Supplementary Table S6 Results of proteome analyses of *Polaribacter* sp. Hel1_33_49 cultures grown on laminarin and chondroitin sulfate vs. D-mannose.

Locus	Product	%NSAF x 1,000			Ratio		
	(detected CAZymes and sulfatase are in bold typeface)	Cho	Man	Lam	Cho/Man	Lam/Man	Cho/Lam
PHEL49_1	chromosomal replication initiator protein DnaA	12.31	24.07	19.45	0.51	0.81	0.63
PHEL49_5	aminodeoxychorismate lyase			6.86			
PHEL49_7	diaminopimelate epimerase	11.67		12.30			0.95
PHEL49_8	HtrA protease/chaperone protein	19.91	67.06	50.69	0.30	0.76	0.39
PHEL49_9	glyceraldehyde-3-phosphate dehydrogenase	79.21	14.57	10.09	5.44	0.69	7.85
PHEL49_13	DNA ligase	16.25	29.42	30.91	0.55	1.05	0.53
PHEL49_15	conserved hypothetical protein	2.71	11.03	12.48	0.25	1.13	0.22
PHEL49_25	MerR HTH family regulatory protein	4.23					
PHEL49_28	ribose-phosphate pyrophosphokinase	85.63	87.61	141.60	0.98	1.62	0.60
PHEL49_29	LSU ribosomal protein L25p	454.61	246.91	437.27	1.84	1.77	1.04
PHEL49_34	peptidase, M23 family	4.23		5.57			0.76
PHEL49_35	nicotinate-nucleotide adenylyltransferase	5.89					
PHEL49_36	guanylate kinase	76.94	20.06	68.89	3.84	3.43	1.12
PHEL49_37	YicC-like domain-containing protein	88.23	50.15	175.60	1.76	3.50	0.50
PHEL49_39	uracil phosphoribosyltransferase	11.28					
PHEL49_44	ATP-binding Mrp / Nbp35 family protein	36.33	32.29	26.09	1.13	0.81	1.39
PHEL49_46	thioredoxin reductase	8.68					
PHEL49_47	homogentisate 1,2-dioxygenase	28.59	4.90		5.83		
PHEL49_48	4-hydroxyphenylpyruvate dioxygenase	23.08	25.07		0.92		
PHEL49_49	tryptophan 2,3-dioxygenase	18.81		7.43			2.53
PHEL49_52	glucose-6-phosphate isomerase	50.49	162.68	87.64	0.31	0.54	0.58
PHEL49_54	conserved hypothetical protein		29.55				
PHEL49_57	1-acylglycerol-3-phosphate O-acyltransferase	27.70		20.26			1.37
PHEL49_58	acyl-ACP desaturase	26.73	69.68	37.54	0.38	0.54	0.71
PHEL49_61	conserved hypothetical protein, PD-(D/E)XK nuclease superfamily	1.27	2.06	3.33	0.61	1.62	0.38
PHEL49_62	universal stress protein UspA	51.91	62.51	104.01	0.83	1.66	0.50
PHEL49_64	two-component system sensor histidine kinase			9.91			
PHEL49_65	enoyl-CoA hydratase			12.74			
PHEL49_68	transcriptional regulator, AraC family			27.02			
PHEL49_72	conserved hypothetical protein (DUF1094)	203.12	125.03	95.10	1.62	0.76	2.14
PHEL49_73	DnaJ-domain protein DjlA	29.02		31.84			0.91

PHEL49_74	isoleucyl-tRNA synthetase	35.42	84.86	29.49	0.42	0.35	1.20
PHEL49_75	DnaK suppressor protein	151.04	237.61	171.45	0.64	0.72	0.88
PHEL49_80	phosphate:sodium symporter	24.85		21.44			1.16
PHEL49_81	phosphate-selective porin O and P	50.05	38.37	56.21	1.30	1.46	0.89
PHEL49_82	TonB-dependent receptor, plug			30.29			
PHEL49_83	conserved hypothetical protein containing pectin lyase domain		3.24	11.80		3.64	
PHEL49_87	peptidase, M16 family	100.21	89.73	128.38	1.12	1.43	0.78
PHEL49_88	peptidase, M16 family	88.02	108.11	130.16	0.81	1.20	0.68
PHEL49_89	LSU ribosomal protein L21	564.23	220.64	336.80	2.56	1.53	1.68
PHEL49_90	LSU ribosomal protein L27p	22.57					
PHEL49_97	molybdopterin-guanine dinucleotide biosynthesis protein MobA	3.47		4.57			0.76
PHEL49_102	single-stranded DNA-binding protein	368.16	199.96	239.60	1.84	1.20	1.54
PHEL49_104	histone-like bacterial DNA-binding protein	216.67	33.10		6.55		
PHEL49_106	ribonuclease G	18.68	19.02	21.52	0.98	1.13	0.87
PHEL49_107	endonuclease/exonuclease/phosphatase family protein		5.38	4.35		0.81	
PHEL49_110	glyoxalase/bleomycin resistance protein/dioxygenase	13.54					
PHEL49_111	cell division protein FtsX	3.98		7.87			0.51
PHEL49_116	large-conductance mechanosensitive channel	112.85					
PHEL49_118	thymidine kinase	14.72					
PHEL49_119	conserved hypothetical protein	11.67	7.61		1.53		
PHEL49_122	conserved hypothetical protein (DUF4252)		42.90				
PHEL49_123	arsenate reductase	29.02					
PHEL49_125	cystathionine gamma-lyase	8.06	5.25	23.35	1.53	4.44	0.35
PHEL49_126	conserved hypothetical protein containing bacterial Ig-like domain	2.22	3.62	2.92	0.61	0.81	0.76
PHEL49_129	glycyl-tRNA synthetase	39.02	44.88	54.40	0.87	1.21	0.72
PHEL49_130	elongation factor Ts	232.14	305.75	303.12	0.76	0.99	0.77
PHEL49_131	SSU ribosomal protein S2p (SAe)	336.36	298.93	411.25	1.13	1.38	0.82
PHEL49_132	SSU ribosomal protein S9p (S16e)	1002.08	455.99	433.88	2.20	0.95	2.31
PHEL49_133	LSU ribosomal protein L13p (L13Ae)	370.40	253.09	388.08	1.46	1.53	0.95
PHEL49_134	**conserved hypothetical protein (DUF1083), N-terminal CBMnc domain**	**1.34**	**8.74**	**2.65**	**0.15**	**0.30**	**0.51**
PHEL49_136	glutaminyl-tRNA synthetase	58.33	52.61	82.29	1.11	1.56	0.71
PHEL49_139	dihydroneopterin aldolase	24.18	126.08	50.94	0.19	0.40	0.47
PHEL49_142	conserved hypothetical protein	20.69	19.92	34.67	1.04	1.74	0.60
PHEL49_149	metallo-beta-lactamase superfamily protein	19.04	55.16	25.07	0.35	0.45	0.76
PHEL49_150	peptidase, S8/S53 family	15.87	62.06	26.47	0.26	0.43	0.60
PHEL49_151	Zn-dependent aminopeptidase, M1 family	26.70	174.03	62.78	0.15	0.36	0.43
PHEL49_155	flavodoxin reductases (ferredoxin-NADPH reductases)	13.89	16.97	9.14	0.82	0.54	1.52
PHEL49_156	aspartate-semialdehyde dehydrogenase		6.13	17.34		2.83	
PHEL49_160	formate acetyltransferase			2.12			

PHEL49_162	PSP1 domain-containing protein	18.23	27.58	25.72	0.66	0.93	0.71
PHEL49_164	**penicillin-binding protein 1A, GT51 family**	**5.58**	**3.89**	**2.10**	**1.43**	**0.54**	**2.66**
PHEL49_165	succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A	52.08	21.22	27.43	2.45	1.29	1.90
PHEL49_170	conserved hypothetical protein	9.15	5.96	9.64	1.53	1.62	0.95
PHEL49_172	tryptophanyl-tRNA synthetase	54.54	55.16	61.91	0.99	1.12	0.88
PHEL49_177	immunoreactive 84kD antigen PG93	1.57		3.11			0.51
PHEL49_179	TonB-dependent receptor, plug		2.37	6.71		2.83	
PHEL49_182	acyl-CoA thioesterase II	6.16					
PHEL49_184	membrane fusion protein of RND family multidrug efflux pump	11.56	78.03	58.71	0.15	0.75	0.20
PHEL49_185	acriflavin resistance protein	28.69	104.71	21.91	0.27	0.21	1.31
PHEL49_186	outer membrane efflux protein	21.67	26.48	37.44	0.82	1.41	0.58
PHEL49_193	hypothetical protein	49.48					
PHEL49_201	conserved hypothetical protein			1.37			
PHEL49_202	lysophospholipase L1-like esterases		8.49				
PHEL49_203	acyl-CoA dehydrogenase	227.75	132.89	91.18	1.71	0.69	2.50
PHEL49_206	conserved hypothetical protein	10.75	15.76	22.64	0.68	1.44	0.47
PHEL49_207	conserved hypothetical protein	60.94	85.50	78.01	0.71	0.91	0.78
PHEL49_208	dTDP-4-dehydrorhamnose 3,5-epimerase	9.15	29.82	24.10	0.31	0.81	0.38
PHEL49_209	CDP-glycerol:poly(glycerophosphate) glycerophosphotransferase	3.47	5.66	9.14	0.61	1.62	0.38
PHEL49_214	bacterial transferase hexapeptide repeat protein	19.35		29.72			0.65
PHEL49_217	**glycosyltransferase, GT2 family**			**5.94**			
PHEL49_218	phosphoribosylamine-glycine ligase	11.78		7.75			1.52
PHEL49_220	two-component system response regulator	88.54	93.35	68.58	0.95	0.73	1.29
PHEL49_223	ABC transporter, ATP-binding protein	6.68	3.11	11.30	2.15	3.64	0.59
PHEL49_224	glucose-1-phosphate thymidylyltransferase	21.96	11.93	26.50	1.84	2.22	0.83
PHEL49_229	small-conductance mechanosensitive channel	24.95	40.64	70.38	0.61	1.73	0.35
PHEL49_230	acyl-CoA thioester hydrolase	64.14	29.03	70.38	2.21	2.42	0.91
PHEL49_233	conserved hypothetical protein			4.25			
PHEL49_235	transcription-repair coupling factor	1.07	8.69	2.81	0.12	0.32	0.38
PHEL49_242	ATP-dependent helicase	6.21	1.84	4.46	3.38	2.42	1.39
PHEL49_243	2-amino-3-ketobutyrate coenzyme A ligase	35.39	25.07	12.16	1.41	0.48	2.91
PHEL49_244	OmpA family protein	607.96	659.62	687.22	0.92	1.04	0.88
PHEL49_245	ATP synthase beta chain	358.60	580.20	487.04	0.62	0.84	0.74
PHEL49_247	ribosome-binding factor A	36.11					
PHEL49_251	peptidase, M28 family	4.51		7.92			0.57
PHEL49_252	WD40-like beta propeller	25.39	63.43	53.49	0.40	0.84	0.47
PHEL49_253	conserved hypothetical protein containing EF-hand calcium-binding domain	47.40					
PHEL49_254	GTP-binding protein LepA	8.08	18.11	25.28	0.45	1.40	0.32
PHEL49_255	peptidase membrane zinc metallopeptidase	27.08	180.93	71.32	0.15	0.39	0.38

PHEL49_257	MotA/TolQ/ExbB proton channel family protein	976.56	865.59	1237.85	1.13	1.43	0.79
PHEL49_259	biopolymer transport ExbD/TolR protein	244.34	220.64	337.23	1.11	1.53	0.72
PHEL49_260	biopolymer transport ExbD/TolR protein	382.35	155.75	346.12	2.45	2.22	1.10
PHEL49_261	conserved hypothetical protein containing outer membrane protein beta-barrel domain			13.21			
PHEL49_263	RNA polymerase sigma-54 factor RpoN	7.25	27.58	9.55	0.26	0.35	0.76
PHEL49_264	asparaginyl-tRNA synthetase	73.86	110.32	89.15	0.67	0.81	0.83
PHEL49_266	inner membrane transporter	3.01		5.94			0.51
PHEL49_267	ribosome recycling factor	98.18	33.10	102.53	2.97	3.10	0.96
PHEL49_268	uridylate kinase	85.94	131.54	120.01	0.65	0.91	0.72
PHEL49_269	FKBP-type peptidyl-prolyl cis-transisomerase (trigger factor)	136.74	175.21	164.32	0.78	0.94	0.83
PHEL49_270	ATP-dependent Clp protease proteolytic subunit	781.46	1264.09	1682.76	0.62	1.33	0.46
PHEL49_271	ATP-dependent Clp protease ATP-binding subunit ClpX	25.58	34.32	21.79	0.75	0.63	1.17
PHEL49_272	DNA primase	1.76		2.32			0.76
PHEL49_274	NAD synthetase	81.72	45.65	73.78	1.79	1.62	1.11
PHEL49_275	gliding motility protein GldB			16.42			
PHEL49_278	polyribonucleotide nucleotidyltransferase	114.21	164.82	163.27	0.69	0.99	0.70
PHEL49_279	SSU ribosomal protein S15p (S13e)	135.42					
PHEL49_280	acetyl-coenzyme A carboxyl transferase beta chain	80.40	34.48	136.52	2.33	3.96	0.59
PHEL49_281	fructose-bisphosphate aldolase class II	60.76	189.52	283.46	0.32	1.50	0.21
PHEL49_282	surface antigen (D15)	4.84	2.25	5.46	2.15	2.42	0.89
PHEL49_283	RNA methyltransferase, TrmH family	17.55					
PHEL49_286	NifU-like protein	3.98	9.73	31.47	0.41	3.23	0.13
PHEL49_287	outer membrane protein transport protein (OMPP1/FadL/TodX)		4.41	39.23		8.89	
PHEL49_290	prolyl-tRNA synthetase	56.83	55.16	68.46	1.03	1.24	0.83
PHEL49_292	SSU ribosomal protein S20p	52.66		59.44			0.89
PHEL49_297	rod shape-determining protein MreB	71.37	71.56	57.83	1.00	0.81	1.23
PHEL49_298	IMP cyclohydrolase / phosphoribosylaminoimidazolecarboxamide formyltransferase	42.32	68.95	105.07	0.61	1.52	0.40
PHEL49_304	heat shock protein 60 family chaperone GroEL	182.11	2957.73	787.00	0.06	0.27	0.23
PHEL49_305	heat shock protein 60 family co-chaperone GroES	27.08	330.96	80.24	0.08	0.24	0.34
PHEL49_307	conserved hypothetical protein	9.34	22.82	12.30	0.41	0.54	0.76
PHEL49_308	conserved hypothetical protein containing lipopolysaccharide-assembly domain	64.14	203.22	79.77	0.32	0.39	0.80
PHEL49_309	transcriptional regulator, Fis family	8.64	42.25	7.59	0.20	0.18	1.14
PHEL49_310	tRNA-i(6)A37 methylthiotransferase			8.10			
PHEL49_311	DNA topoisomerase I	54.02	194.82	103.38	0.28	0.53	0.52
PHEL49_312	arginase		10.03	10.13		1.01	
PHEL49_313	gliding motility protein GldK	55.99	44.55	53.15	1.26	1.19	1.05
PHEL49_314	gliding motility protein GldL	494.56	426.89	717.10	1.16	1.68	0.69

PHEL49_315	gliding motility protein GldM	120.91	128.05	170.35	0.94	1.33	0.71
PHEL49_316	gliding motility protein GldN	110.79	190.55	113.47	0.58	0.60	0.98
PHEL49_319	ABC transporter, ATP-binding protein			3.77			
PHEL49_322	hexapeptide transferase family protein			9.91			
PHEL49_325	endonuclease/exonuclease/phosphatase family protein	14.25	29.03	39.88	0.49	1.37	0.36
PHEL49_327	amidohydrolase 3 family protein	5.55	3.62	8.77	1.53	2.42	0.63
PHEL49_329	S-adenosylmethionine synthetase	8.83	4.80	25.20	1.84	5.25	0.35
PHEL49_330	O-acetylhomoserine sulfhydrylase / O-succinylhomoserine sulfhydrylase		71.10	332.84		4.68	
PHEL49_331	aspartokinase / homoserine dehydrogenase		3.50	12.03		3.43	
PHEL49_332	O-acetylhomoserine sulfhydrylase / O-succinylhomoserine sulfhydrylase			36.47			
PHEL49_333	Rrf2 family transcriptional regulator	8.46					
PHEL49_336	phosphoadenylyl-sulfate reductase [thioredoxin]	47.96	179.27	386.33	0.27	2.16	0.12
PHEL49_337	sulfate adenylyltransferase subunit 2		12.61	76.42		6.06	
PHEL49_338	sulfate adenylyltransferase subunit 1	5.89	69.55	122.10	0.08	1.76	0.05
PHEL49_339	nitrite/sulfite reductase		14.14	46.86		3.31	
PHEL49_341	precorrin-2 dehydrogenase			36.47			
PHEL49_342	pyridine nucleotide-disulphide oxidoreductase	42.76	75.48	150.15	0.57	1.99	0.28
PHEL49_344	serine O-acetyltransferase			25.47			
PHEL49_345	cysteine synthase	42.32	72.40	105.87	0.58	1.46	0.40
PHEL49_346	homocysteine S-methyltransferase	3.66					
PHEL49_347	methionine synthase		2.23	5.40		2.42	
PHEL49_348	5,10-methylenetetrahydrofolate reductase			24.76			
PHEL49_349	thioredoxin	258.52					
PHEL49_359	**glycoside hydrolase, CBM48 domain, GH13 family**	**1.93**					
PHEL49_360	SusE outer membrane protein	2.26					
PHEL49_362	RagB/SusD domain-containing protein	11.67	5.71	9.22	2.05	1.62	1.27
PHEL49_363	TonB-dependent receptor, plug	22.78	28.87	24.16	0.79	0.84	0.94
PHEL49_364	transcriptional regulator, LacI family	12.47					
PHEL49_367	**maltose phosphorylase, GH65 family**	**1.52**		**2.00**			**0.76**
PHEL49_376	prephenate dehydratase			5.75			
PHEL49_377	aminotransferase	14.17	12.83	4.15	1.10	0.32	3.42
PHEL49_378	prephenate dehydrogenase	6.55	7.12	14.38	0.92	2.02	0.46
PHEL49_379	3-deoxy-D-arabino-heptulosonate 7-phosphate synthetase/chorismate mutase type II	13.21	32.29	84.80	0.41	2.63	0.16
PHEL49_380	ribosome-associated GTPase	14.64	17.89	7.23	0.82	0.40	2.03
PHEL49_382	YceI-like domain protein	327.26	712.49	586.92	0.46	0.82	0.56
PHEL49_384	Cys/Met metabolism PLP-dependent enzyme	67.71					
PHEL49_386	Na+/H+ antiporter NhaC type	3.91					
PHEL49_388	conserved hypothetical protein (DUF4289)	5.35	11.61	11.73	0.46	1.01	0.46
PHEL49_390	37-kD nucleoid-associated bacterial protein	9.91	13.45	50.01	0.74	3.72	0.20
PHEL49_391	lipoate-protein ligase B	12.54	12.26	29.72	1.02	2.42	0.42
PHEL49_392	metallo-peptidase, M12B family, reprolysin-like	7.91	12.88	3.90	0.61	0.30	2.03

PHEL49_393	conserved hypothetical protein	13.54	13.24		1.02		
PHEL49_395	peptidase, S41 family	15.36	12.05	3.00	1.27	0.25	5.13
PHEL49_396	delta-1-pyrroline-5-carboxylate dehydrogenase	220.34	321.61	282.57	0.69	0.88	0.78
PHEL49_397	conserved hypothetical protein (DUF833)	5.02					
PHEL49_401	Na(+)-translocating NADH-quinone reductase subunit A	20.73	24.77	40.03	0.84	1.62	0.52
PHEL49_403	Na(+)-translocating NADH-quinone reductase subunit C	17.55		62.74			0.28
PHEL49_406	Na(+)-translocating NADH-quinone reductase subunit F	22.57	34.48	44.58	0.65	1.29	0.51
PHEL49_408	YqeY family protein	46.55					
PHEL49_411	flavin containing amine oxidoreductase	9.87	11.49	18.57	0.86	1.62	0.53
PHEL49_414	RNA polymerase sigma-70 factor, RpoD	192.87	96.95	110.77	1.99	1.14	1.74
PHEL49_417	deoxyadenosine kinase	101.56	73.55	118.87	1.38	1.62	0.85
PHEL49_419	two-component system sensor histidine kinase			2.97			
PHEL49_422	conserved hypothetical protein	61.36	244.77	153.23	0.25	0.63	0.40
PHEL49_423	conserved hypothetical protein (DUF4480)	32.21	175.66	82.23	0.18	0.47	0.39
PHEL49_425	gliding motility protein GldA	9.96	9.73	44.58	1.02	4.58	0.22
PHEL49_427	oxidoreductase, FAD-binding protein	2.71	4.41	24.96	0.61	5.66	0.11
PHEL49_428	DNA polymerase III subunit alpha	11.97	2.02	1.63	5.93	0.81	7.34
PHEL49_429	SSU ribosomal protein S16p	445.45	267.09	347.23	1.67	1.30	1.28
PHEL49_434	saccharopine dehydrogenase	106.77	53.04	37.72	2.01	0.71	2.83
PHEL49_436	phosphoenolpyruvate carboxykinase (ATP)	60.94	18.39	8.92	3.31	0.48	6.84
PHEL49_437	amidohydrolase, M20 family	20.17	14.08	3.79	1.43	0.27	5.32
PHEL49_443	isochorismatase hydrolase	143.54	22.06	64.19	6.51	2.91	2.24
PHEL49_445	pyrophosphate-energized proton pump	43.81	29.85	13.64	1.47	0.46	3.21
PHEL49_446	inorganic pyrophosphatase		31.52	114.63		3.64	
PHEL49_447	pyruvate dehydrogenase E1 component beta subunit	133.54	202.25	260.03	0.66	1.29	0.51
PHEL49_448	electron transfer flavoprotein subunit beta	1120.94	902.99	1254.74	1.24	1.39	0.89
PHEL49_449	electron transfer flavoprotein subunit alpha	1323.38	1450.88	1156.28	0.91	0.80	1.14
PHEL49_450	conserved hypothetical protein (DUF151)	47.10	19.19	50.39	2.45	2.63	0.93
PHEL49_451	Na+ dependent nucleoside transporter domain-containing protein	27.64	4.50	20.01	6.14	4.44	1.38
PHEL49_452	thymidylate synthase	31.74	24.13	27.86	1.32	1.15	1.14
PHEL49_456	Xaa-Pro aminopeptidase, M24 family	18.23	4.24	22.29	4.30	5.25	0.82
PHEL49_459	dipeptidyl-peptidase III	88.81	73.07	94.94	1.22	1.30	0.94
PHEL49_463	NTP pyrophosphohydrolase-like domain	36.11					
PHEL49_464	carbohydrate kinase	3.69		6.48			0.57
PHEL49_468	helix-turn-helix domain protein	10.26		10.81			0.95
PHEL49_472	lysine dehydrogenase	19.56		17.83			1.10
PHEL49_475	2-dehydro-3-deoxyphosphooctonate aldolase	15.80	18.39	53.49	0.86	2.91	0.30
PHEL49_476	peptidase, M28 family	21.96	17.89	24.10	1.23	1.35	0.91
PHEL49_478	alpha-2-macroglobulin domain protein	2.29					
PHEL49_479	UDP-N-acetylmuramate-L-alanine ligase	13.28	10.82	19.23	1.23	1.78	0.69
PHEL49_481	conserved hypothetical protein	9.23	5.01	4.05	1.84	0.81	2.28
PHEL49_485	potassium uptake protein TrkA	12.19		8.92			1.37

PHEL49_488	acyl-CoA N-acyltransferase family protein			4.95			
PHEL49_490	**glycosyltransferase, GT4 family**	**4.72**					
PHEL49_494	conserved hypothetical protein	13.10					
PHEL49_497	23S rRNA (guanosine-2'-O-)-methyltransferase RlmB	92.79	61.29	92.45	1.51	1.51	1.00
PHEL49_498	**arylsulfate sulfotransferase**	**37.24**	**20.23**	**2.97**	**1.84**	**0.15**	**12.53**
PHEL49_499	ASPIC/UnbV-like protein / integrin-like protein	5.50					
PHEL49_500	conserved hypothetical protein	607.26	131.01	158.80	4.64	1.21	3.82
PHEL49_501	RagB/SusD domain-containing protein	1232.29	347.93	526.69	3.54	1.51	2.34
PHEL49_502	TonB-dependent receptor, plug	1829.85	662.87	824.47	2.76	1.24	2.22
PHEL49_504	SSU ribosomal protein S12p (S23e)	24.18					
PHEL49_505	SSU ribosomal protein S7p (S5e)	304.69	269.67	341.75	1.13	1.27	0.89
PHEL49_506	elongation factor EF-G	253.47	217.81	174.88	1.16	0.80	1.45
PHEL49_507	SSU ribosomal protein S10p (S20e)	381.63	130.38	113.47	2.93	0.87	3.36
PHEL49_509	LSU ribosomal protein L3p (L3e)	470.88	446.30	628.12	1.06	1.41	0.75
PHEL49_510	LSU ribosomal protein L4p (L1e)	253.17	278.20	348.86	0.91	1.25	0.73
PHEL49_511	LSU ribosomal protein L23p (L23Ae)	147.73	260.76	243.14	0.57	0.93	0.61
PHEL49_512	LSU ribosomal protein L2p (L8e)	117.36	80.90	109.96	1.45	1.36	1.07
PHEL49_513	SSU ribosomal protein S19p (S15e)	270.83	176.51	178.31	1.53	1.01	1.52
PHEL49_514	LSU ribosomal protein L22p (L17e)	356.60	88.26	219.91	4.04	2.49	1.62
PHEL49_515	SSU ribosomal protein S3p (S3e)	280.86	73.55	323.59	3.82	4.40	0.87
PHEL49_516	LSU ribosomal protein L16p (L10e)	215.82	186.17	356.61	1.16	1.92	0.61
PHEL49_518	SSU ribosomal protein S17p (S11e)	13.54		17.83			0.76
PHEL49_520	LSU ribosomal protein L24p (L26e)	153.88					
PHEL49_521	LSU ribosomal protein L5p (L11e)	660.15	347.51	570.58	1.90	1.64	1.16
PHEL49_522	SSU ribosomal protein S14p (S29e)	74.48	33.10	80.24	2.25	2.42	0.93
PHEL49_523	SSU ribosomal protein S8p (S15Ae)	257.29	169.16	101.04	1.52	0.60	2.55
PHEL49_524	LSU ribosomal protein L6p (L9e)	270.83	347.51	307.58	0.78	0.89	0.88
PHEL49_525	LSU ribosomal protein L18p (L5e)	67.71					
PHEL49_526	SSU ribosomal protein S5p (S2e)	447.63	153.22	326.89	2.92	2.13	1.37
PHEL49_527	LSU ribosomal protein L30p (L7e)	29.02					
PHEL49_528	LSU ribosomal protein L15p (L27Ae)	359.70	131.01	228.45	2.75	1.74	1.57
PHEL49_529	preprotein translocase subunit SecY (TC 3.A.5.1.1)	38.09	45.97	16.72	0.83	0.36	2.28
PHEL49_530	translation initiation factor IF-1	67.71					
PHEL49_532	SSU ribosomal protein S13p (S18e)	270.83	133.96	235.62	2.02	1.76	1.15
PHEL49_533	SSU ribosomal protein S11p (S14e)	67.71		70.05			0.97
PHEL49_534	SSU ribosomal protein S4p (S9e)	403.30	153.49	395.37	2.63	2.58	1.02
PHEL49_535	DNA-directed RNA polymerase alpha subunit	728.32	1753.20	534.92	0.42	0.31	1.36
PHEL49_536	LSU ribosomal protein L17p	650.75	281.93	624.07	2.31	2.21	1.04
PHEL49_539	conserved hypothetical protein	4.84					
PHEL49_540	carbamoyl-phosphate synthase small chain	64.41	37.67	65.23	1.71	1.73	0.99
PHEL49_542	enolase	222.26	942.52	1430.32	0.24	1.52	0.16
PHEL49_543	citrate synthase (si)	189.02	64.35	44.58	2.94	0.69	4.24

PHEL49_546	amidinotransferase	56.42	6.13	4.95	9.21	0.81	11.39
PHEL49_548	type I phosphodiesterase/nucleotide pyrophosphatase precursor	2.22	16.28	19.00	0.14	1.17	0.12
PHEL49_550	methionine ABC transporter ATP-binding protein	30.35	34.24	73.78	0.89	2.16	0.41
PHEL49_552	complex I intermediate-associated protein 30 (CIA30)			32.85			
PHEL49_553	conserved hypothetical membrane protein (DUF389)		14.30				
PHEL49_555	short chain dehydrogenase/reductase	51.46	13.24	39.23	3.89	2.96	1.31
PHEL49_556	amidohydrolase 1 family protein	97.15	47.97	31.01	2.03	0.65	3.13
PHEL49_557	conserved hypothetical protein		12.03	17.83		1.48	
PHEL49_558	glutamine cyclotransferase	27.78	82.03	70.87	0.34	0.86	0.39
PHEL49_559	LSU ribosomal protein L31p	128.65	77.22	240.71	1.67	3.12	0.53
PHEL49_560	glycine dehydrogenase	116.54	171.85	74.58	0.68	0.43	1.56
PHEL49_562	D-3-phosphoglycerate dehydrogenase	17.41	70.92	136.28	0.25	1.92	0.13
PHEL49_563	NlpC/P60 family protein	9.03		9.91			0.91
PHEL49_565	kynurenine 3-monooxygenase			3.18			
PHEL49_566	endoribonuclease L-PSP	22.57					
PHEL49_567	peptidase, M20 family	15.44					
PHEL49_568	aldehyde dehydrogenase family protein	2.56					
PHEL49_569	short chain dehydrogenase/reductase	36.27	11.82	15.92	3.07	1.35	2.28
PHEL49_576	chaperone protein DnaK	210.09	1289.78	382.83	0.16	0.30	0.55
PHEL49_577	conserved hypothetical protein (DUF2853)	713.54	517.66	747.51	1.38	1.44	0.95
PHEL49_579	proteorhodopsin	185.57					
PHEL49_581	conserved hypothetical protein (DUF328)	14.01	15.22	76.86	0.92	5.05	0.18
PHEL49_584	conserved hypothetical protein	8.21	170.50	72.94	0.05	0.43	0.11
PHEL49_589	ribosomal large subunit pseudouridine synthase D	8.68	8.49		1.02		
PHEL49_590	conserved hypothetical protein containing PASTA domain	45.14	52.53	114.63	0.86	2.18	0.39
PHEL49_591	D-alanine-D-alanine ligase			4.95			
PHEL49_595	6-phosphogluconolactonase	3.30		8.70			0.38
PHEL49_597	molybdopterin-binding domain of aldehyde dehydrogenase	3.34	6.81		0.49		
PHEL49_598	sulfate permease (SulP)			3.02			
PHEL49_599	NUDIX hydrolase family protein			7.75			
PHEL49_600	orotate phosphoribosyltransferase	11.28		11.14			1.01
PHEL49_601	conserved hypothetical protein containing START-like domain	275.35	183.87	160.48	1.50	0.87	1.72
PHEL49_603	iojap-like protein	48.36	86.68	38.21	0.56	0.44	1.27
PHEL49_604	cell division protein FtsH	20.41	132.99	84.27	0.15	0.63	0.24
PHEL49_605	conserved hypothetical protein containing 5-formyltetrahydrofolate cyclo-ligase-like domain	58.48	10.03	28.37	5.83	2.83	2.06
PHEL49_607	phosphatidylserine decarboxylase	59.58	26.48	128.38	2.25	4.85	0.46
PHEL49_609	YceI-like domain protein	197.24	167.88	228.70	1.17	1.36	0.86
PHEL49_610	sugar nucleotide epimerase, YfcH	4.23		5.57			0.76
PHEL49_611	conserved hypothetical protein	13.82	131.71	126.45	0.10	0.96	0.11
PHEL49_612	conserved hypothetical protein, von Willebrand factor type A domain	12.60	46.18	14.51	0.27	0.31	0.87
PHEL49_613	magnesium-chelatase subunit ChlI	35.06	204.88	98.70	0.17	0.48	0.36

PHEL49_614	leucine aminopeptidase-related protein	20.73	6.75	3.64	3.07	0.54	5.70
PHEL49_621	conserved hypothetical protein (DUF3050)			14.38			
PHEL49_624	two-component transcriptional regulator sigma-54	8.83	4.80	3.88	1.84	0.81	2.28
PHEL49_629	lipopolysaccharide biosynthesis protein	2.26					
PHEL49_634	**putative mannosyltransferase, GT4 family**		**5.01**				
PHEL49_638	**glycosyltransferase, GT2 family**	**9.03**					
PHEL49_643	heat shock protein 90	115.67	945.39	297.18	0.12	0.31	0.39
PHEL49_645	3-oxoacyl-[acyl-carrier-protein] synthase, KASIII	18.30	23.85	21.69	0.77	0.91	0.84
PHEL49_646	conserved hypothetical protein		8.17				
PHEL49_648	ribonuclease Z		6.30				
PHEL49_650	aspartate carbamoyltransferase		38.94	23.60		0.61	
PHEL49_651	PyrR bifunctional protein	29.02					
PHEL49_654	HlyD family secretion protein			5.09			
PHEL49_659	shikimate 5-dehydrogenase			21.52			
PHEL49_660	conserved hypothetical protein (DUF349)	29.51	36.77	24.00	0.80	0.65	1.23
PHEL49_661	conserved Hypothetical protein (DUF164)	241.49	191.22	136.70	1.26	0.71	1.77
PHEL49_662	NGG1p interacting factor 3 protein, NIF3	47.40	24.82	40.12	1.91	1.62	1.18
PHEL49_663	tetraacyldisaccharide 4'-kinase	3.39	11.03	4.46	0.31	0.40	0.76
PHEL49_665	OmpA family protein	35.47	86.68	70.05	0.41	0.81	0.51
PHEL49_666	exopolyphosphatase	14.36	10.03	16.21	1.43	1.62	0.89
PHEL49_667	phosphoglycerate/bisphosphoglycerate mutase	33.85		19.81			1.71
PHEL49_668	pyridoxamine 5'-phosphate oxidase	40.62		35.66			1.14
PHEL49_670	hypothetical protein containing galactose binding lectin domain		1.89	0.77		0.40	
PHEL49_672	serine/threonine protein phosphatase	7.25					
PHEL49_678	conserved hypothetical protein			5.40			
PHEL49_679	pyridine nucleotide-disulphide oxidoreductase	2.60					
PHEL49_684	transcriptional regulator, LacI family	81.96	60.97	23.46	1.34	0.38	3.49
PHEL49_687	conserved hypothetical protein (DUF2797)	10.92	14.23		0.77		
PHEL49_688	GH3 auxin-responsive promoter	3.50					
PHEL49_689	polyprenyl synthetase	21.96	35.78	26.50	0.61	0.74	0.83
PHEL49_690	ribosomal RNA large subunit methyltransferase N	3.39					
PHEL49_691	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	54.17	68.95	84.70	0.79	1.23	0.64
PHEL49_693	**glycosyltransferase, GHnc family**	**70.63**	**103.66**	**30.74**	**0.68**	**0.30**	**2.30**
PHEL49_698	pyridoxine 5'-phosphate synthase			6.60			
PHEL49_699	CBS domain-containing protein	10.83					
PHEL49_700	NAD kinase	28.72	13.37	27.02	2.15	2.02	1.06
PHEL49_701	conserved hypothetical protein	5.64					
PHEL49_702	undecaprenyl diphosphate synthase	9.34		6.15			1.52
PHEL49_703	outer membrane protein assembly factor YaeT precursor	21.61	65.72	34.14	0.33	0.52	0.63
PHEL49_704	outer membrane protein H precursor	17.92	22.71	39.33	0.79	1.73	0.46
PHEL49_705	outer membrane protein H precursor	295.78	656.12	244.00	0.45	0.37	1.21
PHEL49_706	glutamate racemase	15.80		5.94			2.66

PHEL49_708	sugar transporter	14.25	7.74	3.13	1.84	0.40	4.56
PHEL49_709	**glucosylceramidase, GH30-1 family**	**8.46**	**15.76**	**17.51**	**0.54**	**1.11**	**0.48**
PHEL49_717	conserved hypothetical protein (DUF481)			20.80			
PHEL49_760	GTP-binding protein Era	17.92	84.36	36.71	0.21	0.44	0.49
PHEL49_761	**putative glycoside hydrolase, GH16 family**	**3.17**					
PHEL49_764	S-adenosyl-L-homocysteine hydrolase	117.08	117.22	130.01	1.00	1.11	0.90
PHEL49_765	siderophore (surfactin) biosynthesis regulatory protein	8.46					
PHEL49_770	TonB-dependent receptor, plug	12.65		91.11			0.14
PHEL49_773	metallo-beta-lactamase superfamily protein	5.31	36.77	6.99	0.14	0.19	0.76
PHEL49_775	holliday junction DNA helicase RuvB	48.11	5.81	14.08	8.29	2.42	3.42
PHEL49_777	cytochrome c oxidase polypeptide II	69.44	76.38	52.58	0.91	0.69	1.32
PHEL49_778	conserved hypothetical membrane protein	11.08					
PHEL49_779	cytochrome c family protein	240.36	148.93	205.05	1.61	1.38	1.17
PHEL49_780	ABC-type Fe3+ transport system protein / molybdenum transport protein	37.24		40.12			0.93
PHEL49_781	molybdopterin oxidoreductase	27.81	13.79	7.96	2.02	0.58	3.49
PHEL49_782	molybdopterin oxidoreductase, iron-sulfur binding subunit	68.92	80.77	100.30	0.85	1.24	0.69
PHEL49_783	cytochrome c	49.65	78.45	55.47	0.63	0.71	0.90
PHEL49_784	sporulation domain-containing protein	14.51					
PHEL49_785	translation initiation factor IF-2	120.44	156.99	75.44	0.77	0.48	1.60
PHEL49_786	transcription elongation factor NusA	99.40	169.00	140.37	0.59	0.83	0.71
PHEL49_789	universal stress protein UspA	40.62	8.83	28.53	4.60	3.23	1.42
PHEL49_790	glyceraldehyde-3-phosphate dehydrogenase	52.79	91.62	111.82	0.58	1.22	0.47
PHEL49_792	ketol-acid reductoisomerase	93.75	59.40	192.02	1.58	3.23	0.49
PHEL49_793	acetolactate synthase small subunit			106.98			
PHEL49_794	acetolactate synthase large subunit	31.17	33.27	90.57	0.94	2.72	0.34
PHEL49_795	dihydroxy-acid dehydratase	13.77	14.96	39.29	0.92	2.63	0.35
PHEL49_796	3-isopropylmalate dehydrogenase	3.30					
PHEL49_798	conserved hypothetical protein	5.46		11.50			0.47
PHEL49_799	aspartokinase / homoserine dehydrogenase	9.78	12.26	42.60	0.80	3.47	0.23
PHEL49_800	homoserine kinase			5.57			
PHEL49_801	threonine synthase		11.49	11.14		0.97	
PHEL49_803	conserved hypothetical membrane protein (DUF2723)	15.23	24.82	12.63	0.61	0.51	1.21
PHEL49_806	DNA polymerase I	36.70	48.46	31.66	0.76	0.65	1.16
PHEL49_811	hemolysin	4.91					
PHEL49_814	fructose-1,6-bisphosphatase, type I	55.24	14.52	4.69	3.81	0.32	11.77
PHEL49_815	manganese superoxide dismutase	384.70	391.14	340.40	0.98	0.87	1.13
PHEL49_816	amidophosphoribosyltransferase	36.68	30.64	48.29	1.20	1.58	0.76
PHEL49_817	ribokinase	65.72	107.08	97.02	0.61	0.91	0.68
PHEL49_818	sulfur acceptor protein SufE for iron-sulfur cluster assembly	46.55					
PHEL49_819	FeS assembly SUF protein	62.07					
PHEL49_822	conserved hypothetical protein (DUF3078)	149.78	40.12	121.57	3.73	3.03	1.23
PHEL49_823	CBS domain-containing protein	6.45					

PHEL49_824	GTP-binding protein HflX	14.72	16.79	17.44	0.88	1.04	0.84
PHEL49_827	conserved hypothetical protein	6.45		25.47			0.25
PHEL49_828	conserved hypothetical membrane protein	14.11		29.72			0.47
PHEL49_831	aspartyl-tRNA synthetase	52.32	60.17	77.00	0.87	1.28	0.68
PHEL49_833	rRNA small subunit methyltransferase I			10.70			
PHEL49_834	conserved hypothetical protein	2.88	4.69	9.48	0.61	2.02	0.30
PHEL49_838	nitrate ABC transporter, nitrate-binding protein			55.94			
PHEL49_841	periplasmic nitrate reductase/nitrite reductase			4.08			
PHEL49_842	transcriptional regulator, LuxR family	16.25					
PHEL49_843	multi-sensor signal transduction histidine kinase			6.56			
PHEL49_845	nitrite reductase (NAD(P)H) small subunit			63.68			
PHEL49_846	nitrite reductase (NAD(P)H) large subunit			19.38			
PHEL49_850	UDP-2,3-diacylglucosamine hydrolase			5.75			
PHEL49_852	MoxR-like ATPase in aerotolerance operon	124.44	488.99	238.54	0.25	0.49	0.52
PHEL49_853	conserved hypothetical protein (DUF58)		16.72	10.81		0.65	
PHEL49_854	conserved hypothetical protein	14.36	143.75	43.23	0.10	0.30	0.33
PHEL49_855	BatA		31.93	9.38		0.29	
PHEL49_856	BatB	15.62	42.43	22.86	0.37	0.54	0.68
PHEL49_857	BatC	12.70	17.24	16.72	0.74	0.97	0.76
PHEL49_858	BatD	5.05	34.58	18.63	0.15	0.54	0.27
PHEL49_859	BatE	21.01	60.87	43.04	0.35	0.71	0.49
PHEL49_861	sulfate transporter	3.56	5.81		0.61		
PHEL49_863	carbonic anhydrase	135.42	275.80	48.63	0.49	0.18	2.78
PHEL49_864	sulfate transporter	4.04					
PHEL49_865	carbonic anhydrase	282.61	215.84	201.56	1.31	0.93	1.40
PHEL49_872	methionyl-tRNA synthetase	21.10	40.12	32.42	0.53	0.81	0.65
PHEL49_874	isoquinoline 1-oxidoreductase beta subunit			2.17			
PHEL49_891	two-component system response regulator	22.57	8.49	32.00	2.66	3.77	0.71
PHEL49_892	sensory transduction histidine kinase	2.82	7.66	17.34	0.37	2.26	0.16
PHEL49_910	inosine monophosphate dehydrogenase-related protein	244.50		29.72			8.23
PHEL49_911	peptidase, M28 family	2.33					
PHEL49_912	pyruvate kinase	94.54	154.03	191.76	0.61	1.24	0.49
PHEL49_913	conserved hypothetical protein	15.05		14.86			1.01
PHEL49_915	3-oxoacyl-[acyl-carrier-protein] synthase, KASII	29.24	20.06	36.47	1.46	1.82	0.80
PHEL49_917	phosphoribosylglycinamide formyltransferase	24.62	25.07	52.68	0.98	2.10	0.47
PHEL49_918	ribonuclease HI-related protein 3	8.46					
PHEL49_919	succinate dehydrogenase iron-sulfur protein	50.05	76.74	186.06	0.65	2.42	0.27
PHEL49_920	succinate dehydrogenase flavoprotein subunit	83.26	184.86	208.42	0.45	1.13	0.40
PHEL49_921	succinate dehydrogenase cytochrome b subunit	59.58	35.30	71.32	1.69	2.02	0.84
PHEL49_923	conserved hypothetical protein containing Kelch-type beta propeller domain	3.56	316.45	53.96	0.01	0.17	0.07
PHEL49_926	**glycoside hydrolase, GHnc family**	**7.74**					
PHEL49_928	ATP-dependent RNA helicase RhlE	25.39	20.69	7.43	1.23	0.36	3.42

PHEL49_929	Xaa-Pro aminopeptidase, M24 family	30.40	27.02	34.57	1.13	1.28	0.88
PHEL49_933	beta-lactamase	2.33					
PHEL49_935	**glycoside hydrolase, GHnc family**	**2.02**					
PHEL49_937	thiamine-monophosphate kinase	35.64	43.55	30.50	0.82	0.70	1.17
PHEL49_938	conserved hypothetical protein	67.71	108.28	23.11	0.63	0.21	2.93
PHEL49_940	conserved hypothetical protein, quinonprotein alcohol dehydrogenase-like superfamily		22.98	3.71		0.16	
PHEL49_944	iron-sulfur cluster assembly protein SufB	43.88	24.52	37.97	1.79	1.55	1.16
PHEL49_945	iron-sulfur cluster assembly ATPase protein SufC	67.71	31.52	66.86	2.15	2.12	1.01
PHEL49_946	iron-sulfur cluster assembly protein SufD	23.49	4.50	10.92	5.22	2.42	2.15
PHEL49_949	cysteine desulfurase			5.94			
PHEL49_950	zinc-dependent metalloprotease		29.03				
PHEL49_952	G-D-S-L family lipolytic protein	212.24	55.16	24.00	3.85	0.44	8.84
PHEL49_953	TonB-dependent receptor, plug	580.08	310.81	132.01	1.87	0.42	4.39
PHEL49_955	seryl-tRNA synthetase	43.73	34.48	52.01	1.27	1.51	0.84
PHEL49_958	conserved hypothetical protein (DUF4286)	10.42					
PHEL49_959	dimethyladenosine transferase	4.51					
PHEL49_960	Mg/Co/Ni transporter MgtE / CBS domain	10.83	22.06	19.61	0.49	0.89	0.55
PHEL49_962	histidine kinase			2.20			
PHEL49_963	SpoU rRNA methylase family protein	54.17	82.74	71.32	0.65	0.86	0.76
PHEL49_964	DNA mismatch repair protein MutS	8.89	7.80	3.60	1.14	0.46	2.47
PHEL49_967	conserved hypothetical protein		7.70	4.15		0.54	
PHEL49_969	twin-arginine translocation protein TatA	40.62		17.83			2.28
PHEL49_970	O-methyltransferase	19.75		7.43			2.66
PHEL49_972	RNA polymerase sigma-70 factor	27.70					
PHEL49_973	3-methyl-2-oxobutanoate hydroxymethyltransferase	54.17		56.46			0.96
PHEL49_974	D-3-phosphoglycerate dehydrogenase	3.87					
PHEL49_979	glucose inhibited division protein A	17.66	20.79	23.26	0.85	1.12	0.76
PHEL49_983	glutamyl-tRNA synthetase	21.01	51.36	30.74	0.41	0.60	0.68
PHEL49_985	membrane protease	433.33	633.55	320.95	0.68	0.51	1.35
PHEL49_987	conserved hypothetical protein (DUF2807)	56.87	92.67	260.33	0.61	2.81	0.22
PHEL49_988	ribonuclease R	9.56	18.17	8.39	0.53	0.46	1.14
PHEL49_992	ribose 5-phosphate isomerase B	97.33					
PHEL49_995	aldose 1-epimerase	38.37	36.77	53.49	1.04	1.45	0.72
PHEL49_996	recombinase RecA	167.39	346.28	205.55	0.48	0.59	0.81
PHEL49_998	deoxyuridine 5'-triphosphate nucleotidohydrolase	31.60					
PHEL49_1000	conserved hypothetical protein	148.96	39.72	78.45	3.75	1.98	1.90
PHEL49_1004	glycerol-3-phosphate dehydrogenase (FAD)	15.29	17.79	25.88	0.86	1.45	0.59
PHEL49_1005	pyridoxamine 5'-phosphate oxidase	25.79		16.98			1.52
PHEL49_1013	phenylalanyl-tRNA synthetase subunit alpha	93.75	90.52	114.30	1.04	1.26	0.82
PHEL49_1014	NADP-specific glutamate dehydrogenase	536.25	139.00	92.72	3.86	0.67	5.78
PHEL49_1019	oxidoreductase	25.79	18.39	6.37	1.40	0.35	4.05

PHEL49_1022	naringenin-chalcone synthase	6.94		11.43			0.61
PHEL49_1030	conserved hypothetical protein	21.38		23.46			0.91
PHEL49_1031	thioredoxin	67.71	9.59	54.27	7.06	5.66	1.25
PHEL49_1033	conserved hypothetical protein containing SnoaL-like domain	20.31		17.83			1.14
PHEL49_1035	acriflavin resistance protein	19.79	33.10	17.83	0.60	0.54	1.11
PHEL49_1036	efflux transporter, RND family, MFP subunit	42.51	79.53	130.62	0.53	1.64	0.33
PHEL49_1037	outer membrane efflux protein	7.67	12.49	23.55	0.61	1.89	0.33
PHEL49_1038	transcriptional regulator, TetR family	9.67		16.98			0.57
PHEL49_1039	polyprenyl synthetase	5.49					
PHEL49_1042	prolyl endopeptidase	15.88	20.43	23.11	0.78	1.13	0.69
PHEL49_1049	ABC transporter, ATP-binding protein	5.21					
PHEL49_1050	SprE, gliding motility protein	26.29	24.66	18.88	1.07	0.77	1.39
PHEL49_1054	ATP synthase A chain	17.73	21.01	21.23	0.84	1.01	0.84
PHEL49_1056	ATP synthase B chain	383.68	275.80	421.00	1.39	1.53	0.91
PHEL49_1057	ATP synthase delta chain	109.62	52.53	148.59	2.09	2.83	0.74
PHEL49_1058	ATP synthase alpha chain	261.16	366.42	364.57	0.71	0.99	0.72
PHEL49_1059	ATP synthase gamma chain	86.75	144.80	130.94	0.60	0.90	0.66
PHEL49_1060	conserved hypothetical protein	67.71	42.90	79.25	1.58	1.85	0.85
PHEL49_1062	oxidoreductase, short chain dehydrogenase/reductase family	21.76		28.66			0.76
PHEL49_1066	aldehyde dehydrogenase B	288.07	84.24	118.33	3.42	1.40	2.43
PHEL49_1067	asparaginase	58.30	27.58	42.10	2.11	1.53	1.38
PHEL49_1072	tyrosyl-tRNA synthetase	31.03	25.28	29.72	1.23	1.18	1.04
PHEL49_1073	3-beta hydroxysteroid dehydrogenase/isomerase family protein			7.04			
PHEL49_1075	dihydroorotase	5.42	17.65	3.57	0.31	0.20	1.52
PHEL49_1079	uroporphyrinogen-III synthase HemD, putative	36.27	47.28	105.07	0.77	2.22	0.35
PHEL49_1080	DNA repair protein RadA	16.25	46.33	23.18	0.35	0.50	0.70
PHEL49_1083	pantoate-beta-alanine ligase	6.16					
PHEL49_1084	**glycosyltransferase, GT5 family**	**198.76**	**227.76**	**310.60**	**0.87**	**1.36**	**0.64**
PHEL49_1085	conserved hypothetical protein (DUF4270)	18.23	137.90	24.00	0.13	0.17	0.76
PHEL49_1086	glucosamine-fructose-6-phosphate aminotransferase	20.61	44.77	41.35	0.46	0.92	0.50
PHEL49_1091	deoxyribose-phosphate aldolase	43.53	11.82	35.02	3.68	2.96	1.24
PHEL49_1093	aldo/keto reductase	65.97	87.69	82.29	0.75	0.94	0.80
PHEL49_1094	phosphoglycerate kinase	55.11	156.50	236.36	0.35	1.51	0.23
PHEL49_1095	DNA polymerase III subunit delta	7.87					
PHEL49_1097	4-hydroxythreonine-4-phosphate dehydrogenase	69.49	81.29	103.23	0.85	1.27	0.67
PHEL49_1099	LSU ribosomal protein L32	33.85					
PHEL49_1100	3-oxoacyl-[acyl-carrier-protein] synthase, KASIII	144.82	162.42	89.15	0.89	0.55	1.62
PHEL49_1101	acetyl-CoA carboxylase, biotin carboxyl carrier protein	203.12	227.13	298.92	0.89	1.32	0.68
PHEL49_1102	acetyl-CoA carboxylase, biotin carboxylase	117.81	154.45	149.78	0.76	0.97	0.79
PHEL49_1103	transcriptional regulator, AsnC family	79.66					
PHEL49_1107	carboxymuconolactone decarboxylase	52.32		20.26			2.58
PHEL49_1108	OsmC family protein	38.09					

PHEL49_1110	helicase	7.44	4.85	1.96	1.53	0.40	3.80
PHEL49_1112	2-oxoglutarate dehydrogenase, E2 subunit	111.80	223.21	184.53	0.50	0.83	0.61
PHEL49_1114	2-oxoglutarate dehydrogenase, E1 subunit	37.76	76.38	66.86	0.49	0.88	0.56
PHEL49_1124	tRNA-guanine transglycosylase	18.90	23.09	22.81	0.82	0.99	0.83
PHEL49_1127	acetyl-coenzyme A carboxyl transferase alpha chain	92.16	85.80	153.54	1.07	1.79	0.60
PHEL49_1128	thiol:disulfide interchange protein TlpA	5.21	39.60	93.72	0.13	2.37	0.06
PHEL49_1129	histidine ammonia-lyase	16.30	10.21	3.30	1.60	0.32	4.94
PHEL49_1130	ATP-dependent Clp protease, ATP-binding subunit ClpC	129.77	171.23	87.30	0.76	0.51	1.49
PHEL49_1131	DNA gyrase subunit A	166.39	200.69	87.26	0.83	0.43	1.91
PHEL49_1132	tetratricopeptide repeat family protein	239.14	178.39	73.98	1.34	0.41	3.23
PHEL49_1133	NlpC/P60 family protein	7.25		22.29			0.33
PHEL49_1134	acetyl-CoA acetyltransferase	107.34	166.83	130.47	0.64	0.78	0.82
PHEL49_1135	HD family protein	10.42		2.29			4.56
PHEL49_1139	CHU large protein; gliding motility-related protein; possible adhesin AidA-related	2.05		0.90			2.28
PHEL49_1141	glutamate synthase (NADPH) small chain			61.09			
PHEL49_1142	glutamate synthase (NADPH) large chain	7.25	59.76	215.45	0.12	3.61	0.03
PHEL49_1144	nitrogen regulatory protein P-II	83.33	212.15	212.60	0.39	1.00	0.39
PHEL49_1146	conserved hypothetical protein (DUF1597)			611.33			
PHEL49_1148	butyryl-CoA dehydrogenase	288.57	254.79	101.89	1.13	0.40	2.83
PHEL49_1150	Glu/Leu/Phe/Val dehydrogenase family protein	46.64	51.48	47.55	0.91	0.92	0.98
PHEL49_1152	MotA/TolQ/ExbB proton channel family protein	59.58	83.84	131.95	0.71	1.57	0.45
PHEL49_1155	dihydrofolate synthase / folylpoly glutamate synthase		17.16				
PHEL49_1157	PAP2 superfamily protein			26.50			
PHEL49_1159	UDP-glucose dehydrogenase	25.39	27.58	24.15	0.92	0.88	1.05
PHEL49_1160	oxidoreductase		21.45	9.91		0.46	
PHEL49_1162	glycerol-3-phosphate cytidylyltransferase	127.45	90.85	194.04	1.40	2.14	0.66
PHEL49_1163	GDP-L-fucose synthetase	37.62	6.13	54.48	6.14	8.89	0.69
PHEL49_1165	GDP-mannose 4,6-dehydratase	148.31	126.08	212.27	1.18	1.68	0.70
PHEL49_1166	UDP-glucose 6-dehydrogenase	36.46	19.09	113.16	1.91	5.93	0.32
PHEL49_1167	dTDP-glucose 4,6-dehydratase	266.96	179.66	290.38	1.49	1.62	0.92
PHEL49_1168	UDP-glucuronate 5'-epimerase	35.64	43.55	46.92	0.82	1.08	0.76
PHEL49_1169	dTDP-glucose 4,6-dehydratase	55.86	85.50	111.44	0.65	1.30	0.50
PHEL49_1170	glucose-1-phosphate thymidylyltransferase	75.92	113.66	289.07	0.67	2.54	0.26
PHEL49_1171	dTDP-4-dehydrorhamnose 3,5-epimerase	15.39		8.10			1.90
PHEL49_1172	dTDP-4-dehydrorhamnose reductase	107.91	72.40	164.38	1.49	2.27	0.66
PHEL49_1173	LPS polysaccharide biosynthesis protein	3.98					
PHEL49_1176	**glycosyltransferase WbsX family protein**	**20.00**	**7.52**	**44.58**	**2.66**	**5.93**	**0.45**
PHEL49_1177	**glycosyltransferase WbsX family protein**	**45.14**	**39.40**	**59.44**	**1.15**	**1.51**	**0.76**
PHEL49_1180	**glycosyltransferase, GT4 family**	**18.73**		**26.56**			**0.71**
PHEL49_1182	dTDP-4-dehydrorhamnose reductase	199.02	183.87	316.09	1.08	1.72	0.63
PHEL49_1183	**glycosyltransferase, GT4 family**			**6.37**			

PHEL49_1184	undecaprenyl-phosphate glucose phosphotransferase	36.36					
PHEL49_1185	polysaccharide export outer membrane protein	116.74	95.10	147.56	1.23	1.55	0.79
PHEL49_1186	tyrosine-protein kinase involved in exopolysaccharide biosynthesis	47.93	40.91	72.12	1.17	1.76	0.66
PHEL49_1188	capsular polysaccharide biosynthesis protein	4.67					
PHEL49_1189	conserved hypothetical protein, BadF/BadG/BcrA/BcrD ATPase family	50.78	48.27	147.66	1.05	3.06	0.34
PHEL49_1190	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6- diaminopimelate-D-alanyl-D-alanine ligase	5.76	4.69	9.48	1.23	2.02	0.61
PHEL49_1191	gliding motility protein GldJ	60.53	38.45	58.08	1.57	1.51	1.04
PHEL49_1192	conserved hypothetical protein, putative peptidase, C25 family	15.58	12.26	7.08	1.27	0.58	2.20
PHEL49_1193	conserved hypothetical protein	143.67	166.83	132.64	0.86	0.80	1.08
PHEL49_1196	3-oxoacyl-[acyl-carrier-protein] synthase, KASIII	27.78	14.14	22.86	1.96	1.62	1.22
PHEL49_1197	GMP synthase (glutamine-hydrolyzing)	37.48	47.28	35.02	0.79	0.74	1.07
PHEL49_1198	**peptidoglycan-binding LysM domain protein, CBM50 domain**	**20.75**	**12.46**	**23.01**	**1.67**	**1.85**	**0.90**
PHEL49_1199	conserved hypothetical protein	71.09		71.32			1.00
PHEL49_1200	cytochrome c assembly protein	23.86	8.14	15.35	2.93	1.89	1.56
PHEL49_1201	peptidase, M20 family	48.55	52.04	21.87	0.93	0.42	2.22
PHEL49_1202	cardiolipin synthetase	5.84					
PHEL49_1203	methylmalonyl-CoA mutase large subunit	10.69	10.16	9.38	1.05	0.92	1.14
PHEL49_1204	methylmalonyl-CoA mutase small subunit		6.36	3.43		0.54	
PHEL49_1206	uridine kinase	114.81	163.08	69.77	0.70	0.43	1.65
PHEL49_1207	ABC1 family protein	2.71	39.72	35.66	0.07	0.90	0.08
PHEL49_1208	conserved hypothetical protein		41.37	85.44		2.07	
PHEL49_1210	conserved hypothetical protein	26.67	183.87	83.75	0.15	0.46	0.32
PHEL49_1213	conserved hypothetical protein	236.98	27.58	57.95	8.59	2.10	4.09
PHEL49_1214	glycerol-3-phosphate dehydrogenase (NAD(P)+)	203.12	91.93	99.06	2.21	1.08	2.05
PHEL49_1215	acyltransferase	2.77	2.71	9.50	1.02	3.50	0.29
PHEL49_1218	conserved hypothetical protein, putative acyltransferase	13.74	6.40	18.09	2.15	2.83	0.76
PHEL49_1220	deoxyribodipyrimidine photolyase	39.83	84.36	22.73	0.47	0.27	1.75
PHEL49_1221	conserved hypothetical protein	82.75	79.68	89.15	1.04	1.12	0.93
PHEL49_1224	glutathione peroxidase	142.94	190.00	188.21	0.75	0.99	0.76
PHEL49_1225	short chain dehydrogenase	205.83	397.15	267.46	0.52	0.67	0.77
PHEL49_1226	conserved hypothetical protein	15.05					
PHEL49_1228	GTP cyclohydrolase I	93.75	186.70	257.17	0.50	1.38	0.36
PHEL49_1231	cryptochrome	4.59	14.96	15.11	0.31	1.01	0.30
PHEL49_1232	deoxyribodipyrimidine photolyase	54.64	168.38	51.61	0.32	0.31	1.06
PHEL49_1233	cryptochrome, DASH family	41.16	127.63	54.19	0.32	0.42	0.76
PHEL49_1234	NAD-dependent epimerase/dehydratase	20.06	42.90	33.02	0.47	0.77	0.61
PHEL49_1235	flavin reductase domain-containing FMN-binding protein	76.17	257.41	89.15	0.30	0.35	0.85
PHEL49_1237	thioredoxin reductase	19.91	32.45	18.35	0.61	0.57	1.08
PHEL49_1240	acyl-CoA dehydrogenase	1216.69	666.94	536.27	1.82	0.80	2.27
PHEL49_1241	acetyl-CoA acetyltransferase	1091.20	1416.21	568.09	0.77	0.40	1.92
PHEL49_1242	3-hydroxyacyl-CoA dehydrogenase	844.45	1104.44	507.87	0.76	0.46	1.66

PHEL49_1244	sulfate/thiosulfate import ATP-binding protein CysA	19.35	40.98	45.85	0.47	1.12	0.42
PHEL49_1245	ABC transporter, permease protein	43.22	30.51	43.63	1.42	1.43	0.99
PHEL49_1247	two-component sigma-54 specific transcriptional regulator	3.15	12.83		0.25		
PHEL49_1248	**catalase / peroxidase**	**342.72**	**118.49**	**156.29**	**2.89**	**1.32**	**2.19**
PHEL49_1249	peroxiredoxin	22.57		96.58			0.23
PHEL49_1250	thioredoxin	11.28					
PHEL49_1254	polyphosphate kinase 2	103.68	155.14	97.51	0.67	0.63	1.06
PHEL49_1255	DNA polymerase III subunit epsilon	111.39	110.32	115.04	1.01	1.04	0.97
PHEL49_1256	conserved hypothetical protein	14.25					
PHEL49_1257	**beta-N-acetylglucosaminidase, GH3 family / serine peptidase, S12 family**		**23.07**				
PHEL49_1261	ribosomal RNA small subunit methyltransferase E			23.11			
PHEL49_1262	GTP cyclohydrolase		5.01	12.16		2.42	
PHEL49_1265	conserved hypothetical protein	125.74	157.60	89.15	0.80	0.57	1.41
PHEL49_1266	conserved hypothetical membrane protein	5.15	2.40	5.81	2.15	2.42	0.89
PHEL49_1269	**glycosyltransferase, GT4 family**			**3.71**			
PHEL49_1270	polysaccharide biosynthesis protein	2.38					
PHEL49_1274	signal peptidase I	23.60	28.42	13.51	0.83	0.48	1.75
PHEL49_1275	dihydrodipicolinate reductase	36.46	16.97	44.58	2.15	2.63	0.82
PHEL49_1276	conserved hypothetical protein	12.90		12.74			1.01
PHEL49_1277	chromosome (plasmid) partitioning protein ParB	65.66	147.09	78.35	0.45	0.53	0.84
PHEL49_1278	chromosome (plasmid) partitioning protein ParA	50.78	118.20	85.97	0.43	0.73	0.59
PHEL49_1279	aminoacyl-histidine dipeptidase (peptidase D)	10.03	14.30	29.72	0.70	2.08	0.34
PHEL49_1280	nitroreductase family protein	42.32	45.97		0.92		
PHEL49_1282	conserved hypothetical protein	42.23	79.48	46.01	0.53	0.58	0.92
PHEL49_1283	branched-chain alpha-keto acid dehydrogenase, E1 component, alpha/beta subunit	22.57	10.68	10.54	2.11	0.99	2.14
PHEL49_1284	aminopeptidase N	1.23					
PHEL49_1285	conserved hypothetical protein containing possible lysine decarboxylase motif	102.82	122.58	115.57	0.84	0.94	0.89
PHEL49_1286	excinuclease ABC subunit A	9.03	14.71	7.64	0.61	0.52	1.18
PHEL49_1288	potassium channel protein	3.87		7.64			0.51
PHEL49_1289	Na(+)-linked D-alanine glycine permease	73.65	36.77	28.15	2.00	0.77	2.62
PHEL49_1291	butyryl-CoA dehydrogenase	47.70	22.57	81.05	2.11	3.59	0.59
PHEL49_1295	ribosomal subunit interface protein	299.04					
PHEL49_1300	translation elongation factor Tu	1288.03	2039.65	1331.07	0.63	0.65	0.97
PHEL49_1303	transcription antitermination protein NusG	365.62	231.67	258.54	1.58	1.12	1.41
PHEL49_1304	LSU ribosomal protein L11p (L12e)	591.32	235.35	344.72	2.51	1.46	1.72
PHEL49_1305	LSU ribosomal protein L1p (L10Ae)	372.39	193.06	297.18	1.93	1.54	1.25
PHEL49_1306	LSU ribosomal protein L10p (P0)	894.46	632.89	581.84	1.41	0.92	1.54
PHEL49_1307	LSU ribosomal protein L7/L12 (P1/P2)	2041.66	1281.41	1488.17	1.59	1.16	1.37
PHEL49_1308	DNA-directed RNA polymerase beta subunit	522.25	638.78	250.00	0.82	0.39	2.09

PHEL49_1310	DNA-directed RNA polymerase beta subunit	530.95	607.46	235.86	0.87	0.39	2.25
PHEL49_1314	chorismate synthase	51.67	14.52	23.46	3.56	1.62	2.20
PHEL49_1317	response regulator receiver and SARP domain-containing protein	14.90	17.65	14.26	0.84	0.81	1.04
PHEL49_1323	**sulfatase (S1-51) / glycoside hydrolase (GH99)**	**1.33**					
PHEL49_1332	**sulfatase, S1-15 family**		**4.01**				
PHEL49_1334	**sulfatase, S1-51 family**		**5.61**				
PHEL49_1337	**mannose-6-phosphate isomerase**			**4.82**			
PHEL49_1347	2-dehydro-3-deoxyphosphogluconate aldolase / 4-hydroxy-2-oxoglutarate aldolase	10.83					
PHEL49_1348	2-dehydro-3-deoxygluconate kinase	3.56					
PHEL49_1351	aldehyde dehydrogenase	3.76					
PHEL49_1361	glycerophosphoryl diester phosphodiesterase	4.84					
PHEL49_1363	protein containing pectin lyase domain	7.65	12.47		0.61		
PHEL49_1373	**endo-1,3(4)-beta-glucanase, GH16 family**			**40.21**			
PHEL49_1377	conserved hypothetical protein (DUF4287)	93.50					
PHEL49_1380	ribosomal large subunit pseudouridine synthase F	17.92		13.11			1.37
PHEL49_1385	conserved hypothetical protein	12.31	14.04	6.48	0.88	0.46	1.90
PHEL49_1386	oxidoreductase alpha (molybdopterin) subunit			2.10			
PHEL49_1389	conserved hypothetical membrane protein (DUF20)	5.08					
PHEL49_1390	conserved hypothetical protein			3.64			
PHEL49_1394	gamma-glutamyltranspeptidase	87.37	76.51	94.90	1.14	1.24	0.92
PHEL49_1397	DNA polymerase III subunit beta	166.79	312.13	223.97	0.53	0.72	0.74
PHEL49_1398	**carbohydrate esterase, CE14 family**	**5.76**	**17.60**	**6.64**	**0.33**	**0.38**	**0.87**
PHEL49_1399	sodium iodide symporter	1.91					
PHEL49_1401	conserved hypothetical protein (DUF2911)	336.55	992.88	631.94	0.34	0.64	0.53
PHEL49_1403	dTDP-glucose 4,6-dehydratase			12.30			
PHEL49_1404	gliding motility protein GldG	1.50	4.90	1.98	0.31	0.40	0.76
PHEL49_1408	S-adenosyl-l-methionine hydroxide adenosyltransferase	12.70	13.79	13.93	0.92	1.01	0.91
PHEL49_1409	phosphate starvation-inducible protein PhoH	20.69	58.22	52.01	0.36	0.89	0.40
PHEL49_1411	phosphoribosylaminoimidazole-succinocarboxamide synthase	61.73	38.94	68.18	1.59	1.75	0.91
PHEL49_1413	glyoxylase family protein	53.20					
PHEL49_1417	Na+/solute symporter	2.22					
PHEL49_1418	acetyl-CoA synthetase			3.71			
PHEL49_1420	lipid A export ATP-binding/permease protein MsbA	2.08	42.43	15.09	0.05	0.36	0.14
PHEL49_1421	conserved hypothetical protein		30.43	9.22		0.30	
PHEL49_1423	endoglucanase	204.82	711.57	474.74	0.29	0.67	0.43
PHEL49_1424	ABC transporter, ATP-binding protein	65.66	70.20	83.75	0.94	1.19	0.78
PHEL49_1425	conserved hypothetical membrane protein containing ABC-2 family transporter and peptidase MA domains	5.85	4.76		1.23		
PHEL49_1427	conserved hypothetical protein containing esterase-like activity of phytase domain	4.95		4.35			1.14
PHEL49_1429	dihydrodipicolinate synthase	32.83	20.06	56.73	1.64	2.83	0.58

PHEL49_1430	ferritin 1	388.43	63.87	98.54	6.08	1.54	3.94
PHEL49_1431	lipoprotein	67.71	198.58	99.34	0.34	0.50	0.68
PHEL49_1432	RNA polymerase Rpb6	11.28					
PHEL49_1433	phosphopantothenoylcysteine decarboxylase / phosphopantothenoylcysteine synthetase	32.32	47.64	10.13	0.68	0.21	3.19
PHEL49_1434	conserved hypothetical protein	37.84	22.71	39.33	1.67	1.73	0.96
PHEL49_1435	DNA repair protein RecN	7.64	17.79	11.50	0.43	0.65	0.66
PHEL49_1436	enoyl-(acyl-carrier-protein) reductase [NADH]	516.84	393.48	451.71	1.31	1.15	1.14
PHEL49_1440	copper homeostasis protein CutC	39.06	8.49	6.86	4.60	0.81	5.70
PHEL49_1446	inner membrane protein translocase component YidC	20.69	38.31	29.72	0.54	0.78	0.70
PHEL49_1447	CTP synthase	48.52	40.45	49.03	1.20	1.21	0.99
PHEL49_1449	carbamoyl-phosphate synthase large chain	100.92	56.20	84.95	1.80	1.51	1.19
PHEL49_1450	conserved hypothetical protein	9.67		25.47			0.38
PHEL49_1453	two-component system response regulator	8.26	8.07	8.70	1.02	1.08	0.95
PHEL49_1456	YceI-like domain protein	57.55					
PHEL49_1457	conserved hypothetical protein			11.14			
PHEL49_1460	glucose-1-phosphate thymidylyltransferase	53.86	107.81	89.15	0.50	0.83	0.60
PHEL49_1462	conserved hypothetical protein (DUF2807)	65.10	178.21	106.30	0.37	0.60	0.61
PHEL49_1463	conserved hypothetical protein	11.56	88.79	21.74	0.13	0.24	0.53
PHEL49_1466	conserved hypothetical protein (DUF4380)			4.95			
PHEL49_1468	ATP-dependent protease La	28.59	240.25	58.44	0.12	0.24	0.49
PHEL49_1469	nucleoside triphosphate pyrophosphohydrolase MazG	13.54	7.35	20.80	1.84	2.83	0.65
PHEL49_1470	conserved hypothetical protein	93.10		50.15			1.86
PHEL49_1471	peptide deformylase	44.16		58.14			0.76
PHEL49_1473	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	65.45	77.22	124.81	0.85	1.62	0.52
PHEL49_1474	**lipopolysaccharide core biosynthesis glycosyltransferase, GT2 family**	**9.34**	**7.61**	**55.34**	**1.23**	**7.27**	**0.17**
PHEL49_1477	**sulfatase**	**7.03**		**2.32**			**3.04**
PHEL49_1480	lipid A export ATP-binding/permease protein MsbA	17.92	4.87	26.22	3.68	5.39	0.68
PHEL49_1481	phosphoglucomutase	41.91	52.53	130.19	0.80	2.48	0.32
PHEL49_1482	**undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase, GT2 family**			**4.82**			
PHEL49_1483	LSU ribosomal protein L31 type B	167.49	69.68	197.07	2.40	2.83	0.85
PHEL49_1484	oxidoreductase, short chain dehydrogenase/reductase family			14.86			
PHEL49_1485	conserved hypothetical protein	3.39	33.10	8.92	0.10	0.27	0.38
PHEL49_1486	transaldolase	500.45	589.97	658.96	0.85	1.12	0.76
PHEL49_1487	2-succinyl-5-enolpyruvyl-6-hydroxy-3- cyclohexene-1-carboxylic-acid synthase			2.83			
PHEL49_1488	RNA binding S1 protein	35.64		18.77			1.90
PHEL49_1489	esterase	10.77	15.04		0.72		
PHEL49_1490	naphthoate synthase	69.89	71.17	126.54	0.98	1.78	0.55
PHEL49_1491	formyltetrahydrofolate deformylase			10.81			
PHEL49_1492	fumarylacetoacetate hydrolase family protein	58.88	57.56	73.65	1.02	1.28	0.80

PHEL49_1493	competence/damage-inducible protein CinA-like protein	10.30	9.59	17.44	1.07	1.82	0.59
PHEL49_1494	LSU ribosomal protein L28p	90.28		89.15			1.01
PHEL49_1496	conserved hypothetical protein (DUF4295)	22.57					
PHEL49_1498	signal recognition particle-docking protein FtsY	43.26	70.48	27.24	0.61	0.39	1.59
PHEL49_1503	phosphomannomutase / phosphoglucosamine mutase	48.75	44.13	64.19	1.10	1.45	0.76
PHEL49_1504	conserved hypothetical protein		10.34	19.50		1.89	
PHEL49_1505	cysteine desulfurase	8.62	4.01	9.73	2.15	2.42	0.89
PHEL49_1506	lipid A biosynthesis lauroyl acyltransferase	3.66		19.28			0.19
PHEL49_1509	peptidyl-prolyl cis-trans isomerase	104.64	123.69	121.57	0.85	0.98	0.86
PHEL49_1510	conserved hypothetical protein	8.32		10.95			0.76
PHEL49_1511	peptide chain release factor 3	6.77	3.68		1.84		
PHEL49_1513	isopentenyl-diphosphate delta-isomerase	32.24	31.52	8.49	1.02	0.27	3.80
PHEL49_1514	6-pyruvoyl tetrahydrobiopterin synthase	8.46					
PHEL49_1518	mannose-6-phosphate isomerase	3.66	38.76	31.32	0.09	0.81	0.12
PHEL49_1519	3-deoxy-manno-octulosonate cytidylyltransferase	19.35	23.64	25.47	0.82	1.08	0.76
PHEL49_1520	haloacid delahogenase-like hydrolase	17.55	8.17	6.60	2.15	0.81	2.66
PHEL49_1523	conserved hypothetical protein		23.64				
PHEL49_1526	conserved hypothetical protein	110.03	354.60	159.20	0.31	0.45	0.69
PHEL49_1528	conserved hypothetical protein	111.23		50.94			2.18
PHEL49_1534	conserved hypothetical protein (DUF4870)	33.85					
PHEL49_1535	dihydroorotase	14.72	31.18	34.89	0.47	1.12	0.42
PHEL49_1537	serine carboxypeptidase	30.88	11.61	17.20	2.66	1.48	1.80
PHEL49_1539	lipoprotein-releasing system ATP-binding protein LolD	5.42		14.26			0.38
PHEL49_1541	succinyl-CoA ligase (ADP-forming) subunit beta	168.48	274.52	265.39	0.61	0.97	0.63
PHEL49_1544	excinuclease ABC subunit B	6.24	2.90	8.21	2.15	2.83	0.76
PHEL49_1545	conserved hypothetical protein	55.29	62.01	31.65	0.89	0.51	1.75
PHEL49_1546	excinuclease ABC subunit B		44.82				
PHEL49_1547	ABC transporter, ATP-binding protein	28.72	113.66	45.93	0.25	0.40	0.63
PHEL49_1548	plasmid pRiA4b, Orf3-like protein	14.25		46.92			0.30
PHEL49_1549	thioesterase superfamily protein	12.70					
PHEL49_1551	conserved hypothetical protein (DUF3276)	952.75	575.24	630.44	1.66	1.10	1.51
PHEL49_1552	ABC multidrug transporter, ATP-binding and permease protein	5.13		6.75			0.76
PHEL49_1553	NusB family protein	29.02	12.61	33.11	2.30	2.63	0.88
PHEL49_1554	conserved hypothetical protein (DUF1573)	342.52	707.35	902.02	0.48	1.28	0.38
PHEL49_1555	preprotein translocase subunit YajC (TC 3.A.5.1.1)	677.08	376.93	631.50	1.80	1.68	1.07
PHEL49_1556	conserved hypothetical protein			4.95			
PHEL49_1558	two-component system sensor histidine kinase	4.51	12.87	5.94	0.35	0.46	0.76
PHEL49_1559	two-component system response regulator	273.34	935.68	194.82	0.29	0.21	1.40
PHEL49_1560	Sua5/YciO/YrdC/YwlC family protein	64.76		7.75			8.35
PHEL49_1562	type I restriction enzyme R protein	9.03					
PHEL49_1563	DNA polymerase III subunit delta	10.42	14.14	20.57	0.74	1.45	0.51
PHEL49_1564	long-chain fatty-acid-CoA ligase	42.82	43.80	36.71	0.98	0.84	1.17

PHEL49_1565	long-chain fatty-acid-CoA ligase	8.08	11.53	14.64	0.70	1.27	0.55
PHEL49_1566	conserved hypothetical protein containing pentapeptide repeats	26.21	352.31	227.20	0.07	0.64	0.12
PHEL49_1569	phosphoribosylformylglycinamidine synthase, synthetase subunit / phosphoribosylformylglycinamidine synthase, glutamine amidotransferase subunit	81.65	134.66	51.13	0.61	0.38	1.60
PHEL49_1570	cytochrome c peroxidase	14.32	6.36	3.43	2.25	0.54	4.18
PHEL49_1571	endonuclease I	27.45	47.71	8.43	0.58	0.18	3.25
PHEL49_1572	endonuclease I	42.32	41.37	10.03	1.02	0.24	4.22
PHEL49_1573	tRNA and rRNA cytosine-C5-methylase	20.61	19.19	27.13	1.07	1.41	0.76
PHEL49_1576	CDP-alcohol phosphatidyltransferase	14.01		9.22			1.52
PHEL49_1579	**glycoside hydrolase, GHnc family**	**22.18**	**38.99**	**24.59**	**0.57**	**0.63**	**0.90**
PHEL49_1580	**glycoside hydrolase, GHnc family**	**5.25**		**4.61**			**1.14**
PHEL49_1583	ArgK protein	19.10	22.63	34.29	0.84	1.52	0.56
PHEL49_1584	cysteinyl-tRNA synthetase	14.51	84.71	71.64	0.17	0.85	0.20
PHEL49_1586	prolipoprotein diacylglyceryl transferase			7.87			
PHEL49_1588	conserved hypothetical protein		20.06				
PHEL49_1590	acyltransferase			11.50			
PHEL49_1591	Zn-dependent aminopeptidase, MA superfamily	70.13	101.13	142.22	0.69	1.41	0.49
PHEL49_1592	Zn-dependent aminopeptidase, MA superfamily	19.23	36.77	19.81	0.52	0.54	0.97
PHEL49_1594	conserved hypothetical protein (DUF4480)		14.23				
PHEL49_1597	peptidase S51 family	5.21		6.86			0.76
PHEL49_1598	3,4-dihydroxy-2-butanone 4-phosphate synthase / GTP cyclohydrolase II	43.53	86.68	76.42	0.50	0.88	0.57
PHEL49_1600	conserved hypothetical protein	43.33		42.79			1.01
PHEL49_1601	cell division protein FtsK	19.60	4.35	14.08	4.50	3.23	1.39
PHEL49_1603	thiol peroxidase, Tpx-type	11.28		34.67			0.33
PHEL49_1606	aminopeptidase, M28 family	99.87	157.21	104.75	0.64	0.67	0.95
PHEL49_1609	nucleoside 5-triphosphatase RdgB	18.47					
PHEL49_1611	quinolinate phosphoribosyltransferase	24.03	32.03	14.38	0.75	0.45	1.67
PHEL49_1612	McbG protein	33.85	55.16	28.37	0.61	0.51	1.19
PHEL49_1615	histidyl-tRNA synthetase	54.43	54.08	54.19	1.01	1.00	1.00
PHEL49_1616	GTP cyclohydrolase I	117.19	12.73	137.16	9.21	10.78	0.85
PHEL49_1617	**hypothetical protein containing three putative carbohydrate binding modules, CBM61**			**19.63**			
PHEL49_1618	**putatuve endo-1,3(4)-beta-glucanase, GH81 family**	**1.17**	**4.46**	**18.04**	**0.26**	**4.04**	**0.07**
PHEL49_1620	preprotein translocase subunit SecA	84.24	348.33	100.38	0.24	0.29	0.84
PHEL49_1622	cobalamin adenosyltransferase	21.54	65.19	137.78	0.33	2.11	0.16
PHEL49_1629	fumarate hydratase class II	134.06	145.62	185.44	0.92	1.27	0.72
PHEL49_1631	TonB-dependent receptor, plug	11.78	29.98	20.35	0.39	0.68	0.58
PHEL49_1632	arsenate reductase	41.67					
PHEL49_1633	peptide chain release factor 2	17.73	26.27	14.86	0.68	0.57	1.19
PHEL49_1634	extracellular metal-dependent peptidase	51.34	58.19	36.25	0.88	0.62	1.42
PHEL49_1635	L-allo-threonine aldolase	14.25	23.23	21.12	0.61	0.91	0.68

PHEL49_1637	RNA polymerase sigma-70 factor	28.51					
PHEL49_1638	transcriptional regulator, MerR family	71.47	177.74	126.30	0.40	0.71	0.57
PHEL49_1639	phytoene dehydrogenase	54.17	146.43	89.15	0.37	0.61	0.61
PHEL49_1640	phytoene synthase			27.02			
PHEL49_1642	lycopene cyclase		17.16	3.96		0.23	
PHEL49_1643	NADH:flavin oxidoreductase/NADH oxidase	9.03		17.83			0.51
PHEL49_1644	**carbohydrate binding protein, CBM9 domain**	**11.28**	**9.19**	**22.29**	**1.23**	**2.42**	**0.51**
PHEL49_1646	argininosuccinate lyase		9.19	35.29		3.84	
PHEL49_1648	acetylglutamate kinase			6.37			
PHEL49_1649	ornithine carbamoyltransferase			28.02			
PHEL49_1652	acetylornithine aminotransferase		5.38	4.35		0.81	
PHEL49_1653	pyrroline-5-carboxylate reductase		7.61	110.67		14.55	
PHEL49_1654	N-acetyl-gamma-glutamyl-phosphate reductase			27.24			
PHEL49_1655	argininosuccinate synthase	3.08	17.55	60.79	0.18	3.46	0.05
PHEL49_1658	two-component system sensor histidine kinase	6.39	27.06		0.24		
PHEL49_1664	two-component system response regulator		7.35				
PHEL49_1668	SPFH domain / band 7 family protein	50.78	58.61	125.37	0.87	2.14	0.41
PHEL49_1669	endonuclease	78.99	257.41	115.90	0.31	0.45	0.68
PHEL49_1670	redoxin			13.37			
PHEL49_1671	thioredoxin family protein	32.38	91.13	42.64	0.36	0.47	0.76
PHEL49_1675	conserved hypothetical protein (DUF490)	6.57					
PHEL49_1676	6-phosphofructokinase	21.91	45.43	86.53	0.48	1.90	0.25
PHEL49_1677	glyceraldehyde-3-phosphate dehydrogenase	278.36	637.41	1099.55	0.44	1.73	0.25
PHEL49_1679	conserved hypothetical protein		9.73	4.37		0.45	
PHEL49_1681	MCE family protein	30.09	39.84	52.01	0.76	1.31	0.58
PHEL49_1682	iron-sulphur-binding reductase	17.60		19.61			0.90
PHEL49_1683	iron-sulphur-binding reductase	28.02	34.24	79.93	0.82	2.33	0.35
PHEL49_1687	conserved hypothetical protein	33.85		35.66			0.95
PHEL49_1688	O-succinylbenzoate synthase	17.36	22.63	11.43	0.77	0.51	1.52
PHEL49_1689	abortive infection protein	5.64					
PHEL49_1690	O-succinylbenzoic acid-CoA ligase	5.21	5.66		0.92		
PHEL49_1691	peptidoglycan-binding domain protein	33.85	12.73	51.43	2.66	4.04	0.66
PHEL49_1692	transcriptional regulator, Crp/Fnr family			7.75			
PHEL49_1697	cytochrome c oxidase subunit CcoN/CcoO	1.63					
PHEL49_1704	two-component system response regulator	90.28	93.98	59.44	0.96	0.63	1.52
PHEL49_1709	tRNA modification GTPase TrmE	5.31		5.24			1.01
PHEL49_1712	tRNA-(MS[2]IO[6]A)-hydroxylase	17.66		23.26			0.76
PHEL49_1715	sodium/hydrogen exchanger	3.03					
PHEL49_1716	DNA polymerase III subunit gamma/tau	2.12		4.18			0.51
PHEL49_1717	peptide methionine sulfoxide reductase MsrA		17.65	32.10		1.82	
PHEL49_1719	outer membrane protein H precursor	60.94	99.29	44.58	0.61	0.45	1.37
PHEL49_1723	proline synthase co-transcribed bacterial homolog	5.42					

PHEL49_1724	D-3-phosphoglycerate dehydrogenase	37.84	61.65	31.47	0.61	0.51	1.20
PHEL49_1725	phosphoserine aminotransferase	13.54	38.61	15.60	0.35	0.40	0.87
PHEL49_1726	acyl-CoA reductase	11.56	40.36	45.66	0.29	1.13	0.25
PHEL49_1728	TonB-dependent receptor, plug	1692.03	1416.69	1486.47	1.19	1.05	1.14
PHEL49_1729	TonB-dependent receptor, plug	2.46		1.62			1.52
PHEL49_1732	GTP-binding protein YchF	13.54	13.79	17.83	0.98	1.29	0.76
PHEL49_1733	aminomethyltransferase	32.16	27.58	11.14	1.17	0.40	2.89
PHEL49_1737	DNA topoisomerase III	4.56					
PHEL49_1740	diaminopimelate decarboxylase			11.38			
PHEL49_1741	DNA topoisomerase IV subunit B	26.70	24.86	21.35	1.07	0.86	1.25
PHEL49_1742	DNA topoisomerase IV subunit A	10.32	7.35		1.40		
PHEL49_1745	vitamin B12 ABC transporter, B12-binding component BtuF	3.15					
PHEL49_1746	GMP reductase	55.24	17.42	39.88	3.17	2.29	1.38
PHEL49_1747	TonB-dependent receptor, plug	63.95	102.66	229.07	0.62	2.23	0.28
PHEL49_1749	ATP-dependent DNA helicase UvrD/PcrA	4.62	2.51	12.16	1.84	4.85	0.38
PHEL49_1750	conserved hypothetical protein (DUF4290)	13.02					
PHEL49_1751	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	22.57	25.28	27.86	0.89	1.10	0.81
PHEL49_1752	GrpE nucleotide exchange factor	132.19	409.76	237.74	0.32	0.58	0.56
PHEL49_1753	chaperone protein DnaJ	47.89	368.63	117.42	0.13	0.32	0.41
PHEL49_1754	aconitate hydratase	100.74	197.77	252.24	0.51	1.28	0.40
PHEL49_1755	hypothetical protein	133.00	74.86	57.31	1.78	0.77	2.32
PHEL49_1757	DNA mismatch repair protein MutS	5.64		5.31			1.06
PHEL49_1760	ABC transporter, substrate binding protein, nitrate/sulfonate	18.47		13.51			1.37
PHEL49_1761	purine nucleoside phosphorylase	23.27	24.13	16.72	0.96	0.69	1.39
PHEL49_1763	oxidoreductase	24.45	18.39	61.91	1.33	3.37	0.39
PHEL49_1765	conserved hypothetical protein			10.49			
PHEL49_1767	RNA methyltransferase, TrmA family			8.10			
PHEL49_1768	ornithine aminotransferase	25.02	21.58	19.38	1.16	0.90	1.29
PHEL49_1773	protease II	2.39					
PHEL49_1774	cystathionine beta-synthase	18.30	53.67	45.78	0.34	0.85	0.40
PHEL49_1775	8-amino-7-oxononanoate synthase	85.37	95.93	60.08	0.89	0.63	1.42
PHEL49_1780	TonB-dependent receptor, plug	2.45	13.29	5.37	0.18	0.40	0.46
PHEL49_1781	inosine-5'-monophosphate dehydrogenase	53.39	103.96	161.16	0.51	1.55	0.33
PHEL49_1784	cAMP-binding protein	6.16		16.21			0.38
PHEL49_1786	OstA family protein			8.36			
PHEL49_1790	cytochrome c, class I	7.52		19.81			0.38
PHEL49_1791	adenylosuccinate synthetase	90.76	131.45	134.68	0.69	1.02	0.67
PHEL49_1792	ferric uptake regulation protein FUR	15.05					
PHEL49_1793	GTP pyrophosphokinase, RelA/SpoT family	3.19		13.64			0.23
PHEL49_1796	polyphosphate glucokinase	42.63	77.63	52.83	0.55	0.68	0.81
PHEL49_1797	SpoU rRNA methylase family protein	15.80	14.71	8.92	1.07	0.61	1.77
PHEL49_1798	conserved hypothetical protein	6.30		2.07			3.04

PHEL49_1799	amidohydrolase 1 family protein	95.08	117.36	92.95	0.81	0.79	1.02
PHEL49_1800	amidohydrolase 1 family protein	60.32	101.29	57.54	0.60	0.57	1.05
PHEL49_1801	conserved hypothetical protein (DUF3810)		5.25				
PHEL49_1802	replicative DNA helicase	3.63		6.37			0.57
PHEL49_1803	acylaminoacyl-peptidase	5.35	4.35	4.69	1.23	1.08	1.14
PHEL49_1805	transketolase, N-terminal section	81.25	91.93	142.64	0.88	1.55	0.57
PHEL49_1806	**glycosyltransferase, GT4 family**	**6.45**	**47.28**	**19.10**	**0.14**	**0.40**	**0.34**
PHEL49_1807	conserved hypothetical protein (DUF937)	74.16					
PHEL49_1808	proton/glutamate symporter	16.93	20.69	16.72	0.82	0.81	1.01
PHEL49_1813	ABC transporter, ATP-binding protein	36.46	131.54	85.72	0.28	0.65	0.43
PHEL49_1814	ABC transporter, permease protein	6.02	36.77	27.74	0.16	0.75	0.22
PHEL49_1815	ABC transporter, permease protein	3.01	26.97	5.94	0.11	0.22	0.51
PHEL49_1816	membrane fusion efflux protein	84.22	637.71	219.62	0.13	0.34	0.38
PHEL49_1821	DEAD/DEAH box helicase	19.35	28.89	6.37	0.67	0.22	3.04
PHEL49_1823	peptidase, S41 family	20.92	39.46	14.50	0.53	0.37	1.44
PHEL49_1824	MaoC-like dehydratase	43.81		10.49			4.18
PHEL49_1826	cold shock protein CspG	211.09		94.40			2.24
PHEL49_1827	3-dehydroquinate synthase	6.77	11.03	6.69	0.61	0.61	1.01
PHEL49_1828	proline dehydrogenase	34.61	34.32	51.51	1.01	1.50	0.67
PHEL49_1830	GTP-binding protein TypA/BipA	25.65	25.07	48.63	1.02	1.94	0.53
PHEL49_1834	pyridoxal-dependent decarboxylase	10.42	4.24	3.43	2.45	0.81	3.04
PHEL49_1836	ATP phosphoribosyltransferase	10.92	35.59	69.02	0.31	1.94	0.16
PHEL49_1837	histidinol dehydrogenase		7.19				
PHEL49_1838	histidinol-phosphate aminotransferase	6.77	27.58	22.29	0.25	0.81	0.30
PHEL49_1839	histidinol-phosphatase / imidazole glycerol-phosphate dehydratase		10.26	8.29		0.81	
PHEL49_1841	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase		28.60	19.81		0.69	
PHEL49_1844	phosphoribosyl-AMP cyclohydrolase / phosphoribosyl-ATP pyrophosphatase	17.66		15.50			1.14
PHEL49_1847	YiaAB two helix domain-containing protein	75.23		44.58			1.69
PHEL49_1852	conserved hypothetical protein	23.90		34.09			0.70
PHEL49_1854	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	5.64					
PHEL49_1855	DEAD/DEAH box helicase	5.42		7.13			0.76
PHEL49_1856	ATP-dependent RNA helicase YqfR	5.53		10.92			0.51
PHEL49_1859	conserved hypothetical protein	2.56		16.82			0.15
PHEL49_1860	conserved hypothetical protein (DUF3897)	218.51	426.24	810.48	0.51	1.90	0.27
PHEL49_1864	small-conductance mechanosensitive channel		7.04	3.79		0.54	
PHEL49_1867	spore coat protein CotH	1.68	1.82		0.92		
PHEL49_1869	ABC transporter, ATP-binding protein		79.43	17.83		0.22	
PHEL49_1870	ABC transporter, permease protein	2.18	18.98		0.12		
PHEL49_1877	TonB-dependent receptor, plug			6.48			
PHEL49_1885	zinc-binding dehydrogenase	89.67	47.71	74.70	1.88	1.57	1.20
PHEL49_1886	2-oxoisovalerate dehydrogenase, E1 component, alpha and beta subunit	19.21	5.96		3.22		

PHEL49_1887	transcriptional regulator, AsnC family	579.28	858.05	416.05	0.68	0.48	1.39
PHEL49_1888	carboxypeptidase, M14 family	11.56	16.14	13.05	0.72	0.81	0.89
PHEL49_1892	aminopeptidase, M1 family	2.16	75.11	17.07	0.03	0.23	0.13
PHEL49_1893	conserved hypothetical protein (DUF4252)	47.40	137.90	138.19	0.34	1.00	0.34
PHEL49_1894	conserved hypothetical protein (DUF4252)	163.92	632.89	206.46	0.26	0.33	0.79
PHEL49_1898	carboxyl-terminal protease, S41 family	18.47	12.03	24.31	1.53	2.02	0.76
PHEL49_1900	**conserved hypothetical protein, sialidase domain, GH74 family**			**4.69**			
PHEL49_1901	conserved hypothetical protein			8.10			
PHEL49_1903	acyltransferase	6.77					
PHEL49_1904	DNA recombination protein RmuC	28.59	31.87	25.76	0.90	0.81	1.11
PHEL49_1907	serine hydroxymethyltransferase	145.72	235.03	277.15	0.62	1.18	0.53
PHEL49_1908	fumarylacetoacetase	63.48	195.36	122.59	0.32	0.63	0.52
PHEL49_1910	deoxyhypusine synthase		6.13				
PHEL49_1912	agmatinase	7.74	28.37	28.02	0.27	0.99	0.28
PHEL49_1913	arginine decarboxylase, biosynthetic			4.78			
PHEL49_1914	ATP-dependent helicase	16.07	28.05	28.71	0.57	1.02	0.56
PHEL49_1916	ATP-dependent chaperone ClpB	80.14	373.74	70.05	0.21	0.19	1.14
PHEL49_1917	phosphoglycerate mutase family protein	7.13					
PHEL49_1921	transketolase, C-terminal section	107.54	77.87	141.60	1.38	1.82	0.76
PHEL49_1922	conserved hypothetical proteinc containing outer membrane protein beta-barrel domain	86.17	135.39	137.78	0.64	1.02	0.63
PHEL49_1923	FKBP-type peptidylprolyl isomerase	16.93	110.32		0.15		
PHEL49_1924	ribosome-associated heat shock protein implicated in the recycling of the 50S subunit (S4 paralog)	13.54					
PHEL49_1925	phosphoribosyltransferase	14.25	29.03	18.77	0.49	0.65	0.76
PHEL49_1930	SPFH domain / band 7 family protein	187.84	231.32	816.75	0.81	3.53	0.23
PHEL49_1934	3-oxoacyl-(acyl-carrier protein) reductase	216.14	199.43	229.74	1.08	1.15	0.94
PHEL49_1935	succinyl-CoA synthetase subunit alpha	236.98	250.06	383.36	0.95	1.53	0.62
PHEL49_1936	UDP-3-O-(3-hydroxymyristoyl) glucosamine N-acyltransferase	16.41		8.10			2.03
PHEL49_1937	translation elongation factor P	80.60	31.52	80.66	2.56	2.56	1.00
PHEL49_1938	UDP-N- acetylglucosamine O-acyltransferase	46.70	7.61	64.56	6.14	8.49	0.72
PHEL49_1939	**bifunctional UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase / (3R)-hydroxymyristoyl-[acyl-carrier protein] dehydratase, CE11 family**	**26.04**	**84.86**	**80.58**	**0.31**	**0.95**	**0.32**
PHEL49_1940	UDP-3-O-(3-hydroxymyristoyl) glucosamine N-acyltransferase	27.45		16.87			1.63
PHEL49_1941	phosphohydrolase	14.11	6.90	3.71	2.05	0.54	3.80
PHEL49_1943	response regulator receiver protein	10.16	57.00	28.23	0.18	0.50	0.36
PHEL49_1945	alanine dehydrogenase	9.23	7.52	4.05	1.23	0.54	2.28
PHEL49_1949	two-component system response regulator	7.25		6.37			1.14
PHEL49_1952	fist c domain-containing protein	19.60	23.23	4.69	0.84	0.20	4.18
PHEL49_1953	heme NO binding protein	16.93					
PHEL49_1956	LSU ribosomal protein L9p	507.81	41.37	156.02	12.27	3.77	3.25

PHEL49_1957	SSU ribosomal protein S18p	190.81		72.94			2.62
PHEL49_1958	SSU ribosomal protein S6p	677.08	84.86	260.60	7.98	3.07	2.60
PHEL49_1961	primosomal protein N'	9.27	13.94	7.51	0.66	0.54	1.23
PHEL49_1965	RNA methylase UPF0020 family protein	2.94	4.80	17.44	0.61	3.64	0.17
PHEL49_1968	ATP-dependent DNA helicase RecQ	14.86	8.07	11.96	1.84	1.48	1.24
PHEL49_1969	sugar isomerase	32.89	129.23	91.70	0.25	0.71	0.36
PHEL49_1971	carboxymuconolactone decarboxylase family protein	31.25					
PHEL49_1972	ABC transporter, ATP-binding protein	21.76	55.16	54.13	0.39	0.98	0.40
PHEL49_1973	GAF sensor signal transduction histidine kinase	7.36	19.19	25.20	0.38	1.31	0.29
PHEL49_1977	conserved hypothetical membrane protein (DUF4105)	2.94		3.88			0.76
PHEL49_1978	glutamate formiminotransferase	81.90	33.81	34.51	2.42	1.02	2.37
PHEL49_1982	phosphohydrolase	59.67	80.40	90.66	0.74	1.13	0.66
PHEL49_1984	conserved hypothetical protein	12.31					
PHEL49_1986	TonB-dependent receptor, plug	9.57	13.19	28.10	0.73	2.13	0.34
PHEL49_1987	thiol peroxidase, Bcp-type	278.80	246.60	199.28	1.13	0.81	1.40
PHEL49_1990	excinuclease ABC subunit A	7.74	43.08	18.68	0.18	0.43	0.41
PHEL49_1992	**carbohydrate esterase, CE14 family**	**17.55**	**8.17**	**13.21**	**2.15**	**1.62**	**1.33**
PHEL49_1993	Na+/sulfate symporter			10.65			
PHEL49_1995	O-acetylhomoserine sulfhydrylase / O-succinylhomoserine sulfhydrylase	4.72		10.37			0.46
PHEL49_1997	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase	20.31	22.06	31.20	0.92	1.41	0.65
PHEL49_2000	oxidoreductase, Gfo/Idh/MocA family		12.26	4.95		0.40	
PHEL49_2001	3-hydroxybutyryl-CoA dehydrogenase	76.17	79.29	103.08	0.96	1.30	0.74
PHEL49_2003	transcriptional regulator, LysR family	9.40		4.95			1.90
PHEL49_2004	ABC transporter, ATP-binding protein	20.75	10.68	30.20	1.94	2.83	0.69
PHEL49_2005	conserved hypothetical protein	2.51	16.34	19.81	0.15	1.21	0.13
PHEL49_2006	DEAD/DEAH box helicase	13.14	3.29	10.65	3.99	3.23	1.23
PHEL49_2008	5'-nucleotidase	9.50	17.42	25.03	0.55	1.44	0.38
PHEL49_2009	hydroxymethylglutaryl-CoA lyase	4.23		11.14			0.38
PHEL49_2013	dihydroorotate dehydrogenase	17.36		20.57			0.84
PHEL49_2014	phenylalanyl-tRNA synthetase subunit beta	28.27	41.22	48.01	0.69	1.16	0.59
PHEL49_2016	redoxin			5.69			
PHEL49_2018	peptidyl-prolyl cis-trans isomerase	33.07	48.75	39.39	0.68	0.81	0.84
PHEL49_2019	FKBP-type peptidyl-prolyl isomerase	228.20	482.14	336.80	0.47	0.70	0.68
PHEL49_2021	DHH family protein	5.21	25.46	16.00	0.20	0.63	0.33
PHEL49_2022	nucleoside diphosphate kinase	112.85	58.84	77.27	1.92	1.31	1.46
PHEL49_2023	conserved hypothetical protein	12.09	7.88	25.47	1.53	3.23	0.47
PHEL49_2024	peptidase C45 acyl-coenzyme A:6-aminopenicillanic acid acyl-transferase	22.57	31.87	37.64	0.71	1.18	0.60
PHEL49_2025	hypothetical protein			5.94			
PHEL49_2029	DNA recombination and repair protein RecF		10.76	19.57		1.82	
PHEL49_2030	TPR domain protein	99.14	66.98	114.63	1.48	1.71	0.86
PHEL49_2033	DNA mismatch repair protein MutL	1.99	97.34	38.02	0.02	0.39	0.05
PHEL49_2045	2-nitropropane dioxygenase	17.92					

PHEL49_2047	tRNA (5-methylaminomethy-2-thiouridylate)-methyltransferase	4.51					
PHEL49_2050	adenylosuccinate lyase	65.05	112.48	134.60	0.58	1.20	0.48
PHEL49_2051	conserved hypothetical protein	43.53		70.05			0.62
PHEL49_2053	TonB-dependent receptor, plug	1.49	3.64	8.82	0.41	2.42	0.17
PHEL49_2057	peptidase, M48 family	9.03		29.72			0.30
PHEL49_2061	signal recognition 54 kDa protein (SRP54)	57.83	87.34	72.44	0.66	0.83	0.80
PHEL49_2062	methylenetetrahydrofolate dehydrogenase (NADP+) / methenyltetrahydrofolate cyclohydrolase	88.87	162.03	128.16	0.55	0.79	0.69
PHEL49_2064	conserved hypothetical protein	125.74	84.05	169.81	1.50	2.02	0.74
PHEL49_2065	conserved hypothetical protein (DUF853)	32.07	38.71	39.10	0.83	1.01	0.82
PHEL49_2066	**glycoside hydrolase, GHnc family**	**55.29**	**215.12**	**60.18**	**0.26**	**0.28**	**0.92**
PHEL49_2067	conserved hypothetical protein (DUF2490)	29.02	21.01	33.96	1.38	1.62	0.85
PHEL49_2069	conserved hypothetical protein (DUF4369)	22.57	8.17	52.83	2.76	6.47	0.43
PHEL49_2070	conserved hypothetical protein (DUF255)	5.85	2.72	17.61	2.15	6.47	0.33
PHEL49_2071	**carbohydrate binding protein, CBM4 domain**	**208.89**	**68.07**	**24.66**	**3.07**	**0.36**	**8.47**
PHEL49_2075	MFS/sugar transport protein	3.69		9.73			0.38
PHEL49_2076	**glucosylceramidase, GH30-1 family**			**4.86**			
PHEL49_2077	**glycoside hydrolase, GH17 family**			**36.39**			
PHEL49_2079	conserved hypothetical protein	9.30	54.74	89.15	0.17	1.63	0.10
PHEL49_2080	**endo-1,3(4)-beta-glucanase, GH16 family**			**120.79**			
PHEL49_2081	conserved hypothetical protein, CBM23 and CBM8 domains	18.59	17.31	75.17	1.07	4.34	0.25
PHEL49_2082	**glycoside hydrolase, GHnc family**	**8.68**	**1.89**	**38.10**	**4.60**	**20.20**	**0.23**
PHEL49_2083	conserved hypothetical protein			85.44			
PHEL49_2084	RagB/SusD domain-containing protein	30.35	22.82	236.72	1.33	10.37	0.13
PHEL49_2085	TonB-dependent receptor, plug	21.12	16.19	153.77	1.30	9.50	0.14
PHEL49_2086	ligand-binding sensor protein	7.52	2.04	5.78	3.68	2.83	1.30
PHEL49_2089	conserved hypothetical protein		10.51	8.49		0.81	
PHEL49_2092	conserved hypothetical protein		5.52				
PHEL49_2093	polyphosphate kinase 2	39.31	56.94	48.89	0.69	0.86	0.80
PHEL49_2094	polyphosphate kinase 2	73.68	77.87	76.04	0.95	0.98	0.97
PHEL49_2097	conserved hypothetical protein	273.25	216.70	410.74	1.26	1.90	0.67
PHEL49_2098	conserved hypothetical protein (DUF3822)	4.23	6.90	11.14	0.61	1.62	0.38
PHEL49_2100	ATPase, AAA family	27.08	72.50	35.66	0.37	0.49	0.76
PHEL49_2101	peptidyl-prolyl cis-trans isomerase	23.02	55.16	49.93	0.42	0.91	0.46
PHEL49_2102	conserved hypothetical protein	3.98		7.87			0.51
PHEL49_2103	peptidylprolyl isomerase	12.90	22.76	24.06	0.57	1.06	0.54
PHEL49_2105	AAA family ATPase-like protein	18.47	30.09	36.47	0.61	1.21	0.51
PHEL49_2107	methionyl-tRNA formyltransferase	36.76	31.52	20.38	1.17	0.65	1.80
PHEL49_2108	DNA-binding protein HU-beta	8290.47	1213.53	653.79	6.83	0.54	12.68
PHEL49_2109	conserved hypothetical protein (DUF179)	25.79		8.49			3.04
PHEL49_2110	aminodeoxychorismate lyase	74.06	113.77	47.36	0.65	0.42	1.56
PHEL49_2111	conserved hypothetical protein containing START-like domain	103.82	66.19	65.38	1.57	0.99	1.59

PHEL49_2120	TonB-dependent receptor, plug	4.23					
PHEL49_2127	type I restriction-modification system, DNA-methyltransferase subunit M	25.71	48.88	22.57	0.53	0.46	1.14
PHEL49_2129	type I restriction-modification system, restriction subunit R	3.98	7.42	1.50	0.54	0.20	2.66
PHEL49_2134	hypothetical protein	6.94					
PHEL49_2137	restriction endonuclease	22.08	11.99	5.81	1.84	0.48	3.80
PHEL49_2138	beta-lactamase superfamily protein	4.42		3.88			1.14
PHEL49_2140	type I restriction-modification system, restriction subunit R	8.93	2.42	2.94	3.68	1.21	3.04
PHEL49_2141	type I restriction-modification system, DNA-methyltransferase subunit M	27.34	23.34	29.15	1.17	1.25	0.94
PHEL49_2142	type I restriction-modification system, specificity subunit S	14.20	12.46	10.07	1.14	0.81	1.41
PHEL49_2146	hypothetical protein	158.69	72.40	60.36	2.19	0.83	2.63
PHEL49_2150	transcriptional regulator, crp/fnr family	22.57					
PHEL49_2168	hypothetical protein	9.67					
PHEL49_2169	X-Pro dipeptidyl peptidase, S15 family	5.21					
PHEL49_2172	3-isopropylmalate dehydrogenase	7.13	29.03	49.27	0.25	1.70	0.14
PHEL49_2173	2-isopropylmalate synthase LeuA		3.94	15.92		4.04	
PHEL49_2174	3-isopropylmalate dehydratase small subunit			72.94			
PHEL49_2175	3-isopropylmalate dehydratase large subunit	2.71	4.41	41.01	0.61	9.29	0.07
PHEL49_2176	6-phosphofructokinase II			34.09			
PHEL49_2178	conserved hypothetical protein, DinB superfamily			22.29			
PHEL49_2180	protein secretion chaperonin CsaA	31.25					
PHEL49_2182	carboxypeptidase, M14 family	97.24	86.85	41.73	1.12	0.48	2.33
PHEL49_2183	conserved hypothetical membrane protein (UPF0187)	3.15					
PHEL49_2185	transcriptional regulator, AsnC family	45.14					
PHEL49_2186	FAD-linked oxidase domain protein		5.11	23.94		4.69	
PHEL49_2187	hypothetical protein	11.10	5.43		2.05		
PHEL49_2188	aldo/keto reductase	5.35	5.81	9.38	0.92	1.62	0.57
PHEL49_2189	flagellar motor rotation protein MotB	188.31	279.25	373.33	0.67	1.34	0.50
PHEL49_2190	valyl-tRNA synthetase	40.22	46.97	52.08	0.86	1.11	0.77
PHEL49_2192	aspartate aminotransferase	15.39	22.57	32.42	0.68	1.44	0.47
PHEL49_2193	UDP-N-acetylenolpyruvoylglucosamine reductase			9.38			
PHEL49_2199	**glycosyltransferase, GT2 family**	**4.72**	**10.26**		**0.46**		
PHEL49_2200	RNA polymerase sigma-70 factor	6.16		8.10			0.76
PHEL49_2203	cystathionine beta-synthase	28.44	19.86	30.31	1.43	1.53	0.94
PHEL49_2207	arginyl-tRNA synthetase	5.05	8.23	10.65	0.61	1.29	0.47
PHEL49_2208	dihydrolipoamide dehydrogenase	121.60	272.42	176.49	0.45	0.65	0.69
PHEL49_2210	**glycosyltransferase, GT2 family**	**4.51**					
PHEL49_2211	conserved hypothetical protein containing tetratricopeptide repeats	5.25	5.71	3.07	0.92	0.54	1.71
PHEL49_2214	**carbohydrate binding protein, CBM50 domain**	**72.54**	**23.64**	**31.84**	**3.07**	**1.35**	**2.28**
PHEL49_2216	ribosomal RNA large subunit methyltransferase F	4.10	130.38	45.93	0.03	0.35	0.09
PHEL49_2217	conserved hypothetical protein (DUF2317)	19.35	82.30	31.13	0.24	0.38	0.62
PHEL49_2218	methyltransferase domain protein			32.10			
PHEL49_2219	carboxypeptidase A, M14 family	18.73	46.94	25.61	0.40	0.55	0.73

PHEL49_2220	SSU ribosomal protein S1p	163.30	217.40	226.82	0.75	1.04	0.72
PHEL49_2221	queuosine biosynthesis QueE radical SAM	14.11		33.43			0.42
PHEL49_2222	cytidylate kinase	10.42	42.43	44.58	0.25	1.05	0.23
PHEL49_2229	threonyl-tRNA synthetase	34.32	74.05	70.83	0.46	0.96	0.48
PHEL49_2230	translation initiation factor IF-3	447.63	220.64	297.18	2.03	1.35	1.51
PHEL49_2232	LSU ribosomal protein L20p	307.29	127.29	102.87	2.41	0.81	2.99
PHEL49_2233	conserved hypothetical protein	144.25	43.17	93.03	3.34	2.16	1.55
PHEL49_2234	**capsular glucan synthase, GT4 family**	**3.01**	**4.90**	**3.96**	**0.61**	**0.81**	**0.76**
PHEL49_2235	glucose-1-phosphate adenylyltransferase	17.29	39.90	66.39	0.43	1.66	0.26
PHEL49_2236	**putative alpha-1,4-glucan: phosphate maltosyltransferase, GH13-3 family**	**2.67**					
PHEL49_2237	**1,4-alpha-glucan branching enzyme, CBM48 domain, GH13-9 family**	**11.89**	**31.31**	**15.66**	**0.38**	**0.50**	**0.76**
PHEL49_2239	**alpha-glucosidase, GH31 family**	**22.33**	**71.59**	**200.12**	**0.31**	**2.80**	**0.11**
PHEL49_2240	peptide chain release factor 1	55.86	66.19	62.41	0.84	0.94	0.90
PHEL49_2241	phosphoribosylformylglycinamidine cyclo-ligase	25.19	41.05	58.05	0.61	1.41	0.43
PHEL49_2248	glutamine synthetase type III, GlnN	13.87	13.29	3.22	1.04	0.24	4.30
PHEL49_2249	glutamine synthetase type II	33.85	110.32	769.53	0.31	6.98	0.04
PHEL49_2250	conserved hypothetical protein (DUF4136)	80.60	63.04	144.34	1.28	2.29	0.56
PHEL49_2251	urocanate hydratase	56.73	56.65	20.48	1.00	0.36	2.77
PHEL49_2253	methylmalonyl-CoA mutase	80.30	86.37	11.06	0.93	0.13	7.26
PHEL49_2261	dienelactone hydrolase family protein	10.26					
PHEL49_2265	amidohydrolase 1 family protein	39.02	39.27	25.69	0.99	0.65	1.52
PHEL49_2266	carboxypeptidase A, M14 family	50.08	41.37	26.00	1.21	0.63	1.93
PHEL49_2269	X-Pro dipeptidyl-peptidase, S15 family	17.38		10.84			1.60
PHEL49_2270	X-Pro dipeptidyl-peptidase, S15 family	3.98					
PHEL49_2271	monooxygenase, flavin-binding family	4.92					
PHEL49_2273	conserved hypothetical protein (DUF4197)	117.19	195.18	185.16	0.60	0.95	0.63
PHEL49_2274	**endo-1,3(4)-beta-glucanase, GH16 family**	**4.44**	**10.85**	**2.92**	**0.41**	**0.27**	**1.52**
PHEL49_2275	orotidine 5'-phosphate decarboxylase			11.50			
PHEL49_2277	triosephosphate isomerase	77.38	224.58	703.67	0.34	3.13	0.11
PHEL49_2278	ribosomal protein L11 methyltransferase			8.36			
PHEL49_2287	conserved hypothetical protein (DUF1684)	67.71		69.77			0.97
PHEL49_2289	enoyl-CoA hydratase/isomerase	78.54	26.48	42.79	2.97	1.62	1.84
PHEL49_2291	DoxX family protein			12.38			
PHEL49_2292	conserved hypothetical protein (DUF1599)	74.16	21.01	46.70	3.53	2.22	1.59
PHEL49_2293	lysine decarboxylase family	9.67					
PHEL49_2294	dihydropteroate synthase		7.88	6.37		0.81	
PHEL49_2295	conserved hypothetical protein CHP00159			6.15			
PHEL49_2296	ABC transporter, ATP-binding protein	7.18					
PHEL49_2297	tRNA pseudouridine synthase A		15.76	15.92		1.01	
PHEL49_2299	sensor histidine kinase			2.70			
PHEL49_2300	conserved hypothetical protein	75.23	167.52	23.11	0.45	0.14	3.25

PHEL49_2301	two-component system response regulator, LuxR family			42.79			
PHEL49_2303	transcription termination factor Rho	81.68	68.29	32.55	1.20	0.48	2.51
PHEL49_2304	peptidylprolyl isomerase	101.56	80.62	99.44	1.26	1.23	1.02
PHEL49_2307	lipopolysaccharide assembly, LptC-related protein	12.90					
PHEL49_2308	conserved hypothetical protein containing tetratricopeptide repeats	78.54	388.33	196.14	0.20	0.51	0.40
PHEL49_2309	conserved hypothetical protein, putative outer membrane protein	25.93	82.15	55.01	0.32	0.67	0.47
PHEL49_2313	NAD-dependent epimerase/dehydrogenase	15.48					
PHEL49_2316	ribosomal large subunit pseudouridine synthase B	39.83	22.71	36.71	1.75	1.62	1.08
PHEL49_2318	mevalonate kinase			5.09			
PHEL49_2319	conserved hypothetical protein	54.17		22.29			2.43
PHEL49_2320	diphosphomevalonate decarboxylase	8.26		8.70			0.95
PHEL49_2325	**glycosyltransferase, GT4 family**	**3.15**					
PHEL49_2326	cell division transporter, ATP-binding protein FtsE (TC 3.A.5.1.1)	41.67	63.65	51.43	0.65	0.81	0.81
PHEL49_2327	TPR domain protein	7.52	14.14	22.86	0.53	1.62	0.33
PHEL49_2328	TonB-dependent receptor			10.49			
PHEL49_2330	peptidase M28 family	20.83	12.73	15.43	1.64	1.21	1.35
PHEL49_2332	amidohydrolase 3 family protein	7.77					
PHEL49_2335	tryptophan synthase beta chain			4.15			
PHEL49_2337	indole-3-glycerol phosphate synthase	14.01	26.63	21.52	0.53	0.81	0.65
PHEL49_2339	anthranilate phosphoribosyltransferase	13.17	30.64	12.38	0.43	0.40	1.06
PHEL49_2341	anthranilate synthase component I	33.85	48.80	22.29	0.69	0.46	1.52
PHEL49_2343	aspartyl-tRNA(Asn) amidotransferase subunit A	26.55	64.89	57.69	0.41	0.89	0.46
PHEL49_2344	aspartyl-tRNA synthetase	18.27	70.04	22.64	0.26	0.32	0.81
PHEL49_2345	DNA gyrase subunit B	148.58	165.48	107.73	0.90	0.65	1.38
PHEL49_2346	conserved hypothetical protein	135.42	92.90	84.46	1.46	0.91	1.60
PHEL49_2347	malate dehydrogenase	655.92	555.05	782.87	1.18	1.41	0.84
PHEL49_2348	formate-tetrahydrofolate ligase	41.07	16.28		2.52		
PHEL49_2350	protein-export membrane protein SecD (TC 3.A.5.1.1) / protein-export membrane protein SecF (TC 3.A.5.1.1)	97.80	190.00	113.92	0.51	0.60	0.86
PHEL49_2352	adenylate kinase	45.14	76.17	50.94	0.59	0.67	0.89
PHEL49_2353	GTP-binding protein Obg	3.76					
PHEL49_2358	aminotransferase class III		5.76	1.55		0.27	
PHEL49_2359	amidohydrolase 1 family protein	28.86	9.95	8.77	2.90	0.88	3.29
PHEL49_2361	4-hydroxyproline epimerase	9.15					
PHEL49_2362	conserved hypothetical protein (DUF885)	19.20					
PHEL49_2363	aldehyde dehydrogenase	24.95					
PHEL49_2364	dihydrodipicolinate synthase	113.51					
PHEL49_2366	tetratricopeptide-like helical	4.23					
PHEL49_2371	magnesium and cobalt transport protein CorA		5.81	4.69		0.81	
PHEL49_2373	N-formylkynurenine (aryl-) formamidase	29.02	35.46	31.84	0.82	0.90	0.91
PHEL49_2375	crossover junction endodeoxyribonuclease RuvC	20.31		8.92			2.28
PHEL49_2377	S-adenosyl-L-methionine-dependent methyltransferase			7.13			

PHEL49_2378	conserved hypothetical protein			23.46			
PHEL49_2379	branched-chain amino acid aminotransferase	39.93	73.55	70.87	0.54	0.96	0.56
PHEL49_2382	heavy metal transporter	38.09		50.15			0.76
PHEL49_2384	conserved hypothetical protein		7.88	6.37		0.81	
PHEL49_2385	conserved hypothetical protein (DUF2911)		10.03				
PHEL49_2388	cobalt-zinc-cadmium resistance protein CzcA; cation efflux system protein CusA	1.98	4.03		0.49		
PHEL49_2392	conserved hypothetical protein containing ribosomal protein S5 domain 2-type fold	3.87	12.61	10.19	0.31	0.81	0.38
PHEL49_2393	hydroxymethylglutaryl-CoA reductase		16.72	13.51		0.81	
PHEL49_2394	dipeptidyl peptidase IV, S9 family	17.73	7.88	2.12	2.25	0.27	8.35
PHEL49_2397	thioredoxin family protein			25.47			
PHEL49_2400	**lipid-A-disaccharide synthase, GT19 family**	**3.22**					
PHEL49_2402	stationary-phase survival acid phosphatase			6.37			
PHEL49_2403	peptidase S41 family		39.02				
PHEL49_2404	thioesterase superfamily protein	7.97	38.94		0.20		
PHEL49_2405	zinc-binding dehydrogenase			5.09			
PHEL49_2408	peptidase M20 family	23.90	25.96	24.47	0.92	0.94	0.98
PHEL49_2409	OmpA family protein	55.40	77.73	107.39	0.71	1.38	0.52
PHEL49_2410	peptidyl-prolyl cis-trans isomerase A	62.50		48.01			1.30
PHEL49_2411	lysyl-tRNA synthetase (class II)	50.53	59.28	67.86	0.85	1.14	0.74
PHEL49_2413	glucose inhibited division protein B	64.89	82.74	126.30	0.78	1.53	0.51
PHEL49_2415	aspartate aminotransferase	41.55	75.22	52.68	0.55	0.70	0.79
PHEL49_2417	cell division protein FtsQ	2.94	11.19	15.50	0.26	1.39	0.19
PHEL49_2418	cell division protein FtsA	28.21	29.88	42.72	0.94	1.43	0.66
PHEL49_2419	cell division protein FtsQ	9.67		6.37			1.52
PHEL49_2420	UDP-N-acetylmuramate-L-alanine ligase	4.06	8.83	5.35	0.46	0.61	0.76
PHEL49_2421	**UDP-N-acetylglucosamine-N-acetylmuramyl- (pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase, GT28 family**	**9.91**	**5.38**	**19.57**	**1.84**	**3.64**	**0.51**
PHEL49_2424	phospho-N-acetylmuramoyl-pentapeptide- transferase	2.94		5.81			0.51
PHEL49_2425	UDP-N-acetylmuramoylalanyl-D-glutamate-2,6- diaminopimelate ligase	4.23		9.29			0.46
PHEL49_2428	S-adenosyl-methyltransferase MraW			7.64			
PHEL49_2429	cell division protein MraZ	50.78		52.01			0.98
PHEL49_2430	alpha/beta hydrolase	48.36	51.22	57.31	0.94	1.12	0.84
PHEL49_2431	GTP-binding protein YsxC/EngB	11.28					
PHEL49_2434	nitroreductase family protein	12.09					
PHEL49_2435	penicillin amidase, peptidase S45 family	11.90	7.27	15.68	1.64	2.16	0.76
PHEL49_2436	DegT/DnrJ/EryC1/StrS aminotransferase	29.92	30.79	41.47	0.97	1.35	0.72
PHEL49_2437	UDP-glucose 4-epimerase	135.42	113.22	124.34	1.20	1.10	1.09
PHEL49_2438	conserved hypothetical protein (DUF2911)	27.08	341.99	53.49	0.08	0.16	0.51
PHEL49_2440	ferrous iron transport protein B	4.29		2.26			1.90

PHEL49_2442	SCO1/SenC family protein			24.00			
PHEL49_2444	peptidase M50 family	14.11	39.07	16.72	0.36	0.43	0.84
PHEL49_2445	TonB-dependent receptor, plug	8.08	87.27	162.34	0.09	1.86	0.05
PHEL49_2449	1-deoxy-D-xylulose 5-phosphate synthase	4.17					
PHEL49_2450	**glycoside hydrolase, GH74 family**	**100.97**	**48.39**	**165.79**	**2.09**	**3.43**	**0.61**
PHEL49_2451	deoxyguanosinetriphosphate triphosphohydrolase	22.57	10.82	27.97	2.09	2.59	0.81
PHEL49_2454	ribonucleotide reductase of class Ia (aerobic), alpha subunit	37.20	44.86	39.19	0.83	0.87	0.95
PHEL49_2455	ribonucleotide reductase of class Ia (aerobic), beta subunit	73.05	104.51	84.46	0.70	0.81	0.86
PHEL49_2456	cold shock DNA-binding domain protein CspA	38.69	47.28		0.82		
PHEL49_2461	conserved hypothetical protein containing carboxypeptidase-like regulatory domain	1.44	16.43	5.69	0.09	0.35	0.25
PHEL49_2462	NADP-dependent malic enzyme	23.38	53.85	39.27	0.43	0.73	0.60
PHEL49_2464	gliding motility protein SprA	67.96	82.02	82.52	0.83	1.01	0.82
PHEL49_2465	glycine cleavage system protein H	29.02		31.84			0.91
PHEL49_2467	TonB protein	121.87	101.49	117.68	1.20	1.16	1.04
PHEL49_2469	dodecin	19.35					
PHEL49_2473	outer membrane efflux protein	48.36	96.81	50.94	0.50	0.53	0.95
PHEL49_2476	SCO1/SenC family protein	70.22	24.52	56.13	2.86	2.29	1.25
PHEL49_2477	conserved hypothetical protein	54.69		48.01			1.14
PHEL49_2479	cytochrome c oxidase subunit III	53.07	29.82	31.32	1.78	1.05	1.69
PHEL49_2483	enoyl-CoA hydratase/isomerase	24.18		19.10			1.27
PHEL49_2485	leucyl-tRNA synthetase	34.12	95.55	32.99	0.36	0.35	1.03
PHEL49_2487	malonyl CoA-acyl carrier protein transacylase	32.76	21.35	17.26	1.53	0.81	1.90
PHEL49_2490	carboxymuconolactone decarboxylase	45.14					
PHEL49_2492	SAM-dependent methyltransferase DSY4148 (UbiE paralog)	3.76	6.13	27.24	0.61	4.44	0.14
PHEL49_2496	hemolysin-type calcium-binding protein	0.68	6.65	3.36	0.10	0.51	0.20
PHEL49_2499	recombination protein RecR	11.78					
PHEL49_2501	ferrochelatase	31.25	76.38	70.87	0.41	0.93	0.44
PHEL49_2503	transcriptional regulator, AraC family	11.95	77.87	23.60	0.15	0.30	0.51
PHEL49_2505	glutamyl-tRNA reductase	17.29	4.69	5.69	3.68	1.21	3.04
PHEL49_2506	porphobilinogen deaminase HemC	2.30		3.02			0.76
PHEL49_2507	delta-aminolevulinic acid dehydratase	35.73	27.58	24.76	1.30	0.90	1.44
PHEL49_2508	glutamate-1-semialdehyde aminotransferase	20.61	31.18	13.57	0.66	0.44	1.52
PHEL49_2509	uroporphyrinogen decarboxylase	3.56					
PHEL49_2512	conserved hypothetical protein	2.76					
PHEL49_2514	dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex	66.30	108.02	104.01	0.61	0.96	0.64
PHEL49_2515	conserved hypothetical protein	82.75	73.55	92.45	1.13	1.26	0.90
PHEL49_2517	dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex	125.91	479.99	301.87	0.26	0.63	0.42
PHEL49_2518	pyruvate dehydrogenase E1 component alpha subunit	128.10	199.77	202.40	0.64	1.01	0.63
PHEL49_2522	conserved hypothetical protein (DUF2807)		33.94				

PHEL49_2523	phage shock protein PspC	4.10	6.69	10.81	0.61	1.62	0.38
PHEL49_2527	signal transduction histidine kinase, phosphotransfer (Hpt) domain-containing protein	9.03					
PHEL49_2528	conserved hypothetical protein (DUF28)	60.45	47.28	47.76	1.28	1.01	1.27
PHEL49_2530	phosphate acetyltransferase	4.45		2.35			1.90
PHEL49_2533	methylcrotonyl-CoA carboxylase carboxyl transfer ase subunit	18.06	11.03	16.34	1.64	1.48	1.10
PHEL49_2534	DNA binding helix-turn helix protein	7.00					
PHEL49_2535	malate synthase	160.53					
PHEL49_2536	isocitrate lyase	172.04					
PHEL49_2539	NADPH-dependent FMN reductase	54.17		17.83			3.04
PHEL49_2544	2,4-dienoyl-CoA reductase (NADPH)	122.78	82.37	123.63	1.49	1.50	0.99
PHEL49_2545	UDP-3-O-(3-hydroxymyristoyl) glucosamine N-acyltransferase	69.64		22.93			3.04
PHEL49_2547	ABC transporter, ATP-binding protein	50.51	99.81	90.57	0.51	0.91	0.56
PHEL49_2552	N-acetylmuramic acid 6-phosphate etherase	9.34		9.22			1.01
PHEL49_2553	conserved hypothetical protein (DUF4249)	6.55	96.09	46.01	0.07	0.48	0.14
PHEL49_2554	TonB-dependent receptor, plug	6.02	51.48	42.60	0.12	0.83	0.14
PHEL49_2555	socitrate dehydrogenase i	40.96	65.38	47.33	0.63	0.72	0.87
PHEL49_2556	LSU ribosomal protein L19p	390.62	271.56	500.63	1.44	1.84	0.78
PHEL49_2563	ribosomal S6 modification enzyme RimK	161.63	217.08	301.97	0.74	1.39	0.54
PHEL49_2566	HYR domain-containing protein	12.28					
PHEL49_2567	hypothetical protein	103.82					
PHEL49_2583	phosphoenolpyruvate carboxylase	19.75	101.13	166.23	0.20	1.64	0.12
PHEL49_2587	lysophospholipase			11.50			
PHEL49_2590	dihydrolipoamide dehydrogenase	59.58	130.18	126.60	0.46	0.97	0.47
PHEL49_2591	conserved hypothetical protein containing haem-binding domain	41.38		123.82			0.33
PHEL49_2593	phage tail collar	63.60	86.92	51.33	0.73	0.59	1.24
PHEL49_2594	conserved hypothetical protein	8.21	8.69	1.08	0.94	0.12	7.59
PHEL49_2595	conserved hypothetical protein		22.63				
PHEL49_2596	peptidase, M3 family	2.64	7.16	11.58	0.37	1.62	0.23
PHEL49_2598	phosphoribosylaminoimidazole carboxylase, ATPase subunit	13.85	35.10	28.37	0.39	0.81	0.49
PHEL49_2600	transcription elongation factor GreA	71.47	165.48	108.96	0.43	0.66	0.66
PHEL49_2602	two-component system sensor histidine kinase	6.02	9.81	35.66	0.61	3.64	0.17
PHEL49_2603	flavin reductase domain-containin FMN-binding protein	4.37					
PHEL49_2604	conserved hypothetical protein (DUF3127)	246.65	23.64	12.74	10.43	0.54	19.37
PHEL49_2608	conserved hypothetical protein	49.89	23.23	65.69	2.15	2.83	0.76
PHEL49_2609	conserved hypothetical protein	40.01	20.06	89.15	1.99	4.44	0.45
PHEL49_2612	TatD family hydrolase			6.15			
PHEL49_2613	ATP-dependent RNA helicase			5.14			
PHEL49_2616	two-component transcriptional regulator, LuxR family	22.57					
PHEL49_2621	OmpA family protein	289.87	1034.25	437.41	0.28	0.42	0.66
PHEL49_2622	thiamine biosynthesis lipoprotein ApbE	9.40		12.38			0.76
PHEL49_2624	methionine aminopeptidase	6.77		23.77			0.28

PHEL49_2625	thioredoxin family protein		18.39	78.01		4.24	
PHEL49_2626	phosphoglycerate mutase	14.77	52.15	94.02	0.28	1.80	0.16
PHEL49_2627	phenylalanine 4-monooxygenase	44.11	46.80		0.94		
PHEL49_2629	conserved hypothetical protein		1.47	3.57		2.42	
PHEL49_2630	GSCFA family protein	5.49					
PHEL49_2633	alanyl-tRNA synthetase	34.88	35.66	44.13	0.98	1.24	0.79
PHEL49_2634	peptidase, M23 family	7.32	20.87	26.50	0.35	1.27	0.28
PHEL49_2635	transcriptional regulator, MerR family	10.42					
PHEL49_2636	acyl-CoA dehydrogenase	206.11	186.57	161.26	1.10	0.86	1.28
PHEL49_2637	short chain dehydrogenase	178.94	82.74	95.52	2.16	1.15	1.87
PHEL49_2638	acyl-CoA dehydrogenase	132.47	175.07	81.40	0.76	0.46	1.63
PHEL49_2639	aminoglycoside phosphotransferase	59.24	93.77	42.35	0.63	0.45	1.40
PHEL49_2640	3-oxoacyl-(acyl-carrier protein) reductase	295.91	163.44	204.72	1.81	1.25	1.45
PHEL49_2641	LemA family protein	1333.55	1549.28	1558.24	0.86	1.01	0.86
PHEL49_2642	conserved hypothetical protein (DUF477)	63.73	32.45	15.73	1.96	0.48	4.05
PHEL49_2643	conserved hypothetical protein (DUF477)	18.68					
PHEL49_2644	conserved hypothetical protein	4.10	23.40		0.18		
PHEL49_2646	metallophosphoesterase	13.74	16.79	5.17	0.82	0.31	2.66
PHEL49_2648	**glycosyltransferase, GT4 family**	**7.13**					
PHEL49_2652	conserved hypothetical protein (UPF0061)	4.51					
PHEL49_2653	**glycoside hydrolase, GH26 family / putative mannan endo-1,4-beta-mannosidase**	**25.58**	**41.68**	**43.59**	**0.61**	**1.05**	**0.59**
PHEL49_2654	**glycosyltransferase, GT2 family**	**5.55**		**7.31**			**0.76**
PHEL49_2655	TPR domain containing protein	6.27		9.91			0.63
PHEL49_2656	surface antigen BspA			3.88			
PHEL49_2660	metal-dependent phosphohydrolase, HD subdomain	4.51		19.81			0.23
PHEL49_2661	conserved hypothetical protein	22.81	14.39	13.57	1.59	0.94	1.68
PHEL49_2662	GTP-binding protein EngA	28.44	41.92	39.23	0.68	0.94	0.72
PHEL49_2665	Legionella vir region protein	4.10					