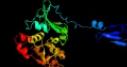
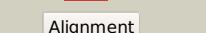
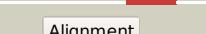
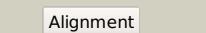
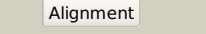
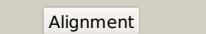
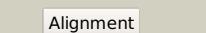
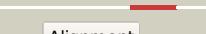
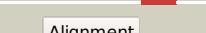


Phyre²

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			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			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			100.0	99	PDB header: transferase Chain: A: PDB Molecule: dna primase; PDBTitle: crystal structure of the rna polymerase domain (rp) of mycobacterium2 tuberculosis primase dnag in complex with double-stranded dna3 gacccgaatgg
4	d1dd9a			100.0	34	Fold: DNA primase core Superfamily: DNA primase core Family: DNA primase DnaG catalytic core
5	c1dd9A			100.0	34	PDB header: transferase Chain: A: PDB Molecule: dna primase; PDBTitle: structure of the dnag catalytic core
6	c4edvA			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			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			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			99.9	51	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: DNA primase zinc finger
10	c1q57G			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			99.8	23	Fold: DNA primase core Superfamily: DNA primase core Family: Primase fragment of primase-helicase protein

12	d1t6t1			99.6	14	Fold: Toprim domain Superfamily: Toprim domain Family: Toprim domain
13	c5z51A			99.5	98	PDB header: transferase Chain: A: PDB Molecule: dna primase; PDBTitle: helicase binding domain of primase from mycobacterium tuberculosis
14	c2r6cG			98.9	9	PDB header: replication Chain: G: PDB Molecule: dna primase, helicase binding domain; PDBTitle: crystal form bh2
15	c2lznA			98.7	13	PDB header: transferase Chain: A: PDB Molecule: dna primase; PDBTitle: solution structure of s. aureus primase c-terminal domain
16	d2fcja1			98.7	18	Fold: Toprim domain Superfamily: Toprim domain Family: Toprim domain
17	c2r5uD			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			97.6	10	PDB header: hydrolase Chain: D: PDB Molecule: replicative dna helicase; PDBTitle: structure of a dodecameric bacterial helicase
19	c4im9C			97.5	19	PDB header: transferase Chain: C: PDB Molecule: dna primase; PDBTitle: cystal structure of dnag primase c-terminal domain from vibrio2 cholerae
20	c6qelB			97.4	6	PDB header: replication Chain: B: PDB Molecule: replicative dna helicase; PDBTitle: e. coli dnabc apo complex
21	c2vyea		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		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		not modelled	97.3	7	PDB header: hydrolase Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: structure of a dodecameric bacterial helicase
24	c2q6tB		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	c3gxxvA		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		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		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		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 PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recr from pseudomonas aeruginosa pao1
30	c5z2vB	Alignment	not modelled	95.9	18	PDB header: recombination Chain: A: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombination mediator protein recr
31	c5zvqA	Alignment	not modelled	94.0	23	Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR
32	d1vdda	Alignment	not modelled	93.8	22	PDB header: recombination Chain: D: PDB Molecule: recombination protein recr; PDBTitle: structure of recombination mediator protein recr16-196 deletion mutant
33	c3ve5D	Alignment	not modelled	93.6	19	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
34	c1vddC	Alignment	not modelled	93.6	22	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
35	c6bbmA	Alignment	not modelled	93.5	7	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
36	c2e9hA	Alignment	not modelled	87.7	23	PDB header: translation Chain: A: PDB Molecule: probable translation initiation factor 2 beta PDBTitle: structure of archaeal translation factor aif2beta from methanobacterium thermoautrophicum
37	c1neeA	Alignment	not modelled	82.9	23	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: architecture of the rna polymerase ii-mediator core transcription2 initiation complex
38	c4v1oM	Alignment	not modelled	82.3	31	PDB header: transcription/dna Chain: Q: PDB Molecule: general transcription factor iie subunit 1; PDBTitle: human holo-pic in the closed state
39	c6o9lQ	Alignment	not modelled	81.2	16	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: DNA primase zinc finger
40	d1nuia2	Alignment	not modelled	79.8	14	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)
41	c6gq3P	Alignment	not modelled	77.9	24	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l13a, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
42	c3zf7o	Alignment	not modelled	77.2	35	PDB header: hydrolyase Chain: A: PDB Molecule: sex4 glucan phosphatase; PDBTitle: structure of a plant phosphatase
43	c3nmeA	Alignment	not modelled	76.6	21	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: transcription initiation complex structures elucidate dna opening (cc)
44	c5fz5M	Alignment	not modelled	76.5	31	PDB header: hydrolyase 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
45	c3emuA	Alignment	not modelled	74.5	20	PDB header: hydrolyase 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
46	c2imgA	Alignment	not modelled	74.3	20	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.
47	c4a17Y	Alignment	not modelled	74.0	36	PDB header: hydrolyase Chain: A: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of the catalytic domain of human mpk5
48	c2oudA	Alignment	not modelled	73.9	20	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
49	c4b6ap	Alignment	not modelled	73.0	29	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: co-crystal structure of anisomycin bound to the 50s ribosomal subunit
50	c3cc4Z	Alignment	not modelled	72.9	30	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
51	d1v3aa	Alignment	not modelled	72.5	19	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
52	c2qa4Z	Alignment	not modelled	71.6	29	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: crystal structure of an rna polymerase ii-tfiiib complex
53	c3k7aM	Alignment	not modelled	71.0	31	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon
54	d1vd4a	Alignment	not modelled	69.6	28	

					Family: Transcriptional factor domain
55	c3j39p	Alignment	not modelled	69.5	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	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	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
58	c3j21i	Alignment	not modelled	69.2	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 (50s ribosomal proteins)
59	c2dcuB	Alignment	not modelled	69.1	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	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 8; PDBTitle: structure of dusp8
61	d1vqoz1	Alignment	not modelled	68.0	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
62	c3rgqA	Alignment	not modelled	67.4	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	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	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	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	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	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	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
69	d1ohea2	Alignment	not modelled	66.5	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
70	d1w0ba	Alignment	not modelled	66.1	Fold: Spectrin repeat-like Superfamily: Alpha-hemoglobin stabilizing protein AHSP Family: Alpha-hemoglobin stabilizing protein AHSP
71	c5xogM	Alignment	not modelled	65.8	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	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	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	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	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	Fold: Spectrin repeat-like Superfamily: Alpha-hemoglobin stabilizing protein AHSP Family: Alpha-hemoglobin stabilizing protein AHSP
77	c4r30C	Alignment	not modelled	64.1	PDB header: hydrolase Chain: C: PDB Molecule: laforin; PDBTitle: structure of human laforin dual specificity phosphatase domain
78	c5oqjW	Alignment	not modelled	63.9	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	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 tmrp
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 (ccdist)
86	d1vhra	Alignment	not modelled	61.4	17	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
87	d1wiaa	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 tfiie 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 factor 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 iiib 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 mmvt 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: ptyr 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	c3hcjB		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	c5ijIA		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	d1xmxa		Alignment	not modelled	50.0	12	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hypothetical protein VC1899