Phyre2

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Description	P0AF90
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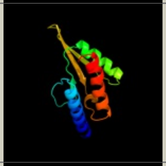
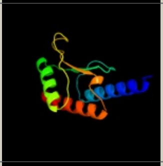
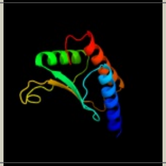
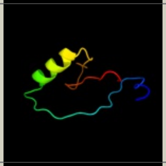
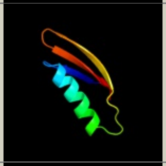
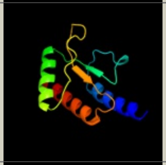
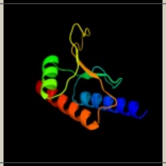
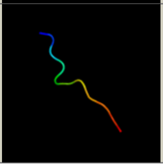
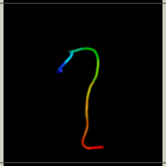
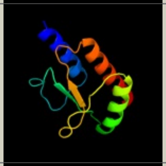
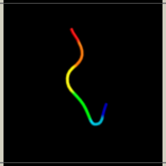
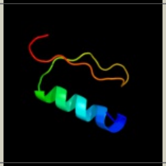
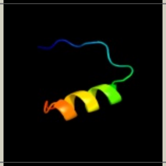
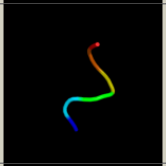
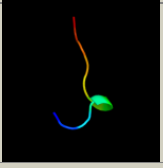
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nxia_	Alignment		100.0	65	**Fold:**Ferredoxin-like **Superfamily:**Hypothetical protein VC0424 **Family:**Hypothetical protein VC0424
2	d1j5ya2	Alignment		47.4	33	**Fold:**HPr-like **Superfamily:**Putative transcriptional regulator TM1602, C-terminal domain **Family:**Putative transcriptional regulator TM1602, C-terminal domain
3	c3tqxA_	Alignment		35.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-amino-3-ketobutyrate coenzyme a ligase; **PDBTitle:** structure of the 2-amino-3-ketobutyrate coenzyme a ligase (kbl) from2 coxiella burnetii
4	d1fc4a_	Alignment		28.6	19	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
5	c3hqtB_	Alignment		27.5	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cai-1 autoinducer synthase; **PDBTitle:** plp-dependent acyl-coa transferase cqsa
6	c2p7pB_	Alignment		26.9	24	**PDB header:**metal binding protein, hydrolase **Chain:** B: **PDB Molecule:**glyoxalase family protein; **PDBTitle:** crystal structure of genomically encoded fosfomycin resistance2 protein, fosx, from listeria monocytogenes complexed with mn(ii) and3 sulfate ion
7	c3qwuA_	Alignment		26.4	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** putative atp-dependent dna ligase from aquifex aeolicus.
8	c3a2bA_	Alignment		25.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
9	d2c0ra1	Alignment		24.7	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
10	c2w8wA_	Alignment		22.1	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** n100y spt with plp-ser
11	d2fhfa3	Alignment		20.5	18	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**PUD-like

12	c2x48B_	Alignment		18.7	24	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**cag38821; **PDBTitle:** orf 55 from sulfolobus islandicus rudivirus 1
13	d2je6i2	Alignment		18.2	27	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**ECR1 N-terminal domain-like
14	c3qm2A_	Alignment		16.8	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** 2.25 angstrom crystal structure of phosphoserine aminotransferase2 (serc) from salmonella enterica subsp. enterica serovar typhimurium
15	c3hz7A_	Alignment		16.3	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the sira-like protein (dsy4693) from2 desulfitobacterium hafniense, northeast structural genomics3 consortium target dhr2a
16	d1o59a1	Alignment		16.3	83	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Allantoicase repeat
17	d1r9ca_	Alignment		15.8	19	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
18	c1zswA_	Alignment		14.8	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**glyoxalase family protein; **PDBTitle:** crystal structure of bacillus cereus metallo protein from glyoxalase2 family
19	c1z64A_	Alignment		14.6	67	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**pleurocidin; **PDBTitle:** nmr solution structure of pleurocidin in dpc micelles
20	d2j44a2	Alignment		14.5	18	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**PUD-like
21	d2j43a1	Alignment	not modelled	13.8	9	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**PUD-like
22	c1w1nA_	Alignment	not modelled	13.7	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol 3-kinase tor1; **PDBTitle:** the solution structure of the fatc domain of the protein2 kinase tor1 from yeast
23	c2qv5A_	Alignment	not modelled	13.1	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu2773; **PDBTitle:** crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58
24	c1j5yA_	Alignment	not modelled	12.5	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, biotin repressor family; **PDBTitle:** crystal structure of transcriptional regulator (tm1602) from2 thermotoga maritima at 2.3 a resolution
25	d2j73a1	Alignment	not modelled	12.4	45	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**PUD-like
26	c2j43A_	Alignment	not modelled	12.2	18	**PDB header:**carbohydrate-binding module **Chain:** A: **PDB Molecule:**spydx; **PDBTitle:** alpha-glucan recognition by family 41 carbohydrate-binding2 modules from streptococcal virulence factors
27	c2ke4A_	Alignment	not modelled	11.8	45	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**cdc42-interacting protein 4; **PDBTitle:** the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
28	d2j43a2	Alignment	not modelled	11.8	25	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**PUD-like

29	c3m2oB_	Alignment	not modelled	11.7	36	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**glyoxalase/bleomycin resistance protein; **PDBTitle:** crystal structure of a putative glyoxalase/bleomycin resistance2 protein from rhodopseudomonas palustris cga009
30	c3dxvA_	Alignment	not modelled	11.6	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alpha-amino-epsilon-caprolactam racemase; **PDBTitle:** the crystal structure of alpha-amino-epsilon-caprolactam racemase from2 achromobacter obae
31	d2j44a1	Alignment	not modelled	11.4	27	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**PUD-like
32	d1utaa_	Alignment	not modelled	11.2	14	**Fold:**Ferredoxin-like **Superfamily:**Sporulation related repeat **Family:**Sporulation related repeat
33	c2j44A_	Alignment	not modelled	11.2	38	**PDB header:**carbohydrate-binding module **Chain:** A: **PDB Molecule:**alkaline amylopullulanase; **PDBTitle:** alpha-glucan binding by a streptococcal virulence factor
34	d1mqta_	Alignment	not modelled	11.0	57	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
35	d1bs0a_	Alignment	not modelled	10.7	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
36	d1x9ba_	Alignment	not modelled	10.1	16	**Fold:**Protozoan pheromone-like **Superfamily:**Hypothetical membrane protein Ta0354, soluble domain **Family:**Hypothetical membrane protein Ta0354, soluble domain
37	c2f06B_	Alignment	not modelled	10.1	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0572 from bacteroides thetaiotaomicron
38	d1oopa_	Alignment	not modelled	9.9	57	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
39	c1z7s1_	Alignment	not modelled	9.7	26	**PDB header:**virus **Chain:** 1: **PDB Molecule:**human coxsackievirus a21; **PDB Fragment:**viral protein 1; **PDBTitle:** the crystal structure of coxsackievirus a21
40	c1wv9B_	Alignment	not modelled	8.9	25	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**rhodanese homolog tt1651; **PDBTitle:** crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermus thermophilus hb8
41	c1zbe1_	Alignment	not modelled	8.7	57	**PDB header:**virus **Chain:** 1: **PDB Molecule:**coat protein vp1; **PDBTitle:** foot-and mouth disease virus serotype a1061
42	d1o59a2	Alignment	not modelled	8.6	80	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Allantoicase repeat
43	c2wff1_	Alignment	not modelled	8.5	57	**PDB header:**virus **Chain:** 1: **PDB Molecule:**p1; **PDB Fragment:**capsid protein vp4, residues 1-80 **PDBTitle:** equine rhinitis a virus
44	d1d4m1_	Alignment	not modelled	7.8	57	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
45	c2jg6A_	Alignment	not modelled	7.8	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna-3-methyladenine glycosidase; **PDBTitle:** crystal structure of a 3-methyladenine dna glycosylase i2 from staphylococcus aureus
46	c2lciA_	Alignment	not modelled	7.7	33	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**protein or36; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or36 (casd3 target)
47	d1jc4a_	Alignment	not modelled	7.6	12	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Methylmalonyl-CoA epimerase
48	c2rbbB_	Alignment	not modelled	7.6	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase; **PDBTitle:** crystal structure of a glyoxalase/bleomycin resistance2 protein/dioxygenase family enzyme from burkholderia phytofirmans psjn
49	d1pvc1_	Alignment	not modelled	7.6	25	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
50	c2gcfA_	Alignment	not modelled	7.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cation-transporting atpase pacs; **PDBTitle:** solution structure of the n-terminal domain of the coppper(i) atpase2 pacs in its apo form
51	c3sviA_	Alignment	not modelled	7.4	36	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**type iii effector hopab2; **PDBTitle:** structure of the pto-binding domain of hoppmal generated by limited2 thermolysin digestion
52	d1rhi1_	Alignment	not modelled	7.4	43	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
53	c1sg3A_	Alignment	not modelled	7.4	56	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**allantoicase; **PDBTitle:** structure of allantoicase
						Fold:PLP-dependent transferase-like

54	d1bjna_	Alignment	not modelled	7.3	9	**Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
55	d2pc6a2	Alignment	not modelled	7.2	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
56	c2kyzA_	Alignment	not modelled	7.2	19	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**heavy metal binding protein; **PDBTitle:** nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima
57	d2qifa1	Alignment	not modelled	7.2	24	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
58	d2f1fa1	Alignment	not modelled	7.2	13	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
59	c2k7wB_	Alignment	not modelled	7.1	19	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-like protein 11; **PDBTitle:** bax activation is initiated at a novel interaction site
60	c2rk0B_	Alignment	not modelled	7.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase domain; **PDBTitle:** crystal structure of glyoxylase/bleomycin resistance2 protein/dioxygenase domain from frankia sp. ean1pec
61	d1xqaa_	Alignment	not modelled	7.0	21	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
62	d1eah1_	Alignment	not modelled	7.0	19	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
63	d1qqp1_	Alignment	not modelled	6.9	29	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
64	c1ik9C_	Alignment	not modelled	6.8	50	**PDB header:**gene regulation/ligase **Chain:** C: **PDB Molecule:**dna ligase iv; **PDBTitle:** crystal structure of a xrcc4-dna ligase iv complex
65	d1zhva2	Alignment	not modelled	6.8	19	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Atu0741-like
66	d1cov1_	Alignment	not modelled	6.8	57	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
67	d2ajta2	Alignment	not modelled	6.7	10	**Fold:**FucI/AraA N-terminal and middle domains **Superfamily:**FucI/AraA N-terminal and middle domains **Family:**AraA N-terminal and middle domain-like
68	c1fi8E_	Alignment	not modelled	6.6	57	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** E: **PDB Molecule:**ecotin; **PDBTitle:** rat granzyme b [n66q] complexed to ecotin [81-84 iepd]
69	c3hgkE_	Alignment	not modelled	6.6	22	**PDB header:**transferase **Chain:** E: **PDB Molecule:**effector protein hopab2; **PDBTitle:** crystal structure of effect protein avrptob complexed with2 kinase pto
70	c2r6uB_	Alignment	not modelled	6.6	45	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of gene product rha04853 from rhodococcus sp. rha1
71	c3eyiB_	Alignment	not modelled	6.6	41	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**z-dna-binding protein 1; **PDBTitle:** the crystal structure of the second z-dna binding domain of2 human dai (zbp1) in complex with z-dna
72	c2jz7A_	Alignment	not modelled	6.5	28	**PDB header:**selenium-binding protein **Chain:** A: **PDB Molecule:**selenium binding protein; **PDBTitle:** solution nmr structure of selenium-binding protein from2 methanococcus vannielii
73	d1zyea1	Alignment	not modelled	6.5	36	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
74	c3q87B_	Alignment	not modelled	6.4	11	**PDB header:**transferase activator/transferase **Chain:** B: **PDB Molecule:**n6 adenine specific dna methylase; **PDBTitle:** structure of eukaryotic translation termination complex2 methyltransferase mtq2-trm112
75	c3kolA_	Alignment	not modelled	6.4	64	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**glyoxalase/bleomycin resistance **PDBTitle:** crystal structure of a glyoxalase/dioxygenase from nostoc2 punctiforme
76	d2e7ja1	Alignment	not modelled	6.4	19	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**SepSecS-like
77	d1aym1_	Alignment	not modelled	6.0	43	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
78	c3oajA_	Alignment	not modelled	5.9	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative ring-cleaving dioxygenase mhqo; **PDBTitle:** crystal structure of putative dioxygenase from bacillus subtilis2 subsp. subtilis str. 168
79	c2nl9B_	Alignment	not modelled	5.9	19	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-like protein 11; **PDBTitle:** crystal structure of the mcl-1:bim bh3 complex
						Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase

80	d1sqia2	Alignment	not modelled	5.9	15	**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
81	c3sk1C_	Alignment	not modelled	5.8	36	**PDB header:**griseoluteate-binding protein **Chain:** C: **PDB Molecule:**ehpr; **PDBTitle:** crystal structure of phenazine resistance protein ehpr from2 enterobacter agglomerans (erwinia herbicola, pantoea agglomerans)3 eh1087, apo form
82	c2l69A_	Alignment	not modelled	5.8	27	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**rossmann 2x3 fold protein; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or28
83	d1elua_	Alignment	not modelled	5.8	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
84	d1tme1_	Alignment	not modelled	5.8	25	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
85	c2cosA_	Alignment	not modelled	5.7	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine protein kinase lats2; **PDBTitle:** solution structure of rsgi ruh-038, a uba domain from mouse2 lats2 (large tumor suppressor homolog 2)
86	d2ggpb1	Alignment	not modelled	5.5	10	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
87	c1yg0A_	Alignment	not modelled	5.5	22	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cop associated protein; **PDBTitle:** solution structure of apo-copp from helicobacter pylori
88	c3h25A_	Alignment	not modelled	5.5	18	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**replication protein b; **PDBTitle:** crystal structure of the catalytic domain of primase repb' in complex2 with initiator dna
89	d1e2ya_	Alignment	not modelled	5.5	36	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
90	d1kn0a_	Alignment	not modelled	5.4	23	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**The homologous-pairing domain of Rad52 recombinase
91	c3q1jA_	Alignment	not modelled	5.3	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 20; **PDBTitle:** crystal structure of tudor domain 1 of human phd finger protein 20
92	c3rriB_	Alignment	not modelled	5.3	18	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase; **PDBTitle:** crystal structure of glyoxalase/bleomycin resistance2 protein/dioxygenase from alicyclobacillus acidocaldarius
93	d1t47a2	Alignment	not modelled	5.2	11	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
94	d1k4na_	Alignment	not modelled	5.2	13	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Hypothetical protein YecM (EC4020)
95	c3e0rC_	Alignment	not modelled	5.2	11	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**c3-degrading proteinase (cppa protein); **PDBTitle:** crystal structure of cppa protein from streptococcus pneumoniae tigr4
96	d1ug7a_	Alignment	not modelled	5.2	50	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain from hypothetical 2610208m17rik protein **Family:**Domain from hypothetical 2610208m17rik protein
97	d1tmf1_	Alignment	not modelled	5.1	15	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
98	c2f1fA_	Alignment	not modelled	5.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase isozyme iii small subunit; **PDBTitle:** crystal structure of the regulatory subunit of2 acetohydroxyacid synthase isozyme iii from e. coli
99	d1kona_	Alignment	not modelled	5.0	20	**Fold:**YebC-like **Superfamily:**YebC-like **Family:**YebC-like