

**Table S1.** Identification of proteins expressed in early stationary phase culture of *Burkholderia pseudomallei* by MALDI-TOF MS.

Gene <sup>a</sup>	Spot number	Accession number	Locus in <i>B. pseudomallei</i> strain K96243 genome	% Seq coverage	Peptides matched	Score	Theo/exp pI	Theo/exp MW (kDa)	Virulence/Potential virulence <sup>b</sup>
<b>Cell envelope biogenesis and outer membrane</b>									
Exopolysaccharide biosynthesis related tyrosine-protein kinase (BceF)	1	YP_111834	BPSS1830	12	9	65	6.61/4.74	79.3/39.3	[1]
UDP-N-acetylmuramoyl-tripeptide D-alanyl-D-alanine ligase (MurF)	2	ZP_01324088	BPSS1239	50	15	152	5.87/5.73	47.8/38.0	[2]
Porin related exported protein (OmpC)	3	YP_111684	BPSS1679	42	13	125	7.78/6.60	40.1/33.9	[3]
UDP-glucose 4-epimerase (GalE)	4	YP_109266	BPSS12670	54	19	223	6.17/6.63	37.2/36.2	[4]
D-alanyl-D-alanine carboxypeptidase (DAP)	5	ZP_00486077	BPSS1239	36	9	91	10.64/4.90	35.6/50.0	[5]
D-alanine-D-alanine ligase B (DalB)	6	YP_109619	BPSS13023	59	14	184	5.26/5.13	33.5/31.1	
Outer membrane protein A (OmpA)	7	YP_109118	BPSS12522	45	18	173	9.51/4.29	24.3/23.8	[6]
Periplasmic/secreted protein	8	ZP_01331873	BPSS10972	61	20	217	8.20/6.28	23.1/21.1	
Acetyltransferase (GNAT) family protein (Gcn5)	9	YP_112313	BPSS2310	34	7	81	9.72/4.73	20.1/45.4	
Phosphatidylethanolamine-binding protein	10	YP_107676	BPSS1049	55	7	106	5.26/5.11	18.3/16.8	
Phosphatidylethanolamine-binding protein	11	YP_107676	BPSS1049	47	7	106	5.26/4.72	18.3/13.7	
Metal-binding periplasmic protein	12	YP_112008	BPSS2003	65	8	134	9.16/6.02	17.8/20.0	
LysM/phospholipid-binding domain protein	13	YP_108071	BPSS1449	38	5	78	4.54/4.54	16.4/16.4	
Exported protein surface antigen	14	ZP_00895393	BPSS2014	85	10	114	9.07/4.71	12.5/17.2	
<b>Energy metabolism</b>									
ATP synthase subunit B (AtpD)	15	YP_109989	BPSS13396	47	19	170	5.26/4.95	50.8/48.2	
ATP synthase subunit B (AtpD)	16	YP_109989	BPSS13396	36	12	118	5.26/5.08	50.8/48.4	
ATP synthase subunit B (AtpD)	17	YP_109989	BPSS13396	58	21	204	5.26/5.13	50.8/48.4	
ATP synthase subunit D (AtpH)	18	YP_109992	BPSS13399	58	11	130	5.30/5.17	19.0/16.4	
ATP synthase subunit epsilon (AtpC)	19	YP_109988	BPSS13395	46	5	75	5.11/5.08	14.9/15.8	
NADH-ubiquinone oxidoreductase subunit E (NuoE)	20	ZP_00440948	BPSS1215	38	5	78	4.85/4.94	15.0/15.1	
NAD(P) transhydrogenase subunit alpha	21	YP_109481	BPSS2887	31	9	102	6.34/6.68	39.3/43.0	
Aldehyde dehydrogenase (NAD) family protein	22	ZP_00487209	BPSS1550	64	24	251	5.46/5.55	50.7/49.1	
Aldehyde dehydrogenase (NAD) family protein	23	ZP_00487209	BPSS1550	54	19	202	5.46/5.65	50.7/49.1	
Aldehyde dehydrogenase (NAD) family protein	24	ZP_00487209	BPSS1550	66	26	275	5.46/5.86	50.7/49.2	
NAD-dependent aldehyde dehydrogenase	25	ZP_00489836	BPSS1354	39	18	167	5.50/5.18	52.4/45.2	
NADH dehydrogenase delta subunit (NuoD)	26	YP_107836	BPSS1214	35	11	148	6.12/5.52	47.6/34.0	
Succinyl-CoA synthetase subunit beta (SucC)	27	YP_107404	BPSS10779	19	8	77	5.25/4.67	41.4/45.6	
Succinate dehydrogenase catalytic subunit (SdhB)	28	YP_106305	BPSS1717	65	23	211	6.00/6.46	27.4/30.5	
Malate dehydrogenase (Mdh)	29	YP_106310	BPSS1722	60	18	204	5.70/6.01	35.1/32.8	
Malate dehydrogenase (Mdh)	30	YP_106310	BPSS1722	56	18	208	5.70/4.46	35.1/32.2	
Electron transfer flavoprotein alpha-subunit (EtfA)	31	YP_109094	BPSS2499	62	14	183	4.86/4.72	31.6/29.5	
Molybdopterin oxidoreductase	32	YP_108802	BPSS2207	25	21	139	8.76/4.96	86.4/32.8	
Ferredoxin-NADP reductase (Fpr)	33	YP_106868	BPSS0241	80	22	238	5.78/6.16	29.0/26.7	
Nitrotriacetate monooxygenase component A (NtaA)	34	YP_110863	BPSS0851	42	15	166	8.94/5.38	48.0/26.2	
2-nitropropane dioxygenase (Npd)	35	ZP_00487498	BPSS0328	40	6	116	5.79/6.24	33.9/29.4	
Phosphate acetyltransferase	36	YP_111961	BPSS1955	70	22	245	5.82/6.21	49.2/49.1	
Phosphate acetyltransferase	37	YP_111961	BPSS1955	29	10	145	5.82/6.31	49.2/29.1	
Inorganic pyrophosphatase (Ppa)	38	YP_107649	BPSS1021	72	23	304	5.37/5.25	19.2/21.0	[7]
Inorganic pyrophosphatase (Ppa)	39	YP_107649	BPSS1021	36	9	125	5.37/5.02	19.2/20.8	
Polyphosphate kinase 2 family (Ppk2)	40	YP_335445	BPSS1281	24	12	131	9.55/4.73	59.9/41.1	
<b>Carbohydrate metabolism</b>									
Carbohydrate porin, OprB family	41	YP_104819	BPSS0294	31	11	116	6.54/5.17	53.0/48.2	[8]
ABC-type sugar transport system	42	YP_110795	BPSS0786	32	9	107	8.82/4.74	35.9/31.5	
ABC-type sugar transport system	43	ZP_00896510	BPSS0787	24	8	88	8.48/4.63	55.3/28.0	
Phosphoglucomutase (Pgm)	44	ZP_00490197	BPSS2666	74	36	118	5.02/5.00	51.1/48.0	[9]
Phosphoglucomutase (Pgm)	45	YP_109262	BPSS2666	70	31	102	5.23/5.07	50.2/47.5	
Mannose-6-phosphate isomerase	46	YP_335985	BPSS1747	17	8	57	10.97/4.73	22.5/21.7	
Glyceraldehyde 3-phosphate dehydrogenase (GapA)	47	YP_109546	BPSS2952	58	13	164	6.37/4.47	36.3/34.9	[10]
Glyceraldehyde 3-phosphate dehydrogenase (GapA)	48	YP_109546	BPSS2952	85	25	282	6.37/6.70	36.3/37.0	

Table S1. Continued

Gene	Spot number	Accession number	Locus in <i>B. pseudomallei</i> strain K96243 genome	% Seq coverage	Peptides matched	Score	Theo/exp pl	Theo/exp MW (kDa)	Virulence/Potential virulence <sup>b</sup>
Phosphoglycerate kinase (Pgk)	49	ZP_00895324	BPSSL0796	61	21	245	5.58/5.72	41.4/43.7	[11]
Phosphoglycerate kinase (Pgk)	50	ZP_00895324	BPSSL0796	50	21	242	5.58/5.18	41.4/28.9	
Phosphopyruvate hydratase (Eno)	51	YP_108866	BPSSL2270	54	25	252	4.81/4.76	45.9/45.4	[12]
Phosphopyruvate hydratase (Eno)	52	YP_108866	BPSSL2270	24	9	98	4.81/4.78	45.9/45.4	
Phosphogluconolactonase (Pgl)	53	ZP_01337223	BPSSL2613	38	7	118	6.15/6.60	24.0/19.8	[13]
Trehalose-6-phosphatase (OstB)	54	ZP_00487870	BPSSL2411	30	10	124	5.61/5.76	26.4/25.0	[14]
Methylisocitrate lyase (PrpB)	55	YP_106412	BPSS0206	77	22	249	5.26/5.14	32.1/27.7	
Nucleoside-diphosphate-sugar epimerases	56	YP_107886	BPSSL1265	54	15	205	5.31/5.26	22.1/24.5	
Lipid metabolism									
Enoyl-CoA hydratase (PaaF)	57	YP_107280	BPSSL0651	49	11	132	6.22/4.67	27.0/35.2	
Enoyl-CoA hydratase (PaaG)	58	YP_105309	BPSSL3043	55	17	193	5.31/5.24	28.5/25.6	
Acetyl-CoA acetyltransferase (PhbA)	59	YP_108155	BPSSL1535	45	20	204	6.62/6.06	40.7/33.0	
Fatty aldehyde dehydrogenase	60	YP_110058	BPSS0034	39	16	154	6.19/6.58	55.1/64.3	
3-hydroxyisobutyrate dehydrogenase (MmsB)	61	ZP_00487155	BPSS0620	39	11	114	5.77/6.11	29.1/28.2	
Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (ScoA)	62	YP_108553	BPSSL1955	50	11	143	5.56/5.89	25.4/25.2	
Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (ScoA)	63	YP_108553	BPSSL1955	34	9	106	5.56/5.34	25.4/24.6	
Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit B (ScoB)	64	YP_108552	BPSSL1954	46	12	126	4.70/4.78	22.3/23.9	
Acetoacetyl-CoA reductase (PhbB)	65	ZP_00490574	BPSS1916	35	8	120	6.07/6.00	25.3/25.7	
Acetoacetyl-CoA reductase (PhbB)	66	YP_111922	BPSS1916	64	21	213	6.30/6.54	26.6/24.8	
Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II (Acs)	67	ZP_01321975	BPSS1274	35	12	129	6.84/5.14	47.2/37.1	
Acyl-carrier-protein S-malonyltransferase (FabD)	68	YP_109033	BPSSL2441	56	14	176	5.46/5.38	32.2/30.2	
Acyl-carrier-protein S-malonyltransferase	69	YP_107960	BPSSL1335	33	6	92	5.76/5.08	32.5/16.4	
Aryl alcohol dehydrogenase	70	ZP_01317539	BPSSL1094	61	7	110	5.29/5.21	16.2/16.1	
4-hydroxy-3-methylbut-2-enyl diphosphate reductase (IspH)	71	YP_107546	BPSSL0919	63	20	215	5.71/6.02	35.4/37.6	
Carboxymuconolactone decarboxylase (PcaC)	72	YP_332204	BPSSL0589	45	8	119	9.80/5.34	22.9/22.7	
Non-ribosomally encoded peptide/polyketide synthase (CmaB)	73	YP_111196	BPSS1183	57	21	247	5.77/6.19	35.6/34.8	
Amino acid metabolism									
Argininosuccinate synthase (ArgG)	74	YP_106925	BPSSL0298	73	33	315	5.37/5.26	49.8/47.2	
Xaa-Pro aminopeptidase	75	ZP_00486035	BPSSL2892	26	12	120	5.30/5.41	51.2/45.5	
Serine-pyruvate aminotransferase	76	ZP_01209494	BPSS0343	32	8	101	6.30/4.76	32.6/40.5	
Phosphoserine aminotransferase (SerC)	77	YP_109115	BPSSL2519	40	12	134	5.94/4.91	39.6/39.2	[15]
L-allo-threonine aldolase (ItaE)	78	YP_110255	BPSS0236	27	8	109	5.65/6.00	35.9/35.5	
Diaminopimelate epimerase (DapF)	79	YP_440730	BPSSL0210	47	12	150	5.58/5.68	31.2/29.0	
Cysteine synthase (CysM)	80	YP_109102	BPSSL2507	61	18	202	5.68/5.87	32.7/31.6	
Imidazole glycerol phosphate synthase subunit (HisH)	81	YP_109728	BPSSL3135	37	7	94	5.73/6.45	23.7/25.7	
Imidazole glycerol phosphate synthase subunit (HisF)	82	YP_109726	BPSSL3133	58	23	225	5.44/5.17	27.7/25.0	
Phosphoribosyl formimino-5-aminoimidazole carboxamide ribonucleotide isomerase (HisA)	83	YP_109727	BPSSL3134	70	21	204	4.37/4.38	26.8/26.5	
Tryptophan synthase subunit alpha (TrpA)	84	YP_111702	BPSS1697	71	18	212	5.30/5.19	28.0/26.5	
3-dehydroquinate synthase (AroB)	85	YP_109761	BPSSL3168	42	15	162	5.60/5.83	38.1/36.3	[16]
2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase (DapD)	86	YP_108764	BPSSL2169	37	10	125	5.68/6.00	29.7/30.5	
Nucleotide metabolism									
Pyrimidine regulatory protein (PyrR)	87	YP_109287	BPSSL2691	56	6	118	5.61/5.64	18.1/16.4	
Orotidine 5'-phosphate decarboxylase (PyrF)	88	YP_109557	BPSSL2963	65	14	179	5.08/4.97	29.9/27.6	[17]
Dihydroorotate dehydrogenase (PyrD)	89	ZP_00488468	BPSSL1866	50	11	142	8.38/4.67	34.7/39.5	[18]
Phosphoribosylaminoimidazole-succinocarboxamide synthase (HemH)	90	YP_107424	BPSSL0799	58	19	216	5.23/5.17	32.9/32.7	[19]
Deoxyribose-phosphate aldolase (DeoC)	91	ZP_00489036	BPSS1962	34	7	90	5.42/5.28	27.1/27.7	[20]
Deoxyribose-phosphate aldolase (DeoC)	92	YP_336226	BPSS1962	87	20	249	5.42/5.53	27.2/27.2	
Nucleoside diphosphate kinase (Ndk)	93	YP_108130	BPSSL1510	56	7	110	5.61/5.88	15.6/16.0	[21]
Thymidylate synthase	94	YP_111119	BPSS1106	34	11	99	6.37/4.91	37.4/37.8	[22]

Table S1. Continued

Gene	Spot number	Accession number	Locus in <i>B. pseudomallei</i> strain K96243 genome	% Seq coverage	Peptides matched	Score	Theo/exp pI	Theo/exp MW (kDa)	Virulence/Potential virulence <sup>b</sup>
Adenylate kinase (Adk)	95	YP_107500	BPSL0875	26	8	85	7.74/4.88	24.2/24.2	[23]
Adenylate cyclase	96	YP_110015	BPSL3422	46	10	159	5.02/4.90	19.7/23.6	[24]
Coenzyme metabolism									
ABC-type siderophores transport systems	97	ZP_00490149	BPSL2723	44	12	155	6.67/6.58	28.6/27.2	
Molybdopterin biosynthesis protein	98	YP_334335	BPSL2480	41	8	120	5.46/5.37	22.3/24.2	
Phosphopantetheine adenylyltransferase (CoaD)	99	YP_107142	BPSL0516	61	12	137	6.12/6.69	18.5/16.4	
Ketopantoate hydroxymethyltransferase (PanB)	100	YP_109419	BPSL2824	61	12	136	5.58/5.67	28.8/27.3	
Riboflavin synthase subunit alpha (RibE)	101	YP_109221	BPSL2625	76	12	145	5.49/5.54	21.7/21.1	
Pyridoxal phosphate biosynthetic protein (PdxJ)	102	YP_334273	BPSL2426	54	10	132	5.78/6.20	27.7/29.4	
Secondary metabolite metabolism									
Cytochrome P450	103	ZP_00440831	BPSS0023	36	17	169	9.13/4.80	44.8/50.0	
Cytochrome P450	104	ZP_00486588	BPSS0023	29	11	123	9.13/5.24	44.8/48.3	
cis-diol dehydrogenase (BenD)	105	YP_111912	BPSS1906	43	12	157	6.66/4.95	27.5/27.7	
Benzoate 1,2-dioxygenase hydroxylase component, beta subunit (BenB)	106	ZP_00490585	BPSS1904	68	10	150	5.13/4.70	19.2/15.1	
Inorganic ion metabolism									
Sulfite reductase, beta subunit	107	ZP_00487414	BPSL1319	41	28	208	6.75/4.92	67.6/53.1	
Rhodanese-related sulfurtransferase	108	YP_105132	BPSS1766	57	17	169	5.98/6.36	31.1/28.9	
Phosphonate metabolism protein (PhnI)	109	YP_334725	BPSL2855	31	13	114	5.15/4.73	43.5/23.0	
ABC-type phosphate/phosphonate transport system (PhnC)	110	ZP_01320985	BPSL2850	43	7	93	11.58/4.81	24.6/32.0	
ABC-type organic solvent resistance	111	ZP_00892628	BPSL3150	40	8	100	5.83/5.93	29.4/34.4	
DNA replication, recombination and repair									
Replicative DNA helicase (DnaB)	112	ZP_01337384	BPSL1462	30	11	110	9.04/4.91	41.9/38.5	
Single-strand DNA-binding protein (Ssb)	113	YP_107172	BPSL0547	55	9	138	5.51/5.68	18.7/20.1	
Mg-dependent DNase	114	ZP_00895143	BPSL1439	29	7	87	6.16/5.73	30.6/49.5	
Integrase core domain protein	115	YP_001074590	BPSS0407	68	11	122	11.22/4.92	21.1/19.9	
Transcription									
DNA-directed RNA polymerase alpha subunit (RpoA)	116	YP_109781	BPSL3187	72	28	297	5.76/6.09	35.8/42.0	
Transcription initiation factor	117	YP_111848	BPSS1844	42	6	76	5.04/4.95	13.1/13.9	
Transcription elongation factor (GreA)	118	YP_107977	BPSL1352	92	15	228	4.50/4.48	17.0/18.2	
Sigma-54 interacting transcriptional regulator	119	YP_112253	BPSL2250	34	14	139	9.57/4.95	35.9/32.2	
Phage shock protein A	120	YP_108702	BPSL2105	62	20	166	5.11/4.97	24.5/25.9	
Phage shock protein A	121	YP_108702	BPSL2105	52	12	147	5.11/4.92	24.5/26.0	
LysR-family transcriptional regulator	122	YP_108192	BPSL1572	27	6	76	6.72/5.72	31.6/45.8	
IcIR regulatory protein	123	YP_108891	BPSL2295	56	19	199	8.45/4.91	29.9/28.0	
Transcriptional regulator, ArsR family	124	YP_336380	BPSS2119	47	7	111	5.75/4.89	24.7/35.5	
Response regulator with putative antiterminator output domain	125	ZP_00486070	BPSS1246	46	17	160	5.24/5.14	22.1/23.7	
Transcriptional regulator, XRE family	126	YP_104861	BPSS0004	47	15	157	9.00/5.39	21.7/23.5	
AsnC-family regulatory protein	127	YP_107935	BPSL1311	65	15	213	6.74/6.53	18.2/28.1	
Transcriptional regulator	128	ZP_00894941	BPSL1269	34	5	70	6.74/5.02	16.2/11.8	
DksA family protein	129	YP_106833	BPSL0205	83	14	191	5.26/5.13	16.1/16.4	
Nucleoside diphosphate kinase regulator	130	YP_110889	BPSS0880	91	16	190	5.04/5.04	15.3/16.0	
Transcriptional activator (FlhD)	131	YP_109907	BPSL3311	54	6	74	5.85/4.95	11.7/17.0	[25]
DNA-binding protein HU-alpha (HupA)	132	YP_106629	BPSL0004	80	10	158	10.20/4.48	9.60/13.1	
Translation									

Table S1. Continued

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tRNA nucleotidyltransferase (cca)	133	YP_106892	BPSSL0265	45	14	159	7.25/4.76	45.2/34.5	
tRNA nucleotidyltransferase (cca)	134	YP_106892	BPSSL0265	44	12	139	7.25/5.23	45.2/38.0	
Elongation factor Tu (Tuf)	135	YP_109809	BPSSL3215	54	18	189	5.36/4.97	43.2/45.4	[26]
Elongation factor Tu (Tuf)	136	YP_109809	BPSSL3215	50	15	143	5.36/4.10	43.2/44.2	
Elongation factor Tu (Tuf)	137	YP_109809	BPSSL3215	53	18	174	5.36/4.16	43.2/45.3	
Elongation factor Tu (Tuf)	138	YP_109809	BPSSL3215	67	24	209	5.36/4.68	43.2/44.3	
Elongation factor Tu (Tuf)	139	YP_109809	BPSSL3215	42	13	131	5.36/4.93	43.2/46.6	
Elongation factor Tu (Tuf)	140	ZP_01320582	BPSSL3215	35	9	139	5.18/4.94	40.3/38.6	
Elongation factor Ts (Tsf)	141	YP_108753	BPSSL2158	72	25	246	5.38/5.19	31.3/30.9	
Elongation factor Ts (Tsf)	142	YP_108753	BPSSL2158	59	21	216	5.38/5.08	31.3/31.4	
GTP-binding GTPase (YchF)	143	YP_105289	BPSSL3062	64	21	251	4.98/4.96	39.4/46.6	[27]
30S ribosomal protein S2 (RpsB)	144	YP_108754	BPSSL2159	84	27	241	7.90/4.23	27.1/30.2	
30S ribosomal protein S3 (RpsC)	145	YP_109801	BPSSL3027	39	8	89	10.56/4.95	29.9/35.2	
30S ribosomal protein S4 (RpsD)	146	YP_109782	BPSSL3188	38	10	125	10.13/6.06	23.2/22.8	
30S ribosomal protein S5 (RpsE)	147	ZP_00439647	BPSSL3196	75	18	183	10.41/4.28	15.8/17.7	
30S ribosomal protein S9 (RpsI)	148	YP_103901	BPSSL2910	66	6	121	10.65/4.13	14.3/16.0	
30S ribosomal protein S9 (RpsI)	149	YP_103901	BPSSL2910	66	10	98	10.65/4.27	14.3/16.0	
50S ribosomal protein L3 (RplC)	150	YP_109807	BPSSL3213	63	15	181	9.99/4.24	23.0/24.5	
50S ribosomal protein L4 (RplD)	151	YP_109806	BPSSL3212	53	8	143	9.62/4.91	22.9/22.4	
50S ribosomal protein L4 (RplD)	152	YP_109806	BPSSL3212	66	11	149	9.62/5.02	22.9/22.3	
50S ribosomal protein L6 (RplF)	153	YP_109792	BPSSL3198	86	16	207	9.63/4.55	18.7/18.0	
50S ribosomal protein L7/L12	154	YP_104175	BPSSL3222	81	9	135	4.90/4.90	12.6/12.6	
2-methylthioadenine synthetase	155	YP_108158	BPSSL1538	35	12	129	5.87/4.69	50.1/31.5	
Post-translational modification									
Molecular chaperone (DnaK)	156	YP_109422	BPSSL2827	39	22	121	4.94/4.93	69.8/80.0	[28]
Chaperonin GroEL	157	AAO46033	BPSSL2697	67	41	121	5.18/4.95	56.5/57.2	[29]
Chaperonin GroEL	158	AAO46033	BPSSL2697	80	44	147	5.18/4.97	56.5/56.5	
Chaperonin GroEL	159	AAO46033	BPSSL2697	77	46	166	5.18/5.00	56.5/56.5	
Chaperonin GroEL	160	AAO46033	BPSSL2697	77	40	126	5.18/5.06	56.5/55.4	
Chaperonin GroES	161	YP_109294	BPSSL2698	91	11	169	5.78/5.21	10.5/14.9	
Chaperonin GroES	162	YP_109294	BPSSL2698	77	11	154	5.78/4.97	10.5/13.8	
Chaperonin GroES	163	YP_109294	BPSSL2698	72	8	122	5.78/4.97	10.5/14.7	
Chaperonin GroES	164	YP_109294	BPSSL2698	72	8	122	5.78/6.00	10.5/14.9	
Heat shock Hsp20-related protein	165	YP_109511	BPSSL2917	57	5	81	6.30/6.51	15.2/19.7	
HSP20/alpha crystallin family protein	166	YP_112291	BPSS2288	76	9	145	5.14/5.00	16.0/15.8	
HSP20/alpha crystallin family protein	167	YP_112291	BPSS2288	60	5	99	5.14/4.78	16.0/15.9	
HSP20/alpha crystallin family protein	168	YP_112291	BPSS2288	76	9	148	5.14/5.00	16.0/16.3	
GrpE heat shock protein	169	YP_109423	BPSSL2829	42	9	124	4.78/4.27	19.7/22.5	
Peptidyl-prolyl cis-trans isomerase, cyclophilin family (PpiA)	170	ZP_00487969	BPSSL2245	50	14	165	9.49/6.59	20.4/18.9	[30]
Peptidyl-prolyl cis-trans isomerase B (PpiB)	171	ZP_01322808	BPSSL2246	45	8	92	6.20/6.02	15.6/19.1	
Peptidyl-prolyl cis-trans isomerase B (PpiB)	172	YP_108841	BPSSL2246	68	18	210	5.94/6.39	17.9/19.2	
Peptidyl-prolyl cis-trans isomerase B (PpiB)	173	YP_108841	BPSSL2246	65	12	161	5.94/6.55	17.9/19.4	
Peptidyl-prolyl cis-trans isomerase B (PpiB)	174	YP_108841	BPSSL2246	69	16	210	5.94/6.28	17.9/19.5	
Peptidyl-prolyl cis-trans isomerase B (PpiB)	175	YP_108841	BPSSL2246	69	16	194	5.94/6.18	17.9/19.2	
Glutathione S-transferase	176	YP_108349	BPSSL1749	50	9	120	6.99/6.67	26.7/28.9	
Glutathione S-transferase	177	YP_108349	BPSSL1749	38	9	104	6.99/6.53	26.7/22.9	
Glutaredoxin-related protein	178	YP_105273	BPSSL3075	48	5	81	4.68/4.74	11.6/12.6	
Thioredoxin	179	ZP_00487706	BPSSL0856	71	18	233	4.59/4.55	31.2/29.4	
Thioredoxin 1 (TrxA)	180	YP_333769	BPSSL1497	63	10	129	8.83/6.06	16.0/15.8	[31]
Thiol peroxidase (Tpx)	181	YP_109581	BPSSL2987	97	15	235	5.12/5.02	17.4/17.9	[32]
ATP-dependent Clp protease ATP-binding subunit (ClpA)	182	ZP_01335014	BPSSL0899	41	14	157	6.02/4.78	35.7/29.0	[33]
Leucyl/phenylalanyl-tRNA protein transferase	183	YP_111202	BPSS1192	31	10	84	6.36/4.92	47.0/49.6	
Protein-L-isoaspartate O-methyltransferase (Pcm)	184	YP_109244	BPSSL2648	75	18	216	5.55/5.57	24.1/24.9	
Xanthine and CO dehydrogenases	185	ZP_00486866	BPSSL0237	22	7	102	5.68/4.92	36.7/27.1	

Table S1. Continued

Gene	Spot number	Accession number	Locus in <i>B. pseudomallei</i> strain K96243 genome	% Seq coverage	Peptides matched	Score	Theo/exp pI	Theo/exp MW (kDa)	Virulence/Potential virulence <sup>b</sup>
Cell motility, intracellular trafficking and secretion									
O-linked N-acetylglucosamine transferase	186	ZP_01325544	BPSL0525	48	26	184	5.75/5.16	63.7/63.6	
O-linked N-acetylglucosamine transferase	187	ZP_01325544	BPSL0525	57	34	115	5.75/5.25	63.7/63.4	
Flagellar biosynthesis/type III secretory pathway ATPase (FliI)	188	ZP_00489093	BPSL0227	29	11	115	6.53/6.02	44.3/46.2	[34]
Type III secretion protein (HrpB1/HrpK)	189	YP_111411	BPSS1399	46	6	84	4.73/4.94	21.0/40.7	
Type III secretion chaperone LcrH/SycD (BicA)	190	YP_335732	BPSS1533	68	7	122	4.88/6.00	18.8/16.0	[35]
BsaU protein (BsaU)	191	ZP_01214210	BPSS1539	65	14	134	10.17/4.83	18.0/17.3	
BipB protein (BipB)	192	YP_106121	BPSS1532	28	23	88	6.03/6.46	64.9/67.4	[36]
Type III secretion system protein (BsaR)	193	YP_111548	BPSS1542	36	4	69	4.61/4.49	15.2/14.1	
Type III effector protein (BipD)	194	YP_111535	BPSS1529	53	11	182	5.13/4.95	34.0/30.0	[37]
Type III/IV secretion system protein	195	ZP_01249703	BPSL3008	43	14	160	8.46/4.38	43.6/32.6	
Type III/IV secretion system protein (PilQ)	196	ZP_01330258	BPSS1597	45	25	204	6.27/6.53	58.8/30.3	[38]
Flp pilus assembly protein	197	ZP_01333163	BPSL1896	36	7	91	9.58/5.18	30.0/24.3	
Export protein translocase (SecB)	198	YP_107071	BPSL0446	92	9	181	4.56/4.46	17.8/19.3	[39]
TadE-like protein	199	YP_001064080	BPSS2194	70	7	97	9.15/5.33	16.4/16.1	
Chemotaxis protein CheW	200	ZP_01335516	BPSL3305	46	6	97	4.99/5.05	16.9/13.9	
Chemotaxis protein CheW	201	ZP_01335516	BPSL3305	54	8	115	4.99/4.99	16.9/13.9	
Cell cycle and division									
Segregation and condensation protein B (ScpB)	202	YP_333310	BPSL1922	32	12	130	4.46/4.16	47.9/44.1	
Cell division protein (FtsZ)	203	YP_109616	BPSL3020	72	24	241	4.87/4.90	41.7/43.3	
Nucleotide-binding protein (Maf)	204	YP_107781	BPSL1159	46	8	110	5.39/5.44	22.0/23.9	
Cobyrinic acid a,c-diamide synthase	205	YP_107617	BPSL0989	47	8	126	6.08/6.52	22.6/24.2	
Stress responses									
Universal stress protein family	206	YP_335264	BPSS1140	70	17	197	5.26/5.36	34.4/33.3	
Universal stress protein family	207	YP_105446	BPSS0839	61	20	224	5.79/6.24	30.4/30.4	
Universal stress protein family	208	YP_104889	BPSS0032	65	10	154	5.78/6.12	16.6/16.1	
Universal stress protein family	209	YP_104981	BPSS1934	47	6	111	6.51/5.26	16.8/16.0	
Universal stress protein family	210	YP_105445	BPSS0838	45	7	74	5.95/5.28	17.6/17.4	
Universal stress protein family	211	ZP_00490462	BPSS0836	70	9	101	5.21/4.96	16.5/16.3	
Phasin (PhaP)	212	YP_108894	BPSL2298	92	20	259	5.96/5.66	19.9/23.5	
Phasin (PhaP)	213	YP_108894	BPSL2298	88	17	214	5.96/5.86	19.9/23.6	
Phasin (PhaP)	214	YP_108894	BPSL2298	91	18	231	5.96/6.30	19.9/23.5	
Phasin (PhaP)	215	YP_108894	BPSL2298	59	9	159	5.96/5.13	19.9/15.4	
Phasin (PhaP)	216	YP_108894	BPSL2298	73	15	174	5.96/4.97	19.9/15.2	
Phasin (PhaP)	217	YP_108894	BPSL2298	74	11	196	5.96/4.90	19.9/15.3	
Phasin (PhaP)	218	YP_108894	BPSL2298	75	13	183	5.96/4.92	19.9/16.7	
Phasin (PhaP)	219	YP_108894	BPSL2298	73	14	185	5.96/4.92	19.9/16.3	
Phasin (PhaP)	220	YP_108894	BPSL2298	50	7	127	5.96/4.79	19.9/14.5	
Alkyl hydroperoxide reductase	221	ZP_00488820	BPSL2096	68	12	179	5.02/4.94	19.1/18.1	
Alkyl hydroperoxide reductase	222	ZP_00488820	BPSL2096	46	9	130	5.02/4.76	19.1/18.3	
Alkyl hydroperoxide reductase	223	ZP_00488820	BPSL2096	50	7	104	5.02/4.70	19.1/13.3	
Alkyl hydroperoxide reductase D	224	YP_108694	BPSL2097	62	13	170	6.30/6.51	18.8/16.7	
Oxidoreductase	225	YP_109344	BPSL2748	54	11	132	5.75/6.19	23.9/24.6	
Oxidoreductase	226	YP_109344	BPSL2748	50	8	111	5.75/5.95	23.9/24.7	
Oxidoreductase	227	YP_109344	BPSL2748	33	6	81	5.75/6.32	23.9/20.5	
Organic hydroperoxide resistance protein (Ohr)	228	YP_111786	BPSS1782	59	6	90	6.28/6.63	14.5/16.2	
Glyoxalase I	229	YP_110250	BPSS0230	74	9	197	5.75/6.11	14.8/15.4	
Glyoxalase I	230	ZP_00485646	BPSS0230	82	10	157	5.77/5.58	14.7/16.1	
Osmotically inducible Y domain protein	231	YP_336221	BPSS1958	32	7	90	5.35/5.34	23.5/24.6	
Osmotically inducible Y domain protein	232	YP_336183	BPSS1924	40	9	129	5.68/5.28	20.9/23.1	

Table S1. Continued

Gene	Spot number	Accession number	Locus in <i>B. pseudomallei</i> strain K96243 genome	% Seq coverage	Peptides matched	Score	Theo/exp pI	Theo/exp MW (kDa)	Virulence/Potential virulence <sup>b</sup>
Osmotically inducible Y domain protein	233	YP_336183	BPSS1924	31	5	88	5.68/5.17	20.9/23.1	[40]
Multidrug efflux pump (AmrA)	234	YP_108403	BPSL1804	43	21	167	9.62/5.08	42.5/33.2	
Multidrug efflux pump (AmrA)	235	YP_108403	BPSL1804	23	10	81	9.62/4.67	42.5/32.6	
Bacterioferritin antioxidant protein	236	YP_108089	BPSL1467	31	5	68	8.85/4.47	17.0/16.3	
Uncharacterized proteins									
Uncharacterized lipoprotein	237	ZP_01249570	BPSS1506	45	10	109	7.21/5.86	22.8/24.7	
Uncharacterized lipoprotein	238	ZP_01317860	BPSS1849	36	3	73	4.94/4.19	14.3/16.0	
Limonene-1,2-epoxide hydrolase	239	YP_110153	BPSS0132	48	7	122	6.43/4.78	14.8/11.6	
NADPH-dependent FMN reductase	240	YP_112348	BPSS2346	40	6	127	6.51/6.32	20.3/18.0	
L-2-Amino-thiazoline-4-carboxylic acid hydrolase	241	ZP_00442057	BPSS0857	75	15	176	5.53/4.91	21.0/18.2	
Family C56 unassigned peptidase	242	YP_106014	BPSS0719	46	9	149	4.72/4.70	23.9/24.5	
Short-chain dehydrogenase	243	YP_109355	BPSL2759	60	12	183	5.74/6.07	26.3/25.7	
Ankyrin repeat protein	244	ZP_01331343	BPSL1440	81	19	208	6.43/5.87	23.5/22.2	
gp30	245	AAO46033	BPSS0387	32	11	127	5.54/5.91	40.5/46.0	
Hypothetical proteins									
Hypothetical protein	246	ZP_01328746	BPSL0086	55	10	152	5.12/4.12	17.3/16.2	
Hypothetical protein	247	YP_106730	BPSL0104	23	3	66	4.48/4.52	20.0/19.2	
Hypothetical protein	248	YP_106975	BPSL0348	59	13	169	6.59/4.52	28.0/23.2	
Hypothetical protein	249	YP_106975	BPSL0348	53	10	149	6.59/4.45	28.0/22.8	
Hypothetical protein	250	YP_106975	BPSL0348	64	18	227	6.59/4.53	28.0/22.7	
Hypothetical protein	251	YP_106975	BPSL0348	47	10	151	6.59/4.57	28.0/22.8	
Hypothetical protein	252	YP_106976	BPSL0349	47	9	111	5.04/4.75	20.3/19.4	
Hypothetical protein	253	YP_106976	BPSL0349	75	13	182	5.04/4.96	20.3/18.9	
Hypothetical protein	254	YP_107036	BPSL0410	77	9	131	5.30/5.29	11.4/15.2	
Hypothetical protein	255	YP_107228	BPSL0599	55	5	99	4.94/4.93	13.9/15.8	
Hypothetical protein	256	YP_107492	BPSL0867	67	16	166	9.17/4.46	18.0/16.5	
Hypothetical protein	257	YP_107677	BPSL1050	37	4	76	6.14/5.36	13.9/21.2	
Hypothetical protein	258	AAU50278	BPSL1067	38	5	65	6.54/7.00	14.5/15.3	
Hypothetical protein	259	YP_107996	BPSL1371	51	12	115	9.94/6.06	20.4/22.0	
Hypothetical protein	260	YP_108169	BPSL1549	30	5	79	5.14/4.98	23.4/22.7	[41]
Hypothetical protein	261	YP_108169	BPSL1549	68	12	159	5.14/5.13	23.4/21.5	
Hypothetical protein	262	YP_108169	BPSL1549	44	7	97	5.14/4.99	23.4/36.8	
Hypothetical protein	263	YP_108201	BPSL1581	61	17	144	5.19/4.98	15.4/16.9	
Hypothetical protein	264	ZP_01213142	BPSL1601	63	10	151	5.61/4.70	15.0/14.6	
Hypothetical protein	265	YP_333132	BPSL2082	76	17	196	9.60/5.28	18.0/28.0	
Hypothetical protein	266	YP_109607	BPSL3012	55	11	128	6.14/5.20	29.0/40.8	
Hypothetical protein	267	YP_110039	BPSS0015	78	10	152	10.47/4.92	17.2/32.2	
Hypothetical protein	268	YP_110050	BPSS0026	42	13	141	8.22/4.65	30.9/23.1	
Hypothetical protein	269	YP_110232	BPSS0212	41	9	109	5.34/5.34	22.5/22.5	
Hypothetical protein	270	YP_110233	BPSS0213	51	13	141	6.65/4.36	21.7/22.1	
Hypothetical protein	271	YP_110696	BPSS0683	55	8	107	5.09/5.00	13.1/14.4	
Hypothetical protein	272	YP_110726	BPSS0712	66	7	110	6.18/5.70	13.9/13.6	
Hypothetical protein	273	YP_110895	BPSS0886	53	9	114	5.89/5.84	15.9/15.0	
Hypothetical protein	274	YP_110940	BPSS0931	26	9	111	9.30/5.17	30.0/36.2	
Hypothetical protein	275	YP_337721	BPSS0961	25	9	83	5.05/4.56	18.3/23.1	
Hypothetical protein	276	YP_111111	BPSS1098	58	6	103	4.57/4.68	9.90/12.5	
Hypothetical protein	277	YP_105479	BPSS1486	63	6	120	5.12/4.75	16.2/15.0	
Hypothetical protein	278	ZP_00489981	BPSS1506	30	12	117	7.21/6.01	22.8/24.8	
Hypothetical protein	279	YP_111596	BPSS1588	20	7	74	6.18/6.04	49.5/49.5	
Hypothetical protein	280	AAO46033	BPSS1923	42	5	80	5.52/5.26	14.2/46.2	
Hypothetical protein	281	ZP_01317823	BPSS2055	30	13	129	5.22/5.13	25.1/22.3	
Hypothetical protein	282	ZP_01327194	BPSS2129	28	5	83	5.63/5.91	20.2/18.3	

<sup>a</sup> Gene abbreviations in the blankets within the biological metabolism categories are used for the metabolic pathways in Figure S4.

<sup>b</sup> Genes whose function has been reported to be involved in virulence are indicated by references.

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