























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2343c_(dnaG)_2620543_2622462
Date	Mon Aug 5 13:25:49 BST 2019
Unique Job ID	4cc3f4de998fc5ad

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2au3A_	 Alignment		100.0	31	PDB header: transferase Chain: A; PDB Molecule: dna primase; PDBTitle: crystal structure of the aquifex aeolicus primase (zinc binding and2 rna polymerase domains)
2	c5gujA_	 Alignment		100.0	30	PDB header: transferase Chain: A; PDB Molecule: dna primase; PDBTitle: crystal structure of the bacillus subtilis dnag rna polymerase domain,2 natural degradation of full length dnag
3	c5w34A_	 Alignment		100.0	99	PDB header: transferase Chain: A; PDB Molecule: dna primase; PDBTitle: crystal structure of the rna polymerase domain (rpd) of mycobacterium2 tuberculosis primase dnag in complex with double-stranded dna3 gaccggaagtgg
4	d1dd9a_	 Alignment		100.0	34	Fold: DNA primase core Superfamily: DNA primase core Family: DNA primase DnaG catalytic core
5	c1dd9A_	 Alignment		100.0	34	PDB header: transferase Chain: A; PDB Molecule: dna primase; PDBTitle: structure of the dnag catalytic core
6	c4edvA_	 Alignment		100.0	27	PDB header: transferase/transferase inhibitor Chain: A; PDB Molecule: dna primase; PDBTitle: the structure of the s. aureus dnag rna polymerase domain bound to2 pppgpp and manganese
7	c5vazB_	 Alignment		100.0	34	PDB header: transferase Chain: B; PDB Molecule: dna primase; PDBTitle: crystal structure of a dna primase domain from pseudomonas aeruginosa
8	c1nuiA_	 Alignment		100.0	24	PDB header: replication Chain: A; PDB Molecule: dna primase/helicase; PDBTitle: crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
9	d1d0qa_	 Alignment		99.9	51	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: DNA primase zinc finger
10	c1q57G_	 Alignment		99.9	27	PDB header: transferase Chain: G; PDB Molecule: dna primase/helicase; PDBTitle: the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
11	d1nuia1	 Alignment		99.8	23	Fold: DNA primase core Superfamily: DNA primase core Family: Primase fragment of primase-helicase protein

12	d1t6t1_	Alignment		99.6	14	Fold: Toprim domain Superfamily: Toprim domain Family: Toprim domain
13	c5z51A_	Alignment		99.5	98	PDB header: transferase Chain: A: PDB Molecule: dna primase; PDBTitle: helicase binding domain of primase from mycobacterium tuberculosis
14	c2r6cG_	Alignment		98.9	9	PDB header: replication Chain: G: PDB Molecule: dnag primase, helicase binding domain; PDBTitle: crystal form bh2
15	c2lznA_	Alignment		98.7	13	PDB header: transferase Chain: A: PDB Molecule: dna primase; PDBTitle: solution structure of s. aureus primase c-terminal domain
16	d2fcja1	Alignment		98.7	18	Fold: Toprim domain Superfamily: Toprim domain Family: Toprim domain
17	c2r5uD_	Alignment		97.8	11	PDB header: hydrolase Chain: D: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of the n-terminal domain of dnab helicase from2 mycobacterium tuberculosis
18	c4zc0D_	Alignment		97.6	10	PDB header: hydrolase Chain: D: PDB Molecule: replicative dna helicase; PDBTitle: structure of a dodecameric bacterial helicase
19	c4im9C_	Alignment		97.5	19	PDB header: transferase Chain: C: PDB Molecule: dna primase; PDBTitle: crystal structure of dnag primase c-terminal domain from vibrio2 cholerae
20	c6qelB_	Alignment		97.4	6	PDB header: replication Chain: B: PDB Molecule: replicative dna helicase; PDBTitle: e. coli dnabc apo complex
21	c2vyeA_	Alignment	not modelled	97.4	8	PDB header: hydrolase/dna Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of the dnac-ssdna complex
22	d1t3wa_	Alignment	not modelled	97.3	15	Fold: DNA primase DnaG, C-terminal domain Superfamily: DNA primase DnaG, C-terminal domain Family: DNA primase DnaG, C-terminal domain
23	c4zc0A_	Alignment	not modelled	97.3	7	PDB header: hydrolase Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: structure of a dodecameric bacterial helicase
24	c2q6tB_	Alignment	not modelled	97.2	11	PDB header: hydrolase Chain: B: PDB Molecule: dnab replication fork helicase; PDBTitle: crystal structure of the thermus aquaticus dnab monomer
25	c3gxvA_	Alignment	not modelled	97.1	7	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
26	c3bgwD_	Alignment	not modelled	97.1	12	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
27	d1jwea_	Alignment	not modelled	97.1	6	Fold: N-terminal domain of DnaB helicase Superfamily: N-terminal domain of DnaB helicase Family: N-terminal domain of DnaB helicase
28	d1b79a_	Alignment	not modelled	96.8	6	Fold: N-terminal domain of DnaB helicase Superfamily: N-terminal domain of DnaB helicase Family: N-terminal domain of DnaB helicase
						PDB header: replication

29	c4nmnA_	Alignment	not modelled	96.6	16	Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: aquifex aeolicus replicative helicase (dnab) complexed with adp, at2 3.3 resolution
30	c5z2vB_	Alignment	not modelled	95.9	18	PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recr from pseudomonas aeruginosa pao1
31	c5zvqA_	Alignment	not modelled	94.0	23	PDB header: recombination Chain: A: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombination mediator protein recr
32	d1vdda_	Alignment	not modelled	93.8	22	Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR
33	c3ve5D_	Alignment	not modelled	93.6	19	PDB header: recombination Chain: D: PDB Molecule: recombination protein recr; PDBTitle: structure of recombination mediator protein recr16-196 deletion mutant
34	c1vddC_	Alignment	not modelled	93.6	22	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
35	c6bbmA_	Alignment	not modelled	93.5	7	PDB header: replication Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: mechanisms of opening and closing of the bacterial replicative2 helicase: the dnab helicase and lambda p helicase loader complex
36	c2e9hA_	Alignment	not modelled	87.7	23	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
37	c1neeA_	Alignment	not modelled	82.9	23	PDB header: translation Chain: A: PDB Molecule: probable translation initiation factor 2 beta PDBTitle: structure of archaeal translation factor aif2beta from2 methanobacterium thermoautotrophicum
38	c4v1oM_	Alignment	not modelled	82.3	31	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: architecture of the rna polymerase ii-mediator core transcription2 initiation complex
39	c6o9lQ_	Alignment	not modelled	81.2	16	PDB header: transcription/dna Chain: Q: PDB Molecule: general transcription factor iie subunit 1; PDBTitle: human holo-pic in the closed state
40	d1nuia2	Alignment	not modelled	79.8	14	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: DNA primase zinc finger
41	c6qg3P_	Alignment	not modelled	77.9	24	PDB header: translation Chain: P: PDB Molecule: eukaryotic translation initiation factor 2 subunit beta; PDBTitle: structure of eif2b-eif2 (phosphorylated at ser51) complex (model b)
42	c3zf7o_	Alignment	not modelled	77.2	35	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l13a, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
43	c3nmeA_	Alignment	not modelled	76.6	21	PDB header: hydrolase Chain: A: PDB Molecule: sex4 glucan phosphatase; PDBTitle: structure of a plant phosphatase
44	c5fz5M_	Alignment	not modelled	76.5	31	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: transcription initiation complex structures elucidate dna opening (cc)
45	c3emuA_	Alignment	not modelled	74.5	20	PDB header: hydrolase Chain: A: PDB Molecule: leucine rich repeat and phosphatase domain containing PDBTitle: crystal structure of a leucine rich repeat and phosphatase domain2 containing protein from entamoeba histolytica
46	c2imgA_	Alignment	not modelled	74.3	20	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
47	c4a17Y_	Alignment	not modelled	74.0	36	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.
48	c2oudA_	Alignment	not modelled	73.9	20	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of the catalytic domain of human mkp5
49	c4b6ap_	Alignment	not modelled	73.0	29	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17-a; PDBTitle: cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
50	c3cc4Z_	Alignment	not modelled	72.9	30	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: co-crystal structure of anisomycin bound to the 50s ribosomal subunit
51	d1v3aa_	Alignment	not modelled	72.5	19	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
52	c2qa4Z_	Alignment	not modelled	71.6	29	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
53	c3k7aM_	Alignment	not modelled	71.0	31	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: crystal structure of an rna polymerase ii-tfiib complex
54	d1vd4a_	Alignment	not modelled	69.6	28	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon

						Family:Transcriptional factor domain
55	c3j39p_	Alignment	not modelled	69.5	25	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
56	c2esbA_	Alignment	not modelled	69.3	20	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 18; PDBTitle: crystal structure of human dusp18
57	d1ffkw_	Alignment	not modelled	69.3	29	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
58	c3j21i_	Alignment	not modelled	69.2	33	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein l13p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
59	c2dcuB_	Alignment	not modelled	69.1	21	PDB header: translation Chain: B: PDB Molecule: translation initiation factor 2 beta subunit; PDBTitle: crystal structure of translation initiation factor aif2betagamma2 heterodimer with gdp
60	c4jmkA_	Alignment	not modelled	69.0	23	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 8; PDBTitle: structure of dusp8
61	d1vqoz1	Alignment	not modelled	68.0	29	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
62	c3rgqA_	Alignment	not modelled	67.4	21	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine phosphatase mitochondrial 1; PDBTitle: crystal structure of ptpmt1 in complex with pi(5)p
63	c1yshD_	Alignment	not modelled	67.4	29	PDB header: structural protein/rna Chain: D: PDB Molecule: ribosomal protein l37a; PDBTitle: localization and dynamic behavior of ribosomal protein l30e
64	c2zkrz_	Alignment	not modelled	67.3	29	PDB header: ribosomal protein/rna Chain: Z: PDB Molecule: e site t-rna; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
65	c3izrm_	Alignment	not modelled	67.1	29	PDB header: ribosome Chain: M: PDB Molecule: 60s ribosomal protein l23 (l14p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
66	c5iy9M_	Alignment	not modelled	67.1	29	PDB header: transcription, transferase/dna/rna Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: human holo-pic in the initial transcribing state (no iis)
67	c2r0bA_	Alignment	not modelled	66.7	20	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
68	d1jj2y_	Alignment	not modelled	66.6	33	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
69	d1ohea2	Alignment	not modelled	66.5	21	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
70	d1w0ba_	Alignment	not modelled	66.1	16	Fold: Spectrin repeat-like Superfamily: Alpha-hemoglobin stabilizing protein AHSP Family: Alpha-hemoglobin stabilizing protein AHSP
71	c5xogM_	Alignment	not modelled	65.8	29	PDB header: transcription Chain: M: PDB Molecule: transcription elongation factor 1 homolog; PDBTitle: rna polymerase ii elongation complex bound with spt5 kow5 and elf1
72	c4qg5D_	Alignment	not modelled	65.6	8	PDB header: isomerase Chain: D: PDB Molecule: putative phosphoglucomutase; PDBTitle: crystal structure of phosphoglucomutase from leishmania major at 3.52 angstrom resolution
73	c6efnA_	Alignment	not modelled	65.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: sporulation killing factor maturation protein skfb; PDBTitle: structure of a ripp maturase, skfb
74	c6byfl_	Alignment	not modelled	64.9	19	PDB header: transferase Chain: I: PDB Molecule: tyrosine-protein phosphatase siw14; PDBTitle: crystal structure of the core catalytic domain of pp-ip phosphatase2 siw14 from s. cerevisiae in complex with citrate
75	c4kyrA_	Alignment	not modelled	64.7	17	PDB header: hydrolase, sugar binding protein Chain: A: PDB Molecule: phosphoglucan phosphatase lsf2, chloroplastic; PDBTitle: structure of a product bound plant phosphatase
76	d1z8ua1	Alignment	not modelled	64.6	16	Fold: Spectrin repeat-like Superfamily: Alpha-hemoglobin stabilizing protein AHSP Family: Alpha-hemoglobin stabilizing protein AHSP
77	c4r30C_	Alignment	not modelled	64.1	19	PDB header: hydrolase Chain: C: PDB Molecule: laforin; PDBTitle: structure of human laforin dual specificity phosphatase domain
78	c5oqjW_	Alignment	not modelled	63.9	21	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
79	c2g6zB_	Alignment	not modelled	63.7	20	PDB header: hydrolase Chain: B: PDB Molecule: dual specificity protein phosphatase 5; PDBTitle: crystal structure of human dusp5
						PDB header: hydrolase

80	c3s4eA	Alignment	not modelled	63.3	18	Chain: A: PDB Molecule: dual specificity protein phosphatase 19; PDBTitle: crystal structure of a novel mitogen-activated protein kinase2 phosphatase, skrp1
81	c2gwoC	Alignment	not modelled	63.3	29	PDB header: hydrolase Chain: C: PDB Molecule: dual specificity protein phosphatase 13; PDBTitle: crystal structure of tmdp
82	c2y96A	Alignment	not modelled	63.0	20	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase dupd1; PDBTitle: structure of human dual-specificity phosphatase 27
83	c6apxA	Alignment	not modelled	62.8	23	PDB header: hydrolase Chain: A: PDB Molecule: maltose-binding periplasmic protein,dual specificity PDBTitle: crystal structure of human dual specificity phosphatase 1 catalytic2 domain (c258s) as a maltose binding protein fusion in complex with3 the monobody ysx1
84	c3k1fM	Alignment	not modelled	62.3	31	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: crystal structure of rna polymerase ii in complex with tfiib
85	c6gymW	Alignment	not modelled	61.6	21	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha, PDBTitle: structure of a yeast closed complex with distorted dna (ccd1st)
86	d1vhra	Alignment	not modelled	61.4	17	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
87	d1wiia	Alignment	not modelled	61.3	37	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Putative zinc binding domain
88	c5oqmW	Alignment	not modelled	61.2	21	PDB header: transcription Chain: W: PDB Molecule: transcription factor tfiie subunit; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
89	c3s4oB	Alignment	not modelled	60.9	27	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein tyrosine phosphatase-like protein; PDBTitle: protein tyrosine phosphatase (putative) from leishmania major
90	c4ki9A	Alignment	not modelled	60.6	26	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 12; PDBTitle: crystal structure of the catalytic domain of human dusp12 at 2.0 a2 resolution
91	d1mkpa	Alignment	not modelled	60.2	14	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
92	c3cw2M	Alignment	not modelled	60.0	15	PDB header: translation Chain: M: PDB Molecule: translation initiation factor 2 subunit beta; PDBTitle: crystal structure of the intact archaeal translation initiation factor2 2 from sulfolobus solfataricus .
93	c6i28A	Alignment	not modelled	60.0	15	PDB header: viral protein Chain: A: PDB Molecule: orf98 ptp-2; PDBTitle: crystal structure of cydia pomonella ptp-2 phosphatase
94	c1yn9B	Alignment	not modelled	59.6	21	PDB header: hydrolase Chain: B: PDB Molecule: polynucleotide 5'-phosphatase; PDBTitle: crystal structure of baculovirus rna 5'-phosphatase2 complexed with phosphate
95	c2f7IA	Alignment	not modelled	59.4	9	PDB header: isomerase Chain: A: PDB Molecule: 455aa long hypothetical phospho-sugar mutase; PDBTitle: crystal structure of sulfolobus tokodaii2 phosphomannomutase/phosphoglucomutase
96	c1s1i9	Alignment	not modelled	58.9	30	PDB header: ribosome Chain: 9: PDB Molecule: 60s ribosomal protein l43; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
97	c3rz2B	Alignment	not modelled	58.9	22	PDB header: hydrolase Chain: B: PDB Molecule: protein tyrosine phosphatase type iva 1; PDBTitle: crystal of prl-1 complexed with peptide
98	c2nt2C	Alignment	not modelled	58.8	20	PDB header: hydrolase Chain: C: PDB Molecule: protein phosphatase slingshot homolog 2; PDBTitle: crystal structure of slingshot phosphatase 2
99	c2i6oA	Alignment	not modelled	58.0	22	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
100	d2fiya1	Alignment	not modelled	57.8	26	Fold: FdhE-like Superfamily: FdhE-like Family: FdhE-like
101	c3jyw9	Alignment	not modelled	57.7	30	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
102	c5xw4A	Alignment	not modelled	57.5	24	PDB header: cell cycle Chain: A: PDB Molecule: tyrosine-protein phosphatase cdc14; PDBTitle: crystal structure of budding yeast cdc14p (wild type) in the apo state
103	c6cnbR	Alignment	not modelled	57.2	15	PDB header: transcription/dna Chain: R: PDB Molecule: transcription factor iib 70 kda subunit,tata-box-binding PDBTitle: yeast rna polymerase iii initial transcribing complex
104	c2pdtD	Alignment	not modelled	57.1	25	PDB header: circadian clock protein Chain: D: PDB Molecule: vivid pas protein vvd; PDBTitle: 2.3 angstrom structure of phosphodiesterase treated vivid

105	c1yz4A_	Alignment	not modelled	56.5	14	PDB header: hydrolase Chain: A; PDB Molecule: dual specificity phosphatase-like 15 isoform a; PDBTitle: crystal structure of dusp15
106	c4rkkA_	Alignment	not modelled	55.8	17	PDB header: hydrolase Chain: A; PDB Molecule: laforin; PDBTitle: structure of a product bound phosphatase
107	c6avjB_	Alignment	not modelled	55.7	24	PDB header: metal binding protein Chain: B; PDB Molecule: cdgsh iron-sulfur domain-containing protein 3, PDBTitle: crystal structure of human mitochondrial inner neet protein (mint)2 /cisd3
108	c2k8dA_	Alignment	not modelled	55.1	36	PDB header: oxidoreductase Chain: A; PDB Molecule: peptide methionine sulfoxide reductase msrb; PDBTitle: solution structure of a zinc-binding methionine sulfoxide reductase
109	d1xria_	Alignment	not modelled	54.5	16	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
110	c6o9l6_	Alignment	not modelled	54.4	8	PDB header: transcription/dna Chain: 6; PDB Molecule: general transcription factor iih subunit 2; PDBTitle: human holo-pic in the closed state
111	c1dsqA_	Alignment	not modelled	54.2	50	PDB header: viral protein Chain: A; PDB Molecule: nucleic acid binding protein p14; PDBTitle: structure of the mmtv nucleocapsid protein (zinc finger 1)
112	c6f42V_	Alignment	not modelled	53.6	15	PDB header: transcription Chain: V; PDB Molecule: transcription factor iiib 70 kda subunit; PDBTitle: rna polymerase iii closed complex cc1.
113	d1i9sa_	Alignment	not modelled	53.4	28	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
114	c2j17A_	Alignment	not modelled	53.2	26	PDB header: hydrolase Chain: A; PDB Molecule: tyrosine-protein phosphatase yil113w; PDBTitle: tyr bound form of sdp-1
115	d1rxda_	Alignment	not modelled	53.1	20	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
116	c2e0tA_	Alignment	not modelled	51.7	29	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
117	c3hcbB_	Alignment	not modelled	51.0	32	PDB header: oxidoreductase Chain: B; PDB Molecule: peptide methionine sulfoxide reductase; PDBTitle: structure of msrb from xanthomonas campestris (oxidized2 form)
118	c2c46B_	Alignment	not modelled	50.9	27	PDB header: transferase Chain: B; PDB Molecule: mrna capping enzyme; PDBTitle: crystal structure of the human rna guanylyltransferase and 5'-2 phosphatase
119	c5ijlA_	Alignment	not modelled	50.1	22	PDB header: transferase Chain: A; PDB Molecule: dna polymerase ii large subunit; PDBTitle: d-family dna polymerase - dp2 subunit (catalytic subunit)
120	d1xmx_	Alignment	not modelled	50.0	12	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hypothetical protein VC1899