

Supplementary Table 3. Database of Pfam IDs that have no equivalent TIGRfam hits and relative abundance per sample.

#ID	Function	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	IC1	V1	V2	V3	V4	V5	V6	V7	V8
1	PF00004_ATPase family associated with various cellular activities (AAA)	-	-	-	-	-	-	-	1.20	-	-	-	-	-	-	-	-	0.55	-	-
2	PF00005_ABC transporter	-	-	-	-	1.49	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3	PF00015_Methyl-accepting chemotaxis protein (MCP) signaling domain	-	-	-	-	2.99	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4	PF00072_Response regulator receiver domain	-	-	-	-	-	-	-	-	-	-	-	-	-	0.69	-	-	0.55	-	-
5	PF00075_RNase H	-	-	-	-	-	-	-	-	4.35	-	-	-	0.58	-	-	-	0.55	-	2.17
6	PF00079_Serpin (serine protease inhibitor)	-	0.94	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
7	PF00092_von Willebrand factor type A domain	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
8	PF00112_Papain family cysteine protease	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-
9	PF00144_Beta-lactamase	-	-	-	-	-	-	-	-	-	-	-	0.84	0.58	0.69	-	-	-	1.69	2.17
10	PF00149_Calcineurin-like phosphoesterase	-	-	-	-	1.49	-	-	1.20	-	-	-	-	-	-	-	-	-	-	-
11	PF00165_Bacterial regulatory helix-turn-helix proteins. AraC family	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1.10	-	-
12	PF00166_Chaperonin 10 Kd subunit	-	-	-	-	1.49	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-
13	PF00176_SNF2 family N-terminal domain	-	0.94	-	0.89	2.99	1.69	-	-	-	-	-	0.84	0.58	0.69	-	-	-	-	-
14	PF00186_Dihydrofolate reductase	-	0.94	-	3.57	-	1.69	-	-	-	-	-	-	-	-	-	-	-	-	-
15	PF00196_Bacterial regulatory proteins. luxR family	-	-	-	0.89	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
16	PF00216_Bacterial DNA-binding protein	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
17	PF00230_Major intrinsic protein	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-
18	PF00239_Resolvase. N terminal domain	-	3.77	-	-	-	-	5.56	1.20	4.35	-	3.70	1.68	2.91	2.76	-	-	-	-	4.35
19	PF00248_Aldo/keto reductase family	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-
20	PF00251_Glycosyl hydrolases family 32 N terminal	-	0.94	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
21	PF00265_Thymidine kinase	-	-	-	1.79	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
22	PF00266_Aminotransferase class-V	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-
23	PF00268_Ribonucleotide reductase. small chain	-	-	-	-	-	-	-	-	-	-	-	0.84	-	-	-	-	-	-	-
24	PF00270_DEAD/DEAH box helicase	-	0.94	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
25	PF00271_Helicase conserved C-terminal domain	-	0.94	-	-	-	-	1.85	-	4.35	-	-	0.84	-	2.07	-	-	0.55	-	-

#ID	Function	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	IC1	V1	V2	V3	V4	V5	V6	V7	V8
52	PF00573_Ribosomal protein L4/L1 family	-	0.94	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
53	PF00574_Clp protease	-	0.94	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	PF00577_Fimbrial Usher protein	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-
55	PF00583_Acetyltransferase (GNAT) family	-	-	-	1.79	-	-	-	1.20	-	-	-	-	-	-	-	-	-	-	-
56	PF00589_Phage integrase family	6.45	1.89	-	-	1.49	3.39	3.70	3.61	-	12.50	-	-	2.33	7.59	-	-	3.87	-	-
57	PF00618_Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif	-	-	-	-	-	1.69	-	-	4.35	-	-	-	-	-	-	-	-	-	-
58	PF00639_PPIC-type PPIASE domain	-	-	-	0.89	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
59	PF00657_GDSL-like Lipase/Acylhydrolase	-	-	-	-	-	-	-	-	-	-	-	-	0.58	0.69	-	-	-	-	-
60	PF00665_Integrase core domain	-	2.83	6.90	1.79	2.99	6.78	3.70	2.41	-	-	3.70	-	2.91	2.07	-	-	2.21	-	8.70
61	PF00672_HAMP domain	-	-	-	-	-	-	-	-	-	-	3.70	-	-	-	-	-	-	-	-
62	PF00675_Insulinase (Peptidase family M16)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
63	PF00691_OmpA family	-	0.94	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
64	PF00703_Glycosyl hydrolases family 2. immunoglobulin-like beta-sandwich domain	-	-	-	-	-	-	-	-	-	-	-	-	0.58	0.69	-	-	-	-	-
65	PF00704_Glycosyl hydrolases family 18	-	-	-	-	-	-	-	-	-	-	-	-	-	0.69	-	-	-	-	-
66	PF00717_Peptidase S24-like	-	0.94	-	0.89	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
67	PF00719_Inorganic pyrophosphatase	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
68	PF00721_Virus coat protein (TMV like)	-	0.94	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
69	PF00753_Metallo-beta-lactamase superfamily	-	-	-	-	-	-	1.85	-	-	-	-	-	-	-	-	-	0.55	-	2.17
70	PF00754_F5/8 type C domain	-	-	-	-	-	-	-	-	-	-	-	-	-	0.69	-	-	-	-	-
71	PF00768_D-alanyl-D-alanine carboxypeptidase	-	-	-	-	-	-	-	-	-	-	-	0.84	0.58	-	-	-	1.10	-	-
72	PF00799_Geminivirus Rep catalytic domain	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1.69	-
73	PF00805_Pentapeptide repeats (8 copies)	-	-	-	-	-	-	-	1.20	-	-	-	-	0.58	0.69	7.69	-	-	-	-
74	PF00814_Glycoprotease family	-	-	-	-	1.49	-	-	1.20	-	-	-	-	-	-	-	-	-	-	-
75	PF00817_impB/mucB/samB family	-	-	-	-	1.49	3.39	-	-	-	-	3.70	-	-	0.69	-	-	-	-	-
76	PF00847_AP2 domain	3.23	0.94	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
77	PF00872_Transposase. Mutator family	-	0.94	3.45	-	-	1.69	-	1.20	-	-	29.63	-	-	0.69	-	-	-	-	-

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78	PF00873_AcrB/AcrD/AcrF family	-	-	-	-	-	-	-	-	-	-	-	0.84	-	-	-	-	0.55	-	-
79	PF00877_NlpC/P60 family	-	0.94	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
80	PF00893_Small Multidrug Resistance protein	-	-	-	-	1.49	-	-	1.20	-	-	-	-	1.16	-	-	-	-	-	-
81	PF00899_ThiF family	-	-	-	-	1.49	-	-	-	-	-	-	-	-	-	-	-	-	-	-
82	PF00903_Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily	-	-	-	-	-	1.69	-	1.20	-	-	-	-	-	-	-	-	-	-	-
83	PF00950_ABC 3 transport family	-	-	-	0.89	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
84	PF00959_Phage lysozyme	-	-	-	5.36	1.49	-	-	1.20	-	-	-	1.68	-	-	-	-	0.55	-	-
85	PF00978_RNA dependent RNA polymerase	-	0.94	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
86	PF01022_Bacterial regulatory protein. arsR family	-	-	-	-	-	-	-	-	-	4.17	-	-	-	-	-	-	0.55	-	-
87	PF01032_FecCD transport family	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-
88	PF01047_MarR family	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
89	PF01051_Initiator Replication protein	-	0.94	3.45	0.89	1.49	1.69	1.85	-	4.35	4.17	-	-	-	-	-	-	0.55	-	-
90	PF01063_Aminotransferase class IV	-	-	-	-	1.49	-	-	-	-	-	-	-	-	-	-	-	-	-	-
91	PF01068_ATP dependent DNA ligase domain	-	-	-	0.89	-	-	-	1.20	-	-	-	-	1.16	-	-	-	-	-	-
92	PF01076_Plasmid recombination enzyme	-	-	-	-	-	1.69	-	1.20	-	-	-	-	1.16	-	-	-	-	-	-
93	PF01107_Viral movement protein (MP)	-	0.94	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
94	PF01136_Peptidase family U32	-	0.94	-	-	-	-	-	-	-	-	-	-	-	0.69	-	-	1.10	-	-
95	PF01183_Glycosyl hydrolases family 25	-	-	-	-	-	-	-	-	-	-	-	5.04	1.74	2.07	-	-	3.31	-	-
96	PF01202_Shikimate kinase	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
97	PF01226_Formate/nitrite transporter	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-
98	PF01228_Glycine radical	-	-	-	0.89	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
99	PF01235_Sodium:alanine symporter family	-	-	-	-	-	3.39	-	2.41	-	-	-	-	-	2.07	-	-	-	-	-
100	PF01244_Membrane dipeptidase (Peptidase family M19)	-	-	-	-	-	-	-	-	-	-	-	-	-	0.69	-	-	-	-	-
101	PF01270_Glycosyl hydrolases family 8	-	-	-	-	-	1.69	-	1.20	-	-	-	-	-	-	-	-	-	-	-
102	PF01297_Periplasmic solute binding protein family	-	-	3.45	2.68	-	-	-	1.20	-	-	-	-	-	0.69	-	-	0.55	-	-
103	PF01336_OB-fold nucleic acid binding domain	-	-	-	-	-	-	-	-	-	-	-	-	-	2.07	-	-	-	-	-
104	PF01339_CheB methylesterase	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-

#ID	Function	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	IC1	V1	V2	V3	V4	V5	V6	V7	V8
105	PF01368_DHH family	-	-	-	-	-	-	3.70	-	-	-	-	-	-	-	-	-	-	-	-
106	PF01370_NAD dependent epimerase/dehydratase family	-	-	-	-	1.49	-	-	1.20	-	-	-	-	-	-	-	-	-	-	-
107	PF01381_Helix-turn-helix	-	1.89	3.45	2.68	7.46	3.39	7.41	3.61	-	8.33	-	3.36	2.91	2.76	-	3.33	7.18	1.69	6.52
108	PF01385_Probable transposase	-	-	-	-	-	-	-	-	-	-	-	-	-	0.69	-	-	-	-	-
109	PF01391_Collagen triple helix repeat (20 copies)	12.90	1.89	-	-	-	-	-	1.20	-	-	-	-	1.74	3.45	-	-	1.66	-	-
110	PF01402_Ribbon-helix-helix protein. copG family	-	0.94	-	-	-	-	1.85	1.20	-	4.17	3.70	0.84	-	-	-	-	-	-	-
111	PF01418_Helix-turn-helix domain. rpiR family	-	-	-	-	-	-	-	-	-	-	-	-	0.58	0.69	-	-	0.55	-	-
112	PF01420_Type I restriction modification DNA specificity domain	-	-	-	0.89	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
113	PF01430_Hsp33 protein	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
114	PF01443_Viral (Superfamily 1) RNA helicase	-	0.94	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
115	PF01446_Replication protein	-	0.94	-	-	2.99	-	-	1.20	-	-	-	0.84	-	-	3.85	-	-	-	-
116	PF01464_Transglycosylase SLT domain	-	-	-	-	1.49	-	-	-	-	-	-	-	1.16	-	-	-	1.10	-	-
117	PF01471_Putative peptidoglycan binding domain	-	-	-	-	-	-	-	-	-	-	-	0.84	-	-	-	-	-	-	-
118	PF01473_Putative cell wall binding repeat	-	-	-	-	2.99	-	-	-	-	-	-	-	-	-	-	-	1.66	-	-
119	PF01476_LysM domain	-	0.94	-	-	-	-	-	-	-	-	-	0.84	-	-	3.85	-	1.10	-	-
120	PF01507_Phosphoadenosine phosphosulfate reductase family	-	-	-	-	-	-	-	1.20	-	-	-	-	0.58	-	-	-	-	-	-
121	PF01510_N-acetylmuramoyl-L-alanine amidase	-	-	-	-	-	1.69	-	-	-	-	-	0.84	2.33	3.45	-	-	1.66	1.69	-
122	PF01520_N-acetylmuramoyl-L-alanine amidase	-	-	-	-	1.49	-	-	2.41	-	-	-	0.84	-	0.69	-	-	-	-	-
123	PF01527_Transposase	-	-	-	-	-	1.69	1.85	-	-	-	3.70	-	0.58	-	-	-	-	-	-
124	PF01541_GIY-YIG catalytic domain	-	0.94	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
125	PF01547_Bacterial extracellular solute-binding protein	-	-	-	-	-	-	-	-	-	-	-	-	-	1.38	-	-	-	-	-
126	PF01551_Peptidase family M23	-	0.94	-	-	-	-	1.85	-	-	-	-	0.84	-	0.69	-	-	1.10	-	-
127	PF01554_MatE	-	-	-	-	-	-	-	-	-	-	-	-	-	0.69	-	-	-	-	-
128	PF01555_DNA methylase	6.45	1.89	-	0.89	1.49	-	1.85	-	4.35	-	-	0.84	0.58	0.69	3.85	-	2.21	-	-
129	PF01569_PAP2 superfamily	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
130	PF01580_FtsK/SpoIIIE family	3.23	-	-	-	-	-	-	-	-	-	-	-	-	0.69	-	-	0.55	-	-
131	PF01584_CheW-like domain	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-

#ID	Function	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	IC1	V1	V2	V3	V4	V5	V6	V7	V8
132	PF01590_GAF domain	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-
133	PF01594_Domain of unknown function DUF20	-	-	-	0.89	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
134	PF01609_Transposase DDE domain	-	0.94	3.45	0.89	-	-	5.56	-	-	4.17	7.41	0.84	1.74	0.69	-	-	-	-	-
135	PF01612_3'-5' exonuclease	-	0.94	-	-	1.49	-	-	-	-	-	-	-	-	-	-	-	-	-	-
136	PF01613_Flavin reductase like domain	-	-	-	-	-	-	-	-	-	-	-	1.68	-	-	-	-	-	-	-
137	PF01660_Viral methyltransferase	-	1.89	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
138	PF01661_Macro domain	-	0.94	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
139	PF01694_Rhomboid family	-	-	-	-	1.49	-	-	1.20	-	-	-	-	-	-	-	-	-	-	-
140	PF01695_IstB-like ATP binding protein	-	-	-	-	-	1.69	3.70	1.20	-	-	-	-	-	0.69	-	-	-	-	-
141	PF01719_Plasmid replication protein	-	1.89	-	-	-	-	3.70	-	-	4.17	3.70	2.52	-	-	-	-	-	-	-
142	PF01734_Patatin-like phospholipase	-	-	-	-	-	-	-	-	-	4.17	-	-	-	-	-	-	-	-	-
143	PF01757_Acyltransferase family	-	-	-	-	-	1.69	-	-	-	-	-	0.84	-	-	-	-	-	-	-
144	PF01797_Transposase IS200 like	-	-	3.45	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
145	PF01832_Mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase	-	-	-	-	-	1.69	-	1.20	-	-	-	0.84	-	-	-	-	-	-	-
146	PF01844_HNH endonuclease	3.23	1.89	-	0.89	1.49	-	-	-	4.35	-	-	2.52	1.74	0.69	-	-	1.10	-	-
147	PF01850_PIN domain	-	-	3.45	0.89	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
148	PF01925_Domain of unknown function DUF81	-	-	-	-	-	-	-	-	-	-	3.70	-	-	-	-	-	-	-	-
149	PF02065_Melibiase	-	-	-	-	-	-	-	-	-	-	-	-	-	0.69	-	-	-	-	-
150	PF02082_Transcriptional regulator	-	-	-	-	-	1.69	-	1.20	-	-	-	-	-	-	-	-	-	-	-
151	PF02086_D12 class N6 adenine-specific DNA methyltransferase	6.45	1.89	-	-	1.49	-	-	-	-	-	-	-	-	-	-	-	-	-	-
152	PF02185_Hr1 repeat	-	-	-	-	-	1.69	-	-	4.35	-	-	-	-	-	-	-	-	-	-
153	PF02190_ATP-dependent protease La (LON) domain	-	-	-	-	1.49	-	-	-	-	-	-	-	-	-	-	-	-	-	-
154	PF02275_Linear amide C-N hydrolases. choloylglycine hydrolase family	-	-	-	-	-	-	-	-	-	-	-	-	0.69	-	-	-	-	-	-
155	PF02305_Capsid protein (F protein)	22.58	1.89	3.45	-	7.46	-	-	6.02	-	-	-	10.08	3.49	3.45	26.9280.00	0.55	54.2439.13	-	-
156	PF02311_AraC-like ligand binding domain	-	-	-	-	-	-	-	-	-	-	-	-	-	0.69	-	-	-	-	-
157	PF02325_YGGT family	-	-	-	-	-	1.69	-	-	-	-	-	-	-	-	-	-	-	-	-
158	PF02368_Bacterial Ig-like domain (group 2)	-	0.94	-	-	-	-	-	-	-	-	-	-	0.58	0.69	-	-	1.10	-	-

#ID	Function	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	IC1	V1	V2	V3	V4	V5	V6	V7	V8
159	PF02371_Transposase IS116/IS110/IS902 family	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
160	PF02384_N-6 DNA Methylase	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1.10	-	-
161	PF02386_Cation transport protein	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
162	PF02391_MoaE protein	-	-	-	-	-	-	-	-	-	-	3.70	-	-	-	-	-	-	-	-
163	PF02413_Caudovirales tail fibre assembly protein	-	-	-	-	-	-	-	-	-	-	-	-	2.33	-	-	-	1.10	-	-
164	PF02424_ApbE family	-	-	-	-	-	-	-	-	-	-	-	0.84	-	-	-	-	-	-	-
165	PF02452_PemK-like protein	-	-	-	-	1.49	-	-	-	-	-	-	-	-	-	-	-	-	-	-
166	PF02498_BRO family. N-terminal domain	-	2.83	-	-	-	-	1.85	-	-	4.17	-	2.52	0.58	2.07	3.85	-	0.55	-	6.52
167	PF02518_Histidine kinase-. DNA gyrase B-. and HSP90-like ATPase	-	-	-	-	-	-	-	-	-	-	-	0.84	-	-	-	-	-	-	-
168	PF02534_TraG/TraD family	-	-	-	-	-	-	-	-	-	-	-	-	-	0.69	-	-	-	-	-
169	PF02557_D-alanyl-D-alanine carboxypeptidase	3.23	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
170	PF02562_Phoh-like protein	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-
171	PF02586_Uncharacterised ACR. COG2135	-	-	-	-	-	-	-	-	-	-	3.70	-	-	0.69	-	-	-	-	-
172	PF02588_Uncharacterized BCR. YitT family COG1284	-	-	-	-	-	-	1.85	-	-	4.17	-	-	-	-	-	-	1.66	-	-
173	PF02600_Disulfide bond formation protein DsbB	-	-	-	-	-	1.69	-	1.20	-	-	-	-	-	-	-	-	-	-	-
174	PF02601_Exonuclease VII. large subunit	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
175	PF02609_Exonuclease VII small subunit	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
176	PF02630_SCO1/SenC	-	-	-	-	-	1.69	-	1.20	-	-	-	-	-	-	-	-	-	-	-
177	PF02661_Fic/DOC family	-	-	-	-	-	-	-	-	-	-	3.70	-	-	-	-	-	-	-	-
178	PF02706_Chain length determinant protein	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-
179	PF02711_E4 protein	-	-	-	0.89	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
180	PF02719_Polysaccharide biosynthesis protein	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
181	PF02732_ERCC4 domain	-	-	-	-	-	-	-	-	-	-	-	0.84	-	-	-	-	-	-	-
182	PF02742_Iron dependent repressor. metal binding and dimerisation domain	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-
183	PF02796_Helix-turn-helix domain of resolvase	-	0.94	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
184	PF02811_PHP domain	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1.10	-	-
185	PF02836_Glycosyl hydrolases family 2. TIM barrel domain	-	-	-	-	-	-	-	-	-	-	-	0.84	1.16	0.69	3.85	-	-	-	-

#ID	Function	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	IC1	V1	V2	V3	V4	V5	V6	V7	V8
239	PF04383_KilA-N domain	-	-	-	-	-	-	-	-	4.35	-	-	-	1.16	-	-	-	-	-	-
240	PF04404_ERF superfamily	-	-	3.45	-	-	-	-	1.20	-	-	-	1.68	1.16	2.07	3.85	-	-	-	-
241	PF04471_Restriction endonuclease	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
242	PF04546_Sigma-70. non-essential region	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-
243	PF04586_Caudovirus prohead protease	-	-	-	-	-	-	-	-	-	-	-	-	1.16	-	-	-	-	-	-
244	PF04606_Ogr/Delta-like zinc finger	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-
245	PF04771_Chicken anaemia virus VP-3 protein	-	-	-	-	-	-	-	-	-	-	-	0.84	-	-	-	-	-	-	-
246	PF04796_Plasmid encoded RepA protein	-	-	-	-	-	1.69	-	1.20	-	-	-	-	-	-	-	-	-	-	-
247	PF04851_Type III restriction enzyme. res subunit	-	-	-	-	-	-	-	-	4.35	-	-	0.84	1.74	0.69	-	-	1.66	-	-
248	PF04861_Gyrovirus VP2 protein	-	-	-	-	-	-	-	-	-	-	-	0.84	-	-	-	-	-	-	-
249	PF04865_Baseplate J-like protein	-	-	-	-	-	-	-	1.20	-	-	-	-	1.16	2.76	-	-	0.55	-	-
250	PF04917_Bacterial shufflon protein. N-terminal constant region	-	-	-	-	-	-	-	1.20	-	-	-	-	-	-	-	-	-	-	-
251	PF04965_Gene 25-like lysozyme	3.23	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
252	PF04984_Phage tail sheath protein	-	-	-	0.89	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
253	PF05036_Sporulation related domain	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-
254	PF05037_Protein of unknown function (DUF669)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
255	PF05063_MT-A70	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
256	PF05065_Phage capsid family	-	0.94	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
257	PF05193_Peptidase M16 inactive domain	-	1.89	-	-	1.49	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-
258	PF05203_Hom_end-associated Hint	-	-	-	-	1.49	-	-	1.20	-	-	-	0.84	-	-	-	-	-	-	-
259	PF05257_CHAP domain	-	-	-	-	-	-	1.85	-	-	-	-	-	-	-	-	-	-	-	-
260	PF05268_Phage tail fibre adhesin Gp38	-	-	-	4.46	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
261	PF05272_Virulence-associated protein E	3.23	0.94	-	2.68	1.49	-	-	-	-	-	-	-	-	0.69	-	-	0.55	-	-
262	PF05282_AAR2 protein	-	-	-	-	-	1.69	-	-	4.35	-	-	-	-	-	-	-	-	-	-
263	PF05352_Phage Connector (GP10)	-	0.94	-	-	-	-	-	-	-	-	-	3.36	0.58	0.69	3.85	-	1.66	-	2.17
264	PF05396_Phage T7 capsid assembly protein	-	-	-	1.79	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
265	PF05534_HicB family	-	-	-	-	-	-	-	-	-	-	-	0.84	-	0.69	-	-	-	-	-

#ID	Function	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	IC1	V1	V2	V3	V4	V5	V6	V7	V8
266	PF05565_Siphovirus Gp157	3.23	-	-	-	1.49	-	-	-	-	-	-	-	-	-	-	-	-	-	-
267	PF05592_Bacterial alpha-L-rhamnosidase	-	-	-	-	-	-	-	-	-	-	-	-	-	0.69	-	-	-	-	-
268	PF05595_Domain of unknown function (DUF771)	-	-	-	-	-	-	1.85	-	-	-	-	-	-	-	-	-	-	-	-
269	PF05666_Fels-1 Prophage Protein-like	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-
270	PF05707_Zonular occludens toxin (Zot)	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-
271	PF05709_Siphovirus tail component protein	-	-	3.45	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
272	PF05713_Bacterial mobilisation protein (MobC)	-	-	-	-	-	1.69	-	1.20	-	-	-	-	-	-	-	-	-	-	-
273	PF05762_VWA domain containing CoxE-like protein	-	-	-	-	-	-	-	-	-	-	-	-	1.16	-	-	-	-	-	-
274	PF05798_Bacteriophage FRD3 protein	-	-	-	0.89	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
275	PF05838_Predicted lysozyme (DUF847)	-	-	-	0.89	1.49	-	-	-	-	-	-	-	-	-	-	-	-	-	-
276	PF05866_Endodeoxyribonuclease RusA	-	-	-	-	-	-	-	-	-	-	-	0.84	1.74	0.69	-	-	0.55	-	-
277	PF05876_Phage terminase large subunit (GpA)	3.23	0.94	-	0.89	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
278	PF05939_Phage minor tail protein	-	-	-	-	1.49	-	-	-	-	-	-	-	-	-	-	-	-	-	-
279	PF05940_NnrS protein	-	-	-	-	-	-	-	-	-	-	3.70	-	-	-	-	-	-	-	-
280	PF05951_Bacterial protein of unknown function (DUF882)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	27.12	-
281	PF05954_Phage late control gene D protein (GPD)	-	-	-	-	-	-	-	-	-	-	-	0.84	-	-	-	-	-	-	-
282	PF05973_Phage derived protein Gp49-like (DUF891)	-	-	-	-	-	1.69	-	-	-	-	-	-	-	-	-	-	-	-	-
283	PF05991_Protein of unknown function (DUF901)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
284	PF06048_Domain of unknown function (DUF927)	-	-	-	-	-	-	1.85	-	-	4.17	-	-	-	-	-	-	0.55	-	-
285	PF06050_2-hydroxyglutaryl-CoA dehydratase. D-component	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-
286	PF06081_Bacterial protein of unknown function (DUF939)	-	-	-	-	-	1.69	-	-	-	-	-	-	-	-	-	-	-	-	-
287	PF06094_AIG2-like family	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
288	PF06114_Domain of unknown function (DUF955)	-	-	-	-	-	-	-	-	-	-	-	-	-	0.69	-	-	1.10	-	2.17
289	PF06123_Inner membrane protein CreD	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-
290	PF06147_Protein of unknown function (DUF968)	3.23	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
291	PF06152_Phage minor capsid protein 2	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	0.55	-	-
292	PF06154_YagB/YeeU/YfjZ family	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-

#ID	Function	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	IC1	V1	V2	V3	V4	V5	V6	V7	V8
293	PF06204_Putative carbohydrate binding domain	-	-	-	-	-	-	-	-	-	-	-	-	-	0.69	-	-	-	-	-
294	PF06250_Protein of unknown function (DUF1016)	-	-	-	-	-	-	-	2.41	-	-	-	-	-	-	-	-	1.10	-	-
295	PF06347_Bacterial SH3 domain	-	-	-	-	-	3.39	-	3.61	4.35	-	-	-	-	-	-	-	-	-	-
296	PF06378_Protein of unknown function (DUF1071)	-	-	-	-	-	-	-	-	-	-	-	-	1.74	-	3.85	-	-	-	-
297	PF06445_Bacterial transcription activator. effector binding domain	-	-	-	-	-	1.69	-	-	-	-	-	-	0.58	-	-	-	-	-	-
298	PF06488_Lactococcus lactis bacteriophage major structural protein	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1.10	-	-
299	PF06491_Protein of unknown function (DUF1094)	-	-	-	-	-	-	-	1.20	-	-	-	-	-	-	-	-	-	-	-
300	PF06520_Protein of unknown function (DUF1105)	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-
301	PF06530_Phage antitermination protein Q	-	-	-	-	-	-	-	-	-	-	-	-	-	0.69	-	-	-	-	-
302	PF06555_Protein of unknown function (DUF1121)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
303	PF06714_Gp5 N-terminal OB domain	-	-	-	1.79	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
304	PF06715_Gp5 C-terminal repeat (3 copies)	-	-	-	1.79	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
305	PF06725_3D domain	-	-	-	-	-	-	-	-	-	-	-	-	1.16	-	-	-	-	-	-
306	PF06737_Transglycosylase-like domain	-	-	-	-	1.49	-	-	-	4.35	-	-	-	-	-	-	-	-	-	-
307	PF06838_Aluminium resistance protein	-	-	-	-	-	-	-	1.20	-	-	-	-	-	-	-	-	-	-	-
308	PF06841_T4-like virus tail tube protein gp19	-	-	-	0.89	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
309	PF06893_Bacteriophage Mu P protein	-	-	-	0.89	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
310	PF06895_Protein of unknown function (DUF1267)	-	0.94	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
311	PF06914_Protein of unknown function (DUF1277)	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-
312	PF06953_Arsenical resistance operon trans-acting repressor ArsD	-	-	-	-	-	-	-	1.20	-	-	-	-	-	-	-	-	-	-	-
313	PF06965_Na+/H+ antiporter 1	-	-	-	-	-	-	1.85	-	-	-	-	-	-	-	-	-	-	-	-
314	PF07031_Protein of unknown function (DUF1321)	-	0.94	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
315	PF07043_Protein of unknown function (DUF1328)	-	-	-	-	-	-	-	-	-	-	3.70	-	-	-	-	-	-	-	-
316	PF07066_Lactococcus phage M3 protein	-	-	3.45	-	-	-	-	-	-	-	-	0.84	-	-	-	-	-	-	-
317	PF07068_Major capsid protein Gp23	-	-	-	1.79	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
318	PF07083_Protein of unknown function (DUF1351)	-	-	-	-	-	-	-	-	-	-	-	-	-	0.69	-	-	-	-	-
319	PF07102_Protein of unknown function (DUF1364)	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-

#ID	Function	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	IC1	V1	V2	V3	V4	V5	V6	V7	V8
347	PF07880_Bacteriophage T4 gp9/10-like protein	-	-	-	0.89	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
348	PF07907_YibE/F-like protein	-	-	-	-	-	-	-	-	-	8.33	-	-	-	-	-	-	-	-	-
349	PF07927_YcfA-like protein	-	-	-	-	-	-	-	-	-	-	-	-	-	0.69	-	-	-	-	-
350	PF07943_Penicillin-binding protein 5. C-terminal domain	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-
351	PF08010_Bacteriophage protein GP30.3	-	-	-	0.89	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
352	PF08199_Bacteriophage E2-like protein	-	-	-	-	-	-	-	-	-	-	-	0.84	-	-	-	-	-	-	-
353	PF08220_DeoR-like helix-turn-helix domain	-	-	-	0.89	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
354	PF08230_Cpl-7 lysozyme C-terminal domain	-	-	-	-	-	-	-	-	-	-	-	-	-	0.69	-	-	0.55	-	-
355	PF08238_Sel1 repeat	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.55	-	-
356	PF08239_Bacterial SH3 domain	-	-	-	-	-	-	-	-	-	-	-	1.68	-	0.69	-	-	-	-	2.17
357	PF08245_Mur ligase middle domain	-	-	-	-	-	-	-	1.20	-	-	-	-	-	-	-	-	-	-	-
358	PF08275_DNA primase catalytic core. N-terminal domain	-	-	-	0.89	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
359	PF08291_Peptidase M15	-	-	41.38	16.07	16.42	1.69	3.70	2.41	21.74	16.67	3.70	1.68	2.91	2.07	7.69	16.67	-	10.17	2.17
360	PF08327_Activator of Hsp90 ATPase homolog 1-like protein	-	-	-	-	-	1.69	-	1.20	-	-	-	-	-	-	-	-	-	-	-
361	PF08333_Protein of unknown function (DUF1725)	-	-	-	-	-	-	-	-	-	-	-	0.84	-	-	-	-	-	-	-
362	PF08346_AntA/AntB antirepressor	-	-	-	-	-	1.69	-	-	-	-	-	1.68	0.58	-	-	-	-	-	-
363	PF08706_D5 N terminal like	-	-	-	-	-	-	-	-	-	-	-	-	-	1.38	-	-	-	-	-
364	PF08707_Primase C terminal 2 (PriCT-2)	-	-	-	-	-	-	-	-	-	4.17	-	-	-	-	-	-	1.66	-	-
365	PF08708_Primase C terminal 1 (PriCT-1)	-	-	-	-	-	-	1.85	-	-	4.17	-	-	-	-	-	-	-	-	-
366	PF08774_VRR-NUC domain	-	-	-	0.89	-	-	-	-	4.35	-	-	0.84	-	-	-	-	0.55	-	-
367	PF08804_gp32 DNA binding protein like	-	-	-	0.89	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
368	PF08818_Domain of unknown function (DU1801)	-	-	-	-	-	1.69	-	-	-	-	-	-	-	-	-	-	-	-	-
369	PF08857_Putative ParB-like nuclease	-	-	-	-	-	1.69	-	-	-	-	-	-	-	-	-	-	-	-	-
370	PF08867_FRG domain	-	-	-	0.89	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
371	PF08890_Phage XkdN-like protein	-	-	-	-	-	-	-	-	-	-	-	-	-	0.69	-	-	-	-	-
372	PF08900_Domain of unknown function (DUF1845)	-	-	-	-	-	-	-	1.20	-	-	-	-	-	-	-	-	-	-	-
373	PF08918_PhoQ Sensor	-	-	-	-	-	-	-	-	-	-	-	-	0.58	-	-	-	-	-	-

