Phyre2

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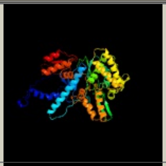
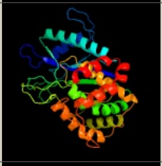
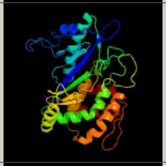
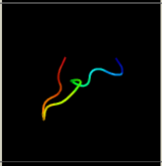
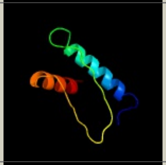
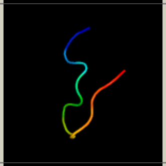
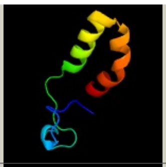
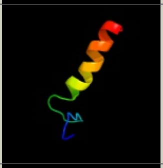
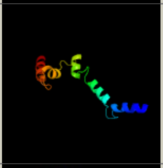
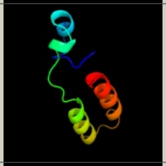
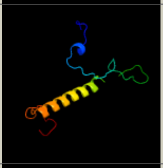
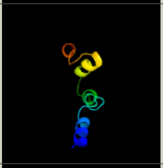
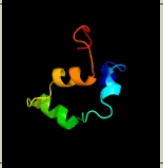
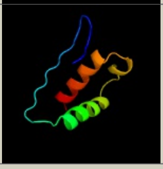
Description	RVBD2097c_(-)_2355327_2356685
Date	Mon Aug 5 13:25:21 BST 2019
Unique Job ID	56eaa2e08237047e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4b0tB_	Alignment		100.0	55	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pup--protein ligase; **PDBTitle:** structure of the pup ligase pafa of the prokaryotic2 ubiquitin-like modification pathway in complex with adp
2	c4bjrA_	Alignment		100.0	54	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pup--protein ligase, prokaryotic ubiquitin-like protein **PDBTitle:** crystal structure of the complex between prokaryotic2 ubiquitin-like protein pup and its ligase pafa
3	c4b0sA_	Alignment		100.0	41	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**deamidase-depupylase dop; **PDBTitle:** structure of the deamidase-depupylase dop of the prokaryotic2 ubiquitin-like modification pathway in complex with atp
4	d1r8ga_	Alignment		96.8	12	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Glutamate-cysteine ligase family 2 (GCS2)
5	d1tt4a_	Alignment		95.7	11	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Glutamate-cysteine ligase family 2 (GCS2)
6	c1tt4B_	Alignment		95.7	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative cytoplasmic protein; **PDBTitle:** structure of np459575, a predicted glutathione synthase from2 salmonella typhimurium
7	c2gwcE_	Alignment		89.7	13	**PDB header:**ligase **Chain:** E: **PDB Molecule:**glutamate cysteine ligase; **PDBTitle:** crystal structure of plant glutamate cysteine ligase in complex with a2 transition state analogue
8	c5cywB_	Alignment		50.9	36	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**interferon antagonist c7; **PDBTitle:** crystal structure of vaccinia virus c7
9	d1ghha_	Alignment		49.2	17	**Fold:**DNA damage-inducible protein DinI **Superfamily:**DNA damage-inducible protein DinI **Family:**DNA damage-inducible protein DinI
10	c5cz3B_	Alignment		49.2	43	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**m64r; **PDBTitle:** crystal structure of myxoma virus m64
11	d2jg0a1	Alignment		40.2	19	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Trehalase-like

12	c2jg0A_	Alignment		40.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**periplasmic trehalase; **PDBTitle:** family 37 trehalase from escherichia coli in complex with 1-2 thiatrehazolin
13	c2kseA_	Alignment		25.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein qsec; **PDBTitle:** backbone structure of the membrane domain of e. coli histidine kinase2 receptor qsec, center for structures of membrane proteins (csmp)3 target 4311c
14	c3ff6D_	Alignment		21.1	24	**PDB header:**ligase **Chain:** D: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** human acc2 ct domain with cp-640186
15	c5m4aA_	Alignment		20.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**neutral trehalase; **PDBTitle:** neutral trehalase nth1 from saccharomyces cerevisiae in complex with2 trehalose
16	c3cvjB_	Alignment		17.3	25	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoheptose isomerase; **PDBTitle:** crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
17	c2x24B_	Alignment		16.2	27	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coa carboxylase; **PDBTitle:** bovine acc2 ct domain in complex with inhibitor
18	c3tadB_	Alignment		15.5	23	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**liprin-alpha-2; **PDBTitle:** crystal structure of the liprin-alpha/liprin-beta complex
19	c4emtB_	Alignment		14.5	42	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**transmembrane protein 173; **PDBTitle:** crystal structure of human sting bound to c-di-gmp
20	c3o2iB_	Alignment		14.3	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of a functionally unknown protein from2 leptospirillum sp. group ii uba
21	d1m65a_	Alignment	not modelled	13.6	16	**Fold:**7-stranded beta/alpha barrel **Superfamily:**PHP domain-like **Family:**PHP domain
22	c5gs5D_	Alignment	not modelled	13.4	37	**PDB header:**immune system **Chain:** D: **PDB Molecule:**stimulator of interferon genes protein; **PDBTitle:** crystal structure of apo rat sting
23	d1uyra2	Alignment	not modelled	13.4	22	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
24	c4wa0A_	Alignment	not modelled	13.3	42	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**possible adhesin; **PDBTitle:** the structure of a possible adhesin c-terminal domain from2 caldicellulosiruptor kronotskyensis
25	d2gc6a1	Alignment	not modelled	12.7	21	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**Folylpolyglutamate synthetase, C-terminal domain
26	c4ef4B_	Alignment	not modelled	12.5	42	**PDB header:**immune system **Chain:** B: **PDB Molecule:**transmembrane protein 173; **PDBTitle:** crystal structure of sting ctd complex with c-di-gmp
27	d2jn4a1	Alignment	not modelled	12.5	50	**Fold:**NifT/FixU barrel-like **Superfamily:**NifT/FixU-like **Family:**NifT/FixU
28	c2jn4A_	Alignment	not modelled	12.5	50	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein fixu, nift; **PDBTitle:** solution nmr structure of protein rp4601 from rhodopseudomonas2 palustris. northeast structural genomics consortium target rpt2;3 ontario center for structural proteomics target rp4601.

29	c2lt5A_	Alignment	not modelled	12.5	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein p-30; **PDBTitle:** zymogen-flg of the onconase
30	c5cqqB_	Alignment	not modelled	12.1	20	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**regulatory protein zeste; **PDBTitle:** crystal structure of the drosophila zeste dna binding domain in2 complex with dna
31	c6mtgB_	Alignment	not modelled	11.6	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homoserine o-succinyltransferase; **PDBTitle:** a single reactive noncanonical amino acid is able to dramatically2 stabilize protein structure
32	c2h2wA_	Alignment	not modelled	11.3	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-succinyltransferase; **PDBTitle:** crystal structure of homoserine o-succinyltransferase (ec 2.3.1.46)2 (homoserine o-transsuccinylase) (hts) (tm0881) from thermotoga3 maritima at 2.52 a resolution
33	d2ghra1	Alignment	not modelled	11.1	31	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**HTS-like
34	d1dy2a_	Alignment	not modelled	11.0	25	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**Endostatin
35	d1u7za_	Alignment	not modelled	10.8	21	**Fold:**Ribokinase-like **Superfamily:**CoaB-like **Family:**CoaB-like
36	c5e2hB_	Alignment	not modelled	10.7	35	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of d-alanine carboxypeptidase ampc from2 mycobacterium smegmatis
37	c5yisC_	Alignment	not modelled	10.3	47	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**ankyrin-2; **PDBTitle:** crystal structure of ankb lir/lc3b complex
38	c4k7cA_	Alignment	not modelled	10.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase c; **PDBTitle:** crystal structure of pepw from lactobacillus rhamnosis hn001 (dr20)2 determined as the selenomet derivative
39	c3btpB_	Alignment	not modelled	10.1	64	**PDB header:**dna binding protein, chaperone **Chain:** B: **PDB Molecule:**protein vire1; **PDBTitle:** crystal structure of agrobacterium tumefaciens vire2 in complex with2 its chaperone vire1: a novel fold and implications for dna binding
40	c3h0jA_	Alignment	not modelled	9.5	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase; **PDBTitle:** crystal structure of the carboxyltransferase domain of2 acetyl-coenzyme a carboxylase in complex with compound 2
41	d1pixa3	Alignment	not modelled	9.4	20	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
42	c5oomv_	Alignment	not modelled	9.2	17	**PDB header:**ribosome **Chain:** V: **PDB Molecule:**39s ribosomal protein l24, mitochondrial; **PDBTitle:** structure of a native assembly intermediate of the human mitochondrial2 ribosome with unfolded interfacial rrna
43	c5gmxA_	Alignment	not modelled	9.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxylesterase; **PDBTitle:** crystal structure of a family viii carboxylesterase
44	d1wo8a1	Alignment	not modelled	9.0	25	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
45	c2pc9B_	Alignment	not modelled	9.0	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoenolpyruvate carboxykinase [atp]; **PDBTitle:** crystal structure of atp-dependent phosphoenolpyruvate carboxykinase2 from thermus thermophilus hb8
46	d2h9fa1	Alignment	not modelled	8.9	14	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PA0793-like
47	c4zqaA_	Alignment	not modelled	8.8	33	**PDB header:**transcription repressor **Chain:** A: **PDB Molecule:**sin3 histone deacetylase corepressor complex component **PDBTitle:** crystal structure of the sds3 dimerization domain
48	d1g5ma_	Alignment	not modelled	8.8	20	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
49	d2hmva1	Alignment	not modelled	8.6	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
50	d1o5za1	Alignment	not modelled	8.5	40	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**Folylpolyglutamate synthetase, C-terminal domain
51	c3ja7L_	Alignment	not modelled	8.5	20	**PDB header:**viral protein **Chain:** L: **PDB Molecule:**portal protein gp20; **PDBTitle:** cryo-em structure of the bacteriophage t4 portal protein assembly at2 near-atomic resolution
52	d1cpqa_	Alignment	not modelled	8.0	50	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
53	d1e85a_	Alignment	not modelled	7.9	50	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
54	c5tgfB_	Alignment	not modelled	7.9	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of putative beta-lactamase from bacteroides dorei2 dsm 17855
						PDB header:ligase **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln)

55	c2g5iB_	Alignment	not modelled	7.8	38	amidotransferase **PDBTitle:** structure of trna-dependent amidotransferase gatcab2 complexed with adp-alf4
56	d1x4ka2	Alignment	not modelled	7.8	40	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
57	c3fy6A_	Alignment	not modelled	7.7	40	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**integron cassette protein; **PDBTitle:** structure from the mobile metagenome of v. cholerae. integron cassette2 protein vch_cass3
58	c3kfuF_	Alignment	not modelled	7.6	38	**PDB header:**ligase/rna **Chain:** F: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; **PDBTitle:** crystal structure of the transamidosome
59	c5yirG_	Alignment	not modelled	7.5	39	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**ankyrin-2; **PDBTitle:** crystal structure of ankb lir/gabarap complex
60	d1s05a_	Alignment	not modelled	7.5	67	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
61	c5yirH_	Alignment	not modelled	7.4	47	**PDB header:**protein binding **Chain:** H: **PDB Molecule:**ankyrin-2; **PDBTitle:** crystal structure of ankb lir/gabarap complex
62	d2f2ab2	Alignment	not modelled	7.3	38	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**GatB/GatE catalytic domain-like
63	c5b3iB_	Alignment	not modelled	7.3	50	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome c prime; **PDBTitle:** homo-dimeric structure of cytochrome c' from thermophilic2 hydrogenophilus thermoluteolus
64	c3ip4B_	Alignment	not modelled	7.3	38	**PDB header:**ligase **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; **PDBTitle:** the high resolution structure of gatcab
65	c3o3vB_	Alignment	not modelled	7.0	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of clbp peptidase domain
66	c4wyoB_	Alignment	not modelled	7.0	19	**PDB header:**ligase/ligase inhibitor **Chain:** B: **PDB Molecule:**acetyl-coa carboxylase; **PDBTitle:** crystal structure of human-yeast chimera acetyl coa carboxylase ct2 domain bound to compound 1
67	d1j3ba2	Alignment	not modelled	7.0	20	**Fold:**PEP carboxykinase N-terminal domain **Superfamily:**PEP carboxykinase N-terminal domain **Family:**PEP carboxykinase N-terminal domain
68	d2j8wa1	Alignment	not modelled	7.0	50	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
69	c5evlA_	Alignment	not modelled	7.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of beta-lactamase/d-alanine carboxypeptidase from2 chromobacterium violaceum
70	c1w8xM_	Alignment	not modelled	7.0	45	**PDB header:**virus **Chain:** M: **PDB Molecule:**protein p30; **PDBTitle:** structural analysis of prd1
71	d2ccya_	Alignment	not modelled	6.9	50	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
72	d1g7oa1	Alignment	not modelled	6.9	13	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
73	c2ebyA_	Alignment	not modelled	6.9	2	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ybaq; **PDBTitle:** crystal structure of a hypothetical protein from e. coli
74	c5m86C_	Alignment	not modelled	6.8	28	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**ta1207; **PDBTitle:** crystal structure of the thermoplasma acidophilum protein ta1207
75	c6njkA_	Alignment	not modelled	6.8	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of beta-lactamase from sulfitobacter sp. ee-36
76	c5n6nC_	Alignment	not modelled	6.7	31	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**neutral trehalase; **PDBTitle:** crystal structure of the 14-3-3:neutral trehalase nth1 complex
77	c3h0mE_	Alignment	not modelled	6.7	38	**PDB header:**ligase **Chain:** E: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase **PDBTitle:** structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
78	c2qz6A_	Alignment	not modelled	6.7	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** first crystal structure of a psychrophile class c beta-2 lactamase
79	c4n0iB_	Alignment	not modelled	6.6	38	**PDB header:**ligase **Chain:** B: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit b, **PDBTitle:** crystal structure of s. cerevisiae mitochondrial gatfab in complex2 with glutamine
80	c5x90A_	Alignment	not modelled	6.6	35	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**icms; **PDBTitle:** structure of dotl(656-783)-icms-icmw-lvga derived from legionella2 pneumophila
						PDB header:ligase/rna

81	c4wj3K_	Alignment	not modelled	6.6	38	**Chain:** K: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; **PDBTitle:** crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
82	c4wj3E_	Alignment	not modelled	6.6	38	**PDB header:**ligase/rna **Chain:** E: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; **PDBTitle:** crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
83	c4wj3H_	Alignment	not modelled	6.6	38	**PDB header:**ligase/rna **Chain:** H: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; **PDBTitle:** crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
84	c4wj3B_	Alignment	not modelled	6.6	38	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; **PDBTitle:** crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
85	c3kfuI_	Alignment	not modelled	6.6	38	**PDB header:**ligase/rna **Chain:** I: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; **PDBTitle:** crystal structure of the transamidosome
86	c4gudA_	Alignment	not modelled	6.6	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**imidazole glycerol phosphate synthase subunit hish; **PDBTitle:** crystal structure of amidotransferase hish from vibrio cholerae
87	c5lcwS_	Alignment	not modelled	6.5	14	**PDB header:**cell cycle **Chain:** S: **PDB Molecule:**mitotic checkpoint serine/threonine-protein kinase bub1 **PDBTitle:** cryo-em structure of the anaphase-promoting complex/cyclosome, in2 complex with the mitotic checkpoint complex (apc/c-mcc) at 4.23 angstrom resolution
88	c3zeyT_	Alignment	not modelled	6.5	17	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**40s ribosomal protein s24; **PDBTitle:** high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
89	d1mqva_	Alignment	not modelled	6.5	33	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
90	c3al0B_	Alignment	not modelled	6.5	38	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; **PDBTitle:** crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
91	c4ulvB_	Alignment	not modelled	6.5	67	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome c, class ii; **PDBTitle:** cytochrome c prime from shewanella frigidimarina
92	c3c85A_	Alignment	not modelled	6.5	36	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative glutathione-regulated potassium-efflux system **PDBTitle:** crystal structure of trka domain of putative glutathione-regulated2 potassium-efflux kefb from vibrio parahaemolyticus
93	c3u5cY_	Alignment	not modelled	6.3	17	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**40s ribosomal protein s24-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
94	c4mupC_	Alignment	not modelled	6.3	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal structure of agrobacterium tumefaciens atu3138 (efi target2 505157), apo structure
95	d1gh6b2	Alignment	not modelled	6.3	15	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Retinoblastoma tumor suppressor domains
96	c3ij3A_	Alignment	not modelled	6.3	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** 1.8 angstrom resolution crystal structure of cytosol aminopeptidase2 from coxiella burnetii
97	c5y88R_	Alignment	not modelled	6.3	60	**PDB header:**splicing **Chain:** R: **PDB Molecule:**protein cwc16; **PDBTitle:** cryo-em structure of the intron-lariat spliceosome ready for2 disassembly from s.cerevisiae at 3.5 angstrom
98	c1sghB_	Alignment	not modelled	6.3	38	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**ezrin-radixin-moesin binding phosphoprotein 50; **PDBTitle:** moesin ferm domain bound to ebp50 c-terminal peptide
99	d2hdsa1	Alignment	not modelled	6.2	27	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase