



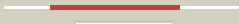

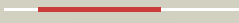
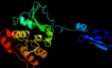













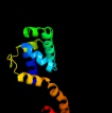











Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2au3A_	 Alignment		100.0	34	PDB header: transferase Chain: A: PDB Molecule: dna primase; PDBTitle: crystal structure of the aquifex aeolicus primase (zinc binding and2 rna polymerase domains)
2	d1dd9a_	 Alignment		100.0	99	Fold: DNA primase core Superfamily: DNA primase core Family: DNA primase DnaG catalytic core
3	c1dd9A_	 Alignment		100.0	99	PDB header: transferase Chain: A: PDB Molecule: dna primase; PDBTitle: structure of the dnag catalytic core
4	c1nuia_	 Alignment		100.0	20	PDB header: replication Chain: A: PDB Molecule: dna primase/helicase; PDBTitle: crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
5	d1d0qa_	 Alignment		100.0	48	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: DNA primase zinc finger
6	c1q57G_	 Alignment		99.9	23	PDB header: transferase Chain: G: PDB Molecule: dna primase/helicase; PDBTitle: the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
7	d1nuia1	 Alignment		99.9	20	Fold: DNA primase core Superfamily: DNA primase core Family: Primase fragment of primase-helicase protein
8	d1t6t1_	 Alignment		99.7	23	Fold: Toprim domain Superfamily: Toprim domain Family: Toprim domain
9	d1t3wa_	 Alignment		99.2	98	Fold: DNA primase DnaG, C-terminal domain Superfamily: DNA primase DnaG, C-terminal domain Family: DNA primase DnaG, C-terminal domain
10	d2fcja1	 Alignment		98.8	20	Fold: Toprim domain Superfamily: Toprim domain Family: Toprim domain
11	c2r6cG_	 Alignment		98.2	14	PDB header: replication Chain: G: PDB Molecule: dnag primase, helicase binding domain; PDBTitle: crystal form bh2

12	c2r5uD	Alignment		96.4	8	PDB header: hydrolase Chain: D: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of the n-terminal domain of dnab helicase from2 mycobacterium tuberculosis
13	c2q6tB	Alignment		96.2	7	PDB header: hydrolase Chain: B: PDB Molecule: dnab replication fork helicase; PDBTitle: crystal structure of the thermus aquaticus dnab monomer
14	d1jwea	Alignment		95.3	11	Fold: N-terminal domain of DnaB helicase Superfamily: N-terminal domain of DnaB helicase Family: N-terminal domain of DnaB helicase
15	c1vddC	Alignment		93.8	19	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
16	d1vdda	Alignment		93.4	19	Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR
17	c3gxvA	Alignment		92.8	8	PDB header: hydrolase/replication Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: three-dimensional structure of n-terminal domain of dnab2 helicase from helicobacter pylori and its interactions with3 primase
18	d1b79a	Alignment		92.6	11	Fold: N-terminal domain of DnaB helicase Superfamily: N-terminal domain of DnaB helicase Family: N-terminal domain of DnaB helicase
19	c2e9hA	Alignment		91.7	29	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: solution structure of the eif-5_eif-2b domain from human2 eukaryotic translation initiation factor 5
20	c3bgwD	Alignment		90.5	8	PDB header: replication Chain: D: PDB Molecule: dnab-like replicative helicase; PDBTitle: the structure of a dnab-like replicative helicase and its interactions2 with primase
21	c1neeA	Alignment	not modelled	86.8	25	PDB header: translation Chain: A: PDB Molecule: probable translation initiation factor 2 beta PDBTitle: structure of archaeal translation factor aif2beta from2 methanobacterium thermoautrophicum
22	c2vyeA	Alignment	not modelled	86.7	10	PDB header: hydrolase Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of the dnac-ssdna complex
23	c2dcuB	Alignment	not modelled	75.6	25	PDB header: translation Chain: B: PDB Molecule: translation initiation factor 2 beta subunit; PDBTitle: crystal structure of translation initiation factor aif2betagamma2 heterodimer with gdp
24	c4a17Y	Alignment	not modelled	73.4	32	PDB header: ribosome Chain: Y: PDB Molecule: rpl37a; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
25	c2pfsA	Alignment	not modelled	71.4	6	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of universal stress protein from nitrosomonas2 europaea
26	c3nmeA	Alignment	not modelled	71.3	17	PDB header: hydrolase Chain: A: PDB Molecule: sex4 glucan phosphatase; PDBTitle: structure of a plant phosphatase
27	c2imgA	Alignment	not modelled	68.4	23	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 23; PDBTitle: crystal structure of dual specificity protein phosphatase2 23 from homo sapiens in complex with ligand malate ion
28	c3cc4Z	Alignment	not modelled	67.6	22	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l37ae;

28	c3cc4z_	Alignment	not modelled	67.6	42	PDBTitle: co-crystal structure of anisomycin bound to the 50s ribosomal subunit
29	d1v3aa_	Alignment	not modelled	67.5	13	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
30	c2oudA_	Alignment	not modelled	67.3	17	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of the catalytic domain of human mkp5
31	c3emuA_	Alignment	not modelled	66.6	23	PDB header: hydrolase Chain: A: PDB Molecule: leucine rich repeat and phosphatase domain PDBTitle: crystal structure of a leucine rich repeat and phosphatase2 domain containing protein from entamoeba histolytica
32	c3k7aM_	Alignment	not modelled	63.8	23	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: crystal structure of an rna polymerase ii-tfiib complex
33	c2qa4Z_	Alignment	not modelled	63.6	21	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: a more complete structure of the the 17/112 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
34	c1yshD_	Alignment	not modelled	63.6	36	PDB header: structural protein/rna Chain: D: PDB Molecule: ribosomal protein l37a; PDBTitle: localization and dynamic behavior of ribosomal protein l30e
35	d1nuia2	Alignment	not modelled	61.4	14	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: DNA primase zinc finger
36	c2esbA_	Alignment	not modelled	61.4	17	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 18; PDBTitle: crystal structure of human dusp18
37	c1oheA_	Alignment	not modelled	61.3	29	PDB header: hydrolase Chain: A: PDB Molecule: cdc14b2 phosphatase; PDBTitle: structure of cdc14b phosphatase with a peptide ligand
38	d1ffkw_	Alignment	not modelled	60.9	25	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
39	c3rggA_	Alignment	not modelled	59.5	17	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine phosphatase mitochondrial 1; PDBTitle: crystal structure of ptptm1 in complex with pi(5)p
40	d1ohea2	Alignment	not modelled	59.2	15	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
41	d1vqoz1	Alignment	not modelled	59.0	21	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
42	d1wiia_	Alignment	not modelled	58.5	29	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Putative zinc binding domain
43	c2zkrz_	Alignment	not modelled	57.8	21	PDB header: ribosomal protein/rna Chain: Z: PDB Molecule: e site t-rna; PDBTitle: structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
44	d1jj2y_	Alignment	not modelled	56.5	25	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
45	c2r0bA_	Alignment	not modelled	56.1	11	PDB header: hydrolase Chain: A: PDB Molecule: serine/threonine/tyrosine-interacting protein; PDBTitle: crystal structure of human tyrosine phosphatase-like2 serine/threonine/tyrosine-interacting protein
46	c1yn9B_	Alignment	not modelled	55.3	20	PDB header: hydrolase Chain: B: PDB Molecule: polynucleotide 5'-phosphatase; PDBTitle: crystal structure of baculovirus rna 5'-phosphatase2 complexed with phosphate
47	c2y96A_	Alignment	not modelled	54.6	20	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase dupd1; PDBTitle: structure of human dual-specificity phosphatase 27
48	c2gwoC_	Alignment	not modelled	54.0	26	PDB header: hydrolase Chain: C: PDB Molecule: dual specificity protein phosphatase 13; PDBTitle: crystal structure of tmdp
49	c3jyw9_	Alignment	not modelled	53.4	36	PDB header: ribosome Chain: 9: PDB Molecule: 60s ribosomal protein l43; PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
50	c3rz2B_	Alignment	not modelled	51.7	16	PDB header: hydrolase Chain: B: PDB Molecule: protein tyrosine phosphatase type iva 1; PDBTitle: crystal of pri-1 complexed with peptide
51	d1vhra_	Alignment	not modelled	50.6	20	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
52	c2g6zB_	Alignment	not modelled	50.2	14	PDB header: hydrolase Chain: B: PDB Molecule: dual specificity protein phosphatase 5; PDBTitle: crystal structure of human dusp5
53	c2i50A_	Alignment	not modelled	49.7	14	PDB header: hydrolase Chain: A: PDB Molecule: ubiquitin carboxyl-terminal hydrolase 16; PDBTitle: solution structure of ubp-m znf-ubp domain
						Fold: (Phosphotyrosine protein) phosphatases II

54	d1i9sa_	Alignment	not modelled	49.7	22	Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
55	c2c46B_	Alignment	not modelled	49.5	22	PDB header: transferase Chain: B: PDB Molecule: mrna capping enzyme; PDBTitle: crystal structure of the human rna guanylyltransferase and2 5'-phosphatase
56	c3cw2M_	Alignment	not modelled	49.5	22	PDB header: translation Chain: M: PDB Molecule: translation initiation factor 2 subunit beta; PDBTitle: crystal structure of the intact archaeal translation2 initiation factor 2 from sulfolobus solfataricus .
57	d1mkpa_	Alignment	not modelled	49.0	14	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
58	cls1i9_	Alignment	not modelled	48.5	29	PDB header: ribosome Chain: 9: PDB Molecule: 60s ribosomal protein l43; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
59	c3fldA_	Alignment	not modelled	47.7	23	PDB header: hydrolase Chain: A: PDB Molecule: protein trai; PDBTitle: crystal structure of the trai c-terminal domain
60	c3s4oB_	Alignment	not modelled	46.2	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein tyrosine phosphatase-like protein; PDBTitle: protein tyrosine phosphatase (putative) from leishmania major
61	d2z3va1	Alignment	not modelled	46.2	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
62	c2k8dA_	Alignment	not modelled	45.6	24	PDB header: oxidoreductase Chain: A: PDB Molecule: peptide methionine sulfoxide reductase msrb; PDBTitle: solution structure of a zinc-binding methionine sulfoxide reductase
63	d1rxda_	Alignment	not modelled	45.3	15	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
64	c3e90B_	Alignment	not modelled	45.2	40	PDB header: hydrolase Chain: B: PDB Molecule: ns3 protease; PDBTitle: west nile vi rus ns2b-ns3protease in complexed with2 inhibitor naph-kkr-h
65	c2e0tA_	Alignment	not modelled	44.9	26	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase 26; PDBTitle: crystal structure of catalytic domain of dual specificity phosphatase2 26, ms0830 from homo sapiens
66	d2ijob1	Alignment	not modelled	44.9	40	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
67	d1xria_	Alignment	not modelled	44.9	23	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
68	c1yz4A_	Alignment	not modelled	44.8	20	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase-like 15 isoform a; PDBTitle: crystal structure of dusp15
69	d1muma_	Alignment	not modelled	44.8	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
70	d1befa_	Alignment	not modelled	44.3	36	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
71	c2i6oA_	Alignment	not modelled	44.3	24	PDB header: hydrolase Chain: A: PDB Molecule: sulfolobus solfataricus protein tyrosine PDBTitle: crystal structure of the complex of the archaeal sulfolobus2 ptp-fold phosphatase with phosphopeptides n-g(p)y-k-n
72	c2nt2C_	Alignment	not modelled	42.6	11	PDB header: hydrolase Chain: C: PDB Molecule: protein phosphatase slingshot homolog 2; PDBTitle: crystal structure of slingshot phosphatase 2
73	c3hcjB_	Alignment	not modelled	41.9	22	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase; PDBTitle: structure of msrb from xanthomonas campestris (oxidized2 form)
74	d1w0ba_	Alignment	not modelled	41.9	20	Fold: Spectrin repeat-like Superfamily: Alpha-hemoglobin stabilizing protein AHSP Family: Alpha-hemoglobin stabilizing protein AHSP
75	d2fp7b1	Alignment	not modelled	41.9	40	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
76	d1z8ua1	Alignment	not modelled	40.5	20	Fold: Spectrin repeat-like Superfamily: Alpha-hemoglobin stabilizing protein AHSP Family: Alpha-hemoglobin stabilizing protein AHSP
77	d1jeva2	Alignment	not modelled	40.2	22	Fold: vWA-like Superfamily: vWA-like Family: Ku70 subunit N-terminal domain
78	d1pnoa_	Alignment	not modelled	39.5	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
						PDB header: transferase Chain: A: PDB Molecule: vaccinia virus capping enzyme d1

79	c2vdwA_	Alignment	not modelled	39.0	9	subunit; PDBTitle: guanosine n7 methyl-transferase sub-complex (d1-d12) of the2 vaccinia virus mrna capping enzyme
80	d1d4oa_	Alignment	not modelled	38.5	18	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
81	c2kxoA_	Alignment	not modelled	37.4	7	PDB header: cell cycle Chain: A: PDB Molecule: cell division topological specificity factor; PDBTitle: solution nmr structure of the cell division regulator mine protein2 from neisseria gonorrhoeae
82	c2pdtD_	Alignment	not modelled	37.3	25	PDB header: circadian clock protein Chain: D: PDB Molecule: vidv pas protein vvd; PDBTitle: 2.3 angstrom structure of phosphodiesterase treated vivid
83	c3lyeA_	Alignment	not modelled	36.0	19	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
84	d1twfj_	Alignment	not modelled	36.0	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: RNA polymerase subunit RPB10 Family: RNA polymerase subunit RPB10
85	d1dl6a_	Alignment	not modelled	36.0	25	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
86	c1pt9B_	Alignment	not modelled	35.7	18	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p) transhydrogenase, mitochondrial; PDBTitle: crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
87	c1zzwA_	Alignment	not modelled	35.4	17	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of catalytic domain of human map kinase2 phosphatase 5
88	d2fomb1	Alignment	not modelled	35.4	33	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
89	c2p3qA_	Alignment	not modelled	35.3	17	PDB header: viral protein,transferase Chain: A: PDB Molecule: type ii methyltransferase; PDBTitle: crystal structure of dengue methyltransferase in complex with gpppg2 and s-adenosyl-l-homocysteine
90	d1ywfa1	Alignment	not modelled	34.5	22	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Mycobacterial PtpB-like
91	d1g26a_	Alignment	not modelled	34.3	50	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Granulin repeat Family: Granulin repeat
92	d1jmva_	Alignment	not modelled	34.0	7	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
93	d1xmx_	Alignment	not modelled	33.8	12	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hypothetical protein VC1899
94	d1ef4a_	Alignment	not modelled	33.7	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: RNA polymerase subunit RPB10 Family: RNA polymerase subunit RPB10
95	c21luA_	Alignment	not modelled	33.3	24	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine-r-sulfoxide reductase b2, mitochondrial; PDBTitle: structure-functional analysis of mammalian msrb2 protein
96	c2j17A_	Alignment	not modelled	32.4	23	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase yil113w; PDBTitle: ptyr bound form of sdp-1
97	c3e0mB_	Alignment	not modelled	32.3	14	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase msra/msrb PDBTitle: crystal structure of fusion protein of msra and msrb
98	c1ee8A_	Alignment	not modelled	32.2	21	PDB header: dna binding protein Chain: A: PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermus thermophilus hb8
99	d1pfta_	Alignment	not modelled	32.1	25	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
100	d1l1da_	Alignment	not modelled	31.5	9	Fold: Mss4-like Superfamily: Mss4-like Family: SelR domain
101	c3gn5B_	Alignment	not modelled	31.2	16	PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator mqsa (ygit/b3021); PDBTitle: structure of the e. coli protein mqsa (ygit/b3021)
102	d2dka2	Alignment	not modelled	31.2	38	Fold: Zinc hairpin stack Superfamily: Zinc hairpin stack Family: Zinc hairpin stack
103	c3ceza_	Alignment	not modelled	30.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine-r-sulfoxide reductase; PDBTitle: crystal structure of methionine-r-sulfoxide reductase from2 burkholderia pseudomallei
104	c2vbcA_	Alignment	not modelled	30.6	33	PDB header: hydrolase Chain: A: PDB Molecule: dengue 4 ns3 full-length protein; PDBTitle: crystal structure of the ns3 protease-helicase from dengue2 virus
105	d1vd4a_	Alignment	not modelled	28.9	14	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon

						Family: Transcriptional factor domain
106	c3r9jD_	Alignment	not modelled	28.8	17	PDB header: cell cycle,hydrolase/cell cycle Chain: D: PDB Molecule: cell division topological specificity factor; PDBTitle: 4.3a resolution structure of a mind-mine(i24n) protein complex
107	d2fiya1	Alignment	not modelled	28.7	19	Fold: FdhE-like Superfamily: FdhE-like Family: FdhE-like
108	c1wrmA_	Alignment	not modelled	28.7	17	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase 22; PDBTitle: crystal structure of jsp-1
109	c3idfA_	Alignment	not modelled	28.1	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: usp-like protein; PDBTitle: the crystal structure of a usp-like protein from wolinella2 succinogenes to 2.0a
110	c1drwA_	Alignment	not modelled	27.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: escherichia coli dhpr/nhdh complex
111	d1di1a_	Alignment	not modelled	27.7	28	Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Aristolochene/pentalenene synthase
112	d1xm0a1	Alignment	not modelled	27.1	11	Fold: Mss4-like Superfamily: Mss4-like Family: SelR domain
113	d1p32a_	Alignment	not modelled	27.1	17	Fold: Mitochondrial glycoprotein MAM33-like Superfamily: Mitochondrial glycoprotein MAM33-like Family: Mitochondrial glycoprotein MAM33-like
114	c3lkwA_	Alignment	not modelled	26.9	24	PDB header: viral protein,hydrolase Chain: A: PDB Molecule: fusion protein of nonstructural protein 2b and PDBTitle: crystal structure of dengue virus 1 ns2b/ns3 protease active2 site mutant
115	c2ysaA_	Alignment	not modelled	26.9	50	PDB header: metal binding protein Chain: A: PDB Molecule: retinoblastoma-binding protein 6; PDBTitle: solution structure of the zinc finger cchc domain from the2 human retinoblastoma-binding protein 6 (retinoblastoma-3 binding q protein 1, rbq-1)
116	d1yqfa1	Alignment	not modelled	26.0	33	Fold: Mitochondrial glycoprotein MAM33-like Superfamily: Mitochondrial glycoprotein MAM33-like Family: Mitochondrial glycoprotein MAM33-like
117	c2pmzN_	Alignment	not modelled	25.8	17	PDB header: translation, transferase Chain: N: PDB Molecule: dna-directed rna polymerase subunit n; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
118	d1vh4a_	Alignment	not modelled	25.7	18	Fold: Single-stranded right-handed beta-helix Superfamily: Stabilizer of iron transporter SufD Family: Stabilizer of iron transporter SufD
119	c3qv0A_	Alignment	not modelled	25.4	39	PDB header: protein binding Chain: A: PDB Molecule: mitochondrial acidic protein mam33; PDBTitle: crystal structure of saccharomyces cerevisiae mam33
120	c3f62A_	Alignment	not modelled	25.1	29	PDB header: cytokine Chain: A: PDB Molecule: interleukin 18 binding protein; PDBTitle: crystal structure of human il-18 in complex with ectromelia virus il-2 18 binding protein