

SUPPLEMENTARY TABLE 2 List of proteins identified by PMF. The scores greater than 45 are significant ($p < 0.05$).

Locus	spot No.	Protein	Description	Score	Sequence coverage%	Gene	NCBI Inr accession no.	Peptides matched	Peptides not-matched
BL0002	241	chaperone		118	18	groEL	gi 23464630	7	22
BL0002	430	chaperone		65	18	groEL	gi 23464630	6	7
BL0002	447	chaperone		118	18	groEL	gi 23464630	6	12
BL0002	290	chaperone		91	21	groEL	gi 23464630	6	20
BL0002	428	chaperone		96	21	groEL	gi 23464630	11	7
BL0002	356	chaperone		113	22	groEL	gi 23464630	10	23
BL0002	357	chaperone		100	22	groEL	gi 23464630	10	33
BL0002	228	chaperone		112	25	groEL	gi 23464630	12	10
BL0002	233	chaperone		108	25	groEL	gi 23464630	10	8
BL0002	583	chaperone		76	25	groEL	gi 23464630	9	12
BL0002	453	chaperone		97	26	groEL	gi 23464630	8	6
BL0002	528	chaperone		78	26	groEL	gi 23464630	8	14
BL0002	415	chaperone		114	29	groEL	gi 23464630	11	35
BL0002	416	chaperone		82	31	groEL	gi 23464630	9	13
BL0002	427	chaperone		98	31	groEL	gi 23464630	9	11
BL0002	586	chaperone		122	31	groEL	gi 23464630	14	13
BL0002	589	chaperone		121	32	groEL	gi 23464630	11	10
BL0002	355	chaperone		120	35	groEL	gi 23464630	14	14
BL0002	425	chaperone		89	36	groEL	gi 23464630	6	11
BL0002	559	chaperone		69	38	groEL	gi 23464630	7	8
BL0002	52	chaperone		96	39	groEL	gi 23464630	10	13
BL0002	591	chaperone		98	42	groEL	gi 23464630	5	4
BL0002	193	chaperone		192	44	groEL	gi 23464630	16	6

BL0002	354	chaperone	181	51	groEL	gi 23464630	19	14
BL0003	394	hypothetical protein BL0003	76	51		gi 23464631	6	2
BL0005	414	response regulator of two-component system	105	41		gi 23464633	9	9
BL0008	336	narrowly conserved hypothetical protein	105	53		gi 23464636	6	1
BL0009	757	hypothetical protein BL0009	223	71		gi 23464637	16	5
BL0017	84	histidyl-tRNA synthetase	250	46	hisS	gi 23464645	20	4
BL0021	800	ATP-binding protein of ABC transporter for glutamate	78	28	gluA	gi 23464649	6	14
BL0022	874	glutamate-binding protein of ABC transporter system	79	23	gluB	gi 23464650	11	3
BL0031	280	histidine kinase sensor of two-component system	80	41		gi 23464659	9	1
BL0033	571	probable solute binding protein of ABC transporter system possibly for sugars	93	30		gi 23464661	7	6
BL0033	381	probable solute binding protein of ABC transporter system possibly for sugars	134	52		gi 23464661	11	7
BL0034	690	ATP binding protein of ABC transporter	143	35		gi 23464662	14	6
BL0038	656	conserved protein with hydroxyacid dehydrogenase catalytic domain	67	22		gi 23464666	5	7
BL0039	342	hypothetical protein BL0039	112	46		gi 23464667	5	3
BL0046	258	narrowly conserved hypothetical protein	96	35		gi 23464674	7	2
BL0049	870	ATP binding protein of ABC transporter	123	24		gi 23464677	6	4
BL0053	168	hypothetical protein with duf059 and 4Fe-4S iron sulfur cluster binding domain	82	29	mrp	gi 23464681	13	26
BL0059	134	narrowly conserved hypothetical protein	117	45		gi 23464686	14	11
BL0065	620	elongation factor P	125	38	efp	gi 23464692	8	2
BL0065	326	elongation factor P	86	47	efp	gi 23464692	9	21

BL0069	826	similar to orotidine 5'-phosphate decarboxylase	152	59		gi 23464696	14	13
BL0077	409	probable solute-binding protein for glutamate/aspartate ABC transporter system	75	36		gi 23464704	8	25
BL0079	613	hypothetical protein with homology to glutaredoxin-like protein	99	80		gi 23464706	6	3
BL0079	878	hypothetical protein with homology to glutaredoxin-like protein	81	80		gi 23464706	5	10
BL0082	8	hypothetical protein BL0082	79	29		gi 23464708	6	2
BL0097	141	1-deoxy-D-xylulose 5-phosphate reductoisomerase	140	43	ispC	gi 23464723	13	4
BL0098	500	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase 1	65	35	ispG	gi 23464724	5	12
BL0098	632	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase 1	86	35	ispG	gi 23464724	5	9
BL0098	198	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase 1	117	58	ispG	gi 23464724	7	17
BL0116	704	glycyl-tRNA synthetase	84	21	glyS	gi 23464742	12	11
BL0118	562	cell division protein FtsZ	113	35	ftsZ	gi 23464744	11	10
BL0118	481	cell division protein FtsZ	146	39	ftsZ	gi 23464744	12	5
BL0119	324	hypothetical protein BL0119	123	84		gi 23464745	11	15
BL0121	553	hypothetical protein BL0121	67	21		gi 23464747	5	3
BL0121	353	hypothetical protein BL0121	172	45		gi 23464747	15	5
BL0121	352	hypothetical protein BL0121	185	48		gi 23464747	17	5
BL0121	351	hypothetical protein BL0121	147	54		gi 23464747	15	13
BL0128	81	narrowly conserved hypothetical protein	134	20		gi 23464754	12	3
BL0140	315	hypothetical protein in PgaM	119	74		gi 23464760	10	20

BL0140	806	phosphoglycerate mutase family hypothetical protein in PgaM	118	79		gi 23464760	11	44
BL0141	369	phosphoglycerate mutase family possible solute binding protein of ABC transporter	87	39		gi 23464761	11	18
BL0159	27	DNA-damage-inducible protein of Escherichia coli	91	32	dinD	gi 23464775	5	19
BL0170	89	methionyl-tRNA synthetase	156	44	metG	gi 23464786	17	12
BL0174	548	narrowly conserved hypothetical protein	98	21		gi 23464790	6	18
BL0175	179	probable AraC/XylS-type transcriptional regulator	110	16		gi 23464791	7	4
BL0175	506	probable AraC/XylS-type transcriptional regulator	96	16		gi 23464791	6	5
BL0197	372	possible ATP binding protein of ABC transporter	96	50		gi 23464812	10	14
BL0204	297	hypothetical protein BL0204	80	35		gi 23464818	7	3
BL0209	436	hypothetical protein with similarity to LicD required for phosphorylcholine incorporation in teicho	84	17		gi 23464823	6	22
BL0216	343	narrowly conserved hypothetical protein	86	20		gi 23464829	5	2
BL0227	227	glucose-1-phosphate thymidyltransferase	178	44	rmlA	gi 23464834	14	3
BL0228	110	possible fused dTDP-4-keto-L-rhamnose reductase and dTDP-4-keto-6-deoxyglucose-3,5-epimerase enzyme	168	42		gi 23464835	17	7
BL0229	793	dTDP-glucose 4,6-dehydratase enzyme involved in rhamnose biosynthesis	60	41	rmlB1	gi 23464836	7	36

BL0239	502	probable integrase/recombinase	101	42		gi 23464845	16	1
BL0255	772	dehydrogenase or reductase protein	176	55		gi 23464858	16	8
BL0256	7	hypothetical protein BL0256	62	72		gi 23464859	6	4
BL0272	515	L-arabinose isomerase	90	35	araA	gi 23464874	5	8
BL0273	815	L-ribulose-5-phosphate 4-epimerase	77	58	araD	gi 23464875	10	36
BL0274	80	probable sugar kinase	76	20		gi 23464876	9	7
BL0279	190	glucose-6-phosphate isomerase	78	22	gpi	gi 23464881	10	12
BL0279	35	glucose-6-phosphate isomerase	227	54	gpi	gi 23464881	21	9
BL0282	788	FemAB-like protein possibly involved in interpeptide bridge formation in peptidoglycan	76	24		gi 23464883	7	36
BL0285	250	widely conserved hypothetical protein in Ham1 family	80	43		gi 23464886	9	8
BL0287	98	hypothetical protein BL0287	110	36		gi 23464888	14	23
BL0290	795	possible reductase	82	37		gi 23464891	8	18
BL0291	858	phosphopantetheine adenylyltransferase	75	57	coaD	gi 23464892	8	12
BL0292	492	hypothetical protein BL0292	72	30		gi 23464893	8	8
BL0292	503	hypothetical protein BL0292	71	31		gi 23464893	6	17
BL0295	319	ribonuclease III	106	21	rncS	gi 23464896	6	12
BL0297	322	acetolactate synthase small subunit	106	38	ilvN	gi 23464898	10	6
BL0309	252	possible oxidoreductase of the aldo/keto reductase family	133	51		gi 23464910	11	5
BL0312	251	probable ATP-binding protein of ABC transporter system for phosphate	130	55	pstB	gi 23464913	15	11
BL0319	710	phospho-2-keto-3-deoxyheptonate aldolase	146	36	aroG	gi 23464920	10	2
BL0320	777	phospho-2-dehydro-3-deoxyheptonate aldolase, phe-sensitive	78	19	aroG2	gi 23464921	7	4
BL0320	146	phospho-2-dehydro-3-deoxyheptonate	169	38	aroG2	gi 23464921	13	2

		aldolase, phe-sensitive						
BL0320	737	phospho-2-dehydro-3-deoxyheptonate aldolase, phe-sensitive	143	41	aroG2	gi 23464921	12	10
BL0320	738	phospho-2-dehydro-3-deoxyheptonate aldolase, phe-sensitive	178	44	aroG2	gi 23464921	14	5
BL0322	489	hypothetical protein BL0322	101	32		gi 23464923	7	9
BL0322	510	hypothetical protein BL0322	74	35		gi 23464923	7	5
BL0322	348	hypothetical protein BL0322	193	45		gi 23464923	26	16
BL0322	349	hypothetical protein BL0322	177	47		gi 23464923	26	28
BL0327	211	tRNA (guanine-N1)-methyltransferase	77	34	trmD	gi 23464928	8	17
BL0331	781	probable PfkB family carbohydrate (sugar) kinase	100	31		gi 23464932	5	24
BL0331	794	probable PfkB family carbohydrate (sugar) kinase	93	53		gi 23464932	11	28
BL0337	265	hypothetical protein possibly in TetR transcriptional regulator family	102	22		gi 23464937	7	1
BL0339	581	hypothetical protein in upf0003	96	30		gi 23464939	10	8
BL0345	371	D-alanine--D-alanine ligase	118	25	ddlA	gi 23464945	5	1
BL0346	525	glycerol-3-phosphate dehydrogenase [NAD(P)+]	97	21		gi 23464946	9	4
BL0346	201	glycerol-3-phosphate dehydrogenase [NAD(P)+]	186	54		gi 23464946	18	8
BL0348	338	hypothetical 14.5 kDa translational inhibitor protein	90	75	psp1	gi 23464948	7	9
BL0350	523	hypothetical protein with marginal similarity to thioredoxin	95	20		gi 23464950	8	8
BL0352	199	hypothetical protein BL0352	95	41		gi 23464951	11	17

BL0356	872	ATP synthase epsilon chain	87	72	atpC	gi 23464955	5	5
BL0357	533	ATP synthase beta chain	85	15	atpD	gi 23464956	5	11
BL0357	363	ATP synthase beta chain	89	17	atpD	gi 23464956	6	10
BL0357	433	ATP synthase beta chain	96	17	atpD	gi 23464956	5	13
BL0357	389	ATP synthase beta chain	88	18	atpD	gi 23464956	6	15
BL0357	575	ATP synthase beta chain	73	18	atpD	gi 23464956	7	3
BL0357	574	ATP synthase beta chain	83	28	atpD	gi 23464956	11	14
BL0357	431	ATP synthase beta chain	61	30	atpD	gi 23464956	7	21
BL0357	411	ATP synthase beta chain	79	31	atpD	gi 23464956	10	10
BL0357	408	ATP synthase beta chain	124	36	atpD	gi 23464956	18	17
BL0357	263	ATP synthase beta chain	173	38	atpD	gi 23464956	16	5
BL0357	577	ATP synthase beta chain	126	39	atpD	gi 23464956	15	13
BL0357	529	ATP synthase beta chain	99	41	atpD	gi 23464956	12	18
BL0357	29	ATP synthase beta chain	255	47	atpD	gi 23464956	29	12
BL0357	53	ATP synthase beta chain	209	57	atpD	gi 23464956	18	7
BL0357	54	ATP synthase beta chain	243	64	atpD	gi 23464956	26	6
BL0358	762	ATP synthase gamma chain	113	28	atpG	gi 23464957	10	3
BL0359	208	ATP synthase alpha chain	87	15	atpA	gi 23464958	5	9
BL0359	450	ATP synthase alpha chain	73	17	atpA	gi 23464958	11	15
BL0359	181	ATP synthase alpha chain	78	18	atpA	gi 23464958	8	8
BL0359	742	ATP synthase alpha chain	85	20	atpA	gi 23464958	7	2
BL0359	185	ATP synthase alpha chain	78	20	atpA	gi 23464958	9	13
BL0359	454	ATP synthase alpha chain	95	22	atpA	gi 23464958	5	3
BL0359	246	ATP synthase alpha chain	90	22	atpA	gi 23464958	9	5
BL0359	207	ATP synthase alpha chain	88	23	atpA	gi 23464958	12	19
BL0359	289	ATP synthase alpha chain	113	24	atpA	gi 23464874	5	1
BL0359	259	ATP synthase alpha chain	74	26	atpA	gi 23464958	13	31

BL0359	271	ATP synthase alpha chain	80	32	atpA	gi 23464958	5	4
BL0359	451	ATP synthase alpha chain	90	38	atpA	gi 23464958	8	11
BL0359	274	ATP synthase alpha chain	90	40	atpA	gi 23464958	5	2
BL0359	592	ATP synthase alpha chain	104	44	atpA	gi 23464958	5	14
BL0369	602	hypothetical protein BL0369	98	21		gi 23464967	6	3
BL0389	599	inorganic pyrophosphatase	90	27	ppa	gi 23464986	12	4
BL0389	597	inorganic pyrophosphatase	112	31	ppa	gi 23464986	8	4
BL0397	623	narrowly conserved hypothetical protein with mutase domain	72	42		gi 23464994	6	8
BL0397	339	narrowly conserved hypothetical protein with mutase domain	125	55		gi 23464994	17	20
BL0401	48	possible acetyltransferase	78	33		gi 23464999	12	15
BL0401	41	possible acetyltransferase	148	46		gi 23464999	15	7
BL0401	43	possible acetyltransferase	138	56		gi 23464999	12	7
BL0402	685	glutamyl-tRNA(Gln) amidotransferase subunit B	132	39	gatB	gi 23465000	11	8
BL0403	883	glutamyl-tRNA(Gln) amidotransferase subunit A	114	43	gatA	gi 23465001	15	29
BL0412	843	histidine-containing phosphocarrier protein (Hpr protein) of Pts transport system	87	51	ptsH	gi 23465010	8	2
BL0416	622	30S ribosomal protein S6	98	38	rpsF	gi 23465014	11	4
BL0416	876	30S ribosomal protein S6	64	52	rpsF	gi 23465014	6	20
BL0419	226	hypothetical protein in upf0001	117	36		gi 23465017	10	6
BL0426	663	LacI-type transcriptional regulator	60	18		gi 23465024	5	6
BL0428	604	hypothetical protein BL0428	98	22		gi 23465026	8	3
BL0429	248	possible cobyrinic acid synthase CobQ	176	51		gi 23465027	14	3
BL0431	95	replicative DNA helicase	68	31	dnaB	gi 23465029	13	28

BL0433	566	protein-pII; uridylyltransferase	96	26	glnD	gi 23465031	5	8
BL0434	877	nitrogen regulatory protein N-II	100	52	glnB	gi 23465032	10	7
BL0441	370	narrowly conserved hypothetical protein	88	18		gi 23465039	8	1
BL0441	619	narrowly conserved hypothetical protein	98	31		gi 23465039	5	17
BL0444	305	6-phosphogluconate dehydrogenase, decarboxylating II	100	23	gnt	gi 23465041	8	4
BL0444	111	6-phosphogluconate dehydrogenase, decarboxylating II	65	34	gnt	gi 23465041	11	35
BL0444	311	6-phosphogluconate dehydrogenase, decarboxylating II	136	38	gnt	gi 23465041	14	13
BL0444	108	6-phosphogluconate dehydrogenase, decarboxylating II	166	41	gnt	gi 23465041	14	4
BL0444	318	6-phosphogluconate dehydrogenase, decarboxylating II	148	45	gnt	gi 23465041	18	23
BL0444	109	6-phosphogluconate dehydrogenase, decarboxylating II	195	59	gnt	gi 23465041	24	25
BL0469	92	glutamyl-tRNA synthetase	231	43	gltX	gi 23465061	28	14
BL0472	774	widely conserved hypothetical protein	130	50		gi 23465064	11	8
BL0478	76	formate--tetrahydrofolate ligase	79	31	fhs	gi 23465070	13	26
BL0478	85	formate--tetrahydrofolate ligase	136	42	fhs	gi 23465070	18	15
BL0492	750	aspartate-semialdehyde dehydrogenase	118	39	asd	gi 23465082	13	15
BL0492	785	aspartate-semialdehyde dehydrogenase	72	39	asd	gi 23465082	12	47
BL0493	596	aspartokinase	89	47	askB	gi 23465083	9	11
BL0514	176	possible acyl protein synthase/acyl-CoA reductase-like protein	173	40		gi 23465104	15	5
BL0519	534	GrpE protein	119	15	grpE	gi 23465108	5	10
BL0519	551	GrpE protein	64	21	grpE	gi 23465108	5	7

BL0520	522	DnaK protein	96	15	dnaK	gi 23465109	6	11
BL0520	569	DnaK protein	85	15	dnaK	gi 23465109	5	11
BL0520	197	DnaK protein	120	20	dnaK	gi 23465109	7	11
BL0520	539	DnaK protein	90	28	dnaK	gi 23465109	6	2
BL0520	378	DnaK protein	86	28	dnaK	gi 23465109	5	6
BL0520	346	DnaK protein	61	30	dnaK	gi 23465109	11	30
BL0520	347	DnaK protein	143	36	dnaK	gi 23465109	15	7
BL0523	851	possible xylosidase or glucosidase	103	15		gi 23465112	5	11
BL0523	798	possible xylosidase or glucosidase	86	16		gi 23465112	7	23
BL0530	178	ketol-acid reductoisomerase	163	51	ilvC1	gi 23465118	20	23
BL0531	188	ketol-acid reductoisomerase	68	18	ilvC2	gi 23465119	5	3
BL0531	219	ketol-acid reductoisomerase	73	18	ilvC2	gi 23465119	6	5
BL0531	756	ketol-acid reductoisomerase	110	20	ilvC2	gi 23465119	6	18
BL0531	145	ketol-acid reductoisomerase	65	28	ilvC2	gi 23465119	8	21
BL0531	189	ketol-acid reductoisomerase	156	43	ilvC2	gi 23465119	13	11
BL0550	148	fructose-bisphosphate aldolase	103	37	fba	gi 23465135	9	8
BL0552	37	probable ferredoxin/ferredoxin-NADP reductase	236	53	fprA	gi 23465137	25	12
BL0576	445	probable Hsp20-family heat shock chaperone	58	32		gi 23465161	7	6
BL0583	538	hypothetical protein with FHA domain	115	42		gi 23465168	7	2
BL0597	166	glycogen phosphorylase	64	15	glgP	gi 23465182	9	14
BL0597	172	glycogen phosphorylase	68	17	glgP	gi 23465182	11	17
BL0597	202	glycogen phosphorylase	64	18	glgP	gi 23465182	10	20
BL0600	102	tryptophanyl-tRNA synthetase	80	22	trpS	gi 23465185	5	7
BL0600	784	tryptophanyl-tRNA synthetase	127	44	trpS	gi 23465185	10	8
BL0603	403	narrowly conserved hypothetical protein	96	31		gi 23465188	6	2
BL0614	214	thioredoxin reductase-like protein	66	17		gi 23465198	8	12

BL0614	77	thioredoxin reductase-like protein	135	27		gi 23465198	12	4
BL0615	608	alkyl hydroperoxide reductase C22 protein	108	20	ahpC	gi 23465199	6	4
BL0615	593	alkyl hydroperoxide reductase C22 protein	168	70	ahpC	gi 23465199	11	6
BL0618	446	hypothetical protein in DPS family	114	59		gi 23465202	8	10
BL0630	432	NADP-specific glutamate dehydrogenase	98	22	gdhA	gi 23465213	7	1
BL0630	113	NADP-specific glutamate dehydrogenase	248	58	gdhA	gi 23465213	22	5
BL0638	272	DNA polymerase III, beta chain	88	18	dnaN	gi 23465221	7	4
BL0638	374	DNA polymerase III, beta chain	132	56	dnaN	gi 23465221	14	16
BL0645	440	narrowly conserved hypothetical protein with possible ssDNA binding domain	95	53	jag	gi 23465228	10	27
BL0646	527	possible glucose inhibited division protein B	89	21	gidB	gi 23465229	9	4
BL0667	329	hypothetical protein BL0667	113	26		gi 23465249	10	3
BL0673	727	ATP binding protein of ABC transporter for sugars	58	18	msiK	gi 23465255	7	5
BL0673	714	ATP binding protein of ABC transporter for sugars	93	29	msiK	gi 23465255	11	7
BL0673	716	ATP binding protein of ABC transporter for sugars	98	38	msiK	gi 23465255	14	26
BL0682	293	protein probably involved in xylan degradation; possible xylan esterase	80	29		gi 23466098	8	3
BL0685	316	HisF cyclase	158	65	hisF	gi 23465266	20	23
BL0686	865	probable phosphoribosyl-AMP cyclohydrolase	90	57	hisI	gi 23465267	8	26
BL0687	39	anthranilate synthase component I	198	55	trpE	gi 23465268	22	11
BL0690	303	hypothetical protein with glucose/ribitol dehydrogenase family signature	67	33		gi 23465271	5	6
BL0699	868	hypothetical myosin-like protein with unknown function	90	27		gi 23465279	6	9

BL0700	898	hypothetical protein BL0700	89	16		gi 23465280	5	1
BL0707	546	phosphoglycerate kinase	98	18	pgk	gi 23465287	7	2
BL0707	554	phosphoglycerate kinase	94	19	pgk	gi 23465287	6	1
BL0707	560	phosphoglycerate kinase	71	23	pgk	gi 23465287	6	7
BL0707	887	phosphoglycerate kinase	62	27	pgk	gi 23465287	7	20
BL0707	60	phosphoglycerate kinase	64	33	pgk	gi 23465287	9	26
BL0707	62	phosphoglycerate kinase	83	38	pgk	gi 23465287	11	20
BL0707	555	phosphoglycerate kinase	139	57	pgk	gi 23465287	9	4
BL0708	832	triosephosphate isomerase	78	40	tpi	gi 23465288	11	36
BL0710	195	L-lactate dehydrogenase	105	31	ldh1	gi 23465290	9	9
BL0715	300	transaldolase	90	17	tal	gi 23465295	6	4
BL0715	474	transaldolase	60	17	tal	gi 23465295	5	4
BL0715	298	transaldolase	90	22	tal	gi 23465295	5	11
BL0715	467	transaldolase	92	22	tal	gi 23465295	7	3
BL0715	288	transaldolase	82	25	tal	gi 23465295	6	3
BL0715	163	transaldolase	80	40	tal	gi 23465295	10	23
BL0715	155	transaldolase	120	46	tal	gi 23465295	13	19
BL0715	159	transaldolase	153	48	tal	gi 23465295	14	11
BL0715	160	transaldolase	212	51	tal	gi 23465295	15	2
BL0715	45	transaldolase	132	57	tal	gi 23465295	16	31
BL0715	273	transaldolase	223	57	tal	gi 23465295	16	5
BL0715	162	transaldolase	203	65	tal	gi 23465295	20	16
BL0716	26	transketolase	68	15	tkt	gi 23465296	7	7
BL0716	72	transketolase	58	15	tkt	gi 23465296	7	7
BL0716	94	transketolase	92	15	tkt	gi 23465296	7	23
BL0716	206	transketolase	64	15	tkt	gi 23465296	10	15
BL0716	282	transketolase	114	18	tkt	gi 23465296	5	5

BL0716	286	transketolase	125	19	tkt	gi 23465296	6	5
BL0716	897	transketolase	119	19	tkt	gi 23465296	6	7
BL0716	69	transketolase	72	21	tkt	gi 23465296	10	20
BL0716	175	transketolase	63	24	tkt	gi 23465296	9	9
BL0716	173	transketolase	62	24	tkt	gi 23465296	10	14
BL0716	249	transketolase	87	25	tkt	gi 23465296	6	10
BL0716	187	transketolase	112	27	tkt	gi 23465296	6	2
BL0716	603	transketolase	67	28	tkt	gi 23465296	6	3
BL0716	171	transketolase	90	28	tkt	gi 23465296	7	7
BL0716	174	transketolase	58	33	tkt	gi 23465296	7	9
BL0716	196	transketolase	62	36	tkt	gi 23465296	7	7
BL0719	790	chaperone protein	110	51	dnaJ	gi 23465298	13	26
BL0720	801	hypothetical protein BL0720	58	39		gi 23465299	7	22
BL0731	448	adenine phosphoribosyltransferase	64	47	apt	gi 23465309	8	21
BL0733	220	succinyl-CoA synthetase alpha chain	90	31	sucD	gi 23465311	10	3
BL0733	766	succinyl-CoA synthetase alpha chain	76	45	sucD	gi 23465311	12	25
BL0735	103	PurH	77	23	purH	gi 23465313	7	4
BL0735	679	PurH	73	23	purH	gi 23465313	8	8
BL0735	780	PurH	112	37	purH	gi 23465313	5	7
BL0735	680	PurH	169	44	purH	gi 23465313	15	5
BL0743	337	narrowly conserved hypothetical protein	90	51		gi 23465320	9	7
BL0744	247	probable hydrolase or phosphatase	95	34		gi 23465321	6	2
BL0751	846	ATP phosphoribosyltransferase	108	57	hisG	gi 23465329	16	26
BL0753	816	ribulose-phosphate 3-epimerase	87	57	rpe	gi 23465331	8	24
BL0774	299	MutT-like protein	127	48		gi 23465350	10	3
BL0783	152	probable aminotransferase	90	32		gi 23465359	8	4
BL0788	836	orotate phosphoribosyltransferase	73	35	pyrE	gi 23465364	7	13

BL0788	841	orotate phosphoribosyltransferase	145	62	pyrE	gi 23465364	14	21
BL0790	422	probable dihydroorotate dehydrogenase electron transfer subunit	101	38	pyrK	gi 23465366	9	6
BL0792	487	dihydroorotase	83	21	pyrC	gi 23465368	6	3
BL0793	866	aspartate carbamoyltransferase regulatory chain	123	51	pyrI	gi 23465369	6	26
BL0794	209	aspartate carbamoyltransferase	92	35	pyrB	gi 23465370	11	15
BL0794	186	aspartate carbamoyltransferase	95	48	pyrB	gi 23465370	13	38
BL0794	180	aspartate carbamoyltransferase	194	58	pyrB	gi 23465370	18	9
BL0796	460	choloylglycine hydrolase	113	22		gi 23465372	5	4
BL0796	459	choloylglycine hydrolase	61	24		gi 23465372	9	6
BL0796	579	choloylglycine hydrolase	62	29		gi 23465372	7	12
BL0796	407	choloylglycine hydrolase	84	32		gi 23465372	7	4
BL0796	580	choloylglycine hydrolase	95	36		gi 23465372	11	5
BL0796	153	choloylglycine hydrolase	80	41		gi 23465372	12	13
BL0796	578	choloylglycine hydrolase	107	41		gi 23465372	12	6
BL0796	396	choloylglycine hydrolase	152	50		gi 23465372	12	4
BL0816	68	hypothetical protein BL0816	92	23		gi 23465391	5	10
BL0816	466	hypothetical protein BL0816	96	68		gi 23465391	8	4
BL0817	507	hypothetical protein BL0817	96	45		gi 23465392	6	4
BL0819	537	hypothetical protein BL0819	100	23		gi 23465394	7	1
BL0833	678	glutamate synthase [NADPH] small subunit	148	30	gltD	gi 23465408	10	1
BL0852	135	probable branched-chain amino acid aminotransferase	127	25	ilvE	gi 23465426	7	16
BL0853	452	probable 50S ribosomal protein L25	97	37	rplY	gi 23465427	8	3
BL0857	59	NAD(P) transhydrogenase subunit alpha part	196	57	pntA	gi 23465431	16	5

BL0863	610	hypothetical protein in Hit family	90	45		gi 23465437	5	4
BL0863	621	hypothetical protein in Hit family	63	66		gi 23465437	7	2
BL0863	895	hypothetical protein in Hit family	78	72		gi 23465437	7	22
BL0864	773	conserved hypothetical protein with similarity to SdrD of <i>S. coelicolor</i>	77	41		gi 23465438	8	15
BL0868	587	hypothetical protein with NifU-like domain	95	29		gi 23465442	5	17
BL0869	724	NifS-like aminotranferase	83	19		gi 23465443	7	4
BL0869	729	NifS-like aminotranferase	172	43		gi 23465443	15	5
BL0869	730	NifS-like aminotranferase	210	49		gi 23465443	19	12
BL0870	779	probable ATP binding protein of ABC transporter	78	28		gi 23465444	5	19
BL0870	771	probable ATP binding protein of ABC transporter	146	54		gi 23465444	13	10
BL0870	776	probable ATP binding protein of ABC transporter	204	66		gi 23465444	20	11
BL0876	859	probable 3-dehydroquinate dehydratase	88	35	aroQ	gi 23465450	6	1
BL0878	789	chorismate synthase	111	32	aroC	gi 23465452	6	34
BL0882	688	alanyl-tRNA synthetase	141	18	alaS	gi 23465456	15	5
BL0882	722	alanyl-tRNA synthetase	92	18	alaS	gi 23465456	12	11
BL0882	723	alanyl-tRNA synthetase	117	28	alaS	gi 23465456	13	5
BL0891	839	xanthine phosphoribosyltransferase	117	57	xpt	gi 23465465	13	35
BL0891	323	xanthine phosphoribosyltransferase	137	72	xpt	gi 23465465	15	25
BL0897	526	probable pyrazinamidase/nicotinamidase	96	27	pncA	gi 23465471	5	4
BL0897	302	probable pyrazinamidase/nicotinamidase	115	62	pncA	gi 23465471	8	10
BL0898	695	hypothetical protein BL0898	152	35		gi 23465472	13	8
BL0921	184	hypothetical protein BL0921	80	17		gi 23465494	7	3
BL0926	437	widely conserved hypothetical GTPase-like	59	30		gi 23465499	5	10

		protein										
BL0926	157	widely conserved hypothetical GTPase-like protein	163	54			gi 23465499	17	14			
BL0927	284	pyrroline-5-carboxylate reductase	86	30	proC		gi 23465500	7	4			
BL0933	333	O-acetylhomoserine (thiol)-lyase	113	24	cysD		gi 23465506	6	17			
BL0933	334	O-acetylhomoserine (thiol)-lyase	88	24	cysD		gi 23465506	6	18			
BL0933	133	O-acetylhomoserine (thiol)-lyase	143	42	cysD		gi 23465506	11	4			
BL0934	395	possible pyridoxine kinase	61	32			gi 23465507	5	9			
BL0944	456	ATP-dependent Clp protease proteolytic subunit 2	82	21	clpP2		gi 23465517	6	1			
BL0944	277	ATP-dependent Clp protease proteolytic subunit 2	131	32	clpP2		gi 23465517	11	4			
BL0945	439	ATP-dependent Clp protease proteolytic subunit 1	84	28	clp1		gi 23465518	8	23			
BL0947	521	trigger factor chaperone	74	19	tig		gi 23465520	9	17			
BL0947	402	trigger factor chaperone	90	21	tig		gi 23465520	8	27			
BL0947	486	trigger factor chaperone	106	21	tig		gi 23465520	9	1			
BL0947	484	trigger factor chaperone	117	31	tig		gi 23465520	11	5			
BL0947	485	trigger factor chaperone	117	31	tig		gi 23465520	11	5			
BL0953	10	glutamine-dependent NAD(+) synthetase	180	43	nadE		gi 23465526	20	8			
BL0954	136	widely conserved hypothetical protein	93	18			gi 23465527	12	4			
BL0959	540	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	108	15			gi 23465532	8	7			
BL0959	797	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	110	15			gi 23465532	7	22			
BL0959	850	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	79	15			gi 23465532	7	19			

BL0959	34	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	73	16	gi 23465532	9	7
BL0959	699	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	106	17	gi 23465532	13	10
BL0959	713	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	83	17	gi 23465532	10	8
BL0959	786	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	110	17	gi 23465532	10	23
BL0959	749	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	97	19	gi 23465532	12	7
BL0959	792	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	184	19	gi 23465532	9	28
BL0959	712	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	99	20	gi 23465532	7	6
BL0959	545	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	89	21	gi 23465532	6	4
BL0959	715	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	137	21	gi 23465532	16	6
BL0959	799	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	127	22	gi 23465532	12	25
BL0959	728	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	86	26	gi 23465532	5	4
BL0959	796	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	111	28	gi 23465532	6	5
BL0959	783	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	77	30	gi 23465532	10	4
BL0959	828	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	111	33	gi 23465532	5	8

		phosphoketolase						
BL0959	782	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	102	38		gi 23465532	7	6
BL0959	543	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	68	39		gi 23465532	6	4
BL0959	36	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	58	51		gi 23465532	9	11
BL0959	33	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	161	56		gi 23465532	9	12
BL0960	78	GMP synthase glutamine amidotransferase	113	30	guaA	gi 23465533	11	8
BL0964	128	UDP-N-acetylglucosamine pyrophosphorylase	75	37	glmU	gi 23465536	9	14
BL0968	682	phosphate acetyltransferase	103	17	pta	gi 23465539	14	4
BL0968	681	phosphate acetyltransferase	154	28	pta	gi 23465539	15	7
BL0969	814	acetate kinase	119	24	ackA	gi 23465540	7	33
BL0969	745	acetate kinase	118	42	ackA	gi 23465540	13	21
BL0969	120	acetate kinase	58	51	ackA	gi 23465540	8	22
BL0969	121	acetate kinase	168	56	ackA	gi 23465540	18	11
BL0969	721	acetate kinase	231	65	ackA	gi 23465540	21	14
BL0970	373	3-phosphoshikimate 1-carboxyvinyltransferase	94	18		gi 23465541	7	1
BL0970	114	3-phosphoshikimate 1-carboxyvinyltransferase	138	33		gi 23465541	12	3
BL0978	115	LacZ	144	15	lacZ	gi 23465547	12	16
BL0978	764	LacZ	72	17	lacZ	gi 23465547	9	6
BL0978	675	LacZ	84	17	lacZ	gi 23465547	9	4
BL0978	93	LacZ	61	18	lacZ	gi 23465547	7	1
BL0978	143	LacZ	112	20	lacZ	gi 23465547	8	4

BL0978	763	LacZ	66	21	lacZ	gi 23465547	12	11
BL0978	758	LacZ	86	21	lacZ	gi 23465547	12	26
BL0978	91	LacZ	60	21	lacZ	gi 23465547	11	17
BL0978	101	LacZ	68	22	lacZ	gi 23465547	10	6
BL0978	86	LacZ	58	23	lacZ	gi 23465547	11	12
BL0978	87	LacZ	63	28	lacZ	gi 23465547	10	12
BL0978	90	LacZ	87	28	lacZ	gi 23465547	13	21
BL0978	127	LacZ	80	29	lacZ	gi 23465547	9	22
BL0978	106	LacZ	120	30	lacZ	gi 23465547	11	10
BL0982	732	probable glycogen operon protein GlgX	66	30	glgX	gi 23465551	9	5
BL0983	268	possible pyrophosphate-releasing NTPase in MutT family	60	36		gi 23465552	8	11
BL0984	216	conserved hypothetical protein with duf34	93	45		gi 23465553	8	13
BL0986	191	conserved hypothetical protein with a response regulator receiver domain	155	56		gi 23465555	16	18
BL0987	321	possible NTP pyrophosphatase in MutT family	73	48		gi 23465556	9	19
BL0988	837	pyruvate kinase	90	18	pyk	gi 23465557	7	4
BL0988	262	pyruvate kinase	100	21	pyk	gi 23465557	10	4
BL0988	686	pyruvate kinase	69	23	pyk	gi 23465557	8	15
BL0988	813	pyruvate kinase	74	25	pyk	gi 23465557	8	11
BL0988	677	pyruvate kinase	111	27	pyk	gi 23465557	8	2
BL0988	834	pyruvate kinase	70	29	pyk	gi 23465557	8	24
BL0988	825	pyruvate kinase	74	32	pyk	gi 23465557	10	33
BL0988	760	pyruvate kinase	187	34	pyk	gi 23465557	16	3
BL0988	105	pyruvate kinase	151	35	pyk	gi 23465557	15	5
BL0988	257	pyruvate kinase	153	35	pyk	gi 23465557	16	5

BL0988	332	pyruvate kinase	121	37	pyk	gi 23465557	6	7
BL0988	221	pyruvate kinase	195	37	pyk	gi 23465557	19	8
BL0988	107	pyruvate kinase	183	41	pyk	gi 23465557	17	4
BL0993	224	bifunctional methylenetetrahydrofolate dehydrogenase and methenyltetrahydrofolate cyclohydrolase	151	43	folD	gi 23465562	12	3
BL0993	803	bifunctional methylenetetrahydrofolate dehydrogenase and methenyltetrahydrofolate cyclohydrolase	144	69	folD	gi 23465562	20	38
BL0999	740	1,4-alpha-glucan branching enzyme	101	17	glgB	gi 23465568	5	7
BL0999	741	1,4-alpha-glucan branching enzyme	62	26	glgB	gi 23465568	8	6
BL0999	122	1,4-alpha-glucan branching enzyme	108	28	glgB	gi 23465568	22	34
BL0999	739	1,4-alpha-glucan branching enzyme	115	34	glgB	gi 23465568	7	9
BL1000	848	response regulator of two-component system	107	55		gi 23465569	13	26
BL1004	829	hypothetical protein with similarity to eukaryotic phosphomannomutases	116	30		gi 23465573	5	23
BL1015	468	transcription elongation factor GreA	115	71	greA	gi 23465584	9	8
BL1016	470	Fk506-binding protein	122	38	fkbP	gi 23465585	9	4
BL1016	462	Fk506-binding protein	74	48	fkbP	gi 23465585	5	8
BL1016	335	Fk506-binding protein	100	97	fkbP	gi 23465585	9	20
BL1022	276	enolase	77	20	eno	gi 23465590	8	7
BL1022	424	enolase	89	30	eno	gi 23465590	10	42
BL1022	361	enolase	139	43	eno	gi 23465590	12	5
BL1022	366	enolase	110	44	eno	gi 23465590	17	28
BL1022	278	enolase	120	52	eno	gi 23465590	7	4
BL1023	426	possible oxidoreductase in aldo-keto reductase family	99	15		gi 23465591	8	2

BL1034	132	gamma-glutamyl phosphate reductase	67	28	proA	gi 23465600	11	34
BL1039	217	hypothetical protein BL1039	110	34		gi 23465605	5	31
BL1043	601	DNA repair protein RecN	86	29	recN	gi 23465610	7	19
BL1046	317	hypothetical protein possibly involved in monovalent cation transport	88	50		gi 23465613	8	45
BL1049	568	conserved hypothetical protein with possible phosphatase function	81	31		gi 23465616	11	14
BL1049	761	conserved hypothetical protein with possible phosphatase function	106	32		gi 23465616	7	42
BL1051	131	tyrosyl-tRNA synthetase	99	35	tyrS	gi 23465618	12	16
BL1056	344	hypothetical protein BL1056	104	35		gi 23465625	10	2
BL1058	242	argininosuccinate synthase	106	15	argG	gi 23465627	5	14
BL1058	130	argininosuccinate synthase	146	47	argG	gi 23465627	21	25
BL1060	734	ornithine carbamoyltransferase, anabolic	67	38	argF	gi 23465629	6	14
BL1064	747	N-acetyl-gamma-glutamyl-phosphate reductase	159	43	argC	gi 23465633	12	2
BL1067	890	phenylalanyl-tRNA synthetase alpha chain	112	25	pheS	gi 23465636	6	15
BL1067	71	phenylalanyl-tRNA synthetase alpha chain	83	43	pheS	gi 23465636	14	25
BL1072	368	widely conserved protein in peptidase or deacetylase family	114	22		gi 23465641	5	3
BL1076	236	glutamine synthetase 1	75	30	glnA1	gi 23465645	13	47
BL1076	32	glutamine synthetase 1	199	48	glnA1	gi 23465645	16	6
BL1090	164	possible alcohol dehydrogenase	71	31		gi 23465659	10	16
BL1097	616	elongation factor Tu	62	16	tuf	gi 23465666	6	3
BL1097	617	elongation factor Tu	109	16	tuf	gi 23465666	6	4
BL1097	283	elongation factor Tu	112	17	tuf	gi 23465666	5	3
BL1097	412	elongation factor Tu	96	17	tuf	gi 23465666	5	5

BL1097	310	elongation factor Tu	100	19	tuf	gi 23465666	5	7
BL1097	421	elongation factor Tu	96	19	tuf	gi 23465666	5	7
BL1097	309	elongation factor Tu	84	22	tuf	gi 23465666	7	23
BL1097	399	elongation factor Tu	88	23	tuf	gi 23465666	5	9
BL1097	270	elongation factor Tu	121	25	tuf	gi 23465666	5	9
BL1097	231	elongation factor Tu	102	26	tuf	gi 23465666	12	4
BL1097	234	elongation factor Tu	79	26	tuf	gi 23465666	6	4
BL1097	292	elongation factor Tu	68	26	tuf	gi 23465666	6	4
BL1097	285	elongation factor Tu	123	27	tuf	gi 23465666	10	4
BL1097	230	elongation factor Tu	68	28	tuf	gi 23465666	7	14
BL1097	232	elongation factor Tu	102	28	tuf	gi 23465666	7	2
BL1097	893	elongation factor Tu	78	30	tuf	gi 23465666	8	14
BL1097	307	elongation factor Tu	67	31	tuf	gi 23465666	9	29
BL1097	708	elongation factor Tu	94	33	tuf	gi 23465666	9	9
BL1097	325	elongation factor Tu	84	34	tuf	gi 23465666	13	20
BL1097	896	elongation factor Tu	66	37	tuf	gi 23465666	10	31
BL1097	237	elongation factor Tu	168	41	tuf	gi 23465666	14	6
BL1097	49	elongation factor Tu	87	42	tuf	gi 23465666	10	23
BL1097	705	elongation factor Tu	160	44	tuf	gi 23465666	12	4
BL1097	51	elongation factor Tu	106	49	tuf	gi 23465666	12	14
BL1097	65	elongation factor Tu	122	49	tuf	gi 23465666	11	8
BL1097	42	elongation factor Tu	119	50	tuf	gi 23465666	13	10
BL1098	99	elongation factor G	82	15	fusA	gi 23465667	12	24
BL1098	281	elongation factor G	80	17	fusA	gi 23465667	10	2
BL1098	364	elongation factor G	88	17	fusA	gi 23465667	10	23
BL1098	393	elongation factor G	101	19	fusA	gi 23465667	14	50
BL1098	63	elongation factor G	95	27	fusA	gi 23465667	18	25

BL1098	413	elongation factor G	90	31	fusA	gi 23465667	8	13
BL1098	266	elongation factor G	80	32	fusA	gi 23465667	12	5
BL1098	2	elongation factor G	190	32	fusA	gi 23465667	23	4
BL1098	67	elongation factor G	63	36	fusA	gi 23465667	10	8
BL1098	576	elongation factor G	103	36	fusA	gi 23465667	7	13
BL1098	1	elongation factor G	209	45	fusA	gi 23465667	28	15
BL1099	698	30S ribosomal protein S7	86	44	rpsG	gi 23465668	16	8
BL1103	194	possible low specificity-threonine aldolase	112	55		gi 23465672	7	7
BL1107	239	phosphoribosylaminoimidazole-succinocarboxamide synthase	164	57	purC	gi 23465675	11	5
BL1114	630	hypothetical protein in ImpB/MucB/SamB family of UV repair proteins	110	32		gi 23465682	5	2
BL1117	552	narrowly conserved hypothetical protein	101	20		gi 23465685	5	6
BL1123	55	phosphoribosylamine--glycine ligase	98	44	purD	gi 23465691	12	23
BL1123	365	phosphoribosylamine--glycine ligase	134	49	purD	gi 23465691	18	19
BL1128	867	probable metal uptake regulator similar to ferric uptake regulator protein	79	29	fur	gi 23465696	10	3
BL1129	696	phosphoribosylaminoimidazole carboxylase ATPase subunit	145	45	purK	gi 23465697	16	6
BL1130	862	phosphoribosylaminoimidazole carboxylase catalytic subunit	111	34	purE	gi 23465698	6	19
BL1132	88	probable 1-deoxyxylulose-5-phosphate synthase	115	29	dxs	gi 23465700	13	9
BL1142	442	L-asparaginase precursor	129	28		gi 23465709	6	11
BL1142	869	L-asparaginase precursor	101	32		gi 23465709	7	20
BL1142	341	L-asparaginase precursor	86	33		gi 23465709	8	10
BL1145	306	conserved hypothetical protein in sno	82	60		gi 23465711	9	32

		glutamine amidotransferase family						
BL1146	254	widely conserved protein in upfoo19 probably involved in pyridoxine biosynthesis	89	32		gi 23465712	9	6
BL1146	891	widely conserved protein in upfoo19 probably involved in pyridoxine biosynthesis	89	36		gi 23465712	10	26
BL1148	590	deoxyguanosinetriphosphate triphosphohydrolase	98	40	dgt	gi 23465714	9	1
BL1149	689	alanine racemase	84	21	alr	gi 23465715	7	4
BL1149	691	alanine racemase	67	28	alr	gi 23465715	11	33
BL1152	330	autoinducer-2 production protein LuxS	81	66		gi 23465718	7	11
BL1152	327	autoinducer-2 production protein LuxS	76	74		gi 23465718	7	25
BL1155	140	cystathionine gamma-synthase	88	25	metB	gi 23465721	7	4
BL1186	243	polypeptide deformylase	76	40		gi 23465752	5	4
BL1187	886	probable phosphoglucomutase or phosphomannomutase	103	44	mrsA	gi 23465753	10	17
BL1187	46	probable phosphoglucomutase or phosphomannomutase	166	63	mrsA	gi 23465753	20	22
BL1193	769	dihydrodipicolinate synthase	89	26	dapA	gi 23465759	5	11
BL1193	218	dihydrodipicolinate synthase	64	40	dapA	gi 23465759	8	17
BL1193	767	dihydrodipicolinate synthase	115	51	dapA	gi 23465759	14	12
BL1194	253	dihydrodipicolinate reductase	174	52	dapB	gi 23465760	11	2
BL1208	811	probable RNA methyltransferase	104	49	yibK	gi 23465775	8	33
BL1209	161	narrowly conserved hypothetical protein	157	49		gi 23465776	25	20
BL1210	881	galactokinase	96	50	galK	gi 23465778	10	21
BL1213	138	dihydroorotate dehydrogenase-like protein	96	34		gi 23465781	9	11
BL1213	124	dihydroorotate dehydrogenase-like protein	122	67		gi 23465781	15	17
BL1216	833	probable transcriptional regulator with cyclic	89	35		gi 23465784	5	26

		nucleotide-binding domain						
BL1216	845	probable transcriptional regulator with cyclic nucleotide-binding domain	111	68		gi 23465784	11	26
BL1222	564	hypothetical protein with N-terminal similarity to NADH pyrophosphatase	97	16		gi 23465790	5	9
BL1222	707	hypothetical protein with N-terminal similarity to NADH pyrophosphatase	112	35		gi 23465790	13	13
BL1222	805	hypothetical protein with N-terminal similarity to NADH pyrophosphatase	86	40		gi 23465790	11	36
BL1222	119	hypothetical protein with N-terminal similarity to NADH pyrophosphatase	142	43		gi 23465790	22	30
BL1223	512	possible alpha beta hydrolase	119	37		gi 23465791	7	13
BL1223	536	possible alpha beta hydrolase	69	37		gi 23465791	9	7
BL1224	438	narrowly conserved hypothetical protein	59	35		gi 23465792	9	22
BL1243	831	hypothetical protein with possible RecF domain	77	20		gi 23465805	5	14
BL1245	137	probable UDP-galactopyranose mutase	244	80	gif	gi 23465807	25	23
BL1247	410	possible 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase in the fumarylacetoacetate hydrolase family	118	27		gi 23465809	7	5
BL1249	687	histidine ammonia-lyase	112	31	hutH	gi 23465811	9	5
BL1252	61	possible phosphodiesterase	74	33		gi 23465814	7	9
BL1254	312	uracil phosphoribosyltransferase	153	83	upp	gi 23465816	18	26
BL1259	491	polyphosphate kinase	89	20	ppk	gi 23465821	7	7
BL1263	296	3-isopropylmalate dehydratase small subunit	172	70	leuD	gi 23465825	13	8
BL1265	64	hypothetical protein with similarity to dihydroorotate dehydrogenase	116	50		gi 23465827	11	9

BL1265	894	hypothetical protein with similarity to dihydroorotate dehydrogenase	187	65		gi 23465827	17	22
BL1267	718	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	189	46	murA	gi 23465829	16	4
BL1272	22	arginyl-tRNA synthetase	90	30	argS	gi 23465834	10	8
BL1272	20	arginyl-tRNA synthetase	169	41	argS	gi 23465834	17	7
BL1274	47	homoserine dehydrogenase	144	43	thrA	gi 23465836	13	5
BL1275	74	possible homoserine kinase	100	28	thrB	gi 23465837	9	8
BL1277	791	ATP-binding protein of ABC transporter system	88	49		gi 23465839	8	19
BL1286	75	aspartate aminotransferase	97	42	aspC	gi 23465848	12	11
BL1288	501	probable transcription antitermination protein	88	20	nusG	gi 23465850	11	4
BL1290	464	50S ribosomal protein L11	91	37	rplK	gi 23465852	7	4
BL1292	822	morphine 6-dehydrogenase	113	49	morA	gi 23465854	6	31
BL1295	882	histidinol dehydrogenase	144	50	hisD	gi 23465857	15	17
BL1296	66	histidinol-phosphate aminotransferase	81	44	hisC	gi 23465858	13	37
BL1297	840	imidazoleglycerol-phosphate dehydratase	118	34	hisB	gi 23465859	9	3
BL1299	291	amidotransferase HisH	86	40	hisH	gi 23465860	7	5
BL1300	449	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase	129	51	hisA	gi 23465861	12	12
BL1302	38	glutamine synthetase 2	153	55	glnA2	gi 23465863	17	11
BL1305	542	ATP-dependent helicase	108	18	hrpA	gi 23465866	9	3
BL1306	264	conserved hypothetical protein possibly in upfoo20	125	18		gi 23465867	5	2
BL1308	150	lactate dehydrogenase	114	25	ldh2	gi 23465869	5	7
BL1308	149	lactate dehydrogenase	71	29	ldh2	gi 23465869	6	2
BL1308	735	lactate dehydrogenase	104	48	ldh2	gi 23465869	9	9

BL1311	498	hypothetical protein with LysM domain of membrane-bound lytic murein transglycosylases	96	21		gi 23465872	8	3
BL1318	535	hypothetical protein possibly involved in cell wall formation	66	30		gi 23465879	12	11
BL1319	82	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanyl ligase	141	43	murF	gi 23465880	18	12
BL1321	40	UDP-N-acetylmuramoylalanine--D-glutamate ligase	95	35	murD	gi 23465882	14	25
BL1326	821	hypothetical protein BL1326	114	25		gi 23465887	11	3
BL1339	192	protein in PfkB family of sugar kinases	150	47		gi 23465900	14	10
BL1344	530	N-acetylglucosamine-6-phosphate deacetylase	97	23	nagA	gi 23465905	9	6
BL1344	711	N-acetylglucosamine-6-phosphate deacetylase	89	35	nagA	gi 23465905	9	15
BL1345	350	probable solute-binding protein of ABC transporter for peptides	146	47		gi 23465906	21	28
BL1348	842	ATP binding protein of ABC transporter	78	16		gi 23465909	6	4
BL1349	598	hypothetical protein containing MutT-like domain	66	49		gi 23465910	6	23
BL1350	294	Xaa-Pro aminopeptidase I	63	20	pepP	gi 23465911	6	7
BL1350	200	Xaa-Pro aminopeptidase I	111	29	pepP	gi 23465911	5	6
BL1350	14	Xaa-Pro aminopeptidase I	130	49	pepP	gi 23465911	25	25
BL1350	30	Xaa-Pro aminopeptidase I	208	51	pepP	gi 23465911	19	3
BL1357	595	RNA polymerase sigma-E factor	95	21	sigH	gi 23465918	9	2
BL1357	607	RNA polymerase sigma-E factor	105	21	sigH	gi 23465918	12	8
BL1357	429	RNA polymerase sigma-E factor	90	23	sigH	gi 23465918	5	12
BL1357	787	RNA polymerase sigma-E factor	56	28	sigH	gi 23465918	13	8
BL1357	765	RNA polymerase sigma-E factor	97	38	sigH	gi 23465918	7	6

BL1360	151	hypothetical protein in aldose epimerase family	97	27		gi 23465921	10	4
BL1360	165	hypothetical protein in aldose epimerase family	87	39		gi 23465921	7	6
BL1363	139	glyceraldehyde 3-phosphate dehydrogenase C	108	42	gap	gi 23465924	13	11
BL1363	123	glyceraldehyde 3-phosphate dehydrogenase C	181	54	gap	gi 23465924	18	9
BL1367	625	50S ribosomal protein L20	95	37	rplT	gi 23465929	8	5
BL1367	509	50S ribosomal protein L20	89	48	rplT	gi 23465929	14	10
BL1374	73	quinolinate synthetase	87	16	nadA	gi 23465936	5	11
BL1379	3	widely conserved protein similar to those annotated as GTP-binding elongation factor TypA/BipA	111	29		gi 23465941	12	5
BL1382	744	probable prephenate dehydrogenase	119	38	tyrA	gi 23465944	10	6
BL1386	203	DppA2	91	15	dppA2	gi 23465947	5	6
BL1386	888	DppA2	114	15	dppA2	gi 23465947	6	22
BL1386	582	DppA2	60	18	dppA2	gi 23465947	7	13
BL1386	156	DppA2	80	23	dppA2	gi 23465947	8	19
BL1386	229	DppA2	96	25	dppA2	gi 23465947	10	7
BL1386	28	DppA2	129	32	dppA2	gi 23465947	11	5
BL1386	213	DppA2	80	39	dppA2	gi 23465947	6	7
BL1386	11	DppA2	119	39	dppA2	gi 23465947	12	8
BL1392	169	narrowly conserved hypothetical protein	120	17		gi 23465952	10	4
BL1392	70	narrowly conserved hypothetical protein	68	36		gi 23465952	9	15
BL1394	697	conserved hypothetical protein with duf90	150	40		gi 23465954	13	6
BL1401	818	hypothetical protein in acetyl transferase family	78	34		gi 23465961	14	10
BL1410	561	hypothetical protein with C-terminal similarity	102	19		gi 23465970	11	5

BL1410	748	to cell (division) filamentation protein Fic hypothetical protein with C-terminal similarity	107	21		gi 23465970	11	4
BL1410	847	to cell (division) filamentation protein Fic hypothetical protein with C-terminal similarity	89	27		gi 23465970	9	31
BL1418	457	to cell (division) filamentation protein Fic hypothetical protein in sigma 54 modulation	96	20		gi 23465978	6	4
BL1419	854	protein / S30ea ribosomal protein family preprotein translocase SecA subunit	80	25	secA	gi 23465979	7	16
BL1422	204	anthranilate phosphoribosyltransferase 1	111	45	trpD	gi 23465980	14	23
BL1424	387	widely conserved hypothetical protein with acyl transferase domain	106	21		gi 23465982	7	3
BL1438	820	deoxyuridine 5'-triphosphate nucleotidohydrolase	60	65	dut	gi 23465996	6	36
BL1442	444	possible peptidyl-prolyl cis-trans isomerase	105	20		gi 23465998	5	3
BL1445	499	narrowly conserved hypothetical protein	97	15		gi 23466001	8	4
BL1445	860	narrowly conserved hypothetical protein	82	49		gi 23466001	8	21
BL1445	863	narrowly conserved hypothetical protein	97	49		gi 23466001	9	20
BL1455	245	hypothetical protein BL1455	163	31		gi 23466011	15	13
BL1457	753	metalloendopeptidase Gcp	174	56	gcp	gi 23466013	13	5
BL1458	629	probable integrase/recombinase	86	53		gi 23466014	6	4
BL1461	384	hypothetical protein BL1461	76	19		gi 23466017	6	2
BL1469	600	DNA topoisomerase III	98	17	topB	gi 23465707	14	9
BL1473	391	modification methylase very similar to EcoRII (cytosine-specific methyltransferase)	108	24		gi 23466029	5	3
BL1483	511	narrowly conserved hypothetical protein	96	27		gi 23466039	5	4
BL1499	609	isocitrate dehydrogenase [NADP]	97	15	icd1	gi 23466055	5	12
BL1500	147	GMP reductase	219	71		gi 23466056	21	10

BL1502	331	polypeptide deformylase	115	69	def	gi 23466058	12	14
BL1504	345	elongation factor TS	89	27	tsf	gi 23466060	9	4
BL1504	210	elongation factor TS	132	48	tsf	gi 23466060	13	19
BL1505	314	uridylyate kinase	171	72	pyrH	gi 23466061	18	14
BL1506	852	ribosome recycling factor	58	33	frr	gi 23466062	5	19
BL1512	320	deoxycytidine triphosphate deaminase	91	36		gi 23466067	5	13
BL1527	709	catabolic threonine dehydratase	143	35	tdcB	gi 23466080	15	16
BL1531	235	narrowly conserved hypothetical protein	124	67		gi 23466084	5	1
BL1535	390	JadJ	143	24	jadJ	gi 23466088	9	1
BL1548	768	hypothetical protein BL1548	107	36		gi 23466101	7	3
BL1549	633	50S ribosomal protein L10	98	27	rplJ	gi 23466102	13	4
BL1550	463	50S ribosomal protein L7/L12	126	38	rplL	gi 23466103	10	5
BL1551	482	hypothetical protein BL1551	118	32		gi 23466104	11	4
BL1551	483	hypothetical protein BL1551	156	45		gi 23466104	16	13
BL1556	853	possible acetyltransferase	102	38		gi 23466108	14	8
BL1558	476	groes	89	35	groES	gi 23466110	13	1
BL1558	477	groes	101	54	groES	gi 23466110	6	3
BL1561	360	UDP-N-acetylenolpyruvoylglucosamine reductase	99	32	murB	gi 23466113	11	13
BL1568	183	possible 2-hydroxyacid dehydrogenase	110	37		gi 23466120	11	9
BL1573	513	probable glycogen operon protein GlgX	96	28		gi 23466125	5	4
BL1592	479	50S ribosomal protein L5	75	21	rplE	gi 23466142	14	7
BL1601	301	adenylate kinase	114	61	adk	gi 23466151	9	5
BL1606	565	DNA-directed RNA polymerase alpha chain	127	28	rpoA	gi 23466156	5	9
BL1606	377	DNA-directed RNA polymerase alpha chain	137	70	rpoA	gi 23466156	11	7
BL1610	770	narrowly conserved hypothetical protein in transglutaminase family	72	35		gi 23466160	8	23

BL1615	725	N utilization substance homolog	84	31	nusA	gi 23466164	9	12
BL1615	726	N utilization substance homolog	190	56	nusA	gi 23466164	16	6
BL1623	240	probable ribose 5-phosphate isomerase	145	35		gi 23466172	10	2
BL1630	420	phosphoglucomutase	126	18	pgm	gi 23466179	8	15
BL1630	340	phosphoglucomutase	86	29	pgm	gi 23466179	7	1
BL1630	31	phosphoglucomutase	141	31	pgm	gi 23466179	11	2
BL1635	702	seryl-tRNA synthetase	117	24	serS	gi 23466184	11	6
BL1635	118	seryl-tRNA synthetase	179	50	serS	gi 23466184	17	9
BL1638	567	solute binding protein of ABC transporter for sugars	108	16		gi 23466186	5	7
BL1643	544	galactose-1-phosphate uridylyltransferase	98	15	galT2	gi 23466191	6	5
BL1644	275	UDP-glucose 4-epimerase	71	23	galE1	gi 23466192	6	6
BL1644	205	UDP-glucose 4-epimerase	66	39	galE1	gi 23466192	9	36
BL1644	177	UDP-glucose 4-epimerase	196	67	galE1	gi 23466192	16	10
BL1645	844	response regulator of two-component system	77	37		gi 23466220	9	25
BL1650	455	hypothetical protein BL1650	85	22		gi 23466198	12	4
BL1654	126	lysyl-tRNA synthetase 1	107	35	lysS	gi 23466201	17	17
BL1656	812	phosphoglycerate mutase	112	30	gpm	gi 23466203	18	7
BL1656	261	phosphoglycerate mutase	182	59	gpm	gi 23466203	12	6
BL1656	313	phosphoglycerate mutase	210	72	gpm	gi 23466203	16	7
BL1660	142	probable phosphoserine aminotransferase	217	60	serC	gi 23466207	17	2
BL1660	733	probable phosphoserine aminotransferase	255	78	serC	gi 23466207	20	7
BL1664	154	widely conserved protein in universal stress protein family	99	42		gi 23466211	9	6
BL1664a	857	hypothetical protein BL1664a	113	54		gi 23466212	14	14
BL1665	225	thymidylate synthase	78	31	thyA	gi 23466213	9	17
BL1665	804	thymidylate synthase	122	33	thyA	gi 23466213	17	13

BL1666	238	dihydrofolate reductase	80	22	dfrA	gi 23466214	7	7
BL1671	441	UDP-glucose 4-epimerase	91	19	galE2	gi 23466219	5	2
BL1671	443	UDP-glucose 4-epimerase	64	23	galE2	gi 23466219	11	4
BL1671	532	UDP-glucose 4-epimerase	97	24	galE2	gi 23466219	10	4
BL1671	504	UDP-glucose 4-epimerase	107	26	galE2	gi 23466219	6	27
BL1671	746	UDP-glucose 4-epimerase	195	45	galE2	gi 23466219	17	3
BL1672	701	possible cyclopropane-fatty-acyl-phospholipid synthase	202	55		gi 23466220	23	14
BL1673	375	possible lactaldehyde reductase	86	21	fucO	gi 23466221	7	2
BL1673	57	possible lactaldehyde reductase	153	58	fucO	gi 23466221	14	6
BL1682	269	ATP-dependent zinc metallopeptidase involved in cell division	109	16	ftsH	gi 23466230	10	2
BL1682	267	ATP-dependent zinc metallopeptidase involved in cell division	121	21	ftsH	gi 23466230	15	5
BL1682	182	ATP-dependent zinc metallopeptidase involved in cell division	84	23	ftsH	gi 23466230	14	22
BL1684	260	dihydropteroate synthase 1	147	54	folP	gi 23466232	14	6
BL1687	775	acyl-CoA thioesterase II	159	54	tesB	gi 23466235	17	11
BL1700	493	polypeptide deformylase	96	20	fms	gi 23466247	7	4
BL1700	423	polypeptide deformylase	96	28	fms	gi 23466247	10	5
BL1707	628	hypothetical protein BL1707	86	32		gi 23466253	7	4
BL1712	359	peptide chain release factor 1	144	51	prfA	gi 23466257	13	8
BL1714	158	solute binding protein of ABC transporter for branched-chain amino acids	143	52		gi 23466259	13	9
BL1717	754	ATP binding protein of ABC transporter for branched-chain amino acids	108	32		gi 23466262	8	2
BL1718	873	ATP binding protein of ABC transporter for	89	23		gi 23466263	5	1

		branched-chain amino acids						
BL1718	618	ATP binding protein of ABC transporter for branched-chain amino acids	115	31		gi 23466263	6	4
BL1723	295	probable oligoribonuclease	99	36	orn	gi 23466268	10	6
BL1728	19	prolyl-tRNA synthetase	242	45	proS	gi 23466273	27	8
BL1732	244	methionine aminopeptidase	78	37	map	gi 23466277	7	9
BL1734	759	widely conserved hypothetical protein	109	32		gi 23466279	9	3
BL1750	605	exonuclease VII, small subunit	132	89	xseB	gi 23466294	11	4
BL1755	96	possible glutamate--cysteine ligase	153	48		gi 23466299	18	16
BL1755	97	possible glutamate--cysteine ligase	150	50		gi 23466299	18	17
BL1786	44	S-adenosylmethionine synthetase	110	28	metK	gi 23466330	11	12
BL1786	358	S-adenosylmethionine synthetase	116	29	metK	gi 23466330	11	10
BL1787	885	probable DNA-directed RNA polymerase omega chain	98	28	rpoZ	gi 23466331	8	3
BL1794	79	probable Aaa-family ATPase	112	34		gi 23466338	12	14
BL1794	256	probable Aaa-family ATPase	87	36		gi 23466338	6	1
BL1795	676	hypothetical proteasome-associated protein	144	31		gi 23466339	12	5
BL1796	802	possible inositol monophosphatase	98	44		gi 23466340	13	20
BL1800	117	adenylosuccinate lyase	113	29	purB	gi 23466344	11	24
BL1800	684	adenylosuccinate lyase	156	44	purB	gi 23466344	11	4