

Table S2. Protein isoforms identified in *Burkholderia pseudomallei* proteome reference map constructed under early stationary phase.

Gene	Spot number	Accession number	% Seq coverage	Peptides matched	Score	Theo/exp pl	Theo/exp MW (kDa)
Cell envelope biogenesis and outer membrane							
Phosphatidylethanolamine-binding protein	10	YP_107676	55	7	106	5.26/5.11	18.3/16.8
Phosphatidylethanolamine-binding protein	11	YP_107676	47	7	106	5.26/4.72	18.3/13.7
Energy metabolism							
ATP synthase subunit B (AtpD)	15	YP_109989	47	19	170	5.26/4.95	50.8/48.2
ATP synthase subunit B (AtpD)	16	YP_109989	36	12	118	5.26/5.08	50.8/48.4
ATP synthase subunit B (AtpD)	17	YP_109989	58	21	204	5.26/5.13	50.8/48.4
Aldehyde dehydrogenase (NAD) family protein	22	ZP_00487209	64	24	251	5.46/5.55	50.7/49.1
Aldehyde dehydrogenase (NAD) family protein	23	ZP_00487209	54	19	202	5.46/5.65	50.7/49.1
Aldehyde dehydrogenase (NAD) family protein	24	ZP_00487209	66	26	275	5.46/5.86	50.7/49.2
Malate dehydrogenase (Mdh)	29	YP_106310	60	18	204	5.70/6.01	35.1/32.8
Malate dehydrogenase (Mdh)	30	YP_106310	56	18	208	5.70/4.46	35.1/32.2
Phosphate acetyltransferase	36	YP_111961	70	22	245	5.82/6.21	49.2/49.1
Phosphate acetyltransferase	37	YP_111961	29	10	145	5.82/6.31	49.2/29.1
Inorganic pyrophosphatase (Ppa)	38	YP_107649	72	23	304	5.37/5.25	19.2/21.0
Inorganic pyrophosphatase (Ppa)	39	YP_107649	36	9	125	5.37/5.02	19.2/20.8
Carbohydrate metabolism							
Glyceraldehyde 3-phosphate dehydrogenase (GapA)	47	YP_109546	58	13	164	6.37/4.47	36.3/34.9
Glyceraldehyde 3-phosphate dehydrogenase (GapA)	48	YP_109546	85	25	282	6.37/6.70	36.3/37.0
Phosphoglycerate kinase (Pgk)	49	ZP_00895324	61	21	245	5.58/5.72	41.4/43.7
Phosphoglycerate kinase (Pgk)	50	ZP_00895324	50	21	242	5.58/5.18	41.4/28.9
Phosphopyruvate hydratase (Eno)	51	YP_108866	54	25	252	4.81/4.76	45.9/45.4
Phosphopyruvate hydratase (Eno)	52	YP_108866	24	9	98	4.81/4.78	45.9/45.4
Lipid metabolism							
Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (ScoA)	62	YP_108553	50	11	143	5.56/5.89	25.4/25.2
Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (ScoA)	63	YP_108553	34	9	106	5.56/5.34	25.4/24.6
Acetoacetyl-CoA reductase (PhbB)	65	ZP_00490574	35	8	120	6.07/6.00	25.3/25.7
Acetoacetyl-CoA reductase (PhbB)	66	YP_111922	64	21	213	6.30/6.54	26.6/24.8
Acyl-carrier-protein S-malonyltransferase (FabD)	68	YP_109033	56	14	176	5.46/5.38	32.2/30.2
Acyl-carrier-protein S-malonyltransferase (FabD)	69	YP_107960	33	6	92	5.76/5.08	32.5/16.4
Nucleotide metabolism							
Deoxyribose-phosphate aldolase (DeoC)	91	ZP_00489036	34	7	90	5.42/5.28	27.1/27.7
Deoxyribose-phosphate aldolase (DeoC)	92	YP_336226	87	20	249	5.42/5.53	27.2/27.2
Secondary metabolite metabolism							
Cytochrome P450	103	ZP_00440831	36	17	169	9.13/4.80	44.8/50.0
Cytochrome P450	104	ZP_00486588	29	11	123	9.13/5.24	44.8/48.3
Transcription							
Phage shock protein A	120	YP_108702	62	20	166	5.11/4.97	24.5/25.9
Phage shock protein A	121	YP_108702	52	12	147	5.11/4.92	24.5/26.0
Translation							
tRNA nucleotidyltransferase	133	YP_106892	45	14	159	7.25/4.76	45.2/34.5

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Gene	Spot number	Accession number	% Seq coverage	Peptides matched	Score	Theo/exp pl	Theo/exp MW (kDa)
tRNA nucleotidyltransferase	134	YP_106892	44	12	139	7.25/5.23	45.2/38.0
Elongation factor Tu (Tuf)	135	YP_109809	54	18	189	5.36/4.97	43.2/45.4
Elongation factor Tu (Tuf)	136	YP_109809	50	15	143	5.36/4.10	43.2/44.2
Elongation factor Tu (Tuf)	137	YP_109809	53	18	174	5.36/4.16	43.2/45.3
Elongation factor Tu (Tuf)	138	YP_109809	67	24	209	5.36/4.68	43.2/44.3
Elongation factor Tu (Tuf)	139	YP_109809	42	13	131	5.36/4.93	43.2/46.6
Elongation factor Tu (Tuf)	140	ZP_01320582	35	9	139	5.18/4.94	40.3/38.6
Elongation factor Ts (Tsf)	141	YP_108753	72	25	246	5.38/5.19	31.3/30.9
Elongation factor Ts (Tsf)	142	YP_108753	59	21	216	5.38/5.08	31.3/31.4
30S ribosomal protein S9 (Rpsl)	148	YP_103901	66	6	121	10.65/4.13	14.3/16.0
30S ribosomal protein S9 (Rpsl)	149	YP_103901	66	10	98	10.65/4.27	14.3/16.0
50S ribosomal protein L4 RplD)	151	YP_109806	53	8	143	9.62/4.91	22.9/22.4
50S ribosomal protein L4 RplD)	152	YP_109806	66	11	149	9.62/5.02	22.9/22.3
Post-translational modification							
Chaperonin GroEL	157	AAO46033	67	41	121	5.18/4.95	56.5/57.2
Chaperonin GroEL	158	AAO46033	80	44	147	5.18/4.97	56.5/56.5
Chaperonin GroEL	159	AAO46033	77	46	166	5.18/5.00	56.5/56.5
Chaperonin GroEL	160	AAO46033	77	40	126	5.18/5.06	56.5/55.4
Chaperonin GroES	161	YP_109294	91	11	169	5.78/5.21	10.5/14.9
Chaperonin GroES	162	YP_109294	77	11	154	5.78/4.97	10.5/13.8
Chaperonin GroES	163	YP_109294	72	8	122	5.78/4.97	10.5/14.7
Chaperonin GroES	164	YP_109295	72	8	122	5.78/6.00	10.5/14.9
HSP20/alpha crystallin family protein	166	YP_112291	76	9	145	5.14/5.00	16.0/15.8
HSP20/alpha crystallin family protein	167	YP_112291	60	5	99	5.14/4.78	16.0/15.9
HSP20/alpha crystallin family protein	168	YP_112291	76	9	148	5.14/5.00	16.0/16.3
Peptidyl-prolyl cis-trans isomerase B (PpiB)	171	ZP_01322808	45	8	92	6.20/6.02	15.6/19.1
Peptidyl-prolyl cis-trans isomerase B (PpiB)	172	YP_108841	68	18	210	5.94/6.39	17.9/19.2
Peptidyl-prolyl cis-trans isomerase B (PpiB)	173	YP_108841	65	12	161	5.94/6.55	17.9/19.4
Peptidyl-prolyl cis-trans isomerase B (PpiB)	174	YP_108841	69	16	210	5.94/6.28	17.9/19.5
Peptidyl-prolyl cis-trans isomerase B (PpiB)	175	YP_108841	69	16	194	5.94/6.18	17.9/19.2
Glutathione S-transferase	176	YP_108349	50	9	120	6.99/6.67	26.7/28.9
Glutathione S-transferase	177	YP_108349	38	9	104	6.99/6.53	26.7/22.9
Cell motility, intracellular trafficking and secretion							
O-linked N-acetylglucosamine transferase	186	ZP_01325544	48	26	184	5.75/5.16	63.7/63.6
O-linked N-acetylglucosamine transferase	187	ZP_01325544	57	34	115	5.75/5.25	63.7/63.4
Chemotaxis protein CheW	200	ZP_01335516	46	6	97	4.99/5.05	16.9/13.9
Chemotaxis protein CheW	201	ZP_01335516	54	8	115	4.99/4.99	16.9/13.9
Stress responses							
Phasin (PhaP)	212	YP_108894	92	20	259	5.96/5.66	19.9/23.5
Phasin (PhaP)	213	YP_108894	88	17	214	5.96/5.86	19.9/23.6
Phasin (PhaP)	214	YP_108894	91	18	231	5.96/6.30	19.9/23.5
Phasin (PhaP)	215	YP_108894	59	9	159	5.96/5.13	19.9/15.4
Phasin (PhaP)	216	YP_108894	73	15	174	5.96/4.97	19.9/15.2
Phasin (PhaP)	217	YP_108894	74	11	196	5.96/4.90	19.9/15.3
Phasin (PhaP)	218	YP_108894	75	13	183	5.96/4.92	19.9/16.7
Phasin (PhaP)	219	YP_108894	73	14	185	5.96/4.92	19.9/16.3
Phasin (PhaP)	220	YP_108894	50	7	127	5.96/4.79	19.9/14.5
Alkyl hydroperoxide reductase	221	ZP_00488820	68	12	179	5.02/4.94	19.1/18.1
Alkyl hydroperoxide reductase	222	ZP_00488820	46	9	130	5.02/4.76	19.1/18.3
Alkyl hydroperoxide reductase	223	ZP_00488820	50	7	104	5.02/4.70	19.1/13.3

Table S2. Continued

Gene	Spot number	Accession number	% Seq coverage	Peptides matched	Score	Theo/exp pI	Theo/exp MW (kDa)
Oxidoreductase	225	YP_109344	54	11	132	5.75/6.19	23.9/24.6
Oxidoreductase	226	YP_109344	50	8	111	5.75/5.95	23.9/24.7
Oxidoreductase	227	YP_109344	33	6	81	5.75/6.32	23.9/20.5
Glyoxalase I	229	YP_110250	74	9	197	5.75/6.11	14.8/15.4
Glyoxalase I	230	ZP_00485646	82	10	157	5.77/5.58	14.7/16.1
Osmotically inducible Y domain protein	232	YP_336183	40	9	129	5.68/5.28	20.9/23.1
Osmotically inducible Y domain protein	233	YP_336183	31	5	88	5.68/5.17	20.9/23.1
Multidrug efflux pump	234	YP_108403	43	21	167	9.62/5.08	42.5/33.2
Multidrug efflux pump	235	YP_108403	23	10	81	9.62/4.67	42.5/32.6
Hypothetical proteins							
Hypothetical protein BPSL0348	248	YP_106975	59	13	169	6.59/4.52	28.0/23.2
Hypothetical protein BPSL0348	249	YP_106975	53	10	149	6.59/4.45	28.0/22.8
Hypothetical protein BPSL0348	250	YP_106975	64	18	227	6.59/4.53	28.0/22.7
Hypothetical protein BPSL0348	251	YP_106975	47	10	151	6.59/4.57	28.0/22.8
Hypothetical protein BPSL0349	252	YP_106976	47	9	111	5.04/4.75	20.3/19.4
Hypothetical protein BPSL0349	253	YP_106976	75	13	182	5.04/4.96	20.3/18.9
Hypothetical protein BPSL1549	260	YP_108169	30	5	79	5.14/4.98	23.4/22.7
Hypothetical protein BPSL1549	261	YP_108169	68	12	159	5.14/5.13	23.4/21.5
Hypothetical protein BPSL1549	262	YP_108169	44	7	97	5.14/4.99	23.4/36.8