

Phyre2

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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4g7oN_	Alignment		100.0	49	PDB header: transcription, transferase/dna Chain: N: PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: crystal structure of thermus thermophilus transcription initiation2 complex containing 2 nt of rna
2	d1smyd_	Alignment		100.0	48	Fold: beta and beta-prime subunits of DNA dependent RNA-polymerase Superfamily: beta and beta-prime subunits of DNA dependent RNA-polymerase Family: RNA-polymerase beta-prime
3	c5tw1D_	Alignment		100.0	87	PDB header: transcription activator/transferase/dna Chain: D: PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpA
4	c2o5jN_	Alignment		100.0	49	PDB header: transferase/dna-rna hybrid Chain: N: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: crystal structure of the t. thermophilus rnap polymerase elongation2 complex with the ntp substrate analog
5	c5x22D_	Alignment		100.0	52	PDB header: transferase/dna Chain: D: PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: crystal structure of thermus thermophilus transcription initiation2 complex with gpa and cmpcpp
6	c4wqsD_	Alignment		100.0	53	PDB header: transferase/dna/rna Chain: D: PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: thermus thermophilus rna polymerase backtracked complex
7	c2o5iD_	Alignment		100.0	48	PDB header: transferase/dna-rna hybrid Chain: D: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: crystal structure of the t. thermophilus rna polymerase elongation2 complex
8	c5xj0D_	Alignment		100.0	49	PDB header: transferase/transcription Chain: D: PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: t. thermophilus rna polymerase holoenzyme bound with gp39 and gp76
9	c6cceD_	Alignment		100.0	85	PDB header: transcription/dna/antibiotic Chain: D: PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: crystal structure of a mycobacterium smegmatis rna polymerase2 transcription initiation complex with inhibitor kanglemycin a
10	c3aoiN_	Alignment		100.0	47	PDB header: transcription, transferase/dna/rna Chain: N: PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: rna polymerase-gfh1 complex (crystal type 2)
11	c4xsxl_	Alignment		100.0	49	PDB header: transcription/antibiotic Chain: J: PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: crystal structure of cbr 703 bound to escherichia coli rna polymerase2 holoenzyme

12	c3aoil_	Alignment		100.0	47	PDB header: transcription, transferase/dna/rna Chain: I: PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: rna polymerase-gfh1 complex (crystal type 2)
13	c1l9uD_	Alignment		100.0	49	PDB header: transcription Chain: D: PDB Molecule: rna polymerase, beta-prime subunit; PDBTitle: thermus aquaticus rna polymerase holoenzyme at 4 a2 resolution
14	c3h0gA_	Alignment		100.0	23	PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase ii subunit rpb1; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
15	c6j9eD_	Alignment		100.0	52	PDB header: transcription Chain: D: PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: cryo-em structure of xanthomonos oryzae transcription elongation2 complex with nusa and the bacteriophage protein p7
16	c4iqcD_	Alignment		100.0	51	PDB header: transcription, transferase Chain: D: PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: x-ray crystal structure of escherichia coli sigma70 holoenzyme
17	c3iydD_	Alignment		100.0	48	PDB header: transcription/dna Chain: D: PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: three-dimensional em structure of an intact activator-dependent2 transcription initiation complex
18	c1i6vD_	Alignment		100.0	49	PDB header: transcription Chain: D: PDB Molecule: dna-directed rna polymerase; PDBTitle: thermus aquaticus core rna polymerase-rifampicin complex
19	d1i6vd_	Alignment		100.0	49	Fold: beta and beta-prime subunits of DNA dependent RNA-polymerase Superfamily: beta and beta-prime subunits of DNA dependent RNA-polymerase Family: RNA-polymerase beta-prime
20	c6gmIA_	Alignment		100.0	25	PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase subunit; PDBTitle: structure of paused transcription complex pol ii-dsif-nelf
21	c6dcfD_	Alignment	not modelled	100.0	86	PDB header: transcription/dna/antibiotic Chain: D: PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rifampicin-resistant rna polymerase and bound3 to kanglemycin a
22	d1twfa_	Alignment	not modelled	100.0	25	Fold: beta and beta-prime subunits of DNA dependent RNA-polymerase Superfamily: beta and beta-prime subunits of DNA dependent RNA-polymerase Family: RNA-polymerase beta-prime
23	c4llgJ_	Alignment	not modelled	100.0	52	PDB header: transferase Chain: J: PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: crystal structure analysis of the e.coli holoenzyme/gp2 complex
24	c5flmA_	Alignment	not modelled	100.0	26	PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase; PDBTitle: structure of transcribing mammalian rna polymerase ii
25	c5tbzD_	Alignment	not modelled	100.0	52	PDB header: transcription/rna Chain: D: PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: e. coli rna polymerase complexed with nusg
26	c4c3iA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase i subunit rpa190; PDBTitle: structure of 14-subunit rna polymerase i at 3.0 a resolution, crystal2 form c2-100
27	c5m3fA_	Alignment	not modelled	100.0	21	PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase i subunit rpa190; PDBTitle: yeast rna polymerase i elongation complex at 3.8a PDB header: transcription/dna-rna hybrid

28	c1i6hA_	Alignment	not modelled	100.0	25	Chain: A: PDB Molecule: dna-directed rna polymerase ii largest subunit; PDBTitle: rna polymerase ii elongation complex
29	c5fjaA_	Alignment	not modelled	100.0	22	PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase iii subunit rpc1; PDBTitle: cryo-em structure of yeast rna polymerase iii at 4.7 a
30	d1ynjd1	Alignment	not modelled	100.0	48	Fold: beta and beta-prime subunits of DNA dependent RNA-polymerase Superfamily: beta and beta-prime subunits of DNA dependent RNA-polymerase Family: RNA-polymerase beta-prime
31	c1twaA_	Alignment	not modelled	100.0	24	PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase ii largest subunit; PDBTitle: rna polymerase ii complexed with atp
32	c5lmxA_	Alignment	not modelled	100.0	20	PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase i subunit rpa190; PDBTitle: monomeric rna polymerase i at 4.9 a resolution
33	c4b1pW_	Alignment	not modelled	100.0	27	PDB header: transferase/dna Chain: W: PDB Molecule: dna-directed rna polymerase; PDBTitle: archaeal rnap-dna binary complex at 4.32ang
34	c4qiwaA_	Alignment	not modelled	100.0	26	PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase; PDBTitle: crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
35	c2pmzQ_	Alignment	not modelled	100.0	31	PDB header: translation, transferase Chain: Q: PDB Molecule: dna-directed rna polymerase subunit a; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
36	c6drdA_	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase ii subunit rpb1; PDBTitle: rna pol ii(g)
37	c3qqcA_	Alignment	not modelled	100.0	28	PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase subunit b, dna-directed rna PDBTitle: crystal structure of archaeal spt4/5 bound to the rnap clamp domain
38	c4qiwcA_	Alignment	not modelled	100.0	24	PDB header: transcription Chain: C: PDB Molecule: dna-directed rna polymerase subunit a"; PDBTitle: crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
39	c2wb1Y_	Alignment	not modelled	100.0	19	PDB header: transcription Chain: Y: PDB Molecule: dna-directed rna polymerase rpo1c subunit; PDBTitle: the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
40	c2pmzG_	Alignment	not modelled	100.0	24	PDB header: translation, transferase Chain: G: PDB Molecule: dna-directed rna polymerase subunit a"; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
41	c2aujD_	Alignment	not modelled	96.6	14	PDB header: transferase Chain: D: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of thermus aquaticus rna polymerase beta'-subunit2 insert
42	c3e7hA_	Alignment	not modelled	96.4	21	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: the crystal structure of the beta subunit of the dna-directed rna2 polymerase from vibrio cholerae o1 biovar eltor
43	c2lmcB_	Alignment	not modelled	95.8	16	PDB header: transcription Chain: B: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: structure of t7 transcription factor gp2-e. coli rnap jaw domain2 complex
44	c2aukA_	Alignment	not modelled	93.9	13	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of e. coli rna polymerase beta' g/g' insert
45	c5fswC_	Alignment	not modelled	89.0	29	PDB header: transferase Chain: C: PDB Molecule: rna dependent rna polymerase qde-1; PDBTitle: rna dependent rna polymerase qde-1 from thielavia terrestris
46	c2j7nA_	Alignment	not modelled	88.7	25	PDB header: hydrolase Chain: A: PDB Molecule: rna-dependent rna polymerase; PDBTitle: structure of the rna polymerase from neurospora crassa
47	c3mkrB_	Alignment	not modelled	80.1	29	PDB header: transport protein Chain: B: PDB Molecule: coatome subunit alpha; PDBTitle: crystal structure of yeast alpha/epsilon-cop subcomplex of the copi2 vesicular coat
48	c3mv2A_	Alignment	not modelled	74.3	15	PDB header: protein transport Chain: A: PDB Molecule: coatome subunit alpha; PDBTitle: crystal structure of a-cop in complex with e-cop
49	d1odha_	Alignment	not modelled	68.4	29	Fold: GCM domain Superfamily: GCM domain Family: GCM domain
50	c4iqzD_	Alignment	not modelled	63.1	21	PDB header: unknown function Chain: D: PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: the crystal structure of a large insert in rna polymerase (rpoC)2 subunit from e. coli
51	c4zlhB_	Alignment	not modelled	54.9	16	PDB header: metal binding protein Chain: B: PDB Molecule: lipopolysaccharide assembly protein b; PDBTitle: structure of the lapb cytoplasmic domain at 2 angstroms
52	c2lcaA_	Alignment	not modelled	50.6	30	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
53	c2hcrB_	Alignment	not modelled	48.4	43	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase;

53	c3ncjB	Alignment	not modelled	48.4	42	PDBTitle: structure of msrb from xanthomonas campestris (oxidized2 form)
54	d1xm0a1	Alignment	not modelled	47.7	17	Fold: Mss4-like Superfamily: Mss4-like Family: SelR domain
55	c3ky9B	Alignment	not modelled	45.6	25	PDB header: apoptosis Chain: B: PDB MOLECULE: proto-oncogene vav; PDBTitle: autoinhibited vav1
56	c2l1uA	Alignment	not modelled	44.7	42	PDB header: oxidoreductase Chain: A: PDB MOLECULE: methionine-r-sulfoxide reductase b2, mitochondrial; PDBTitle: structure-functional analysis of mammalian msrb2 protein
57	c3cezA	Alignment	not modelled	44.4	42	PDB header: oxidoreductase Chain: A: PDB MOLECULE: methionine-r-sulfoxide reductase; PDBTitle: crystal structure of methionine-r-sulfoxide reductase from2 burkholderia pseudomallei
58	c2k8dA	Alignment	not modelled	43.8	42	PDB header: oxidoreductase Chain: A: PDB MOLECULE: peptide methionine sulfoxide reductase msrb; PDBTitle: solution structure of a zinc-binding methionine sulfoxide reductase
59	c6g5iy	Alignment	not modelled	43.1	29	PDB header: ribosome Chain: Y: PDB MOLECULE: 40s ribosomal protein s24; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state r
60	c2hr5B	Alignment	not modelled	42.4	27	PDB header: metal binding protein Chain: B: PDB MOLECULE: rubrerythrin; PDBTitle: pf1283- rubrerythrin from pyrococcus furiosus iron bound form
61	c3e0mB	Alignment	not modelled	42.1	17	PDB header: oxidoreductase Chain: B: PDB MOLECULE: peptide methionine sulfoxide reductase msra/msrb PDBTitle: crystal structure of fusion protein of msra and msrb
62	d1l1da	Alignment	not modelled	41.9	17	Fold: Mss4-like Superfamily: Mss4-like Family: SelR domain
63	c5a1vK	Alignment	not modelled	41.6	26	PDB header: transport protein Chain: K: PDB MOLECULE: coatomer subunit alpha; PDBTitle: the structure of the copi coat linkage i
64	c2gj2A	Alignment	not modelled	39.3	29	PDB header: metal binding protein Chain: A: PDB MOLECULE: wsv230; PDBTitle: crystal structure of vp9 from white spot syndrome virus
65	c5fa9B	Alignment	not modelled	39.2	25	PDB header: oxidoreductase Chain: B: PDB MOLECULE: peptide methionine sulfoxide reductase msra; PDBTitle: bifunctional methionine sulfoxide reductase ab (msrab) from treponema2 denticola
66	c1yuzB	Alignment	not modelled	38.2	30	PDB header: oxidoreductase Chain: B: PDB MOLECULE: nigerythrin; PDBTitle: partially reduced state of nigerythrin
67	c3t6pA	Alignment	not modelled	36.9	25	PDB header: apoptosis Chain: A: PDB MOLECULE: baculoviral iap repeat-containing protein 2; PDBTitle: iap antagonist-induced conformational change in ciap1 promotes e32 ligase activation via dimerization
68	c3uc9A	Alignment	not modelled	35.3	38	PDB header: recombination Chain: A: PDB MOLECULE: increased recombination centers protein 6; PDBTitle: crystal structure of yeast irc6p - a novel type of conserved clathrin2 accessory protein
69	c2vrwB	Alignment	not modelled	34.8	24	PDB header: signaling protein Chain: B: PDB MOLECULE: proto-oncogene vav; PDBTitle: critical structural role for the ph and c1 domains of the2 vav1 exchange factor
70	c2bx9J	Alignment	not modelled	34.6	46	PDB header: transcription regulation Chain: J: PDB MOLECULE: tryptophan rna-binding attenuator protein-inhibitory PDBTitle: crystal structure of b.subtilis anti-trap protein, an2 antagonist of trap-rna interactions
71	c5zb8B	Alignment	not modelled	34.5	25	PDB header: dna binding protein Chain: B: PDB MOLECULE: pfuendoq; PDBTitle: crystal structure of the novel lesion-specific endonuclease pfuendoq2 from pyrococcus furiosus
72	d2gmga1	Alignment	not modelled	33.4	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PF0610-like
73	c2kaoA	Alignment	not modelled	33.1	16	PDB header: oxidoreductase Chain: A: PDB MOLECULE: methionine-r-sulfoxide reductase b1; PDBTitle: structure of reduced mouse methionine sulfoxide reductase b12 (sec95cys mutant)
74	d1x64a2	Alignment	not modelled	32.7	20	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
75	d2eppa1	Alignment	not modelled	31.0	36	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
76	d2g9ha2	Alignment	not modelled	30.2	71	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
77	c4u3eA	Alignment	not modelled	30.1	22	PDB header: oxidoreductase Chain: A: PDB MOLECULE: ribonucleoside triphosphate reductase; PDBTitle: anaerobic ribonucleotide reductase
78	c4rasC	Alignment	not modelled	29.9	19	PDB header: oxidoreductase Chain: C: PDB MOLECULE: oxidoreductase, nad-binding/iron-sulfur cluster-binding

						PDBTitle: reductive dehalogenase structure suggests a mechanism for b12-2 dependent dehalogenation
79	c5ey2A	Alignment	not modelled	29.5	21	PDB header: transcription Chain: A: PDB Molecule: gtp-sensing transcriptional pleiotropic repressor cody; PDBTitle: crystal structure of cody from bacillus cereus
80	c2eppA	Alignment	not modelled	29.3	36	PDB header: transcription Chain: A: PDB Molecule: poz-, at hook-, and zinc finger-containing PDBTitle: solution structure of the first c2h2 type zinc finger2 domain of zinc finger protein 278
81	d1s9va2	Alignment	not modelled	29.1	57	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
82	c1q68B	Alignment	not modelled	28.8	30	PDB header: membrane protein/transferase Chain: B: PDB Molecule: proto-oncogene tyrosine-protein kinase lck; PDBTitle: solution structure of t-cell surface glycoprotein cd4 and2 proto-oncogene tyrosine-protein kinase lck fragments
83	c1v9pB	Alignment	not modelled	28.1	16	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
84	c1q69B	Alignment	not modelled	27.6	30	PDB header: membrane protein/transferase Chain: B: PDB Molecule: proto-oncogene tyrosine-protein kinase lck; PDBTitle: solution structure of t-cell surface glycoprotein cd8 alpha2 chain and proto-oncogene tyrosine-protein kinase lck3 fragments
85	c1bi6H	Alignment	not modelled	27.6	26	PDB header: cysteine protease inhibitor Chain: H: PDB Molecule: bromelain inhibitor vi; PDBTitle: nmr structure of bromelain inhibitor vi from pineapple stem
86	c2bi6H	Alignment	not modelled	27.6	26	PDB header: cysteine protease inhibitor Chain: H: PDB Molecule: bromelain inhibitor vi; PDBTitle: nmr study of bromelain inhibitor vi from pineapple stem
87	c5y06A	Alignment	not modelled	27.5	27	PDB header: unknown function Chain: A: PDB Molecule: msmeg_4306; PDBTitle: structural characterization of msmeg_4306 from mycobacterium smegmatis
88	c3imkA	Alignment	not modelled	26.9	19	PDB header: metal binding protein Chain: A: PDB Molecule: putative molybdenum carrier protein; PDBTitle: crystal structure of putative molybdenum carrier protein (yp_461806.1)2 from syntrophus aciditrophicus sb at 1.45 a resolution
89	d1x62a1	Alignment	not modelled	26.8	27	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
90	d1hk8a	Alignment	not modelled	26.8	22	Fold: PFL-like glycy radical enzymes Superfamily: PFL-like glycy radical enzymes Family: Class III anaerobic ribonucleotide reductase NRDD subunit
91	c1hk8A	Alignment	not modelled	26.8	22	PDB header: oxidoreductase Chain: A: PDB Molecule: anaerobic ribonucleotide-triphosphate reductase; PDBTitle: structural basis for allosteric substrate specificity regulation in2 class iii ribonucleotide reductases: nrdd in complex with dntp
92	c5kl1B	Alignment	not modelled	26.7	21	PDB header: rna binding protein/rna Chain: B: PDB Molecule: protein nanos; PDBTitle: crystal structure of the pumilio-nos-hunchback rna complex
93	c3bjia	Alignment	not modelled	26.3	26	PDB header: signaling protein Chain: A: PDB Molecule: proto-oncogene vav; PDBTitle: structural basis of promiscuous guanine nucleotide exchange2 by the t-cell essential vav1
94	c5ijlA	Alignment	not modelled	26.2	22	PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii large subunit; PDBTitle: d-family dna polymerase - dp2 subunit (catalytic subunit)
95	c2f9iD	Alignment	not modelled	25.5	11	PDB header: transferase Chain: D: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl transferase subunit PDBTitle: crystal structure of the carboxyltransferase subunit of acc from2 staphylococcus aureus
96	d2vnud2	Alignment	not modelled	25.0	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
97	c1dvaA	Alignment	not modelled	24.8	27	PDB header: electron transport Chain: A: PDB Molecule: rubrerythrin; PDBTitle: rubrerythrin
98	c5xodB	Alignment	not modelled	24.6	35	PDB header: transcription Chain: B: PDB Molecule: ski oncogene; PDBTitle: crystal structure of human smad2-ski complex
99	d1eb7a1	Alignment	not modelled	24.4	17	Fold: Cytochrome c Superfamily: Cytochrome c Family: Di-heme cytochrome c peroxidase
100	c2kc1A	Alignment	not modelled	24.2	22	PDB header: structural protein Chain: A: PDB Molecule: mkiaa1027 protein; PDBTitle: nmr structure of the f0 domain (residues 0-85) of the talin2 ferm domain
101	c2lvuA	Alignment	not modelled	24.1	40	PDB header: transcription Chain: A: PDB Molecule: zinc finger and btb domain-containing protein 17; PDBTitle: solution structure of miz-1 zinc finger 10
102	d1nvmb2	Alignment	not modelled	23.8	28	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like PDB header: ligase/ligase inhibitor/dna

103	c4glxA	Alignment	not modelled	23.3	16	Chain: A; PDB Molecule: dna ligase; PDBTitle: dna ligase a in complex with inhibitor
104	d1nmla1	Alignment	not modelled	23.3	17	Fold: Cytochrome c Superfamily: Cytochrome c Family: Di-heme cytochrome c peroxidase
105	d6rxna	Alignment	not modelled	23.1	30	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
106	d1iqca1	Alignment	not modelled	22.8	17	Fold: Cytochrome c Superfamily: Cytochrome c Family: Di-heme cytochrome c peroxidase
107	d2coba1	Alignment	not modelled	22.7	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Psq domain
108	d1jk8a2	Alignment	not modelled	22.4	40	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
109	c4jn6B	Alignment	not modelled	22.2	34	PDB header: lyase/oxidoreductase Chain: B; PDB Molecule: acetaldehyde dehydrogenase; PDBTitle: crystal structure of the aldolase-dehydrogenase complex from <i>Mycobacterium tuberculosis</i> hrv37
110	c3uk2B	Alignment	not modelled	21.9	24	PDB header: ligase Chain: B; PDB Molecule: pantothenate synthetase; PDBTitle: the structure of pantothenate synthetase from <i>Burkholderia thailandensis</i>
111	c3j3v0	Alignment	not modelled	21.9	44	PDB header: ribosome Chain: 0; PDB Molecule: 50s ribosomal protein l32; PDBTitle: atomic model of the immature 50s subunit from <i>Bacillus subtilis</i> (state2 i-a)
112	c2j04C	Alignment	not modelled	21.7	25	PDB header: transcription Chain: C; PDB Molecule: hypothetical protein ypl007c; PDBTitle: the tau60-tau91 subcomplex of yeast transcription factor iiic
113	c2f9yB	Alignment	not modelled	21.7	28	PDB header: ligase Chain: B; PDB Molecule: acetyl-coenzyme a carboxylase carboxyl transferase subunit PDBTitle: the crystal structure of the carboxyltransferase subunit of acc from <i>Escherichia coli</i>
114	d2f9yb1	Alignment	not modelled	21.7	28	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
115	c1pqrA	Alignment	not modelled	21.7	43	PDB header: toxin Chain: A; PDB Molecule: alpha-a-conotoxin eiva; PDBTitle: solution conformation of alphaa-conotoxin eiva
116	c5fmfR	Alignment	not modelled	21.6	27	PDB header: transcription Chain: R; PDB Molecule: transcription initiation factor iie subunit alpha, tfa1; PDBTitle: the p-lobe of rna polymerase ii pre-initiation complex
117	c5f4hF	Alignment	not modelled	21.2	15	PDB header: hydrolase Chain: F; PDB Molecule: nucleotide binding protein pinc; PDBTitle: archaeal ruvb-like holiday junction helicase
118	d1es0a2	Alignment	not modelled	21.2	40	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
119	d1muja2	Alignment	not modelled	21.1	40	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
120	c2fugC	Alignment	not modelled	21.1	9	PDB header: oxidoreductase Chain: C; PDB Molecule: nadh-quinone oxidoreductase chain 3; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from <i>Thermus thermophilus</i>