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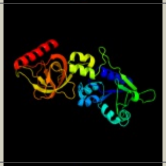
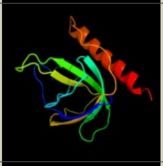
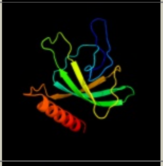
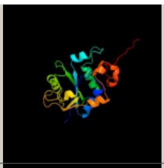
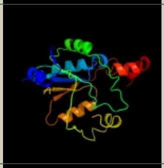
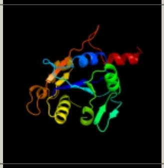
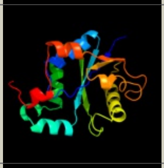
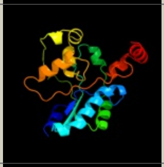
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2x0kB_	Alignment		100.0	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin biosynthesis protein ribf; **PDBTitle:** crystal structure of modular fad synthetase from2 corynebacterium ammoniagenes
2	c3op1A_	Alignment		100.0	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**macrolide-efflux protein; **PDBTitle:** crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
3	c1t6zB_	Alignment		100.0	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin kinase/fmn adenylyltransferase; **PDBTitle:** crystal structure of riboflavin bound tm379
4	d1nb9a_	Alignment		100.0	27	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin kinase-like **Family:**ATP-dependent riboflavin kinase-like
5	d1n08a_	Alignment		100.0	30	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin kinase-like **Family:**ATP-dependent riboflavin kinase-like
6	c3bnwA_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin kinase, putative; **PDBTitle:** crystal structure of riboflavin kinase from trypanosoma brucei
7	d1mrza1	Alignment		100.0	43	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin kinase-like **Family:**ATP-dependent riboflavin kinase-like
8	d1mrza2	Alignment		100.0	27	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
9	c3guzB_	Alignment		99.9	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** structural and substrate-binding studies of pantothenate2 synthenate (ps)provide insights into homotropic inhibition3 by pantoate in ps's
10	c3glvB_	Alignment		99.8	19	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**lipopolysaccharide core biosynthesis protein; **PDBTitle:** crystal structure of the lipopolysaccharide core biosynthesis protein2 from thermoplasma volcanium gss1
11	d1coza_	Alignment		99.7	20	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Cytidylyltransferase

12	c1lw7A_	Alignment		99.7	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulator nadr; **PDBTitle:** nadr protein from haemophilus influenzae
13	c3uk2B_	Alignment		99.7	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** the structure of pantothenate synthetase from burkholderia2 thailandensis
14	c2ejcA_	Alignment		99.6	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantoate--beta-alanine ligase; **PDBTitle:** crystal structure of pantoate--beta-alanine ligase (panc)2 from thermotoga maritima
15	d1v8fa_	Alignment		99.6	23	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
16	d1ihoa_	Alignment		99.6	24	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
17	c3h05A_	Alignment		99.6	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein vpa0413; **PDBTitle:** the crystal structure of a putative nicotinate-nucleotide2 adenylyltransferase from vibrio parahaemolyticus
18	d1lw7a1	Alignment		99.6	10	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
19	c3n8hA_	Alignment		99.6	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantoate-beta-alanine ligase from francisella2 tularensis
20	c3e27B_	Alignment		99.5	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nicotinate (nicotinamide) nucleotide **PDBTitle:** nicotinic acid mononucleotide (namn) adenylyltransferase2 from bacillus anthracis: product complex
21	c3elbA_	Alignment	not modelled	99.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ethanolamine-phosphate cytidylyltransferase; **PDBTitle:** human ctp: phosphoethanolamine cytidylyltransferase in complex with2 cmp
22	c3ag5A_	Alignment	not modelled	99.5	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantothenate synthetase from staphylococcus2 aureus
23	c2h29A_	Alignment	not modelled	99.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable nicotinate-nucleotide **PDBTitle:** crystal structure of nicotinic acid mononucleotide2 adenylyltransferase from staphylococcus aureus: product3 bound form 1
24	c3innB_	Alignment	not modelled	99.5	25	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantoate-beta-alanine-ligase in complex2 with atp at low occupancy at 2.1 a resolution
25	c2b7lD_	Alignment	not modelled	99.5	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glycerol-3-phosphate cytidylyltransferase; **PDBTitle:** crystal structure of ctp:glycerol-3-phosphate2 cytidylyltransferase from staphylococcus aureus
26	c3nv7A_	Alignment	not modelled	99.5	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphopantetheine adenylyltransferase; **PDBTitle:** crystal structure of h.pylori phosphopantetheine adenylyltransferase2 mutant i4v/n76y
27	c3mxtA_	Alignment	not modelled	99.4	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantoate-beta-alanine ligase from campylobacter2 jejuni
						Fold: Adenine nucleotide alpha hydrolase-like

28	d1f9aa_	Alignment	not modelled	99.4	16	**Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
29	d1qjca_	Alignment	not modelled	99.4	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
30	d2a84a1	Alignment	not modelled	99.4	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
31	d1kr2a_	Alignment	not modelled	99.4	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
32	d1nuua_	Alignment	not modelled	99.4	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
33	d1tfua_	Alignment	not modelled	99.3	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
34	d1o6ba_	Alignment	not modelled	99.3	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
35	d1ej2a_	Alignment	not modelled	99.3	23	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
36	c3ikzA_	Alignment	not modelled	99.2	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphopantetheine adenylyltransferase; **PDBTitle:** crystal structure of phosphopantetheine adenylyltransferase from2 burkholderia pseudomallei
37	c3hl4B_	Alignment	not modelled	99.2	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**choline-phosphate cytidylyltransferase a; **PDBTitle:** crystal structure of a mammalian ctp:phosphocholine2 cytidylyltransferase with cdp-choline
38	d1vlha_	Alignment	not modelled	99.1	20	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
39	c3nd5D_	Alignment	not modelled	98.9	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**phosphopantetheine adenylyltransferase; **PDBTitle:** crystal structure of phosphopantetheine adenylyltransferase (ppat)2 from enterococcus faecalis
40	d1od6a_	Alignment	not modelled	98.9	22	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
41	c2r5wA_	Alignment	not modelled	98.9	14	**PDB header:**hydrolase, transferase **Chain:** A: **PDB Molecule:**nicotinamide-nucleotide adenylyltransferase; **PDBTitle:** crystal structure of a bifunctional nmn2 adenylyltransferase/adp ribose pyrophosphatase from3 francisella tularensis
42	c2qjoB_	Alignment	not modelled	98.8	16	**PDB header:**transferase, hydrolase **Chain:** B: **PDB Molecule:**bifunctional nmn adenylyltransferase/nudix hydrolase; **PDBTitle:** crystal structure of a bifunctional nmn adenylyltransferase/adp ribose2 pyrophosphatase (nadm) complexed with adprp and nad from3 synechocystis sp.
43	c1yunB_	Alignment	not modelled	98.8	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable nicotinate-nucleotide **PDBTitle:** crystal structure of nicotinic acid mononucleotide2 adenylyltransferase from pseudomonas aeruginosa
44	c3f3mA_	Alignment	not modelled	98.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphopantetheine adenylyltransferase; **PDBTitle:** six crystal structures of two phosphopantetheine2 adenylyltransferases reveal an alternative ligand binding3 mode and an associated structural change
45	d1kama_	Alignment	not modelled	98.7	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
46	d1k4ma_	Alignment	not modelled	98.6	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
47	c3gmiA_	Alignment	not modelled	98.6	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0348 protein mj0951; **PDBTitle:** crystal structure of a protein of unknown function from2 methanocaldococcus jannaschii
48	c3do8B_	Alignment	not modelled	98.6	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphopantetheine adenylyltransferase; **PDBTitle:** the crystal structure of the protein with unknown function2 from archaeoglobus fulgidus
49	d1jhda2	Alignment	not modelled	97.9	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**ATP sulfurylase catalytic domain
50	c2qjfB_	Alignment	not modelled	97.4	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional 3'-phosphoadenosine 5'- **PDBTitle:** crystal structure of atp-sulfurylase domain of human paps2 synthetase 1
51	c1xnjB_	Alignment	not modelled	97.3	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional 3'-phosphoadenosine 5'-phosphosulfate **PDBTitle:** aps complex of human paps synthetase 1
52	d1x6va2	Alignment	not modelled	97.3	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**ATP sulfurylase catalytic domain
53	d1g8fa2	Alignment	not modelled	96.7	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase

						Family:ATP sulfurylase catalytic domain
54	c1r6xA_	Alignment	not modelled	96.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp:sulfate adenylyltransferase; **PDBTitle:** the crystal structure of a truncated form of yeast atp2 sulfurylase, lacking the c-terminal aps kinase-like domain,3 in complex with sulfate
55	c1jhdA_	Alignment	not modelled	96.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfate adenylyltransferase; **PDBTitle:** crystal structure of bacterial atp sulfurylase from the2 riftia pachyptila symbiont
56	d1v47a2	Alignment	not modelled	96.3	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**ATP sulfurylase catalytic domain
57	d1m8pa2	Alignment	not modelled	96.1	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**ATP sulfurylase catalytic domain
58	c1g8gB_	Alignment	not modelled	96.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfate adenylyltransferase; **PDBTitle:** atp sulfurylase from s. cerevisiae: the binary product complex with2 aps
59	c1m8pB_	Alignment	not modelled	95.5	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfate adenylyltransferase; **PDBTitle:** crystal structure of p. chrysogenum atp sulfurylase in the t-state
60	c3cr8C_	Alignment	not modelled	94.5	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sulfate adenylyltranferase, adenylylsulfate **PDBTitle:** hexameric aps kinase from thiobacillus denitrificans
61	c2gksB_	Alignment	not modelled	94.4	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional sat/aps kinase; **PDBTitle:** crystal structure of the bi-functional atp sulfurylase-aps kinase from2 aquifex aeolicus, a chemolithotrophic thermophile
62	c1v47B_	Alignment	not modelled	92.1	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**atp sulfurylase; **PDBTitle:** crystal structure of atp sulfurylase from thermus2 thermophillus hb8 in complex with aps
63	c3ih5A_	Alignment	not modelled	79.9	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**electron transfer flavoprotein alpha-subunit; **PDBTitle:** crystal structure of electron transfer flavoprotein alpha-2 subunit from bacteroides thetaiotaomicron
64	c1dkrB_	Alignment	not modelled	68.8	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase; **PDBTitle:** crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
65	d2g2ca1	Alignment	not modelled	64.2	22	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
66	c3bdkB_	Alignment	not modelled	60.2	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-mannonate dehydratase; **PDBTitle:** crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
67	c3lx4B_	Alignment	not modelled	57.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**fe-hydrogenase; **PDBTitle:** stepwise [fefe]-hydrogenase h-cluster assembly revealed in the2 structure of hyda(deltaefg)
68	c3dahB_	Alignment	not modelled	55.9	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
69	d1jvna1	Alignment	not modelled	55.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
70	d2nqra3	Alignment	not modelled	53.9	15	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
71	c3rfqC_	Alignment	not modelled	53.3	22	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**pterin-4-alpha-carbinolamine dehydratase moab2; **PDBTitle:** crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
72	c2is8A_	Alignment	not modelled	50.2	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis enzyme, moab; **PDBTitle:** crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus theromophilus hb8
73	c1cvrA_	Alignment	not modelled	50.0	15	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**gingipain r; **PDBTitle:** crystal structure of the arg specific cysteine proteinase gingipain r2 (rgpb)
74	d2h85a2	Alignment	not modelled	49.5	15	**Fold:**EndoU-like **Superfamily:**EndoU-like **Family:**Nsp15 C-terminal domain-like
75	c3jxeB_	Alignment	not modelled	46.2	10	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of pyrococcus horikoshii tryptophanyl-trna2 synthetase in complex with trpamp
76	c2ip1A_	Alignment	not modelled	46.1	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure analysis of s. cerevisiae tryptophanyl trna2 synthetase
77	c3eb2A_	Alignment	not modelled	44.8	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
						PDB header:structural genomics, unknown function

78	c3kbqA_	Alignment	not modelled	44.4	15	**Chain:** A: **PDB Molecule:**protein ta0487; **PDBTitle:** the crystal structure of the protein cina with unknown function from2 thermoplasma acidophilum
79	c1uz5A_	Alignment	not modelled	42.6	17	**PDB header:**molybdopterin biosynthesis **Chain:** A: **PDB Molecule:**402aa long hypothetical molybdopterin **PDBTitle:** the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikosii
80	c3focB_	Alignment	not modelled	41.6	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from giardia lamblia
81	c2fu3A_	Alignment	not modelled	40.9	21	**PDB header:**biosynthetic protein/structural protein **Chain:** A: **PDB Molecule:**gephyrin; **PDBTitle:** crystal structure of gephyrin e-domain
82	d2ozka2	Alignment	not modelled	40.5	23	**Fold:**EndoU-like **Superfamily:**EndoU-like **Family:**Nsp15 C-terminal domain-like
83	c3hv0A_	Alignment	not modelled	40.2	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from cryptosporidium parvum
84	d2choa2	Alignment	not modelled	40.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
85	c1jvnB_	Alignment	not modelled	39.6	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional histidine biosynthesis protein hishf; **PDBTitle:** crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
86	d1xxxa1	Alignment	not modelled	39.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
87	d1np7a2	Alignment	not modelled	39.0	11	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
88	c2hqxB_	Alignment	not modelled	38.4	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**p100 co-activator tudor domain; **PDBTitle:** crystal structure of human p100 tudor domain conserved2 region
89	d2hqxa1	Alignment	not modelled	38.4	11	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
90	c1gcyA_	Alignment	not modelled	37.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucan 1,4-alpha-maltotetrahydrolase; **PDBTitle:** high resolution crystal structure of maltotetraose-forming2 exo-amylase
91	c2r8wB_	Alignment	not modelled	37.4	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**agr_c_1641p; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
92	d1y5ea1	Alignment	not modelled	36.8	21	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
93	d1xi8a3	Alignment	not modelled	36.7	14	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
94	d1mkza_	Alignment	not modelled	35.0	19	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
95	c2zskA_	Alignment	not modelled	34.8	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**226aa long hypothetical aspartate racemase; **PDBTitle:** crystal structure of ph1733, an aspartate racemase2 homologue, from pyrococcus horikoshii ot3
96	d2gtia2	Alignment	not modelled	34.7	21	**Fold:**EndoU-like **Superfamily:**EndoU-like **Family:**Nsp15 C-terminal domain-like
97	c2g4rB_	Alignment	not modelled	34.5	13	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**molybdopterin biosynthesis mog protein; **PDBTitle:** anomalous substructure of moga
98	d1o5ka_	Alignment	not modelled	34.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
99	c2eqkA_	Alignment	not modelled	34.0	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tudor domain-containing protein 4; **PDBTitle:** solution structure of the tudor domain of tudor domain-2 containing protein 4
100	c2ya0A_	Alignment	not modelled	33.6	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alkaline amylopullulanase; **PDBTitle:** catalytic module of the multi-modular glycogen-degrading2 pneumococcal virulence factor spua
101	c2xrzA_	Alignment	not modelled	33.6	17	**PDB header:**lyase/dna **Chain:** A: **PDB Molecule:**deoxyribodipyrimidine photolyase; **PDBTitle:** x-ray structure of archaeal class ii cpd photolyase from2 methanosarcina mazei in complex with intact cpd-lesion
102	d1uz5a3	Alignment	not modelled	33.3	13	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
103	d1owla2	Alignment	not modelled	33.1	15	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
						PDB header:ligase

104	c2el7A_	Alignment	not modelled	32.3	15	**Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from thermus2 thermophilus
105	d3clsd1	Alignment	not modelled	31.9	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
106	c2rfgB_	Alignment	not modelled	31.6	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
107	c2qlcC_	Alignment	not modelled	31.4	12	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**dna repair protein radc homolog; **PDBTitle:** the crystal structure of dna repair protein radc from chlorobium2 tepidum tls
108	d1hf2a2	Alignment	not modelled	31.3	20	**Fold:**Cell-division inhibitor MinC, N-terminal domain **Superfamily:**Cell-division inhibitor MinC, N-terminal domain **Family:**Cell-division inhibitor MinC, N-terminal domain
109	c2nqqA_	Alignment	not modelled	31.3	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis protein moea; **PDBTitle:** moea r137q
110	d1lwha2	Alignment	not modelled	31.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
111	d1wu2a3	Alignment	not modelled	31.2	16	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
112	d2f7wa1	Alignment	not modelled	30.4	15	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
113	c3i05B_	Alignment	not modelled	30.1	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from trypanosoma brucei
114	c1ehaA_	Alignment	not modelled	29.7	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyltrehalose trehalohydrolase; **PDBTitle:** crystal structure of glycosyltrehalose trehalohydrolase2 from sulfolobus solfataricus
115	d1r6ta2	Alignment	not modelled	29.6	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
116	c3cvyA_	Alignment	not modelled	29.6	12	**PDB header:**lyase/dna **Chain:** A: **PDB Molecule:**re11660p; **PDBTitle:** drosophila melanogaster (6-4) photolyase bound to repaired2 ds dna
117	c1wu2B_	Alignment	not modelled	29.5	15	**PDB header:**structural genomics,biosynthetic protein **Chain:** B: **PDB Molecule:**molybdopterin biosynthesis moea protein; **PDBTitle:** crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikoshii ot3
118	c3zt5D_	Alignment	not modelled	29.5	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative glucanohydrolase pep1a; **PDBTitle:** glge isoform 1 from streptomyces coelicolor with maltose2 bound
119	c2gtiA_	Alignment	not modelled	29.4	16	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**replicase polyprotein 1ab; **PDBTitle:** mutation of mhv coronavirus non-structural protein nsp15 (f307l)
120	c2by0A_	Alignment	not modelled	29.2	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**maltooligosyltrehalose trehalohydrolase; **PDBTitle:** is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection