

**SUPPLEMENTARY TABLE 1** Summary of *B. longum* NCC2705 proteins on the 2-D gels

Locus	NCBI GI identifier	spot No.	COG	Protein Description	Theor. mass	Theor. pI	Location*e	Gene	Exp.MW (kd )	Exp. pI	Abundance
BL0002 <sup>a1-1</sup>	gi 23464630 <sup>c</sup>	52	O	chaperone	56803	4.72	C	groEL	70.738	4.76	32,698 <sup>b-2</sup>
BL0002 <sup>a1-2</sup>	gi 23464630 <sup>c</sup>	193	O	chaperone	56860	4.72	C	groEL	41.074	4.91	32,600 <sup>b-2</sup>
BL0002 <sup>a1-3</sup>	gi 23464630	228	O	chaperone	56860	4.72	C	groEL	33.633	4.81	28,793 <sup>b-2</sup>
BL0002 <sup>a1-4</sup>	gi 23464630	233	O	chaperone	56860	4.72	C	groEL	32.849	4.86	29,076 <sup>b-2</sup>
BL0002 <sup>a1-5</sup>	gi 23464630	241	O	chaperone	56860	4.72	C	groEL	29.583	4.84	2,971 <sup>b-2</sup>
BL0002 <sup>a1-6</sup>	gi 23464630	290	O	chaperone	56860	4.72	C	groEL	27.125	4.94	123,974 <sup>b-2</sup>
BL0002 <sup>a1-7</sup>	gi 23464630	354	O	chaperone	56803	4.72	C	groEL	71.344	4.69	21,555 <sup>b-2</sup>
BL0002 <sup>a1-8</sup>	gi 23464630	355	O	chaperone	56803	4.72	C	groEL	70.14	4.72	68,548 <sup>b-2</sup>
BL0002 <sup>a1-9</sup>	gi 23464630	356	O	chaperone	56803	4.72	C	groEL	68.845	4.74	19,0268 <sup>b-2</sup>

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BL0002 <sup>a1-10</sup>	gi 23464630	357	O	chaperone	56803	4.72	C	groEL	57.094	4.81	26,967 <sup>b-2</sup>
BL0002 <sup>a1-11</sup>	gi 23464630	415	O	chaperone	56803	4.72	C	groEL	30.621	4.63	17,191 <sup>b-2</sup>
BL0002 <sup>a1-12</sup>	gi 23464630	416	O	chaperone	56803	4.72	C	groEL	32.696	4.78	29,486 <sup>b-2</sup>
BL0002 <sup>a1-13</sup>	gi 23464630	425	O	chaperone	56803	4.72	C	groEL	31.697	4.74	28,952 <sup>b-2</sup>
BL0002 <sup>a1-14</sup>	gi 23464630	427	O	chaperone	56860	4.72	C	groEL	27.467	4.68	35,471 <sup>b-2</sup>
BL0002 <sup>a1-15</sup>	gi 23464630	428	O	chaperone	56860	4.72	C	groEL	28.556	4.7	41,863 <sup>b-2</sup>
BL0002 <sup>a1-16</sup>	gi 23464630	430	O	chaperone	56860	4.72	C	groEL	26.2	4.62	21,585 <sup>b-2</sup>
BL0002 <sup>a1-17</sup>	gi 23464630	447	O	chaperone	56860	4.72	C	groEL	26.97	4.7	3,582 <sup>b-2</sup>
BL0002 <sup>a1-18</sup>	gi 23464630	453	O	chaperone	56861	4.72	C	groEL	26.492	4.83	17,763 <sup>b-2</sup>
BL0002 <sup>a1-19</sup>	gi 23464630	528	O	chaperone	56860	4.72	C	groEL	26.483	4.61	17,007 <sup>b-2</sup>
BL0002 <sup>a1-20</sup>	gi 23464630	559	O	chaperone	56860	4.72	C	groEL	25.294	4.54	27,538 <sup>b-2</sup>
BL0002 <sup>a1-21</sup>	gi 23464630	583	O	chaperone	56860	4.72	C	groEL	28.661	4.63	11,846 <sup>b-2</sup>
BL0002 <sup>a1-22</sup>	gi 23464630	586	O	chaperone	56860	4.72	C	groEL	28.271	4.55	111,399 <sup>b-2</sup>

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BL0002 <sup>a1-23</sup>	gi 23464630	589	O	chaperone	56860	4.72	C	groEL	24.847	4.59	21,541 <sup>b-2</sup>
BL0002 <sup>a1-24</sup>	gi 23464630	591	O	chaperone	56860	4.72	C	groEL	22.605	4.53	43,672 <sup>b-2</sup>
BL0003	gi 23464631	394	S	hypothetical protein BL0003	10425	4.81	E		33.158	4.67	24,679
BL0005	gi 23464633	414	T	response regulator of two-component system	27203	4.69	C		30.454	4.73	25,544
BL0008	gi 23464636	336	++	narrowly conserved hypothetical protein	43374	3.97	C		18.13	5.13	8,736
BL0009	gi 23464637	757	T	hypothetical protein BL0009	34522	5.39	C		36.397	5.76	26,520
BL0017	gi 23464645	84	J	histidyl-tRNA synthetase	50363	5.01	C	hisS	59.717	5.09	11,308
BL0021	gi 23464649	800	E	ATP-binding protein of ABC transporter for glutamate	30005	6.09	CM	gluA	30.59	6.34	8,145
BL0022	gi 23464650	874	E	glutamate-binding protein of AB transporter system	28671	4.86	U	gluB	18.371	4.88	13,128
BL0031	gi 23464659	280	T	histidine kinase sensor of two-component system	61968	5.12	CM		25.084	4.87	15,160
BL0033 <sup>a2-1</sup>	gi 23464661 <sup>c</sup>	381	G	probable solute binding protein of ABC transporter system possibly for sugars	34668	4.72	U		38.921	4.59	49,913
BL0033 <sup>a2-2</sup>	gi 23464661 <sup>c</sup>	571	G	probable solute binding protein of ABC transporter system possibly	34782	4.72	U		38.038	4.57	5,309

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BL0034	gi 23464662	690	G	ATP binding protein of ABC transporter	55857	5.82	CM		70.329	6.29	11,585
BL0038	gi 23464666	656	E	conserved protein with hydroxyacid dehydrogenase catalytic domain	32598	5.78	C		32.587	6.7	10,557
BL0039	gi 23464667	342	++	hypothetical protein BL0039	19072	6.73	C		18.594	5.3	25,893
BL0046	gi 23464674	258	C	narrowly conserved hypothetical protein	28848	5.08	C		29.899	5.18	69,292
BL0049	gi 23464677	870	P	ATP binding protein of ABC transporter	29774	6.16	CM		30.524	6.87	8,185
BL0053	gi 23464681	168	D	hypothetical protein with duf059 and 4Fe-4S iron sulfur cluster binding domain	39265	4.9	C	mrp	43.118	4.94	3,745
BL0059	gi 23464686	134	++	narrowly conserved hypothetical protein	40822	5.06	C		48.558	5.17	23,783
BL0065 <sup>a3-1</sup>	gi 23464692	326	J	elongation factor P	20641	5.05	C	efp	21.043	5.11	117,174 <sup>b-38</sup>
BL0065 <sup>a3-2</sup>	gi 23464692	620	J	elongation factor P	20698	5.05	C	efp	21.75	5.11	45,207 <sup>b-38</sup>
BL0069	gi 23464696	826	F	similar to orotidine 5'-phosphate decarboxylase	32734	5.72	C		29.003	6.21	22,168

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BL0077	gi 23464704	409	E	probable solute-binding protein for glutamate/aspartate ABC transporter system	32183	4.88	U		33.474	4.7	51,384
BL0079 <sup>a4-1</sup>	gi 23464706	613	O	hypothetical protein with homology to glutaredoxin-like protein	9219	4.55	U		17.342	4.53	25,828
BL0079 <sup>a4-2</sup>	gi 23464706	878	O	hypothetical protein with homology to glutaredoxin-like protein	9219	4.55	U		17.306	4.42	13,828
BL0082	gi 23464708	8	++	hypothetical protein BL0082	20264	9.65	C		77.232	4.74	9,314
BL0097	gi 23464723	141	I	1-deoxy-D-xylulose 5-phosphate reductoisomerase	41987	5.2	C	ispC	43.98	5.34	18,442
BL0098 <sup>a5-1</sup>	gi 23464724	198	I	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase 1	43050	5.76	C	ispG	36.851	4.94	21,152
BL0098 <sup>a5-2</sup>	gi 23464724	500	I	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase 1	43050	6.07	C	ispG	40.213	4.42	13,433
BL0098 <sup>a5-3</sup>	gi 23464724	632	I	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase 1	43050	5.76	C	ispG	17.003	4.97	21,074
BL0116	gi 23464742	704	J	glycyl-tRNA synthetase	56216	5.42	C	glyS	65.183	5.73	15,617
BL0118 <sup>a6-1</sup>	gi 23464744	481	D	cell division protein FtsZ	41524	4.35	C	ftsZ	57.644	4.32	27,355
BL0118 <sup>a6-2</sup>	gi 23464744	562	D	cell division protein FtsZ	41524	4.35	C	ftsZ	51.109	4.46	10,405
BL0119	gi 23464745	324	S	hypothetical protein BL0119	17046	4.82	U		21.373	5.07	33,352

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BL0121 <sup>a7-1</sup>	gi 23464747	351	D	hypothetical protein BL0121	50596	4.66	E		64.601	4.59	27,311 <sup>b-40</sup>
BL0121 <sup>a7-2</sup>	gi 23464747	352	D	hypothetical protein BL0121	50596	4.66	E		64.601	4.61	41,567 <sup>b-40</sup>
BL0121 <sup>a7-3</sup>	gi 23464747	353	D	hypothetical protein BL0121	50596	4.66	E		63.437	4.64	35,944 <sup>b-40</sup>
BL0121 <sup>a7-4</sup>	gi 23464747	553	D	hypothetical protein BL0121	50596	4.66	E		24.931	4.48	42,072 <sup>b-40</sup>
BL0128	gi 23464754	81	++	narrowly conserved hypothetical protein	16527	8.43	C		65.357	5.09	11,899
BL0140 <sup>a8-1</sup>	gi 23464760	315	G	hypothetical protein in PgaM phosphoglycerate mutase family	23624	5.44	C		26.508	5.67	5,868
BL0140 <sup>a8-2</sup>	gi 23464760	806	G	hypothetical protein in PgaM phosphoglycerate mutase family	23738	5.44	C		28.035	5.67	30,146
BL0141	gi 23464761	369	G	possible solute binding protein of ABC transporter	48605	4.68	U		52.22	4.59	38,405
BL0159	gi 23464775	27	++	DNA-damage-inducible protein of Escherichia coli	21427	8.83	C	dinD	80.262	4.89	2,481
BL0170	gi 23464786	89	J	methionyl-tRNA synthetase	69047	5.08	C	metG	90.758	5.21	1,623
BL0174	gi 23464790	548	S	narrowly conserved hypothetical protein	82166	4.97	C		25.492	4.45	27,622
BL0175 <sup>a9-1</sup>	gi 23464791	179	K	probable AraC/XylS-type transcriptional regulator	36946	6.07	C		40.136	5.23	9,383
BL0175 <sup>a9-2</sup>	gi 23464791	506	K	probable AraC/XylS-type transcriptional regulator	36946	6.07	C		32.857	4.48	20,207

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BL0197	gi 23464812	372	G	possible ATP binding protein of ABC transporter	26079	5.97	CM		53.862	4.64	20,188
BL0204	gi 23464818	297	L	hypothetical protein BL0204	14851	11.93	C		26.893	5.1	15,819
BL0209	gi 23464823	436	M	hypothetical protein with similarity to LicD required for phosphorylcholine incorporation in teicho	41567	4.74	C		25.302	4.65	26,272
BL0216	gi 23464829	343	R	narrowly conserved hypothetical protein	74391	5.78	U		18.291	5.3	22,813
BL0227	gi 23464834	227	M	glucose-1-phosphate thymidyltransferase	33377	5.2	C	rmlA	31.293	5.52	19,973
BL0228	gi 23464835	110	M	possible fused dTDP-4-keto-L-rhamnose reductase and dTDP-4-keto-6- deoxyglucose-3,5-epimerase enzyme	52894	5.19	C		57.642	5.34	25,662
BL0229	gi 23464836	793	M	dTDP-glucose 4,6-dehydratase enzyme involved in rhamnose biosynthesis	39535	5.88	C	rmlB1	39.308	6.63	10,962
BL0239	gi 23464845	502	L	probable integrase/recombinase	43548	9.82	C		40.759	4.44	11,065
BL0255	gi 23464858	772	R	dehydrogenase or reductase protein	31825	5.51	C		32.72	5.97	31,375
BL0256	gi 23464859	7	++	hypothetical protein BL0256	14223	10.2	U		16.325	6.38	43,095

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BL0272	gi 23464874	515	G	L-arabinose isomerase	56174	4.99	C	araA	22.064	4.23	22,558
BL0273	gi 23464875	815	G	L-ribulose-5-phosphate 4-epimerase	25172	5.42	C	araD	26.904	5.83	35,933
BL0274	gi 23464876	80	G	probable sugar kinase	59005	5.02	C		68.845	5.09	14,642
BL0279 <sup>a10-1</sup>	gi 23464881	35	G	glucose-6-phosphate isomerase	62959	4.85	C	gpi	66.791	4.87	13,308
BL0279 <sup>a10-2</sup>	gi 23464881	190	G	glucose-6-phosphate isomerase	62959	4.85	C	gpi	40.19	4.86	6,579
BL0282	gi 23464883	788	V	FemAB-like protein possibly involved in interpeptide bridge formation in peptidoglycan	47700	5.93	C		44.394	6.58	41,043
BL0285	gi 23464886	250	F	widely conserved hypothetical protein in Ham1 family	26459	4.94	C		31.878	5.03	57,030
BL0287	gi 23464888	98	H	hypothetical protein BL0287	49004	5.23	U		52.705	5.1	28,105
BL0290	gi 23464891	795	C	possible reductase	37447	5.8	U		38.216	6.32	36,072
BL0291	gi 23464892	858	H	phosphopantetheine adenylyltransferase	18054	5.56	C	coaD	20.305	5.86	34,533
BL0292 <sup>a11-1</sup>	gi 23464893	492	D	hypothetical protein BL0292	31977	4.57	U		40.698	4.5	27,006
BL0292 <sup>a11-2</sup>	gi 23464893	503	D	hypothetical protein BL0292	31977	4.57	U		40.213	4.45	8,084

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BL0295	gi 23464896	319	K	ribonuclease III	29958	5.91	C	rncS	25.686	5.57	32,354
BL0297	gi 23464898	322	E	acetolactate synthase small subunit	19960	6.86	C	ilvN	24.652	5.79	7,009
BL0309	gi 23464910	252	C	possible oxidoreductase of the aldo/keto reductase family	31939	5.02	C		31.697	5.07	52,153
BL0312	gi 23464913	251	P	probable ATP-binding protein of ABC transporter system for phosphate	28990	4.94	CM	pstB	29.646	5.01	79,471
BL0319	gi 23464920	710	E	phospho-2-keto-3-deoxyheptonate aldolase	45025	5.51	C	aroG	54.102	5.94	14,804
BL0320 <sup>a12-1</sup>	gi 23464921	146	E	phospho-2-dehydro-3-deoxyheptonate aldolase, phe-sensitive	41387	5.36	C	aroG2	51.965	5.7	40,479
BL0320 <sup>a12-2</sup>	gi 23464921	737	E	phospho-2-dehydro-3-deoxyheptonate aldolase, phe-sensitive	41729	5.36	C	aroG2	46.031	5.68	4,582
BL0320 <sup>a12-3</sup>	gi 23464921	738	E	phospho-2-dehydro-3-deoxyheptonate aldolase, phe-sensitive	41729	5.36	C	aroG2	45.709	5.7	4,136
BL0320 <sup>a12-4</sup>	gi 23464921	777	E	phospho-2-dehydro-3-deoxyheptonate aldolase, phe-sensitive	41729	5.36	C	aroG2	30.921	5.98	17,490
BL0322 <sup>a13-1</sup>	gi 23464923	348	D	hypothetical protein BL0322	56799	4.62	E		77.908	4.59	41,941 <sup>b-28</sup>
BL0322 <sup>a13-2</sup>	gi 23464923	349	D	hypothetical protein BL0322	56799	4.62	E		77.097	4.61	120,651 <sup>b-28</sup>
BL0322 <sup>a13-3</sup>	gi 23464923	489	D	hypothetical protein BL0322	56799	4.62	E		45.991	4.46	7,463 <sup>b-28</sup>

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BL0322 <sup>a13-4</sup>	gi 23464923	510	D	hypothetical protein BL0322	56799	4.62	E		30.216	4.27	25,161 <sup>b-28</sup>
BL0327	gi 23464928	211	J	tRNA (guanine-N1)-methyltransferase	27388	5.27	C	trmD	35.178	5.15	13,888
BL0331 <sup>a14-1</sup>	gi 23464932	781	G	probable PfkB family carbohydrate (sugar) kinase	36120	5.71	C		38.509	6.19	15,429
BL0331 <sup>a14-2</sup>	gi 23464932	794	G	probable PfkB family carbohydrate (sugar) kinase	36120	5.71	C		36.987	6.3	12,964
BL0337	gi 23464937	265	K	hypothetical protein possibly in TetR transcriptional regulator family	27422	5.16	U		29	5.23	29,065
BL0339	gi 23464939	581	M	hypothetical protein in upf0003	27985	5.87	CM		31.142	4.63	21,626
BL0345	gi 23464945	371	M	D-alanine--D-alanine ligase	46016	4.88	C	ddlA	54.284	4.62	20,993
BL0346 <sup>a15-1</sup>	gi 23464946	201	C	glycerol-3-phosphate dehydrogenase [NAD(P)+]	34880	5.09	U		36.021	5.02	10,757
BL0346 <sup>a15-2</sup>	gi 23464946	525	C	glycerol-3-phosphate dehydrogenase [NAD(P)+]	34880	5.09	U		30.851	4.6	21,195
BL0348	gi 23464948	338	J	hypothetical 14.5 kDa translational inhibitor protein	13430	4.9	C	psp1	17.284	4.88	41,688
BL0350	gi 23464950	523	O	hypothetical protein with marginal similarity to thioredoxin	35227	4.6	C		34.915	4.53	20,452
BL0352	gi 23464951	199	++	hypothetical protein BL0352	36634	5.38	U		34.833	4.91	22,828

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BL0356	gi 23464955	872	C	ATP synthase epsilon chain	10383	4.76	U	atpC	16.695	4.63	15,265
BL0357 <sup>a16-1</sup>	gi 23464956	29	C	ATP synthase beta chain	53277	4.77	C	atpD	66.679	4.81	206,305 <sup>b-4</sup>
BL0357 <sup>a16-2</sup>	gi 23464956	53	C	ATP synthase beta chain	53277	4.77	C	atpD	72.326	4.78	34,651 <sup>b-4</sup>
BL0357 <sup>a16-3</sup>	gi 23464956	54	C	ATP synthase beta chain	53277	4.77	C	atpD	68.151	4.78	39,130 <sup>b-4</sup>
BL0357 <sup>a16-4</sup>	gi 23464956	263	C	ATP synthase beta chain	53448	4.77	C	atpD	29.427	5.23	41,217 <sup>b-4</sup>
BL0357 <sup>a16-5</sup>	gi 23464956	363	C	ATP synthase beta chain	53277	4.77	C	atpD	46.591	4.8	11,370 <sup>b-4</sup>
BL0357 <sup>a16-6</sup>	gi 23464956	389	C	ATP synthase beta chain	53448	4.77	C	atpD	30.96	4.59	8,569 <sup>b-4</sup>
BL0357 <sup>a16-7</sup>	gi 23464956	408	C	ATP synthase beta chain	53448	4.77	C	atpD	38.613	4.75	10,140 <sup>b-4</sup>
BL0357 <sup>a16-8</sup>	gi 23464956	411	C	ATP synthase beta chain	53448	4.77	C	atpD	32.431	4.69	30,227 <sup>b-4</sup>
BL0357 <sup>a16-9</sup>	gi 23464956	431	C	ATP synthase beta chain	53448	4.77	C	atpD	25.391	4.59	21,084 <sup>b-4</sup>
BL0357 <sup>a16-10</sup>	gi 23464956	433	C	ATP synthase beta chain	53448	4.77	C	atpD	24.518	4.59	17,573 <sup>b-4</sup>
BL0357 <sup>a16-11</sup>	gi 23464956	529	C	ATP synthase beta chain	53448	4.77	C	atpD	29.447	4.54	98,797 <sup>b-4</sup>
BL0357 <sup>a16-12</sup>	gi 23464956	533	C	ATP synthase beta chain	53448	4.77	C	atpD	29.158	4.52	51,927 <sup>b-4</sup>

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BL0357 <sup>a16-13</sup>	gi 23464956	574	C	ATP synthase beta chain	53448	4.77	C	atpD	33.232	4.56	17,662 <sup>b-4</sup>
BL0357 <sup>a16-14</sup>	gi 23464956	575	C	ATP synthase beta chain	53448	4.77	C	atpD	31.936	4.54	20,319 <sup>b-4</sup>
BL0357 <sup>a16-15</sup>	gi 23464956	577	C	ATP synthase beta chain	53448	4.77	C	atpD	33.487	4.59	25,001 <sup>b-4</sup>
BL0358	gi 23464957	762	C	ATP synthase gamma chain	33902	5.65	C	atpG	38.119	5.98	24,837
BL0359 <sup>a17-1</sup>	gi 23464958	181	C	ATP synthase alpha chain	58602	4.99	C	atpA	41.7	5.29	11,531 <sup>b-11</sup>
BL0359 <sup>a17-2</sup>	gi 23464958	185	C	ATP synthase alpha chain	58602	4.99	C	atpA	37.183	5.37	13,804 <sup>b-11</sup>
BL0359 <sup>a17-3</sup>	gi 23464958	207	C	ATP synthase alpha chain	58602	4.99	C	atpA	41.187	5.15	15,974 <sup>b-11</sup>
BL0359 <sup>a17-4</sup>	gi 23464958	208	C	ATP synthase alpha chain	58602	4.99	C	atpA	39.813	5.15	4,713 <sup>b-11</sup>
BL0359 <sup>a17-5</sup>	gi 23464958	246	C	ATP synthase alpha chain	58602	4.99	C	atpA	29.458	4.9	33,734 <sup>b-11</sup>
BL0359 <sup>a17-6</sup>	gi 23464958	259	C	ATP synthase alpha chain	58602	4.99	C	atpA	30.256	5.24	15,460 <sup>b-11</sup>
BL0359 <sup>a17-7</sup>	gi 23464958	271	C	ATP synthase alpha chain	58602	4.7	C	atpA	28.297	4.89	21,757 <sup>b-11</sup>
BL0359 <sup>a17-8</sup>	gi 23464958	274	C	ATP synthase alpha chain	58602	4.99	C	atpA	27.441	4.85	43,932 <sup>b-11</sup>
BL0359 <sup>a17-9</sup>	gi 23464958	289	C	ATP synthase alpha chain	58602	4.99	C	atpA	24.277	4.93	19,814 <sup>b-11</sup>

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BL0359 <sup>a17-10</sup>	gi 23464958	450	C	ATP synthase alpha chain	58602	4.99	C	atpA	26.248	4.77	37,725 <sup>b-11</sup>
BL0359 <sup>a17-11</sup>	gi 23464958	451	C	ATP synthase alpha chain	58602	4.99	C	atpA	26.97	4.78	44,735 <sup>b-11</sup>
BL0359 <sup>a17-12</sup>	gi 23464958	454	C	ATP synthase alpha chain	58605	4.99	C	atpA	25.939	4.83	15,362 <sup>b-11</sup>
BL0359 <sup>a17-13</sup>	gi 23464958	592	C	ATP synthase alpha chain	58602	5.99	C	atpA	22.575	4.54	62,871 <sup>b-11</sup>
BL0359 <sup>a17-14</sup>	gi 23464958	742	C	ATP synthase alpha chain	58602	4.99	C	atpA	43.667	5.72	17,409 <sup>b-11</sup>
BL0369	gi 23464967	602	++	hypothetical protein BL0369	18117	12.14	U		17.856	4.45	34,158
BL0389 <sup>a18-1</sup>	gi 23464986	597	C	inorganic pyrophosphatase	18473	4.41	C	ppa	19.363	4.4	391,954 <sup>b-8</sup>
BL0389 <sup>a18-2</sup>	gi 23464986	599	C	inorganic pyrophosphatase	18473	4.41	C	ppa	19.337	4.36	42,744 <sup>b-8</sup>
BL0397 <sup>a19-1</sup>	gi 23464994	339	E	narrowly conserved hypothetical protein with mutase domain	14140	5.17	C		16.915	5.22	14,571
BL0397 <sup>a19-2</sup>	gi 23464994	623	E	narrowly conserved hypothetical protein with mutase domain	14140	5.17	C		17.543	5.17	16,186
BL0401 <sup>a20-1</sup>	gi 23464999	41	J	possible acetyltransferase	38322	5.03	C		58.667	4.95	52,264
BL0401 <sup>a20-2</sup>	gi 23464999	43	J	possible acetyltransferase	38322	5.03	C		55.929	5.02	17,554
BL0401 <sup>a20-3</sup>	gi 23464999	48	J	possible acetyltransferase	38322	5.03	C		51.519	5.04	48,371

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BL0402	gi 23465000	685	J	glutamyl-tRNA(Gln) amidotransferase subunit B	55137	5.44	C	gatB	63.845	5.83	25,355
BL0403	gi 23465001	883	J	glutamyl-tRNA(Gln) amidotransferase subunit A	54136	4.96	U	gatA	63.646	4.95	30,216
BL0412	gi 23465010	843	G	histidine-containing phosphocarrier protein (Hpr protein) of Pts transport system	9394	5.02	C	ptsH	25.823	6.38	18,470
BL0416 <sup>a21-1</sup>	gi 23465014	622	J	30S ribosomal protein S6	11167	5.22	C	rpsF	16.493	5.34	156,606 <sup>b-32</sup>
BL0416 <sup>a21-2</sup>	gi 23465014	876	J	30S ribosomal protein S6	11167	5.22	C	rpsF	16.601	5.06	19,408 <sup>b-32</sup>
BL0419	gi 23465017	226	R	hypothetical protein in upf0001	31168	5.33	C		30.074	5.52	13,954
BL0426	gi 23465024	663	K	LacI-type transcriptional regulator	36972	6.01	C		33.489	6.74	1,356
BL0428	gi 23465026	604	S	hypothetical protein BL0428	11141	5.26	U		17.776	4.56	45,370
BL0429	gi 23465027	248	R	possible cobyric acid synthase CobQ	27693	4.95	C		28.94	4.94	39,506
BL0431	gi 23465029	95	L	replicative DNA helicase	55887	5.19	C	dnaB	57.55	5.14	4,358
BL0433	gi 23465031	566	O	protein-pII; uridylyltransferase	67827	5.71	C	glnD	45.991	4.6	10,099
BL0434	gi 23465032	877	E	nitrogen regulatory protein N-II	11716	5.52	U	glnB	16.409	5.14	28,054

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BL0441 <sup>a22-1</sup>	gi 23465039	370	G	narrowly conserved hypothetical protein	37499	4.56	C		52.624	4.6	31,881
BL0441 <sup>a22-2</sup>	gi 23465039	619	G	narrowly conserved hypothetical protein	37670	4.56	C		19.27	5.14	23,320
BL0444 <sup>a23-1</sup>	gi 23465041	108	G	6-phosphogluconate dehydrogenase, decarboxylating II	52282	5.16	C	gnt	57.735	5.22	14,226
BL0444 <sup>a23-2</sup>	gi 23465041	109	G	6-phosphogluconate dehydrogenase, decarboxylating II	52282	5.16	C	gnt	58.198	5.29	11,495
BL0444 <sup>a23-3</sup>	gi 23465041	111	G	6-phosphogluconate dehydrogenase, decarboxylating II	52282	5.16	C	gnt	57.276	5.31	9,667
BL0444 <sup>a23-4</sup>	gi 23465041	305	G	6-phosphogluconate dehydrogenase, decarboxylating II	52511	5.16	C	gnt	24.139	5.15	7,627
BL0444 <sup>a23-5</sup>	gi 23465041	311	G	6-phosphogluconate dehydrogenase, decarboxylating II	52282	5.16	C	gnt	23.336	5.3	7,836
BL0444 <sup>a23-6</sup>	gi 23465041	318	G	6-phosphogluconate dehydrogenase, decarboxylating II	52282	5.16	C	gnt	26.879	5.58	27,588
BL0469	gi 23465061	92	J	glutamyl-tRNA synthetase	56646	5.04	C	gltX	64.175	5.15	8,976
BL0472	gi 23465064	774	G	widely conserved hypothetical protein	33145	5.36	U		31.055	5.88	31,326
BL0478 <sup>a24-1</sup>	gi 23465070	76	F	formate--tetrahydrofolate ligase	53994	5.04	C	fhs	61.994	5.07	4,730
BL0478 <sup>a24-2</sup>	gi 23465070	85	F	formate--tetrahydrofolate ligase	53994	5.04	C	fhs	62.198	5.13	15,104
BL0492 <sup>a25-1</sup>	gi 23465082	750	E	aspartate-semialdehyde dehydrogenase	40442	5.76	C	asd	41.928	6.17	17,199

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BL0492 <sup>a25-2</sup>	gi 23465082	785	E	aspartate-semialdehyde dehydrogenase	40442	5.76	C	asd	41.537	6.31	22,391
BL0493	gi 23465083	596	E	aspartokinase	18650	4.55	U	askB	20.827	4.48	33,194
BL0514	gi 23465104	176	++	possible acyl protein synthase/acyl-CoA reductase-like protein	42667	5.12	C		45.651	5.2	5,727
BL0519 <sup>a26-1</sup>	gi 23465108	534	O	GrpE protein	23687	4.54	C	grpE	26.889	4.51	31,879
BL0519 <sup>a26-2</sup>	gi 23465108	551	O	GrpE protein	23687	4.54	C	grpE	26.76	4.48	20,848
BL0520 <sup>a27-1</sup>	gi 23465109	197	O	DnaK protein	67073	4.72	C	dnaK	38.818	4.96	9,506 <sup>b-26</sup>
BL0520 <sup>a27-2</sup>	gi 23465109	346	O	DnaK protein	66902	4.72	C	dnaK	80.971	4.7	27,987 <sup>b-26</sup>
BL0520 <sup>a27-3</sup>	gi 23465109	347	O	DnaK protein	66902	4.72	C	dnaK	79.98	4.72	73,694 <sup>b-26</sup>
BL0520 <sup>a27-4</sup>	gi 23465109	378	O	DnaK protein	66902	4.72	C	dnaK	42.876	4.58	22,697 <sup>b-26</sup>
BL0520 <sup>a27-5</sup>	gi 23465109	522	O	DnaK protein	67073	4.72	C	dnaK	34.321	4.54	45,581 <sup>b-26</sup>
BL0520 <sup>a27-6</sup>	gi 23465109	539	O	DnaK protein	67073	4.72	C	dnaK	27.781	4.44	26,891 <sup>b-26</sup>
BL0520 <sup>a27-7</sup>	gi 23465109	569	O	DnaK protein	67073	4.72	C	dnaK	40.033	4.57	9,519 <sup>b-26</sup>
BL0523 <sup>a28-1</sup>	gi 23465112	798	G	possible xylosidase or glucosidase	77430	4.94	C		36.442	6.39	12,572

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BL0523 <sup>a28-2</sup>	gi 23465112	851	G	possible xylosidase or glucosidase	77430	4.94	C		23.441	6.9	26,156
BL0530	gi 23465118	178	E	ketol-acid reductoisomerase	39049	5.1	C	ilvC1	38.21	5.21	5,708
BL0531 <sup>a29-1</sup>	gi 23465119	145	E	ketol-acid reductoisomerase	38527	5.3	C	ilvC2	45.138	5.57	3,612 <sup>b-31</sup>
BL0531 <sup>a29-2</sup>	gi 23465119	188	E	ketol-acid reductoisomerase	38698	5.3	C	ilvC2	34.919	5.35	15,589 <sup>b-31</sup>
BL0531 <sup>a29-3</sup>	gi 23465119	189	E	ketol-acid reductoisomerase	38698	5.3	C	ilvC2	35.011	5.62	136,892 <sup>b-31</sup>
BL0531 <sup>a29-4</sup>	gi 23465119	219	E	ketol-acid reductoisomerase	38698	5.3	C	ilvC2	34.886	5.55	9,875 <sup>b-31</sup>
BL0531 <sup>a29-5</sup>	gi 23465119	756	E	ketol-acid reductoisomerase	38698	5.3	C	ilvC2	35.606	5.73	15,353 <sup>b-31</sup>
BL0550	gi 23465135	148	G	fructose-bisphosphate aldolase	38325	5.31	C	fba	40.989	5.65	43,528
BL0552	gi 23465137	37	E	probable ferredoxin/ferredoxin-NADP reductase	52996	4.83	C	fprA	64.175	4.9	1,852
BL0576	gi 23465161	445	O	probable Hsp20-family heat shock chaperone	19039	4.54	U**		20.046	4.57	45,053
BL0583	gi 23465168	538	T	hypothetical protein with FHA domain	25423	4.46	C		26.608	4.45	88,963
BL0597 <sup>a30-1</sup>	gi 23465182	166	G	glycogen phosphorylase	94676	5.34	U	glgP	44.231	4.92	5,774
BL0597 <sup>a30-2</sup>	gi 23465182	172	G	glycogen phosphorylase	94676	5.34	U	glgP	45.453	4.97	9,478

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BL0597 <sup>a30-3</sup>	gi 23465182	202	G	glycogen phosphorylase	94676	5.34	U	glgP	43.669	5.1	20,146
BL0600 <sup>a31-1</sup>	gi 23465185	102	J	tryptophanyl-tRNA synthetase	39941	5.76	C	trpS	73.959	5.32	5,996
BL0600 <sup>a31-2</sup>	gi 23465185	784	J	tryptophanyl-tRNA synthetase	40055	5.76	C	trpS	42.267	6.25	6,169
BL0603	gi 23465188	403	S	narrowly conserved hypothetical protein	69016	5.89	CM		41.989	4.77	33,740
BL0614 <sup>a32-1</sup>	gi 23465198	77	O	thioredoxin reductase-like protein	66191	4.96	C		61.893	5.1	8,772
BL0614 <sup>a32-2</sup>	gi 23465198	214	O	thioredoxin reductase-like protein	66590	4.96	C		33.674	5.3	15,345
BL0615 <sup>a33-1</sup>	gi 23465199 <sup>c</sup>	593	O	alkyl hydroperoxide reductase C22 protein	21426	4.44	C	ahpC	21.598	4.43	200,042 <sup>b-25</sup>
BL0615 <sup>a33-2</sup>	gi 23465199	608	O	alkyl hydroperoxide reductase C22 protein	21426	4.44	C	ahpC	18.153	4.4	15,994 <sup>b-25</sup>
BL0618	gi 23465202	446	P	hypothetical protein in DPS family	17765	4.57	C		20.111	4.65	279,793 <sup>b-20</sup>
BL0630 <sup>a34-1</sup>	gi 23465213	113	E	NADP-specific glutamate dehydrogenase	48747	5.25	C	gdhA	54.796	5.3	31,320
BL0630 <sup>a34-2</sup>	gi 23465213	432	E	NADP-specific glutamate dehydrogenase	48918	5.25	C	gdhA	26.665	4.56	16,820
BL0638 <sup>a35-1</sup>	gi 23465221	272	L	DNA polymerase III, beta chain	40999	4.54	C	dnaN	27.467	4.89	39,785
BL0638 <sup>a35-2</sup>	gi 23465221	374	L	DNA polymerase III, beta chain	40942	4.54	C	dnaN	50.113	4.6	36,406

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				narrowly conserved hypothetical protein with possible ssDNA								
BL0645	gi 23465228	440	R	binding domain	20124	4.56	C	jag	23.775	4.6	31,233	
BL0646	gi 23465229	527	M	possible glucose inhibited division protein B	24319	8.48	C	gidB	26.533	4.59	38,377	
BL0667	gi 23465249	329	++	hypothetical protein BL0667	8856	9.88	U		18.49	5.09	26,861	
BL0673 <sup>a36-1</sup>	gi 23465255	714	G	ATP binding protein of ABC transporter for sugars	40759	5.85	CM	msiK	49.654	6.15	11,608	
BL0673 <sup>a36-2</sup>	gi 23465255	716	G	ATP binding protein of ABC transporter for sugars	40759	5.85	CM	msiK	52.119	6.35	98,834	
BL0673 <sup>a36-3</sup>	gi 23465255	727	G	ATP binding protein of ABC transporter for sugars	40759	5.85	CM	msiK	52.979	5.99	3,446	
				protein probably involved in xylan degradation; possible xylan								
BL0682	gi 23465264	293	I	esterase	32931	5.34	C		27.021	5.05	40,022	
BL0685	gi 23465266	316	E	HisF cyclase	27534	5.34	C	hisF	25.985	5.52	15,928	
BL0686	gi 23465267	865	E	probable phosphoribosyl-AMP cyclohydrolase	14766	5.9	C	hisI	18.511	6.48	20,618	
BL0687	gi 23465268	39	E	anthranilate synthase component I	56644	4.94	C	trpE	66.568	4.96	5,599	
BL0690	gi 23465271	303	R	hypothetical protein with glucose/ribitol dehydrogenase family	25521	5.03	U		24.158	5.13	49,952	

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BL0699	gi 23465279	868	S	hypothetical myosin-like protein with unknown function	131144	5.09	C		38.216	6.74	12,770
BL0700	gi 23465280	898	S	hypothetical protein BL0700	45135	6	C		82.558	5.06	50,882
BL0707 <sup>a37-1</sup>	gi 23465287	60	G	phosphoglycerate kinase	46545	5.22	C	pgk	52.95	4.86	8,062 <sup>b-39</sup>
BL0707 <sup>a37-2</sup>	gi 23465287	62	G	phosphoglycerate kinase	46545	5.22	C	pgk	49.142	4.91	5,030 <sup>b-39</sup>
BL0707 <sup>a37-3</sup>	gi 23465287	546	G	phosphoglycerate kinase	46659	5.22	C	pgk	22.757	4.37	30,054 <sup>b-39</sup>
BL0707 <sup>a37-4</sup>	gi 23465287	554	G	phosphoglycerate kinase	46659	5.22	C	pgk	23.301	4.46	41,909 <sup>b-39</sup>
BL0707 <sup>a37-5</sup>	gi 23465287	555	G	phosphoglycerate kinase	46659	5.22	C	pgk	23.733	4.48	27,930 <sup>b-39</sup>
BL0707 <sup>a37-6</sup>	gi 23465287	560	G	phosphoglycerate kinase	46659	5.22	C	pgk	25.142	4.5	35,821 <sup>b-39</sup>
BL0707 <sup>a37-7</sup>	gi 23465287	887	G	phosphoglycerate kinase	46659	5.22	C	pgk	51.347	4.91	6,850 <sup>b-39</sup>
BL0708	gi 23465288	832	G	triosephosphate isomerase	29296	5.71	C	tpi	27.339	6.24	26,053
BL0710	gi 23465290	195	C	L-lactate dehydrogenase	34078	4.92	C	ldh1	37.375	4.94	6,748
BL0715 <sup>a38-1</sup>	gi 23465295 <sup>c</sup>	45	G	transaldolase	39682	4.87	C	tal	55.664	4.86	49,007 <sup>b-5</sup>

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BL0715 <sup>a38-2</sup>	gi 23465295	155	G	transaldolase	39682	4.87	C	tal	43.731	4.75	41,244 <sup>b-5</sup>
BL0715 <sup>a38-3</sup>	gi 23465295	159	G	transaldolase	39682	4.87	C	tal	42.577	4.9	16,345 <sup>b-5</sup>
BL0715 <sup>a38-4</sup>	gi 23465295	160	G	transaldolase	39682	4.87	C	tal	42.518	4.81	118,150 <sup>b-5</sup>
BL0715 <sup>a38-5</sup>	gi 23465295	162	G	transaldolase	39682	4.87	C	tal	46.864	4.85	10,613 <sup>b-5</sup>
BL0715 <sup>a38-6</sup>	gi 23465295	163	G	transaldolase	39682	4.87	C	tal	48.269	4.85	21,566 <sup>b-5</sup>
BL0715 <sup>a38-7</sup>	gi 23465295	273	G	transaldolase	39739	4.87	C	tal	42.106	4.86	255,063 <sup>b-5</sup>
BL0715 <sup>a38-8</sup>	gi 23465295	288	G	transaldolase	39739	4.87	C	tal	24.977	4.92	15,610 <sup>b-5</sup>
BL0715 <sup>a38-9</sup>	gi 23465295	298	G	transaldolase	39739	4.87	C	tal	24.316	5.03	24,587 <sup>b-5</sup>
BL0715 <sup>a38-10</sup>	gi 23465295	300	G	transaldolase	39739	4.87	C	tal	23.608	4.96	20,951 <sup>b-5</sup>
BL0715 <sup>a38-11</sup>	gi 23465295	467	G	transaldolase	39739	4.87	C	tal	17.365	4.71	22,069 <sup>b-5</sup>
BL0715 <sup>a38-12</sup>	gi 23465295	474	G	transaldolase	39739	4.87	C	tal	17.152	4.8	24,904 <sup>b-5</sup>
BL0716 <sup>a39-1</sup>	gi 23465296	26	G	transketolase	75868	4.97	C	tkl	85.848	5	14,521 <sup>b-10</sup>
BL0716 <sup>a39-2</sup>	gi 23465296	69	G	transketolase	75868	4.97	C	tkl	47.071	4.98	17,329 <sup>b-10</sup>

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BL0716 <sup>a39-3</sup>	gi 23465296	72	G	transketolase	75868	4.97	C	tk	44.868	5.03	28,752 <sup>b-10</sup>
BL0716 <sup>a39-4</sup>	gi 23465296	94	G	transketolase	75868	4.97	C	tk	60.3	5.15	2,565 <sup>b-10</sup>
BL0716 <sup>a39-5</sup>	gi 23465296	171	G	transketolase	76096	4.96	C	tk	43.423	4.96	36,834 <sup>b-10</sup>
BL0716 <sup>a39-6</sup>	gi 23465296	173	G	transketolase	76096	4.97	C	tk	42.4	5	36,033 <sup>b-10</sup>
BL0716 <sup>a39-7</sup>	gi 23465296	174	G	transketolase	76096	4.97	C	tk	42.047	5.13	40,472 <sup>b-10</sup>
BL0716 <sup>a39-8</sup>	gi 23465296	175	G	transketolase	76096	4.97	C	tk	43.793	5.16	13,976 <sup>b-10</sup>
BL0716 <sup>a39-9</sup>	gi 23465296	187	G	transketolase	76096	4.97	C	tk	36.571	5.32	4,512 <sup>b-10</sup>
BL0716 <sup>a39-10</sup>	gi 23465296	196	G	transketolase	76096	4.97	C	tk	39.442	4.94	16,668 <sup>b-10</sup>
BL0716 <sup>a39-11</sup>	gi 23465296	206	G	transketolase	76096	4.97	C	tk	36.524	5.11	38,303 <sup>b-10</sup>
BL0716 <sup>a39-12</sup>	gi 23465296	249	G	transketolase	76096	4.97	C	tk	28.644	4.97	24,555 <sup>b-10</sup>
BL0716 <sup>a39-13</sup>	gi 23465296	282	G	transketolase	76096	4.97	C	tk	29.242	4.79	12,962 <sup>b-10</sup>
BL0716 <sup>a39-14</sup>	gi 23465296	286	G	transketolase	76096	4.97	C	tk	26.152	4.96	16,708 <sup>b-10</sup>
BL0716 <sup>a39-15</sup>	gi 23465296	603	G	transketolase	76100	4.97	C	tk	18.061	4.54	30,084 <sup>b-10</sup>

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BL0716 <sup>a39-16</sup>	gi 23465296	897	G	transketolase	76096	4.97	C	tkt	84.034	5.03	28,294 <sup>b-10</sup>
BL0719	gi 23465298	790	O	chaperone protein	41138	6.07	C	dnaJ	54.924	6.79	13,530
BL0720	gi 23465299	801	S	hypothetical protein BL0720	29205	5.77	C		29.791	6.36	32,704
BL0731	gi 23465309	448	F	adenine phosphoribosyltransferase	20239	4.71	C	apt	25.084	4.73	29,268
BL0733 <sup>a40-1</sup>	gi 23465311	220	C	succinyl-CoA synthetase alpha chain	30823	5.33	C	sucD	33.713	5.56	16,293
BL0733 <sup>a40-2</sup>	gi 23465311	766	C	succinyl-CoA synthetase alpha chain	30823	5.33	C	sucD	31.089	5.63	18,278
BL0735 <sup>a41-1</sup>	gi 23465313	103	F	PurH	58377	5.36	C	purH	65.904	5.43	1,642
BL0735 <sup>a41-2</sup>	gi 23465313	679	F	PurH	58377	5.36	C	purH	66.236	5.59	18,499
BL0735 <sup>a41-3</sup>	gi 23465313	680	F	PurH	58377	5.36	C	purH	66.236	5.66	47,924
BL0735 <sup>a41-4</sup>	gi 23465313	780	F	PurH	58719	5.36	C	purH	36.442	6.14	23,481
BL0743	gi 23465320	337	++	narrowly conserved hypothetical protein	13165	4.84	C		17.569	4.85	54,497
BL0744	gi 23465321	247	R	probable hydrolase or phosphatase	27126	4.91	C		28.614	4.91	48,899
BL0751	gi 23465329	846	E	ATP phosphoribosyltransferase	30930	5.81	C	hisG	28.454	6.51	38,214

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BL0753	gi 23465331 <sup>c</sup>	816	G	ribulose-phosphate 3-epimerase	24364	5.35	C	rpe	25.732	5.67	21,574
BL0774	gi 23465350	299	F	MutT-like protein	23647	4.97	C		24.477	4.96	10,378
BL0783	gi 23465359	152	E	probable aminotransferase	43079	4.74	C		43.855	4.79	27,121
BL0788 <sup>a42-1</sup>	gi 23465364	836	F	orotate phosphoribosyltransferase	24928	5.77	U	pyrE	24.469	5.95	21,490
BL0788 <sup>a42-2</sup>	gi 23465364	841	F	orotate phosphoribosyltransferase	24928	5.77	U	pyrE	24.27	6.26	66,133
BL0790	gi 23465366	422	H	probable dihydroorotate dehydrogenase electron transfer subunit	29959	4.72	C	pyrK	28.702	4.76	24,201
BL0792	gi 23465368	487	F	dihydroorotase	53620	4.5	C	pyrC	69.988	4.49	29,903
BL0793	gi 23465369	866	F	aspartate carbamoyltransferase regulatory chain	15736	5.8	C	pyrI	17.955	6.34	51,648
BL0794 <sup>a43-1</sup>	gi 23465370	180	F	aspartate carbamoyltransferase	36145	5.17	C	pyrB	37.375	5.29	29,944
BL0794 <sup>a43-2</sup>	gi 23465370	186	F	aspartate carbamoyltransferase	36145	5.17	C	pyrB	34.876	5.28	1,792
BL0794 <sup>a43-3</sup>	gi 23465370	209	F	aspartate carbamoyltransferase	36145	5.17	C	pyrB	38.563	5.19	4,533
BL0796 <sup>a44-1</sup>	gi 23465372 <sup>c</sup>	153	M	choloylglycine hydrolase	35102	4.71	C		46.727	4.78	23,150 <sup>b-3</sup>
BL0796 <sup>a44-2</sup>	gi 23465372	396	M	choloylglycine hydrolase	35274	4.71	C		35.005	4.71	260,484 <sup>b-3</sup>

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BL0796 <sup>a44-3</sup>	gi 23465372	407	M	choloylglycine hydrolase	35276	4.71	C		33.544	4.77	328,963 <sup>b-3</sup>
BL0796 <sup>a44-4</sup>	gi 23465372	459	M	choloylglycine hydrolase	35274	4.71	C		21.427	4.85	30,180 <sup>b-3</sup>
BL0796 <sup>a44-5</sup>	gi 23465372	460	M	choloylglycine hydrolase	35274	4.71	C		20.325	4.82	16,858 <sup>b-3</sup>
BL0796 <sup>a44-6</sup>	gi 23465372	578	M	choloylglycine hydrolase	35274	4.71	C		34.411	4.63	55,922 <sup>b-3</sup>
BL0796 <sup>a44-7</sup>	gi 23465372	579	M	choloylglycine hydrolase	35274	4.71	C		33.702	4.63	44,366 <sup>b-3</sup>
BL0796 <sup>a44-8</sup>	gi 23465372	580	M	choloylglycine hydrolase	35274	4.71	C		34.638	4.65	57,891 <sup>b-3</sup>
BL0816 <sup>a45-1</sup>	gi 23465391	68	S	hypothetical protein BL0816	28898	5.1	C		47.912	4.99	30,076
BL0816 <sup>a45-2</sup>	gi 23465391	466	S	hypothetical protein BL0816	29240	5.1	C		17.491	4.69	29,035
BL0817	gi 23465392	507	++	hypothetical protein BL0817	19077	4.54	C		31.591	4.46	12,690
BL0819	gi 23465394	537	C	hypothetical protein BL0819	12256	8.2	C		28.301	4.49	35,136
BL0833	gi 23465408	678	E	glutamate synthase [NADPH] small subunit	56879	5.3	C	gltD	67.203	5.56	12,714
BL0852	gi 23465426	135	E	probable branched-chain amino acid aminotransferase	41448	5.05	C	ilvE	46.05	5.1	41,990
BL0853	gi 23465427	452	J	probable 50S ribosomal protein L25	21801	4.68	C	rplY	24.828	4.8	162,645 <sup>b-37</sup>

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BL0857	gi 23465431	59	C	NAD(P) transhydrogenase subunit alpha part 1	39547	4.78	CM	pntA	50.341	4.85	49,162
BL0863 <sup>a46-1</sup>	gi 23465437	610	F	hypothetical protein in Hit family	12461	5.21	C		17.584	4.38	26,023
BL0863 <sup>a46-2</sup>	gi 23465437	621	F	hypothetical protein in Hit family	12461	5.21	C		16.692	5.28	40,607
BL0863 <sup>a46-3</sup>	gi 23465437	895	F	hypothetical protein in Hit family	12461	5.21	C		16.648	5.06	5,661
BL0864	gi 23465438	773	S	conserved hypothetical protein with similarity to SdrD of <i>S. coelicolor</i>	28844	5.6	C		32.028	5.96	8,900
BL0868	gi 23465442	587	C	hypothetical protein with NifU-like domain	19629	4.61	C		25.88	4.59	27,840
BL0869 <sup>a47-1</sup>	gi 23465443	724	E	NifS-like aminotranferase	45561	5.74	C		47.285	6	12,641
BL0869 <sup>a47-2</sup>	gi 23465443	729	E	NifS-like aminotranferase	45561	5.74	C		46.817	6.13	17,140
BL0869 <sup>a47-3</sup>	gi 23465443	730	E	NifS-like aminotranferase	45561	5.74	C		46.161	6.23	52,930
BL0870 <sup>a48-1</sup>	gi 23465444	771	O	probable ATP binding protein of ABC transporter	28189	5.54	CM		31.293	5.82	12,490 <sup>b-35</sup>
BL0870 <sup>a48-2</sup>	gi 23465444	776	O	probable ATP binding protein of ABC transporter	28189	5.54	CM		30.821	6.07	151,687 <sup>b-35</sup>
BL0870 <sup>a48-3</sup>	gi 23465444	779	O	probable ATP binding protein of ABC transporter	28189	5.54	CM		31.225	6.24	4,686 <sup>b-35</sup>

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BL0876	gi 23465450	859	E	probable 3-dehydroquinate dehydratase	16512	5.3	C	aroQ	17.922	5.65	19,042
BL0878	gi 23465452	789	E	chorismate synthase	42337	6.06	C	aroC	56.706	6.75	7,141
BL0882 <sup>a49-1</sup>	gi 23465456	688	J	alanyl-tRNA synthetase	97611	5.13	C	alaS	64.664	5.9	1,284
BL0882 <sup>a49-2</sup>	gi 23465456	722	J	alanyl-tRNA synthetase	97611	5.13	C	alaS	51.506	5.8	11,590
BL0882 <sup>a49-3</sup>	gi 23465456	723	J	alanyl-tRNA synthetase	97611	5.13	C	alaS	47.352	5.94	28,878
BL0891 <sup>a50-1</sup>	gi 23465465	323	F	xanthine phosphoribosyltransferase	20756	5.33	C	xpt	21.599	5.54	12,419
BL0891 <sup>a50-2</sup>	gi 23465465	839	F	xanthine phosphoribosyltransferase	20927	5.33	C	xpt	22.602	5.63	30,108
BL0897 <sup>a51-1</sup>	gi 23465471	302	Q	probable pyrazinamidase/nicotinamidase	21962	4.98	C	pncA	24.061	5.03	30,039
BL0897 <sup>a51-2</sup>	gi 23465471	526	Q	probable pyrazinamidase/nicotinamidase	21962	4.98	C	pncA	27.178	4.61	28,321
BL0898	gi 23465472	695	K	hypothetical protein BL0898	54362	5.37	C		57.672	5.7	1,832
BL0921	gi 23465494	184	H	hypothetical protein BL0921	11205	10.35	U		40.518	5.34	8,632
BL0926 <sup>a52-1</sup>	gi 23465499	157	J	widely conserved hypothetical GTPase-like protein	39566	4.65	C		49.216	4.74	33,816
BL0926 <sup>a52-2</sup>	gi 23465499	437	J	widely conserved hypothetical GTPase-like protein	39623	4.65	C		24.437	4.64	25,044

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BL0927	gi 23465500	284	E	pyrroline-5-carboxylate reductase	28043	4.87	C	proC	26.057	4.92	42,034
BL0933 <sup>a53-1</sup>	gi 23465506	133	E	O-acetylhomoserine (thiol)-lyase	47571	5.1	C	cysD	53.279	5.24	22,559
BL0933 <sup>a53-2</sup>	gi 23465506	333	E	O-acetylhomoserine (thiol)-lyase	47571	5.1	C	cysD	22.397	5.3	22,161
BL0933 <sup>a53-3</sup>	gi 23465506	334	E	O-acetylhomoserine (thiol)-lyase	47571	5.1	C	cysD	21.984	5.3	30,688
BL0934	gi 23465507	395	H	possible pyridoxine kinase	31432	4.61	C		31.237	4.66	32,245
BL0944 <sup>a54-1</sup>	gi 23465517	277	O	ATP-dependent Clp protease proteolytic subunit 2	25869	5.11	C	clpP2	26.641	4.85	42,822
BL0944 <sup>a54-2</sup>	gi 23465517	456	O	ATP-dependent Clp protease proteolytic subunit 2	25870	5.11	C	clpP2	23.195	4.81	49,501
BL0945	gi 23465518	439	O	ATP-dependent Clp protease proteolytic subunit 1	22823	4.61	C	clp1	23.7	4.57	33,649
BL0947 <sup>a55-1</sup>	gi 23465520	402	O	trigger factor chaperone	49611	4.43	C	tig	41.7	4.74	33,682 <sup>b-14</sup>
BL0947 <sup>a55-2</sup>	gi 23465520	484	O	trigger factor chaperone	49611	4.43	C	tig	68.774	4.44	76,881 <sup>b-14</sup>
BL0947 <sup>a55-3</sup>	gi 23465520	485	O	trigger factor chaperone	49611	4.43	C	tig	67.2	4.46	138,987 <sup>b-14</sup>
BL0947 <sup>a55-4</sup>	gi 23465520	486	O	trigger factor chaperone	49611	4.43	C	tig	69.042	4.47	31,344 <sup>b-14</sup>
BL0947 <sup>a55-5</sup>	gi 23465520	521	O	trigger factor chaperone	49611	4.43	C	tig	46.903	4.58	39,959 <sup>b-14</sup>

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BL0953	gi 23465526	10	H	glutamine-dependent NAD(+) synthetase	60925	4.75	C	nadE	72.326	4.94	18,064
BL0954	gi 23465527	136	R	widely conserved hypothetical protein	41543	5.12	C		48.558	5.24	3,796
BL0959 <sup>a56-1</sup>	gi 23465532 <sup>c</sup>	33	G	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	92469	5.06	U		62.096	4.81	5,312 <sup>b-15</sup>
BL0959 <sup>a56-2</sup>	gi 23465532	34	G	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	92469	5.06	U		63.228	4.86	1,171 <sup>b-15</sup>
BL0959 <sup>a56-3</sup>	gi 23465532	36	G	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	92469	5.06	U		66.346	4.9	18,597 <sup>b-15</sup>
BL0959 <sup>a56-4</sup>	gi 23465532	540	G	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	92697	5.06	U		26.261	4.43	37,419 <sup>b-15</sup>
BL0959 <sup>a56-5</sup>	gi 23465532	543	G	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	92697	5.06	U		25.036	4.35	36,577 <sup>b-15</sup>
BL0959 <sup>a56-6</sup>	gi 23465532	545	G	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	92697	5.06	U		24.042	4.34	28,719 <sup>b-15</sup>
BL0959 <sup>a56-7</sup>	gi 23465532	699	G	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	92697	5.06	U		58.118	5.98	13,268 <sup>b-15</sup>
BL0959 <sup>a56-8</sup>	gi 23465532	712	G	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	92697	5.06	U		57.849	6.08	10,052 <sup>b-15</sup>
BL0959 <sup>a56-9</sup>	gi 23465532	713	G	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	92697	5.06	U		52.9	6.14	19,358 <sup>b-15</sup>
BL0959 <sup>a56-10</sup>	gi 23465532	715	G	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	92697	5.06	U		52.979	6.2	4,005 <sup>b-15</sup>
BL0959 <sup>a56-11</sup>	gi 23465532	728	G	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	92697	5.06	U		47.217	6.06	15,395 <sup>b-15</sup>

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BL0959 <sup>a56-12</sup>	gi 23465532	749	G	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	92697	5.06	U		43.787	6.09	10,180 <sup>b-15</sup>
BL0959 <sup>a56-13</sup>	gi 23465532	782	G	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	92697	5.06	U		44.888	6.31	9,702 <sup>b-15</sup>
BL0959 <sup>a56-14</sup>	gi 23465532	783	G	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	92697	5.06	U		43.548	6.26	22,048 <sup>b-15</sup>
BL0959 <sup>a56-15</sup>	gi 23465532	786	G	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	92697	5.06	U		46.096	6.38	13,612 <sup>b-15</sup>
BL0959 <sup>a56-16</sup>	gi 23465532	792	G	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	92697	5.06	U		40.665	6.69	10,891 <sup>b-15</sup>
BL0959 <sup>a56-17</sup>	gi 23465532	796	G	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	92697	5.06	U		34.514	6.7	3,959 <sup>b-15</sup>
BL0959 <sup>a56-18</sup>	gi 23465532	797	G	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	92697	5.06	U		33.518	6.7	5,213 <sup>b-15</sup>
BL0959 <sup>a56-19</sup>	gi 23465532	799	G	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	92697	5.06	U		32.063	6.38	2,535 <sup>b-15</sup>
BL0959 <sup>a56-20</sup>	gi 23465532	828	G	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	92697	5.06	U		28.257	6.16	14,933 <sup>b-15</sup>
BL0959 <sup>a56-21</sup>	gi 23465532	850	G	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	92697	5.06	U		24.191	6.9	34,865 <sup>b-15</sup>
BL0960	gi 23465533	78	F	GMP synthase glutamine amidotransferase	57830	5.16	C	guaA	70.618	5.03	12,469
BL0964	gi 23465536	128	M	UDP-N-acetylglucosamine pyrophosphorylase	49064	5.12	C	glmU	57.827	5.2	2,819
BL0968 <sup>a57-1</sup>	gi 23465539	681	C	phosphate acetyltransferase	60854	5.59	U	pta	67.53	5.77	14,509

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BL0968 <sup>a57-2</sup>	gi 23465539	682	C	phosphate acetyltransferase	60854	5.59	U	pta	67.203	5.91	14,222
BL0969 <sup>a58-1</sup>	gi 23465540 <sup>c</sup>	120	C	acetate kinase	44172	5.47	C	ackA	50.09	5.57	5,043 <sup>b-27</sup>
BL0969 <sup>a58-2</sup>	gi 23465540	121	C	acetate kinase	44172	5.47	C	ackA	47.623	5.72	45,227 <sup>b-27</sup>
BL0969 <sup>a58-3</sup>	gi 23465540	721	C	acetate kinase	44287	5.47	C	ackA	46.422	5.83	129,992 <sup>b-27</sup>
BL0969 <sup>a58-4</sup>	gi 23465540	745	C	acetate kinase	44287	5.47	C	ackA	51.506	5.72	19,323 <sup>b-27</sup>
BL0969 <sup>a58-5</sup>	gi 23465540	814	C	acetate kinase	44287	5.47	C	ackA	27.576	5.75	13,415 <sup>b-27</sup>
BL0970 <sup>a59-1</sup>	gi 23465541	114	E	3-phosphoshikimate 1-carboxyvinyltransferase	48013	5.24	C		52.821	5.47	19,719
BL0970 <sup>a59-2</sup>	gi 23465541	373	E	3-phosphoshikimate 1-carboxyvinyltransferase	48013	5.24	C		53.362	4.62	14,541
BL0978 <sup>a60-1</sup>	gi 23465547	86	G	LacZ	114378	4.86	C	lacZ	70.859	5.13	10,968 <sup>b-36</sup>
BL0978 <sup>a60-2</sup>	gi 23465547	87	G	LacZ	114378	4.86	C	lacZ	78.867	5.17	9,202 <sup>b-36</sup>
BL0978 <sup>a60-3</sup>	gi 23465547	90	G	LacZ	114378	4.86	C	lacZ	72.326	5.19	7,581 <sup>b-36</sup>
BL0978 <sup>a60-4</sup>	gi 23465547	91	G	LacZ	114378	4.86	C	lacZ	69.665	5.19	9,148 <sup>b-36</sup>
BL0978 <sup>a60-5</sup>	gi 23465547	93	G	LacZ	114378	4.86	C	lacZ	62.71	5.17	14,175 <sup>b-36</sup>

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BL0978 <sup>a60-6</sup>	gi 23465547	101	G	LacZ	114378	4.86	C	lacZ	76.83	5.32	5,916 <sup>b-36</sup>
BL0978 <sup>a60-7</sup>	gi 23465547	106	G	LacZ	114378	4.86	C	lacZ	63.124	5.33	11,695 <sup>b-36</sup>
BL0978 <sup>a60-8</sup>	gi 23465547	115	G	LacZ	114378	4.86	C	lacZ	56.462	5.37	13,294 <sup>b-36</sup>
BL0978 <sup>a60-9</sup>	gi 23465547	127	G	LacZ	114378	4.86	C	lacZ	71.466	5.24	2,872 <sup>b-36</sup>
BL0978 <sup>a60-10</sup>	gi 23465547	143	G	LacZ	114378	4.86	C	lacZ	39.77	5.51	11,735 <sup>b-36</sup>
BL0978 <sup>a60-11</sup>	gi 23465547	675	G	LacZ	114777	4.86	C	lacZ	74.008	5.44	13,404 <sup>b-36</sup>
BL0978 <sup>a60-12</sup>	gi 23465547	758	G	LacZ	114777	4.86	C	lacZ	35.867	5.82	21,755 <sup>b-36</sup>
BL0978 <sup>a60-13</sup>	gi 23465547	763	G	LacZ	114777	4.86	C	lacZ	34.844	6.04	12,416 <sup>b-36</sup>
BL0978 <sup>a60-14</sup>	gi 23465547	764	G	LacZ	114777	4.86	C	lacZ	34.03	6.03	19,268 <sup>b-36</sup>
BL0982	gi 23465551	732	G	probable glycogen operon protein GlgX	81707	5.3	C	glgX	46.95	5.53	6,547
BL0983	gi 23465552	268	L	possible pyrophosphate-releasing NTPase in MutT family	25286	4.95	C		30.621	5.07	7,915
BL0984	gi 23465553	216	S	conserved hypothetical protein with duf34	34001	5.25	C		31.377	5.31	39,927
BL0986	gi 23465555	191	T	conserved hypothetical protein with a response regulator receiver	29189	4.85	C		37.136	4.89	84,861

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BL0987	gi 23465556	321	L	possible NTP pyrophosphatase in MutT family	28229	5.91	C		24.036	5.65	86,051
BL0988 <sup>a61-1</sup>	gi 23465557	105	G	pyruvate kinase	55233	5.49	C	pyk	64.816	5.3	67,004 <sup>b-6</sup>
BL0988 <sup>a61-2</sup>	gi 23465557	107	G	pyruvate kinase	55233	5.49	C	pyk	63.857	5.36	176,347 <sup>b-6</sup>
BL0988 <sup>a61-3</sup>	gi 23465557	221	G	pyruvate kinase	55518	5.49	C	pyk	32.832	5.57	14,786 <sup>b-6</sup>
BL0988 <sup>a61-4</sup>	gi 23465557	257	G	pyruvate kinase	55518	5.49	C	pyk	30.587	5.12	49,221 <sup>b-6</sup>
BL0988 <sup>a61-5</sup>	gi 23465557	262	G	pyruvate kinase	55518	5.49	C	pyk	28.063	5.52	35,838 <sup>b-6</sup>
BL0988 <sup>a61-6</sup>	gi 23465557	332	G	pyruvate kinase	55233	5.49	C	pyk	22.853	5.3	1,344 <sup>b-6</sup>
BL0988 <sup>a61-7</sup>	gi 23465557	677	G	pyruvate kinase	55233	5.49	C	pyk	66.45	5.51	9,428 <sup>b-6</sup>
BL0988 <sup>a61-8</sup>	gi 23465557	686	G	pyruvate kinase	55233	5.49	C	pyk	66.13	5.86	9,176 <sup>b-6</sup>
BL0988 <sup>a61-9</sup>	gi 23465557	760	G	pyruvate kinase	55518	5.49	C	pyk	33.402	5.63	16,922 <sup>b-6</sup>
BL0988 <sup>a61-10</sup>	gi 23465557	813	G	pyruvate kinase	55518	5.49	C	pyk	28.229	5.83	31,081 <sup>b-6</sup>
BL0988 <sup>a61-11</sup>	gi 23465557	825	G	pyruvate kinase	55518	5.49	C	pyk	29.241	6.11	27,510 <sup>b-6</sup>

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BL0988 <sup>a61-12</sup>	gi 23465557	834	G	pyruvate kinase	55518	5.49	C	pyk	27.682	6.07	32,083 <sup>b-6</sup>
BL0988 <sup>a61-13</sup>	gi 23465557	837	G	pyruvate kinase	55518	5.49	C	pyk	26.387	6.06	18,882 <sup>b-6</sup>
BL0993 <sup>a62-1</sup>	gi 23465562	224	H	bifunctional methylenetetrahydrofolate dehydrogenase and methenyltetrahydrofolate cyclohydrolase	31384	5.32	C	folD	28.654	5.62	41,336
BL0993 <sup>a62-2</sup>	gi 23465562	803	H	bifunctional methylenetetrahydrofolate dehydrogenase and methenyltetrahydrofolate cyclohydrolase	31384	5.32	C	folD	29.979	5.63	33,268
BL0999 <sup>a63-1</sup>	gi 23465568	122	G	1,4-alpha-glucan branching enzyme	82998	5.11	U	glgB	96.009	5.22	815
BL0999 <sup>a63-2</sup>	gi 23465568	739	G	1,4-alpha-glucan branching enzyme	83055	5.11	U	glgB	45.013	5.74	1,523
BL0999 <sup>a63-3</sup>	gi 23465568	740	G	1,4-alpha-glucan branching enzyme	83055	5.11	U	glgB	45.773	5.87	3,480
BL0999 <sup>a63-4</sup>	gi 23465568	741	G	1,4-alpha-glucan branching enzyme	83055	5.11	U	glgB	44.826	5.85	5,276
BL1000	gi 23465569	848	T	response regulator of two-component system	26340	6.13	C		26.779	6.8	7,197
BL1004	gi 23465573	829	R	hypothetical protein with similarity to eukaryotic phosphomannomutases	29549	5.77	U		28.369	6.35	20,174

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BL1015	gi 23465584	468	K	transcription elongation factor GreA	17125	4.82	C	greA	17.405	4.76	217,840 <sup>b-24</sup>
BL1016 <sup>a64-1</sup>	gi 23465585	335	O	Fk506-binding protein	14453	4.86	U	fkpP	18.333	4.84	206,071 <sup>b-22</sup>
BL1016 <sup>a64-2</sup>	gi 23465585	462	O	Fk506-binding protein	14453	4.86	U	fkpP	18.447	4.69	12,517 <sup>b-22</sup>
BL1016 <sup>a64-3</sup>	gi 23465585	470	O	Fk506-binding protein	14453	4.86	U	fkpP	17.996	4.84	17,585 <sup>b-22</sup>
BL1022 <sup>a65-1</sup>	gi 23465590	276	G	enolase	46600	4.7	C	eno	27.494	4.87	43,882 <sup>b-9</sup>
BL1022 <sup>a65-2</sup>	gi 23465590	278	G	enolase	46600	4.7	C	eno	25.892	4.88	59,763 <sup>b-9</sup>
BL1022 <sup>a65-3</sup>	gi 23465590	361	G	enolase	46486	4.7	C	eno	51.425	4.8	176,309 <sup>b-9</sup>
BL1022 <sup>a65-4</sup>	gi 23465590	366	G	enolase	46486	4.7	C	eno	51.741	4.76	82,496 <sup>b-9</sup>
BL1022 <sup>a65-5</sup>	gi 23465590	424	G	enolase	46486	4.7	C	eno	29.427	4.63	27,617 <sup>b-9</sup>
BL1023	gi 23465591	426	C	possible oxidoreductase in aldo-keto reductase family	35184	4.85	C		27.334	4.62	45,507
BL1034	gi 23465600	132	E	gamma-glutamyl phosphate reductase	49606	5.07	C	proA	52.462	5.22	15,534
BL1039	gi 23465605	217	++	hypothetical protein BL1039	28804	10.52	U		33.513	5.35	9,364
BL1043	gi 23465610	601	L	DNA repair protein RecN	62844	4.44	C	recN	17.991	4.46	38,258

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BL1046	gi 23465613	317	P	hypothetical protein possibly involved in monovalent cation transport	23693	5.27	C		27.339	5.52	6,651
BL1049 <sup>a66-1</sup>	gi 23465616	568	G	conserved hypothetical protein with possible phosphatase function	37336	4.56	C		41.827	4.56	6,852
BL1049 <sup>a66-2</sup>	gi 23465616	761	G	conserved hypothetical protein with possible phosphatase function	37336	4.56	C		33.713	5.62	15,717
BL1051	gi 23465618	131	J	tyrosyl-tRNA synthetase	48413	5.08	C	tyrS	55.228	5.22	11,192
BL1056	gi 23465625	344	++	hypothetical protein BL1056	9622	9.13	U		18.177	5.3	14,547
BL1058 <sup>a67-1</sup>	gi 23465627	130	E	argininosuccinate synthase	45478	5.14	C	argG	53.114	5.2	26,357
BL1058 <sup>a67-2</sup>	gi 23465627	242	E	argininosuccinate synthase	45820	5.14	C	argG	27.958	4.81	11,290
BL1060	gi 23465629	734	E	ornithine carbamoyltransferase, anabolic	35503	5.32	C	argF	41.043	5.51	32,992
BL1064	gi 23465633	747	E	N-acetyl-gamma-glutamyl-phosphate reductase	38108	5.53	U	argC	42.381	5.96	17,123
BL1067 <sup>a68-1</sup>	gi 23465636	71	J	phenylalanyl-tRNA synthetase alpha chain	38848	4.96	C	pheS	44.168	5.02	21,107
BL1067 <sup>a68-2</sup>	gi 23465636	890	J	phenylalanyl-tRNA synthetase alpha chain	38962	4.96	C	pheS	46.05	5.05	1,927
BL1072	gi 23465641	368	E	widely conserved protein in peptidase or deacetylase family	48309	4.56	C		55.84	4.58	22,133

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BL1076 <sup>a69-1</sup>	gi 23465645 <sup>c</sup>	32	E	glutamine synthetase 1	53206	4.81	C	glnA1	66.124	4.84	77,109 <sup>b-49</sup>
BL1076 <sup>a69-2</sup>	gi 23465645	236	E	glutamine synthetase 1	53321	4.81	C	glnA1	31.377	4.86	47,016 <sup>b-49</sup>
BL1090	gi 23465659	164	E	possible alcohol dehydrogenase	36851	4.82	C		45.322	4.86	9,947
BL1097 <sup>a70-1</sup>	gi 23465666	42	J	elongation factor Tu	43909	4.88	C	tuf	60.792	4.99	109,233 <sup>b-01</sup>
BL1097 <sup>a70-2</sup>	gi 23465666	49	J	elongation factor Tu	43909	4.88	C	tuf	60.398	4.97	8,089 <sup>b-01</sup>
BL1097 <sup>a70-3</sup>	gi 23465666	51	J	elongation factor Tu	43909	4.88	C	tuf	53.528	4.94	98,342 <sup>b-01</sup>
BL1097 <sup>a70-4</sup>	gi 23465666	65	J	elongation factor Tu	43909	4.88	C	tuf	53.611	4.99	686,147 <sup>b-01</sup>
BL1097 <sup>a70-5</sup>	gi 23465666	230	J	elongation factor Tu	44137	4.88	C	tuf	31.59	4.83	23,121 <sup>b-01</sup>
BL1097 <sup>a70-6</sup>	gi 23465666	231	J	elongation factor Tu	44137	4.88	C	tuf	34.162	4.83	10,613 <sup>b-01</sup>
BL1097 <sup>a70-7</sup>	gi 23465666	232	J	elongation factor Tu	44137	4.88	C	tuf	31.951	4.91	51,602 <sup>b-01</sup>
BL1097 <sup>a70-8</sup>	gi 23465666	234	J	elongation factor Tu	44137	4.88	C	tuf	32.134	4.93	34,306 <sup>b-01</sup>
BL1097 <sup>a70-9</sup>	gi 23465666	237	J	elongation factor Tu	44137	4.88	C	tuf	30.388	4.79	5,439 <sup>b-01</sup>
BL1097 <sup>a70-10</sup>	gi 23465666	270	J	elongation factor Tu	44137	4.88	C	tuf	28.268	5	41,639 <sup>b-01</sup>

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BL1097 <sup>a70-11</sup> gi 23465666	283	J	elongation factor Tu	44137	4.88	C	tuf	26.128	4.91	40,782 <sup>b-01</sup>
BL1097 <sup>a70-12</sup> gi 23465666	285	J	elongation factor Tu	44137	4.88	C	tuf	25.986	4.94	18,384 <sup>b-01</sup>
BL1097 <sup>a70-13</sup> gi 23465666	292	J	elongation factor Tu	44137	4.88	C	tuf	25.986	5	5,130 <sup>b-01</sup>
BL1097 <sup>a70-14</sup> gi 23465666	307	J	elongation factor Tu	43909	4.88	C	tuf	23.125	5.2	146,502 <sup>b-01</sup>
BL1097 <sup>a70-15</sup> gi 23465666	309	J	elongation factor Tu	43909	4.88	C	tuf	21.095	5.19	64,768 <sup>b-01</sup>
BL1097 <sup>a70-16</sup> gi 23465666	310	J	elongation factor Tu	43909	4.88	C	tuf	20.816	5.19	11,366 <sup>b-01</sup>
BL1097 <sup>a70-17</sup> gi 23465666	325	J	elongation factor Tu	43909	4.88	C	tuf	22.622	5.02	23,387 <sup>b-01</sup>
BL1097 <sup>a70-18</sup> gi 23465666	399	J	elongation factor Tu	44137	4.88	C	tuf	46.796	4.74	22,181 <sup>b-01</sup>
BL1097 <sup>a70-19</sup> gi 23465666	412	J	elongation factor Tu	44137	4.88	C	tuf	31.063	4.69	11,259 <sup>b-01</sup>
BL1097 <sup>a70-20</sup> gi 23465666	421	J	elongation factor Tu	43909	4.88	C	tuf	30.223	4.77	28,667 <sup>b-01</sup>
BL1097 <sup>a70-21</sup> gi 23465666	616	J	elongation factor Tu	44137	4.88	C	tuf	18.053	5.08	25,055 <sup>b-01</sup>
BL1097 <sup>a70-22</sup> gi 23465666	617	J	elongation factor Tu	44137	4.88	C	tuf	17.947	5.08	17,183 <sup>b-01</sup>
BL1097 <sup>a70-23</sup> gi 23465666	705	J	elongation factor Tu	44137	4.88	C	tuf	51.888	5.58	8,406 <sup>b-01</sup>

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BL1097 <sup>a70-24</sup> gi 23465666	708	J	elongation factor Tu	44137	4.88	C	tuf	54.102	5.82	15,351 <sup>b-01</sup>
BL1097 <sup>a70-25</sup> gi 23465666	893	J	elongation factor Tu	44137	4.88	C	tuf	21.469	5.11	18,431 <sup>b-01</sup>
BL1097 <sup>a70-26</sup> gi 23465666	896	J	elongation factor Tu	44137	4.88	C	tuf	33.08	4.93	19,660 <sup>b-01</sup>
BL1098 <sup>a71-1</sup> gi 23465667	1	J	elongation factor G	78087	4.83	C	fusA	92.413	4.83	15,350 <sup>b-23</sup>
BL1098 <sup>a71-2</sup> gi 23465667	2	J	elongation factor G	78087	4.83	C	fusA	91.581	4.86	35,335 <sup>b-23</sup>
BL1098 <sup>a71-3</sup> gi 23465667	63	J	elongation factor G	78087	4.83	C	fusA	45.717	4.92	13,835 <sup>b-23</sup>
BL1098 <sup>a71-4</sup> gi 23465667	67	J	elongation factor G	78087	4.83	C	fusA	49.29	4.98	6,179 <sup>b-23</sup>
BL1098 <sup>a71-5</sup> gi 23465667	99	J	elongation factor G	78087	4.83	C	fusA	51.662	5.09	13,971 <sup>b-23</sup>
BL1098 <sup>a71-6</sup> gi 23465667	266	J	elongation factor G	78429	4.83	C	fusA	30.028	5.05	24,755 <sup>b-23</sup>
BL1098 <sup>a71-7</sup> gi 23465667	281	J	elongation factor G	78429	4.83	C	fusA	24.08	4.84	11,726 <sup>b-23</sup>
BL1098 <sup>a71-8</sup> gi 23465667	364	J	elongation factor G	78087	4.83	C	fusA	57.367	4.77	17,276 <sup>b-23</sup>
BL1098 <sup>a71-9</sup> gi 23465667	393	J	elongation factor G	78429	4.83	C	fusA	34.08	4.67	47,632 <sup>b-23</sup>
BL1098 <sup>a71-10</sup> gi 23465667	413	J	elongation factor G	78087	4.83	C	fusA	29.583	4.69	18,990 <sup>b-23</sup>

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BL1098 <sup>a71-11</sup>	gi 23465667	576	J	elongation factor G	78429	4.83	C	fusA	35.338	4.6	18,420 <sup>b-23</sup>
BL1099	gi 23465668	698	J	30S ribosomal protein S7	17542	9.99	U	rpsG	61.372	5.97	12,817
BL1103	gi 23465672	194	E	possible low specificity-threonine aldolase	37465	4.94	C		40.136	4.94	10,111
BL1107	gi 23465675	239	F	phosphoribosylaminoimidazole-succinocarboxamide synthase	28374	4.85	C	purC	30.093	4.85	86,891
BL1114	gi 23465682	630	L	hypothetical protein in ImpB/MucB/SamB family of UV repair proteins	58689	6.55	C		17.792	5.04	10,484
BL1117	gi 23465685	552	S	narrowly conserved hypothetical protein	16914	4.44	U		26.941	4.49	26,433
BL1123	gi 23465691	55	F	phosphoribosylamine--glycine ligase	45229	4.68	C	purD	56.017	4.79	13,816
BL1123	gi 23465691	365	F	phosphoribosylamine--glycine ligase	45229	4.68	C	purD	54.71	4.77	31,461
BL1128	gi 23465696	867	P	probable metal uptake regulator similar to ferric uptake regulator protein	16593	5.89	C	fur	17.774	6.39	17,316
BL1129	gi 23465697	696	F	phosphoribosylaminoimidazole carboxylase ATPase subunit	42922	5.41	C	purK	56.62	5.83	11,484
BL1130	gi 23465698	862	F	phosphoribosylaminoimidazole carboxylase catalytic subunit	17707	5.47	U	purE	17.969	5.76	16,564

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BL1132	gi 23465700	88	H	probable 1-deoxyxylulose-5-phosphate synthase	81804	5.25	U	dxs	89.782	5.18	3,959
BL1142 <sup>a72-1</sup>	gi 23465709	341	E	L-asparaginase precursor	31838	4.75	C		17.121	5.26	27,711 <sup>b-34</sup>
BL1142 <sup>a72-2</sup>	gi 23465709	442	E	L-asparaginase precursor	32009	4.75	C		22.18	4.59	83,051 <sup>b-34</sup>
BL1142 <sup>a72-3</sup>	gi 23465709	869	E	L-asparaginase precursor	32009	4.75	C		17.034	5.8	53,536 <sup>b-34</sup>
BL1145	gi 23465711	306	H	conserved hypothetical protein in sno glutamine amidotransferase family	22683	5.09	C		22.903	5.19	12,277
BL1146 <sup>a73-1</sup>	gi 23465712	254	H	widely conserved protein in upfoo19 probably involved in pyridoxine biosynthesis	35011	5.6	C		32.964	5.16	21,173
BL1146 <sup>a73-2</sup>	gi 23465712	891	H	widely conserved protein in upfoo19 probably involved in pyridoxine biosynthesis	35011	5.6	C		32.171	5.15	27,009
BL1148	gi 23465714	590	F	deoxyguanosinetriphosphate triphosphohydrolase	12656	10.15	C	dgt	22.896	4.52	33,121
BL1149 <sup>a74-1</sup>	gi 23465715	689	M	alanine racemase	48493	5.58	C	alr	64.458	5.96	735
BL1149 <sup>a74-2</sup>	gi 23465715	691	M	alanine racemase	48493	5.58	C	alr	64.049	6.00	13,271

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BL1152 <sup>a75-1</sup>	gi 23465718	327	T	autoinducer-2 production protein LuxS	15643	5.29	C		18.984	5.11	144,928 <sup>b-30</sup>
BL1152 <sup>a75-2</sup>	gi 23465718	330	T	autoinducer-2 production protein LuxS	15643	5.29	C		18.926	5.27	37,657 <sup>b-30</sup>
BL1155	gi 23465721	140	E	cystathionine gamma-synthase	41893	5.26	C	metB	44.868	5.36	9,161
BL1186	gi 23465752	243	J	polypeptide deformylase	24542	4.75	C		28.354	4.86	44,859
BL1187 <sup>a76-1</sup>	gi 23465753	46	G	probable phosphoglucomutase or phosphomannomutase	48630	4.93	C	mrsA	55.84	4.88	35,475 <sup>b-43</sup>
BL1187 <sup>a76-2</sup>	gi 23465753	886	G	probable phosphoglucomutase or phosphomannomutase	48858	4.93	C	mrsA	54.71	4.95	104,999 <sup>b-43</sup>
BL1193 <sup>a77-1</sup>	gi 23465759	218	E	dihydrodipicolinate synthase	31830	5.37	U	dapA	35.265	5.38	46,081
BL1193 <sup>a77-2</sup>	gi 23465759	767	E	dihydrodipicolinate synthase	31830	5.37	U	dapA	32.609	5.68	49,941
BL1193 <sup>a77-3</sup>	gi 23465759	769	E	dihydrodipicolinate synthase	31830	5.37	U	dapA	33.635	5.7	10,943
BL1194	gi 23465760	253	E	dihydrodipicolinate reductase	26229	5.08	C	dapB	31.133	5.14	28,314
BL1208	gi 23465775	811	J	probable RNA methyltransferase	18928	6.14	U	yibK	29.791	5.88	2,633
BL1209	gi 23465776	161	S	narrowly conserved hypothetical protein	47575	4.9	C		42.756	4.84	30,886
BL1210	gi 23465778	881	G	galactokinase	44560	4.93	C	galK	53.032	4.96	166,888 <sup>b-33</sup>

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BL1213 <sup>a78-1</sup>	gi 23465781	124	F	dihydroorotate dehydrogenase-like protein	37251	5.14	C	47.217	5.59	53,459
BL1213 <sup>a78-2</sup>	gi 23465781	138	F	dihydroorotate dehydrogenase-like protein	37251	5.14	C	48.63	5.28	10,416
BL1216 <sup>a79-1</sup>	gi 23465784	833	T	probable transcriptional regulator with cyclic nucleotide-binding domain	26870	5.72	C	27.656	6.02	9,426
BL1216 <sup>a79-2</sup>	gi 23465784	845	T	probable transcriptional regulator with cyclic nucleotide-binding domain	26870	5.72	C	28.09	6.45	8,765
BL1222 <sup>a80-1</sup>	gi 23465790	119	L	hypothetical protein with N-terminal similarity to NADH pyrophosphatase	45238	5.39	C	54.51	5.54	8,434
BL1222 <sup>a80-2</sup>	gi 23465790	564	L	hypothetical protein with N-terminal similarity to NADH pyrophosphatase	45466	5.39	C	38.59	4.63	22,368
BL1222 <sup>a80-3</sup>	gi 23465790	707	L	hypothetical protein with N-terminal similarity to NADH pyrophosphatase	45466	5.39	C	50.383	5.8	16,706
BL1222 <sup>a80-4</sup>	gi 23465790	805	L	hypothetical protein with N-terminal similarity to NADH pyrophosphatase	45466	5.39	C	30.427	6.01	15,382

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pyrophosphatase											
BL1223 <sup>a81-1</sup>	gi 23465791	512	R	possible alpha beta hydrolase	30528	4.51	U		29.158	4.4	29,853 <sup>b-29</sup>
BL1223 <sup>a81-2</sup>	gi 23465791	536	R	possible alpha beta hydrolase	30528	4.51	U		29.032	4.49	161,867 <sup>b-29</sup>
BL1224	gi 23465792	438	F	narrowly conserved hypothetical protein	23145	4.64	C		24.336	4.67	64,234
BL1243	gi 23465805	831	R	hypothetical protein with possible RecF domain	54586	5.25	C		28.145	6.3	22,481
BL1245	gi 23465807	137	M	probable UDP-galactopyranose mutase	44819	5.16	C	gif	47.771	5.25	24,985
BL1247	gi 23465809	410	Q	possible 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase in the fumarylacetoacetate hydrolase family	32022	5	C		32.658	4.71	34,768
BL1249	gi 23465811	687	E	histidine ammonia-lyase	54343	5.54	C	hutH	62.543	5.84	11,485
BL1252	gi 23465814	61	C	possible phosphodiesterase	40005	4.83	C		48.849	4.87	7,663
BL1254	gi 23465816	312	F	uracil phosphoribosyltransferase	22646	5.27	C	upp	24.198	5.37	54,266
BL1259	gi 23465821	491	P	polyphosphate kinase	84143	5.98	C	ppk	44.389	4.52	68,695
BL1263	gi 23465825	296	E	3-isopropylmalate dehydratase small subunit	26088	4.98	C	leuD	26.369	5.08	21,042

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BL1265 <sup>a82-1</sup>	gi 23465827	64	F	hypothetical protein with similarity to dihydroorotate dehydrogenase	38946	4.87	C		45.062	4.91	5,981
BL1265 <sup>a82-2</sup>	gi 23465827	894	F	hypothetical protein with similarity to dihydroorotate dehydrogenase	39174	4.87	C		47.349	4.94	22,459
BL1267	gi 23465829	718	M	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	47438	5.93	C	murA	53.376	6.61	11,243
BL1272 <sup>a83-1</sup>	gi 23465834	20	J	arginyl-tRNA synthetase	67164	4.88	C	argS	72.824	4.81	10,157
BL1272 <sup>a83-2</sup>	gi 23465834	22	J	arginyl-tRNA synthetase	67164	4.88	C	argS	80.403	5.08	6,787
BL1274	gi 23465836	47	E	homoserine dehydrogenase	45901	4.87	U	thrA	51.19	4.89	103,317
BL1275	gi 23465837	74	E	possible homoserine kinase	38535	4.94	U	thrB	49.662	5.04	15,390
BL1277	gi 23465839	791	V	ATP-binding protein of ABC transporter system	37045	6.13	CM		43.251	6.75	145,022 <sup>b-41</sup>
BL1286	gi 23465848	75	E	aspartate aminotransferase	42774	4.97	C	aspC	48.558	5.07	35,640
BL1288	gi 23465850	501	K	probable transcription antitermination protein	32120	4.4	C	nusG	40.153	4.42	20,540
BL1290	gi 23465852	464	J	50S ribosomal protein L11	15291	9.21	C	rplK	17.569	4.61	13,554

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BL1292	gi 23465854	822	R	morphine 6-dehydrogenase	30318	5.55	U	morA	28.974	5.97	40,950
BL1295	gi 23465857	882	E	histidinol dehydrogenase	50397	4.93	C	hisD	62.607	4.94	29,071
BL1296	gi 23465858	66	E	histidinol-phosphate aminotransferase	42509	4.95	C	hisC	50.418	5	24,427
BL1297	gi 23465859	840	E	imidazoleglycerol-phosphate dehydratase	21804	5.62	C	hisB	24.152	6.18	25,033
BL1299	gi 23465860	291	E	amidotransferase HisH	23382	4.96	C	hisH	25.869	4.99	32,534
BL1300	gi 23465861	449	E	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase	25788	4.77	C	hisA	25.916	4.75	39,766
BL1302	gi 23465863	38	E	glutamine synthetase 2	50041	4.84	C	glnA2	62.917	4.9	2,583
BL1305	gi 23465866	542	L	ATP-dependent helicase	153089	7.24	C	hrpA	25.426	4.4	24,993
BL1306	gi 23465867	264	J	conserved hypothetical protein possibly in upfoo20	23597	5.07	U		28.527	5.18	41,744
BL1308 <sup>a84-1</sup>	gi 23465869	149	C	lactate dehydrogenase	34219	5.3	C	ldh2	41.097	5.69	19,771 <sup>b-18</sup>
BL1308 <sup>a84-2</sup>	gi 23465869	150	C	lactate dehydrogenase	34219	5.3	C	ldh2	39.718	5.68	60,464 <sup>b-18</sup>
BL1308 <sup>a84-3</sup>	gi 23465869	735	C	lactate dehydrogenase	34390	5.3	C	ldh2	41.097	5.56	38,751 <sup>b-18</sup>

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BL1311	gi 23465872	498	M	hypothetical protein with LysM domain of membrane-bound lytic murein transglycosylases	12260	6.82	U		38.815	4.27	13,536
BL1318	gi 23465879	535	M	hypothetical protein possibly involved in cell wall formation	30600	4.42	U		29.19	4.47	37,644
BL1319	gi 23465880	82	M	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanyl ligase	50616	5.04	C	murF	61.792	5.09	22,688
BL1321	gi 23465882	40	M	UDP-N-acetylmuramoylalanine--D-glutamate ligase	51022	4.93	C	murD	65.904	4.98	23,120
BL1326	gi 23465887	821	J	hypothetical protein BL1326	17296	5.29	C		22.008	5.71	15,542
BL1339	gi 23465900	192	G	protein in PfkB family of sugar kinases	32533	4.88	C		38.972	4.92	7,883
BL1344 <sup>a85-1</sup>	gi 23465905	530	G	N-acetylglucosamine-6-phosphate deacetylase	45536	5.51	C	nagA	28.63	4.54	46,187
BL1344 <sup>a85-2</sup>	gi 23465905	711	G	N-acetylglucosamine-6-phosphate deacetylase	45536	5.51	C	nagA	51.811	5.93	15,117
BL1345	gi 23465906	350	E	probable solute-binding protein of ABC transporter for peptides	58524	4.66	CW		67.922	4.6	22,780
BL1348	gi 23465909	842	R	ATP binding protein of ABC transporter	62455	6.05	CM		25.007	6.35	19,844
BL1349	gi 23465910	598	L	hypothetical protein containing MutT-like domain	19248	4.53	C		19.952	4.54	41,734

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BL1350 <sup>a86-1</sup>	gi 23465911	14	E	Xaa-Pro aminopeptidase I	58260	4.84	C	pepP	66.903	5.05	122,229 <sup>b-19</sup>
BL1350 <sup>a86-2</sup>	gi 23465911	30	E	Xaa-Pro aminopeptidase I	58260	4.84	C	pepP	70.021	4.87	137,669 <sup>b-19</sup>
BL1350 <sup>a86-3</sup>	gi 23465911	200	E	Xaa-Pro aminopeptidase I	58488	4.84	C	pepP	35.751	4.97	10,167 <sup>b-19</sup>
BL1350 <sup>a86-4</sup>	gi 23465911	294	E	Xaa-Pro aminopeptidase I	58488	4.84	C	pepP	26.152	5.03	13,165 <sup>b-19</sup>
BL1357 <sup>a87-1</sup>	gi 23465918	429	K	RNA polymerase sigma-E factor	29353	5.39	C	sigH	26.616	4.58	38,332 <sup>b-42</sup>
BL1357 <sup>a87-2</sup>	gi 23465918	595	K	RNA polymerase sigma-E factor	29353	5.39	C	sigH	22.62	4.41	37,451 <sup>b-42</sup>
BL1357 <sup>a87-3</sup>	gi 23465918	607	K	RNA polymerase sigma-E factor	29353	5.39	C	sigH	17.758	4.3	35,144 <sup>b-42</sup>
BL1357 <sup>a87-4</sup>	gi 23465918	765	K	RNA polymerase sigma-E factor	29353	5.39	C	sigH	34.03	5.76	13,055 <sup>b-42</sup>
BL1357 <sup>a87-5</sup>	gi 23465918	787	K	RNA polymerase sigma-E factor	29353	5.39	C	sigH	42.61	6.5	18,111 <sup>b-42</sup>
BL1360 <sup>a88-1</sup>	gi 23465921	151	G	hypothetical protein in aldose epimerase family	34815	4.82	C		40.299	4.8	11,038
BL1360 <sup>a88-2</sup>	gi 23465921	165	G	hypothetical protein in aldose epimerase family	34815	4.82	C		42.106	4.87	19,013
BL1363 <sup>a89-1</sup>	gi 23465924	123	G	glyceraldehyde 3-phosphate dehydrogenase C	37693	5.23	C	gap	50.879	5.38	87,993
BL1363 <sup>a89-2</sup>	gi 23465924	139	G	glyceraldehyde 3-phosphate dehydrogenase C	37693	5.23	C	gap	51.035	5.27	31,859



BL1367 <sup>a90-1</sup>	gi 23465929	509	J	50S ribosomal protein L20	14596	11.08	C	rplT	29.032	4.22	25,925
BL1367 <sup>a90-2</sup>	gi 23465929	625	J	50S ribosomal protein L20	14596	11.08	C	rplT	16.536	5.15	20,024
BL1374	gi 23465936	73	H	quinolinate synthetase	46449	5.33	C	nadA	49.29	5.05	35,940
BL1379	gi 23465941	3	T	widely conserved protein similar to those annotated as GTP-binding elongation factor TypA/BipA	70172	4.92	C		89.62	5.07	16,663
BL1382	gi 23465944	744	E	probable prephenate dehydrogenase	38123	5.45	C	tyrA	44.517	5.81	7,739
BL1386 <sup>a91-1</sup>	gi 23465947	11	E	DppA2	59024	5	CW	dppA2	69.547	5	46,520 <sup>b-12</sup>
BL1386 <sup>a91-2</sup>	gi 23465947	28	E	DppA2	59024	5	CW	dppA2	70.859	4.83	188,246 <sup>b-12</sup>
BL1386 <sup>a91-3</sup>	gi 23465947	156	E	DppA2	59024	5	CW	dppA2	41.018	4.76	8,866 <sup>b-12</sup>
BL1386 <sup>a91-4</sup>	gi 23465947	203	E	DppA2	59252	5	CW	dppA2	42.282	5.08	20,238 <sup>b-12</sup>
BL1386 <sup>a91-5</sup>	gi 23465947	213	E	DppA2	59252	5	CW	dppA2	34.791	5.21	21,518 <sup>b-12</sup>
BL1386 <sup>a91-6</sup>	gi 23465947	229	E	DppA2	59252	5	CW	dppA2	32.658	4.8	35,533 <sup>b-12</sup>
BL1386 <sup>a91-7</sup>	gi 23465947	582	E	DppA2	59252	5	CW	dppA2	29.126	4.62	23,895 <sup>b-12</sup>

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BL1386 <sup>a91-8</sup>	gi 23465947	888	E	DppA2	59252	5	CW	dppA2	43.98	5.01	11,110 <sup>b-12</sup>
BL1392 <sup>a92-1</sup>	gi 23465952 <sup>c</sup>	70	++	narrowly conserved hypothetical protein	30557	4.88	U		44.484	5.01	75,465
BL1392 <sup>a92-2</sup>	gi 23465952	169	++	narrowly conserved hypothetical protein	30557	4.88	U		47.489	4.9	5,157
BL1394	gi 23465954	697	J	conserved hypothetical protein with duf90	47731	5.6	C		57.672	5.9	16,460
BL1401	gi 23465961	818	K	hypothetical protein in acetyl transferase family	24737	5.68	C		23.369	5.74	13,494
BL1410 <sup>a93-1</sup>	gi 23465970	561	D	hypothetical protein with C-terminal similarity to cell (division) filamentation protein Fic	34022	6.07	C		31.29	4.57	29,190
BL1410 <sup>a93-2</sup>	gi 23465970	748	D	hypothetical protein with C-terminal similarity to cell (division) filamentation protein Fic	34022	6.07	C		44.332	6.01	7,612
BL1410 <sup>a93-3</sup>	gi 23465970	847	D	hypothetical protein with C-terminal similarity to cell (division) filamentation protein Fic	34022	6.07	C		26.754	6.51	32,895
BL1418	gi 23465978	457	J	hypothetical protein in sigma 54 modulation protein / S30ea ribosomal protein family	24668	5.85	C		23.907	4.74	16,561

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BL1419	gi 23465979	854	U	preprotein translocase SecA subunit	107651	5.18	C	secA	20.146	5.68	12,163
BL1422	gi 23465980	204	E	anthranilate phosphoribosyltransferase 1	36015	5	U	trpD	38.461	5.12	50,530
BL1424	gi 23465982	387	I	widely conserved hypothetical protein with acyl transferase domain	25401	9.39	C		31.987	4.59	68,175
BL1438	gi 23465996	820	F	deoxyuridine 5'-triphosphate nucleotidohydrolase	16737	5.42	C	dut	21.728	5.74	32,630
BL1442	gi 23465998	444	O	possible peptidyl-prolyl cis-trans isomerase	19925	4.7	C		21.636	4.7	77,729
BL1445 <sup>a94-1</sup>	gi 23466001	499	R	narrowly conserved hypothetical protein	22058	8.98	C		39.678	4.33	21,231 <sup>b-21</sup>
BL1445 <sup>a94-2</sup>	gi 23466001	860	R	narrowly conserved hypothetical protein	22058	8.98	C		17.876	5.62	17,602 <sup>b-21</sup>
BL1445 <sup>a94-3</sup>	gi 23466001	863	R	narrowly conserved hypothetical protein	22058	8.98	C		17.889	6.03	218,402 <sup>b-21</sup>
BL1455	gi 23466011	245	O	hypothetical protein BL1455	51878	6.11	C		30.19	4.9	25,087
BL1457	gi 23466013	753	O	metalloendopeptidase Gcp	36448	5.42	E	gcp	38.411	5.73	21,888
BL1458	gi 23466014	629	L	probable integrase/recombinase	35693	9.27	C		18.418	5.08	18,551
BL1461	gi 23466017	384	L	hypothetical protein BL1461	22798	6.32	C		38.664	4.66	14,089
BL1139	gi 23465707	600	L	hypothetical protein BL1139	12717	11.11	C		18.445	4.41	28,347

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BL1473	gi 23466029	391	L	modification methylase very similar to EcoRII (cytosine-specificmethyltransferase)	35970	6.76	U		32.208	4.64	21,533
BL1483	gi 23466039	511	O	narrowly conserved hypothetical protein	55584	5.71	C		30.251	4.31	35,392
BL1499	gi 23466055	609	C	isocitrate dehydrogenase [NADP]	45530	5.35	C	icd1	18.026	4.4	21,198
BL1500	gi 23466056	147	F	GMP reductase	39478	5.35	U		43.847	5.66	37,816
BL1502	gi 23466058	331	J	polypeptide deformylase	18357	5.31	C	def	18.862	5.59	42,626
BL1504 <sup>a95-1</sup>	gi 23466060	210	J	elongation factor TS	29961	5.07	C	tsf	33.513	5.13	318,381 <sup>b-13</sup>
BL1504 <sup>a95-2</sup>	gi 23466060	345	J	elongation factor TS	29961	5.07	C	tsf	20.242	5.24	7,091 <sup>b-13</sup>
BL1505	gi 23466061	314	F	uridylate kinase	26603	5.42	C	pyrH	27.986	5.45	39,405
BL1506	gi 23466062	852	J	ribosome recycling factor	20117	5.77	C	frr	21.933	6.17	133,949 <sup>b-47</sup>
BL1512	gi 23466067	320	F	deoxycytidine triphosphate deaminase	21451	5.27	C		25.028	5.62	23,225
BL1527	gi 23466080	709	E	catabolic threonine dehydratase	45466	5.39	C	tdcB	44.237	5.97	4,642
BL1531	gi 23466084	235	T	narrowly conserved hypothetical protein	30646	4.92	C		31.554	4.9	5,508

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BL1535	gi 23466088	390	I	JadJ	70379	5.75	C	jadJ	31.307	4.61	41,161
BL1548	gi 23466101	768	++	hypothetical protein BL1548	35788	5.98	U		32.171	5.73	34,671
BL1549	gi 23466102	633	J	50S ribosomal protein L10	18735	8.67	C	rplJ	16.854	4.96	5,893
BL1550	gi 23466103	463	J	50S ribosomal protein L7/L12	13239	4.56	U	rplL	17.491	4.63	306,381 <sup>b-17</sup>
BL1551 <sup>a96-1</sup>	gi 23466104	482	T	hypothetical protein BL1551	54780	4.54	U		76.644	4.43	3,736
BL1551 <sup>a96-2</sup>	gi 23466104	483	T	hypothetical protein BL1551	54780	4.54	U		76.186	4.45	7,154
BL1556	gi 23466108	853	J	possible acetyltransferase	25908	8	C		21.106	5.72	29,984
BL1558 <sup>a97-1</sup>	gi 23466110	476	O	groes	10594	5.1	C	groES	16.444	4.7	93,596 <sup>b-46</sup>
BL1558 <sup>a97-2</sup>	gi 23466110	477	O	groes	10594	5.1	C	groES	16.515	4.83	41,420 <sup>b-46</sup>
BL1561	gi 23466113	360	M	UDP-N-acetylenolpyruvoylglucosamine reductase	38210	4.88	U	murB	52.06	4.83	31,080
BL1568	gi 23466120	183	E	possible 2-hydroxyacid dehydrogenase	36945	5.21	C		42.4	5.31	3,682
BL1573	gi 23466125	513	G	probable glycogen operon protein GlgX	95917	5.08	C		24.484	4.29	75,781
BL1592	gi 23466142	479	J	50S ribosomal protein L5	21394	8.71	C	rplE	39.678	4.68	23,476

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BL1601	gi 23466151	301	F	adenylate kinase	20545	4.93	C	adk	22.803	4.95	112,380
BL1606 <sup>a98-1</sup>	gi 23466156	377	K	DNA-directed RNA polymerase alpha chain	36131	4.6	C	rpoA	49.216	4.66	125,129 <sup>b-48</sup>
BL1606 <sup>a98-2</sup>	gi 23466156	565	K	DNA-directed RNA polymerase alpha chain	36246	4.6	C	rpoA	49.394	4.65	5,119 <sup>b-48</sup>
BL1610	gi 23466160	770	E	narrowly conserved hypothetical protein in transglutaminase family	29995	5.42	C		32.572	5.81	3,684
BL1615 <sup>a99-1</sup>	gi 23466164	725	K	N utilization substance homolog	38002	5.64	C	nusA	52.664	6.03	13,555
BL1615 <sup>a99-2</sup>	gi 23466164	726	K	N utilization substance homolog	38002	5.64	C	nusA	51.128	6.1	12,521
BL1623	gi 23466172	240	G	probable ribose 5-phosphate isomerase	25253	4.83	C		28.44	4.84	60,867
BL1630 <sup>a100-1</sup>	gi 23466179	31	G	phosphoglucomutase	60385	4.92	C	pgm	71.588	4.9	50,150
BL1630 <sup>a100-2</sup>	gi 23466179	340	G	phosphoglucomutase	60385	4.92	C	pgm	17.612	5.26	12,892
BL1630 <sup>a100-3</sup>	gi 23466179	420	G	phosphoglucomutase	60385	4.92	C	pgm	30.688	4.83	12,564
BL1635 <sup>a101-1</sup>	gi 23466184	118	J	seryl-tRNA synthetase	47926	5.39	C	serS	54.428	5.73	54,820
BL1635 <sup>a101-2</sup>	gi 23466184	702	J	seryl-tRNA synthetase	48154	5.39	C	serS	54.428	5.63	17,162
BL1638	gi 23466186	567	G	solute binding protein of ABC transporter for sugars	46246	4.75	U		42.742	4.56	15,822

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BL1643	gi 23466191	544	G	galactose-1-phosphate uridylyltransferase	57118	4.74	C	galT2	23.895	4.32	21,946
BL1644 <sup>a102-1</sup>	gi 23466192	177	M	UDP-glucose 4-epimerase	37281	5.13	C	galE1	40.684	5.19	60,381 <sup>b-45</sup>
BL1644 <sup>a102-2</sup>	gi 23466192	205	M	UDP-glucose 4-epimerase	37281	5.13	C	galE1	40.463	5.12	70834 <sup>b-45</sup>
BL1644 <sup>a102-3</sup>	gi 23466192	275	M	UDP-glucose 4-epimerase	37281	5.13	C	galE1	23.462	5.15	7006 <sup>b-45</sup>
BL1645	gi 23466193	844	T	response regulator of two-component system	24488	5.76	C		26.754	6.43	23,787
BL1650	gi 23466198	455	++	hypothetical protein BL1650	24043	4.8	U		24.417	4.8	9,456
BL1654	gi 23466201	126	J	lysyl-tRNA synthetase 1	61835	4.86	C	lysS	79.421	4.94	3,286
BL1656 <sup>a103-1</sup>	gi 23466203 <sup>c</sup>	261	G	phosphoglycerate mutase	28817	5.8	U	gpm	28.88	5.33	80,047 <sup>b-16</sup>
BL1656 <sup>a103-2</sup>	gi 23466203 <sup>c</sup>	313	G	phosphoglycerate mutase	28703	5.8	U	gpm	29.09	5.45	199,202 <sup>b-16</sup>
BL1656 <sup>a103-3</sup>	gi 23466203	812	G	phosphoglycerate mutase	28817	5.8	U	gpm	28.711	5.87	28,800 <sup>b-16</sup>
BL1660 <sup>a104-1</sup>	gi 23466207	142	H	probable phosphoserine aminotransferase	40607	5.28	C	serC	44.089	5.48	11,620
BL1660 <sup>a104-2</sup>	gi 23466207	733	H	probable phosphoserine aminotransferase	40835	5.28	C	serC	43.075	5.52	30,017
BL1664	gi 23466211	154	T	widely conserved protein in universal stress protein family	36490	4.69	U		44.42	4.75	49,578

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BL1664a	gi 23466212	857	O	hypothetical protein BL1664a	15161	5.32	U		19.321	5.76	67,782
BL1665 <sup>a105-1</sup>	gi 23466213	225	F	thymidylate synthase	30897	5.56	C	thyA	27.844	5.79	11,710
BL1665 <sup>a105-2</sup>	gi 23466213	804	F	thymidylate synthase	30897	5.56	C	thyA	30.137	5.69	7,395
BL1666	gi 23466214	238	H	dihydrofolate reductase	24295	4.81	C	dfrA	29.427	4.82	2,537
BL1671 <sup>a106-1</sup>	gi 23466219	441	M	UDP-glucose 4-epimerase	37329	5.5	C	galE2	24.022	4.62	26,898 <sup>b-44</sup>
BL1671 <sup>a106-2</sup>	gi 23466219	443	M	UDP-glucose 4-epimerase	37329	5.5	C	galE2	21.693	4.64	36,852 <sup>b-44</sup>
BL1671 <sup>a106-3</sup>	gi 23466219	504	M	UDP-glucose 4-epimerase	37329	5.5	C	galE2	37.236	4.46	17,880 <sup>b-44</sup>
BL1671 <sup>a106-4</sup>	gi 23466219	532	M	UDP-glucose 4-epimerase	37329	5.5	C	galE2	30.011	4.52	48,713 <sup>b-44</sup>
BL1671 <sup>a106-5</sup>	gi 23466219	746	M	UDP-glucose 4-epimerase	37329	5.5	C	galE2	40.989	5.83	8,761 <sup>b-44</sup>
BL1672	gi 23466220	701	M	possible cyclopropane-fatty-acyl-phospholipid synthase	49138	5.8	C		57.055	6.39	9,592
BL1673 <sup>a107-1</sup>	gi 23466221	57	C	possible lactaldehyde reductase	40598	4.74	C	fucO	48.63	4.8	102,723 <sup>b-50</sup>
BL1673 <sup>a107-2</sup>	gi 23466221	375	C	possible lactaldehyde reductase	40598	4.74	C	fucO	50.038	4.63	17,940 <sup>b-50</sup>
BL1682 <sup>a108-1</sup>	gi 23466230	182	O	ATP-dependent zinc metallopeptidase involved in cell division	75961	5.54	CM	ftsH	41.074	5.31	7,593

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BL1682 <sup>a108-2</sup>	gi 23466230	267	O	ATP-dependent zinc metallopeptidase involved in cell division	75961	5.54	CM	ftsH	29.458	5.05	18,523
BL1682 <sup>a108-3</sup>	gi 23466230	269	O	ATP-dependent zinc metallopeptidase involved in cell division	75961	5.54	CM	ftsH	30.995	5.1	13,953
BL1684	gi 23466232	260	H	dihydropteroate synthase I	30520	5.19	C	folP	29.365	5.31	51,138
BL1687	gi 23466235	775	I	acyl-CoA thioesterase II	32992	5.52	C	tesB	31.604	6	21,877
BL1700 <sup>a109-1</sup>	gi 23466247	423	J	polypeptide deformylase	15554	6.29	C	fms	28.325	4.76	25,629
BL1700 <sup>a109-2</sup>	gi 23466247	493	J	polypeptide deformylase	15725	6.29	C	fms	43.553	4.43	6,557
BL1707	gi 23466253	628	++	hypothetical protein BL1707	14590	11.22	U		16.461	5.01	34,850
BL1712	gi 23466257	359	J	peptide chain release factor I	40029	4.74	C	prfA	55.228	4.83	34,324
BL1714	gi 23466259	158	E	solute binding protein of ABC transporter for branched-chain amino acids	41373	5.08	U		41.815	4.92	11,882
BL1717	gi 23466262	754	E	ATP binding protein of ABC transporter for branched-chain amino acids	31517	5.24	CM		39.006	5.58	14,548
BL1718 <sup>a110-1</sup>	gi 23466263	618	E	ATP binding protein of ABC transporter for branched-chain amino acids	25520	8.54	CM		16.479	5.09	401,113 <sup>b-7</sup>

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				acids								
				ATP binding protein of ABC transporter for branched-chain amino acids								
BL1718 <sup>a110-2</sup>	gi 23466263	873	E		25520	8.54	CM		16.463	5.92	52,971 <sup>b-7</sup>	
				acids								
BL1723	gi 23466268	295	A	probable oligoribonuclease	24345	4.98	C	orn	26.345	5.05	11,150	
BL1728	gi 23466273	19	J	prolyl-tRNA synthetase	66113	4.84	C	proS	76.963	4.8	5,879	
BL1732	gi 23466277	244	J	methionine aminopeptidase	28589	4.91	C	map	30.454	4.87	5,564	
BL1734	gi 23466279	759	E	widely conserved hypothetical protein	35705	5.59	C		39.207	5.91	20,497	
BL1750	gi 23466294	605	L	exonuclease VII, small subunit	10899	4.4	U	xseB	18.042	4.32	29,435	
BL1755 <sup>a111-1</sup>	gi 23466299	96	H	possible glutamate--cysteine ligase	43607	4.8	C		55.577	5.13	12,692	
BL1755 <sup>a111-2</sup>	gi 23466299	97	H	possible glutamate--cysteine ligase	43607	4.8	C		52.624	5.11	11,402	
BL1786 <sup>a112-1</sup>	gi 23466330	44	H	S-adenosylmethionine synthetase	43748	4.85	C	metK	58.762	4.87	73,793	
BL1786 <sup>a112-2</sup>	gi 23466330	358	H	S-adenosylmethionine synthetase	43748	4.85	C	metK	59.911	4.83	18,447	
BL1787	gi 23466331	885	K	probable DNA-directed RNA polymerase omega chain	10360	4.22	C	rpoZ	52.06	4.98	38,593	

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BL1794 <sup>a113-1</sup>	gi 23466338	79	O	probable Aaa-family ATPase	56443	4.99	CM	66.457	5.06	4,445	
BL1794 <sup>a113-2</sup>	gi 23466338	256	O	probable Aaa-family ATPase	56557	4.99	CM	31.59	5.22	11,949	
BL1795	gi 23466339	676	++	hypothetical proteasome-associated protein	61597	5.19	C	68.299	5.46	12,181	
BL1796	gi 23466340	802	G	possible inositol monophosphatase	33641	6	C	29.211	6.75	9,389	
BL1800 <sup>a114-1</sup>	gi 23466344	117	F	adenylosuccinate lyase	53708	5.33	C	purB	54.796	5.35	8,178
BL1800 <sup>a114-2</sup>	gi 23466344	684	F	adenylosuccinate lyase	53708	5.33	C	purB	61.469	5.74	12,809

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- Spots representing the same protein were labeled with upper letter such as a1-1 on the right of locus name. “a” means a protein distributing more than one spot on the gel. The first “1” means the no. of the 115 proteins distributing more than one spot from 1 to 115. The second “1” means that the no. of spot representing the protein.
- The 50 most abundant proteins were labeled with upper letter such as b-1 on the right of abundance value. The number behind “b” is used to mark the 50 most abundant proteins.
- The proteins conformed by ESI-MS/MS were labeled with upper letter c.
- Abbreviation of cellular role categories. Categories were taken from the TIGR-CMR ([www.tigr.org](http://www.tigr.org)) and the abbreviation was used to mark the

categories. A: amino acid biosynthesis; B: biosynthesis of cofactors, prosthetic groups, and carriers; C1: cell envelope; C2: cellular processes; C3: central intermediary metabolism; D: DNA metabolism; E: energy metabolism; F: fatty acid and phospholipid metabolism; H: hypothetical proteins; P1: protein fate; P2: protein synthesis; P3: purines, pyrimidines, nucleosides, and nucleotides; R: regulatory functions; S: signal transduction; T1: transcription; T2: transport and binding proteins; U: unknown function and the blank in this column representing the category not classified.

5. Abbreviation of cellular locations. Protein cellular location was annotated by psort v.2.0 ([www.psort.org](http://www.psort.org)). C: cytoplasmic; CM: cytoplasmic membrane; E: extracellular; U: unknown. U\*\*: This protein may have multiple localization site.