4_6593G0003	165 hypothetical protein													
UBABSL4_6593G0004	336 Putative permease					0.0086							UBAL3_95680120	76
UBABSL4_6942G0001	115 Conserved hypothetical protein												UBAL3_93200091	47
UBABSL4_6942G0002	325 Conserved hypothetical protein					0.0044							UBAL3_93200092	85
UBABSL4_6942G0003	147 Conserved hypothetical protein												UBAL3_95450136	68
UBABSL4_6942G0004	186 thiazole biosynthesis family protein ThiG	0.01934	0.12842			0.0931							UBAL3_93200094	89
UBABSL4_7131G0001	241 cell shape determining protein, MreB/Mrl family	0.08209	0.01802			0.1018							UBAL3_94530045	95
UBABSL4_7131G0002	99 Conserved protein of unknown function					0.0291							UBAL3_94530046	54
UBABSL4_7131G0003	228 Ribulose-phosphate 3-epimerase					0.0443							UBAL3_94530047	74
UBABSL4_7131G0004	252 peptidase M48					0.1088							UBAL3_94530048	85
UBABSL4_7671G0001	202 Putative peptidyl-prolyl cis-trans isomerase												UBAL3_79520065	56
UBABSL4_7671G0002	155 Probable peptidyl-prolyl cis-trans isomerase												UBAL3_79520066	70
UBABSL4_7671G0003	103 Probable peptidyl-prolyl cis-trans isomerase	0.03492											UBAL3_79520066	69
UBABSL4_7671G0004	291 transcription-repair coupling factor					0.0099							UBAL3_79520067	74
UBABSL4_8194G0001	277 Probable cytochrome b/b6, C-terminal	0.12216	0.11038	0.03528		0.2396							UBAL3_94170024	97
UBABSL4_8194G0002	72 Conserved protein of unknown function												UBAL3_94170025	94
UBABSL4_8194G0002a	233 Probable cytochrome c, class I					0.3034							UBAL3_94170026	82
UBABSL4_8194G0003	225 transposase					0.0577								
UBABSL4_8268G0001	197 UTP-glucose-1-phosphate uridylyltransferase GalU	0.01826	0.03307			0.022							UBAL3_94320058	84
UBABSL4_8268G0002	331 thiamine-monophosphate kinase					0.0305							UBAL3_94320057	56
UBABSL4_8268G0002a	152 Conserved hypothetical protein					0.0095							UBAL3_94320056	65
UBABSL4_8268G0003	214 OmpA family protein												UBAL3_94320055	58
UBABSL4_8752G0001	132 hypothetical protein													
UBABSL4_8752G0002	126 hypothetical protein					0.1485								
UBABSL4_8752G0004	191 Putative phosphatidylethanolamine binding protein					0.0453							UBAL3_94530001a	73
UBABSL4_8752G0005	145 4-hydroxybenzoate polyprenyl transferase												UBAL3_94530001	67
UBABSL4_8800G0001	234 Precorrin-3B methylase (EC 2.1.1.131)		0.17168			0.0308							UBAL3_79520031	69
UBABSL4_8800G0002	57 Precorrin-3B methylase (EC 2.1.1.131)												UBAL3_79520031	80
UBABSL4_8800G0003	181 cob(I)alamin adenosyltransferase		0.07198			0.0319							UBAL3_79520032	81

UBABSL4_10355G0003	87 hypothetical protein								0.1161													
UBABSL4_10355G0004	354 Vesicle-fusing ATPase		0.01016						0.0571										UBAL3_92050098			73
UBABSL4_10381G0001	408 isoleucyl-tRNA synthetase								0.0177										UBAL3_79520011			53
UBABSL4_10381G0002	555 isoleucyl-tRNA synthetase								0.0234										UBAL3_79520011			
UBABSL4_10381G0003	tRNA-Val-CAC tRNA Val CAC																					
UBABSL4_10381G0003	100 DNA polymerase III, epsilon subunit																		UBAL3_79520016			35
UBABSL4_10473G0001	464 Putative adenylylsulfate reductase, subunit A		0.04914						0.028										UBAL3_79160037			77
UBABSL4_10473G0002	116 Probable adenylylsulfate reductase, subunit B								0.0249										UBAL3_79160036			86
UBABSL4_10473G0003	402 sulfate adenylyltransferase		0.05816	0.17015					0.0754										UBAL3_79160035			87
UBABSL4_10473G0004	65 hypothetical protein (transcriptional regulator)								0.1776													
UBABSL4_10576G0001	98 Conserved hypothetical protein																		UBAL3_95450061			86
UBABSL4_10576G0002	293 Putative ATPase, AAA family								0.0098										UBAL3_95680106			68
UBABSL4_10576G0003	337 Conserved hypothetical protein																		UBAL3_95680107			62
UBABSL4_10576G0004	203 Conserved hypothetical protein																		UBAL3_95680108			68
UBABSL4_10595G0001	90 Conserved hypothetical protein												0.4227	0.038	0.0243				UBAL3_96270025			59
UBABSL4_10595G0002	147 Conserved hypothetical protein											0.2157	0.0352	0.1708	0.0466	0.0149			UBAL3_96270024			86
UBABSL4_10595G0003	53 Conserved hypothetical protein											0.1196	0.1954	0.3554	0.0323	0.0206			UBAL3_96270023			98
UBABSL4_10595G0004	189 Isb-like ATP-binding protein		0.34257	0.47107	10.557	2.3365	2.5766	5.4484	6.4296	6.1047	3.3433	9.7131	17.427	8.6867	12.969	6.1884						
UBABSL4_10760G0001	204 Acetoacetylase		0.03193						0.0141										UBAL3_94240042			92
UBABSL4_10760G0002	169 acetolactate synthase, small subunit			0.10922					0.0341										UBAL3_94240043			86
UBABSL4_10760G0003	533 acetolactate synthase, large subunit		0.02539	0.11472	0.12222				0.0541										UBAL3_94240044			87
UBABSL4_10760G0004	67 acetolactate synthase, large subunit																		UBAL3_94240044			97
UBABSL4_10769G0001	487 Probable conjugal transfer protein (TrbE)																		UBAL3_44810040			78
UBABSL4_10769G0002	103 Probable conjugal transfer protein (TrbD)																		UBAL3_44810041			72
UBABSL4_10769G0003	101 Conserved hypothetical protein																		UBAL3_44810042			65
UBABSL4_10769G0004	148 Putative conjugal transfer protein (TrbB)																		UBAL3_44810043			87
UBABSL4_10788G0001	554 periplasmic sensor signal transduction histidine kinase								0.0078										UBAL3_93200046			63
UBABSL4_10788G0002	176 Probable hexapeptide transferase family protein								0.0246										UBAL3_93200045			82
UBABSL4_10788G0003	243 Conserved protein of unknown function								0.0059										UBAL3_93200044			66
UBABSL4_10788G0004	21 hypothetical protein																					
UBABSL4_10802G0001	246 UDP-glucose 6-dehydrogenase (EC 1.1.1.22)		0.0662						0.0645										UBAL3_94240095			89
UBABSL4_10802G0002	483 glucosamine--fructose-6-phosphate aminotransferase [isomerizing] (EC: 2.4.1.15)			0.02248					0.0388										UBAL3_94240096			85
UBABSL4_10802G0003	76 hypothetical protein																					
UBABSL4_10802G0004	364 Putative endonuclease																		UBAL3_94530056			74
UBABSL4_10971G0001	62 Conserved hypothetical protein																		UBAL3_94170075			71
UBABSL4_10971G0002	218 3-isopropylmalate dehydratase, small subunit			0.10957					0.0132										UBAL3_94170076			79
UBABSL4_10971G0003	468 3-isopropylmalate dehydratase, large subunit		0.04227	0.38744					0.0493										UBAL3_94170077			82
UBABSL4_10971G0005	257 transcriptional regulator, LysR family																		UBAL3_94170078			63
UBABSL4_11269G0001	257 Probable lipopolysaccharide heptosyltransferase II																		UBAL3_95680058			55
UBABSL4_11269G0002	343 Putative heptosyltransferase family protein								0.0084										UBAL3_95680057			66
UBABSL4_11269G0003	245 polysaccharide deacetylase																		UBAL3_95680056			65
UBABSL4_11269G0004	310 glycosyl transferase, family 1								0.014										UBAL3_95680055			63
UBABSL4_11296G0001	225 cytidylate kinase		0.00965						0.0385										UBAL3_95320017			65
UBABSL4_11296G0002	447 3-phosphoshikimate 1-carboxyvinyltransferase			0.08501					0.0194										UBAL3_95320016			73
UBABSL4_11296G0003	297 Prephenate dehydrogenase			0.06946					0.0146										UBAL3_95320015			61
UBABSL4_11296G0004	231 phospho-2-dehydro-3-deoxyheptonate aldolase		0.11719	0.51385	0.90714				0.0625										UBAL3_95320014			93
UBABSL4_11309G0001	258 glycosyl transferase, group 1																		UBAL3_94240109			76
UBABSL4_11309G0002	393 glycosyl transferase, group 1								0.0037										UBAL3_94240110			86
UBABSL4_11309G0003	267 polysaccharide deacetylase								0.0378										UBAL3_94240111			70
UBABSL4_11309G0004	269 protein tyrosine phosphatase								0.0054										UBAL3_94240112			58
UBABSL4_11790G0001	710 Putative helicase, Snf2 family																		UBAL3_95950014			36

UBABSL4_11790G0002	149 Conserved protein of unknown function		0.0097		UBAL3_95950013	75	
UBABSL4_11790G0003	223 transcriptional repressor, LexA family		0.0129		UBAL3_95950012	37	
UBABSL4_11790G0004	373 putative chemotaxis phosphatase, CheZ	0.03375 0.06113	0.0812		UBAL3_95950011	59	
UBABSL4_12069G0001	553 [NifE] hydrogenase large subunit HydB		0.0496				
UBABSL4_12069G0002	369 [NifE] hydrogenase small subunit HydA	0.01951	0.0274				
UBABSL4_12069G0003	197 thymidylate kinase		0.022		UBAL3_94530007	76	
UBABSL4_12069G0004	221 Thymidylate kinase	0.07369			UBAL3_94530008	87	
rRNA-16S	16S rRNA						
rRNA-Ile-GAT	rRNA Ile GAT						
rRNA-Ala-TGC	rRNA Ala TGC						
rRNA-23S	23S rRNA						
UBABSL4_13359G0001	264 Conserved hypothetical protein		0.0219				
UBABSL4_13359G0002	185 Deoxyribonuclease, TatD family		0.0156		UBAL3_94240088	74	
UBABSL4_13359G0003	93 methionyl-tRNA synthetase				UBAL3_94240087	84	
UBABSL4_13359G0004	294 hypothetical protein		0.0294				
UBABSL4_17890G0001	211 Putative endonuclease III				UBAL3_95680141	35	
UBABSL4_17890G0002	657 glycoside hydrolase, family 15		0.0154		UBAL3_95950017	68	
UBABSL4_17890G0003	591 diguanylate cyclase/phosphodiesterase		0.0024		UBAL3_74420053	45	
UBABSL4_17890G0004	166 transposase						
UBABSL4_17891G0001	239 methyl-accepting chemotaxis sensory transducer		0.0664		UBAL3_94240159	41	
UBABSL4_17891G0002	159 Thiamine biosynthesis protein (ThiC)	0.03414	0.1542		UBAL3_80290068	87	
UBABSL4_17891G0003	286 Probably 5-methyltetrahydrofolate--homocysteine methyltransferase		0.0101		UBAL3_80290067	83	
UBABSL4_17891G0004	266 5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)	0.04898			UBAL3_80290066	83	
UBABSL4_2740G0001	112 Conserved hypothetical protein			0.0098			
UBABSL4_2740G0002	191 N-acetyl-gamma-glutamyl-phosphate reductase			0.0164	0.0458	UBAL3_94530032	42
UBABSL4_2740G0003	259 arginine biosynthesis bifunctional protein ArgJ		0.0245	0.0121	0.0211	UBAL3_94530029	41
UBABSL4_3307G0001	130 Conserved hypothetical protein				UBAL3_95680111	66	
UBABSL4_3307G0002	152 Conserved hypothetical protein				UBAL3_95680112	75	
UBABSL4_3307G0003	472 hypothetical protein		0.0031				
UBABSL4_3660G0001	194 Conserved hypothetical protein				UBAL3_80290077	52	
UBABSL4_3660G0002	180 Conserved protein of unknown function				UBAL3_80290076	86	
UBABSL4_3660G0003	463 Conserved protein of unknown function				UBAL3_80290076		
UBABSL4_3690G0001	40 hypothetical protein						
UBABSL4_3690G0002	235 TPR-domain containing protein		0.1412		UBAL3_79520009	80	
UBABSL4_3690G0003	87 TPR-domain containing protein		0.1327		UBAL3_79520009	83	
UBABSL4_3990G0001	257 cobyrinic acid synthase CobQ				UBAL3_95450140	52	
UBABSL4_3990G0002	180 cobalamin biosynthesis protein CobD/CbiB				UBAL3_95450139	61	
UBABSL4_3990G0003	320 Putative L-threonine-O-3-phosphate decarboxylase				UBAL3_95450138	54	
UBABSL4_4294G0001	106 Conserved hypothetical protein				UBAL3_78920092	72	
UBABSL4_4294G0002	106 Putative iron-sulfur cofactor synthesis protein (NifZ)				UBAL3_78920093	86	
UBABSL4_4294G0003	82 Conserved hypothetical protein				UBAL3_78920094	68	
UBABSL4_4393G0001	211 Putative hydrogenase-4 subunit (HyfF)				UBAL3_79520044	56	
UBABSL4_4393G0002	86 Probable hydrogenase-4 membrane component (HyfE)				UBAL3_79520045	65	
UBABSL4_4393G0003	231 respiratory-chain NADH dehydrogenase, subunit 1						
UBABSL4_4489G0001	197 Conserved protein of unknown function				UBAL3_44810079	55	
UBABSL4_4489G0002	119 Conserved hypothetical protein				UBAL3_44810080	69	
UBABSL4_4489G0003	200 3-dehydroquinate synthase				UBAL3_44810082	64	
UBABSL4_6289G0001	183 UDP-3-O-acetyl-N-acetylglucosamine deacetylase		0.0315		UBAL3_79520053	68	
UBABSL4_6289G0002	103 ferredoxin				UBAL3_79520054	65	
UBABSL4_6289G0003	199 Conserved protein of unknown function		0.029		UBAL3_79520055	60	

UBABSL4_10523G0001	601 Peptidase S1C, Do	0.54051	0.23341	0.06684						0.1008		UBAL3_93200048	86
UBABSL4_10523G0002	214 Probable holliday junction DNA helicase (RuvA)			0.01015						0.0202		UBAL3_93200050	66
UBABSL4_10523G0003	204 Holliday junction DNA helicase RuvB									0.0424		UBAL3_93200051	87
UBABSL4_11228G0001	169 Conserved hypothetical protein									0.0939	0.0306	0.0405	0.0065
UBABSL4_11228G0002	84 hypothetical protein									0.0515			
UBABSL4_11228G0003	424 Aminopeptidase N (EC 3.4.11.2)			0.06146						0.0204		UBAL3_92050078	55
UBABSL4_11254G0001	124 amidophosphoribosyltransferase									0.0233		UBAL3_95320044	77
UBABSL4_11254G0002	742 phosphoribosylformylglycinamide synthase II			0.03658						0.0078		UBAL3_95320045	75
UBABSL4_11254G0003	236 phosphoribosylformylglycinamide synthase I									0.0917		UBAL3_95320046	66
UBABSL4_11334G0001	597 deoxyxylulose-5-phosphate synthase		0.00603	0.04365						0.0169		UBAL3_60500022	83
UBABSL4_11334G0002	184 Probable hemolysin									0.0078		UBAL3_60500021	60
UBABSL4_11334G0003	126 NAD-dependent epimerase/dehydratase									0.0114		UBAL3_60500020	63
UBABSL4_11454G0001	360 peptidase C14, caspase catalytic subunit p20											UBAL3_95450007	31
UBABSL4_11454G0002	235 peptidase C14, caspase catalytic subunit p20											UBAL3_95450007	34
UBABSL4_11454G0003	115 Cellulose synthase catalytic subunit (UDP-forming)												
UBABSL4_11504G0001	92 Dihydroliipoamide dehydrogenase (EC 1.8.1.4)											UBAL3_94170054	63
UBABSL4_11504G0002	470 glutamine synthetase, type I	0.27359	0.52806	0.69303						0.1842		UBAL3_94170056	90
UBABSL4_11504G0003	391 transcriptional regulator, NifA, Fis Family			0.0361						0.0037		UBAL3_94170057	85
UBABSL4_11710G0001	90 hypothetical protein												
UBABSL4_11710G0002	476 Conserved protein of unknown function	2.6445	0.68765	0.49725						0.0697	0.0133	0.0109	0.0066
UBABSL4_11710G0003	245 ammonium transporter									0.0353			UBAL3_92050069
													96
UBABSL4_12343G0001	134 Transposase-like												UBAL3_94240057
UBABSL4_12343G0002	417 transposase									0.3494	0.0124		
UBABSL4_12343G0003	87 hypothetical protein												
UBABSL4_12576G0001	252 Conserved hypothetical protein											UBAL3_80290017	55
UBABSL4_12576G0002	228 Conserved protein of unknown function											UBAL3_80290016	74
UBABSL4_12576G0003	233 transposase			0.15844						0.0124		UBAL3_93670016	46
UBABSL4_12683G0001	408 Dihydroliipoamide dehydrogenase			0.01064						0.0389		UBAL3_79160026	58
UBABSL4_12683G0002	447 Conserved hypothetical protein			0.01214								UBAL3_95950035	56
UBABSL4_12683G0003	53 hypothetical protein												
UBABSL4_17877G0001	95 hypothetical protein												
UBABSL4_17877G0002	432 Adenylosuccinate synthase		0.08743	0.09551		0.1563				0.1069		UBAL3_94320006	85
UBABSL4_17877G0003	83 Conserved protein of unknown function											UBAL3_94320007	46
UBABSL4_17899G0001	136 Homoserine dehydrogenase									0.0212		UBAL3_95450115	77
UBABSL4_17899G0002	93 threonine synthase											UBAL3_95450114	80
UBABSL4_17899G0003	187 Probable phosphoglycerate mutase									0.0231		UBAL3_95450113	42
UBABSL4_684G0001	213 NAD-dependent epimerase/dehydratase									0.0068		UBAL3_95450095	75
UBABSL4_684G0002	288 Conserved protein of unknown function									0.02		UBAL3_95450093	62
UBABSL4_802G0001	314 Putative filamentous haemagglutinin family protein			0.097		0.1021	0.0276	0.1919	0.2144	0.09	0.3107	0.6371	UBAL3_78920045
UBABSL4_802G0002	303 Putative filamentous haemagglutinin family protein						0.019	0.0732	0.0342	0.0518	0.2203	0.5267	UBAL3_78920046
													44
UBABSL4_2328G0001	182 Conserved protein of unknown function									0.5469		UBAL3_96150002	70
UBABSL4_2328G0002	239 phosphoglucomutase, alpha-D-glucose			0.00909						0.0362		UBAL3_96150004	68
UBABSL4_3153G0001	123 Probable rieske iron-sulfur family protein									0.0938		UBAL3_92050216	90
UBABSL4_3153G0002	206 Cytochrome b/b6, N-terminal domain									0.042		UBAL3_92050217	91
UBABSL4_4391G0001	145 peptidase M23B									0.0099		UBAL3_60500018	73
UBABSL4_4391G0002	113 preprotein translocase, SecA subunit									0.0511		UBAL3_60500017	77

UBABSL4_4579G0001	72 Probable N-acetyltransferase family protein							UBAL3_94170066	57	
UBABSL4_4579G0002	204 peptide chain release factor 2		0.03193			0.0212		UBAL3_94170067	89	
UBABSL4_4962G0001	130 Putative sulfite synthesis pathway protein (CysQ)					0.0111		UBAL3_78920010	64	
UBABSL4_4962G0002	295 Conserved hypothetical protein					0.0098		UBAL3_78920011	55	
UBABSL4_6076G0001	103 riboflavin biosynthesis protein RibD (EC:3.5.4.26 1.1.1.193)									
UBABSL4_6076G0002	195 riboflavin synthase, alpha subunit							UBAL3_95450154	44	
UBABSL4_6180G0001	181 Polyribonucleotide nucleotidyltransferase							UBAL3_92050205	50	
UBABSL4_6180G0002	44 Ribosomal protein S15							UBAL3_92050204		
UBABSL4_6185G0001	244 Conserved hypothetical protein									
UBABSL4_6185G0002	228 Conserved protein of unknown function							UBAL3_95680069	41	
UBABSL4_7122G0001	184 NADH dehydrogenase (quinone) F subunit		0.07819	0.15932			0.149	UBAL3_60500011	91	
UBABSL4_7122G0002	189 Putative NADH dehydrogenase (ubiquinone), E subunit	0.14323	0.26644	0.22979			0.0687	UBAL3_60500012	85	
UBABSL4_7607G0001	321 putative aconitate hydratase	1.1174	1.26621	1.02486			0.1528	UBAL3_92050122	95	
UBABSL4_7607G0002	213 hypothetical protein						0.1151			
UBABSL4_7720G0001	232 Cystathionine gamma-synthase			0.06552			0.0062	UBAL3_92050065	68	
UBABSL4_7720G0002	50 transposase						0.1731			
UBABSL4_8065G0001	323 Putative general secretion pathway protein K							UBAL3_80290004	79	
UBABSL4_8065G0002	322 Conserved protein of unknown function						0.009	UBAL3_80290003	70	
UBABSL4_8108G0001	204 Conserved hypothetical protein			0.0747			0.0786	0.0933	UBAL3_95390017	84
UBABSL4_8108G0002	37 hypothetical protein							0.0848		
UBABSL4_8247G0001	128 Conserved protein of unknown function							UBAL3_92050231	70	
UBABSL4_8247G0002	231 Conserved protein of unknown function							UBAL3_92050232	53	
UBABSL4_8572G0001	187 UDP-glucose 4-epimerase (EC 5.1.3.2)			0.0987			0.0077	UBAL3_94240092	92	
UBABSL4_8572G0002	162 Conserved protein of unknown function						0.1069	UBAL3_94240093	55	
UBABSL4_9030G0001	59 hypothetical protein									
UBABSL4_9030G0002	617 GTP-binding protein						0.0468	UBAL3_94240168	84	
UBABSL4_9383G0001	496 UDP-N-acetylmuramoylalanine--D-glutamate ligase			0.01532				UBAL3_92050139	62	
UBABSL4_9383G0002	356 phospho-N-acetylmuramoyl-pentapeptide-transferase						0.0081	UBAL3_92050138	83	
UBABSL4_9559G0001	930 NADH dehydrogenase, subunit F (EC 1.6.99.5)		0.05415	0.13426			0.1427	UBAL3_95680142	94	
UBABSL4_9559G0002	247 NADH dehydrogenase, subunit F (EC 1.6.99.5)			0.02637			0.0584	UBAL3_95680142		
UBABSL4_9818G0001	277 Conserved protein of unknown function						0.0156	UBAL3_94530059	46	
UBABSL4_9818G0002	431 transposase						0.0703			
UBABSL4_9882G0001	321 metal dependent phosphohydrolase		0.09525	0.17927			0.0135	UBAL3_79160020	77	
UBABSL4_9882G0002	488 glycosyl transferase, family protein			0.02892			0.0059	UBAL3_79160019	51	
UBABSL4_11135G0001	375 Transcription termination factor (NusA)			0.1199	0.14477		0.1885	UBAL3_92050199	85	
UBABSL4_11135G0002	753 translation initiation factor IF-2	0.06291	0.09792	0.17014			0.0632	UBAL3_92050200	77	
UBABSL4_11310G0001	884 Conserved protein of unknown function						0.0033	UBAL3_74420059	68	
UBABSL4_11310G0002	117 nitrogen regulatory protein P-II							UBAL3_74420058	89	
UBABSL4_17913G0001	94 CRISPR-associated protein, Cas2		0.3241	0.797		0.1705		UBAL3_78920062	67	
UBABSL4_17913G0002	307 Conserved hypothetical protein		0.2481	0.8541	0.1973	1.3049	0.0047	0.0056	0.0071	
UBABSL4_2192G0001	282 Probable TPR-domain containing protein							UBAL3_94240129	71	
UBABSL4_4241G0001	296 Conserved protein of unknown function	0.09145	0.09721				0.078	UBAL3_69480020	69	

UBABSL4_10441G0001	348 Organic solvent tolerance protein OstA				0.0083		UBAL3_94170018	75
UBABSL4_11460G0001	1228 Glutamate synthase (ferredoxin)	0.01102	0.0703	0.06278	0.0399		UBAL3_95680085	83

