Phyre2

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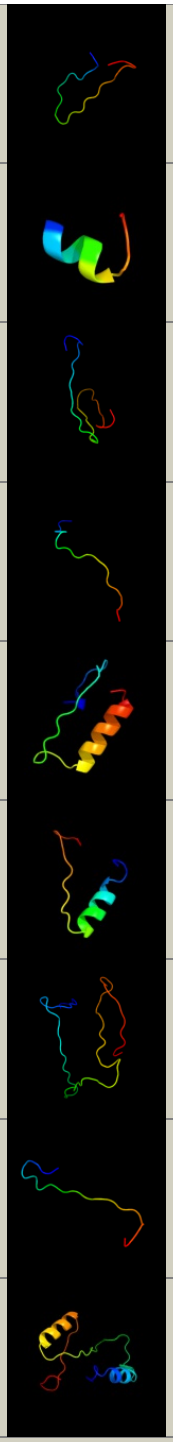
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1smyc_	Alignment		100.0	54	**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
2	c3iydC_	Alignment		100.0	58	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** three-dimensional em structure of an intact activator-dependent2 transcription initiation complex
3	d1ynjc1	Alignment		100.0	55	**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
4	c2pmzB_	Alignment		100.0	29	**PDB header:**translation, transferase **Chain:** B: **PDB Molecule:**dna-directed rna polymerase subunit b; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
5	c3h0gN_	Alignment		100.0	26	**PDB header:**transcription **Chain:** N: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb2; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
6	d1twfb_	Alignment		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
7	c3mlqD_	Alignment		100.0	62	**PDB header:**transferase/transcription **Chain:** D: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** crystal structure of the thermus thermophilus transcription-repair2 coupling factor rna polymerase interacting domain with the thermus3 aquaticus rna polymerase beta1 domain
8	c3mlqB_	Alignment		100.0	63	**PDB header:**transferase/transcription **Chain:** B: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** crystal structure of the thermus thermophilus transcription-repair2 coupling factor rna polymerase interacting domain with the thermus3 aquaticus rna polymerase beta1 domain
9	c3tbiB_	Alignment		99.9	44	**PDB header:**transcription **Chain:** B: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** crystal structure of t4 gp33 bound to e. coli rnap beta-flap domain
10	c3ltiA_	Alignment		99.9	60	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** crystal structure of the escherichia coli rna polymerase beta subunit2 beta2-betai4 domains
11	c3qqcA_	Alignment		99.2	24	**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

12	d1r46a1	Alignment		47.4	16	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
13	d1zq1c1	Alignment		36.0	42	**Fold:**GatB/YqeY motif **Superfamily:**GatB/YqeY motif **Family:**GatB/GatE C-terminal domain-like
14	d1n26a2	Alignment		31.4	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
15	d1d02a_	Alignment		30.3	17	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease MunI
16	d1nbwa1	Alignment		27.4	14	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Swiveling domain of dehydratase reactivase alpha subunit **Family:**Swiveling domain of dehydratase reactivase alpha subunit
17	d1uj4a2	Alignment		27.3	24	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
18	c2gtiA_	Alignment		26.9	16	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**replicase polyprotein 1ab; **PDBTitle:** mutation of mhv coronavirus non-structural protein nsp15 (f307l)
19	d1gm5a4	Alignment		23.9	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
20	c1uj6A_	Alignment		23.2	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of thermus thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate
21	d2d0oa1	Alignment	not modelled	21.9	13	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Swiveling domain of dehydratase reactivase alpha subunit **Family:**Swiveling domain of dehydratase reactivase alpha subunit
22	c3lvwA_	Alignment	not modelled	21.4	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamate--cysteine ligase; **PDBTitle:** glutathione-inhibited scgcl
23	c3mjhD_	Alignment	not modelled	21.4	50	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**early endosome antigen 1; **PDBTitle:** crystal structure of human rab5a in complex with the c2h2 zinc finger2 of eea1
24	c3kdeC_	Alignment	not modelled	21.2	16	**PDB header:**dna binding protein/dna **Chain:** C: **PDB Molecule:**transposable element p transposase; **PDBTitle:** crystal structure of the thap domain from d. melanogaster p-element2 transposase in complex with its natural dna binding site
25	d1lk5a2	Alignment	not modelled	21.2	12	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
26	c3cwiA_	Alignment	not modelled	21.1	22	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**thiamine-biosynthesis protein this; **PDBTitle:** crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
27	c2c2lD_	Alignment	not modelled	20.6	24	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**carboxy terminus of hsp70-interacting protein; **PDBTitle:** crystal structure of the chip u-box e3 ubiquitin ligase
28	d1y4oa1	Alignment	not modelled	20.0	47	**Fold:**Profilin-like **Superfamily:**Roadblock/LC7 domain **Family:**Roadblock/LC7 domain

29	d1ujpa_	Alignment	not modelled	19.8	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
30	c2db3D_	Alignment	not modelled	19.8	43	**PDB header:**hydrolase/rna **Chain:** D: **PDB Molecule:**atp-dependent rna helicase vasa; **PDBTitle:** structural basis for rna unwinding by the dead-box protein2 drosophila vasa
31	d2eyqa5	Alignment	not modelled	19.4	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
32	c2q8nB_	Alignment	not modelled	19.0	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of glucose-6-phosphate isomerase (ec2 5.3.1.9) (tm1385) from thermotoga maritima at 1.82 a3 resolution
33	c1nbwA_	Alignment	not modelled	18.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerol dehydratase reactivase alpha subunit; **PDBTitle:** glycerol dehydratase reactivase
34	d1jbja1	Alignment	not modelled	18.2	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
35	c2pjmA_	Alignment	not modelled	17.7	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
36	d1xiwb_	Alignment	not modelled	16.9	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
37	d1cf2o2	Alignment	not modelled	16.6	34	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
38	d1zcea1	Alignment	not modelled	16.6	17	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
39	d1prtc1	Alignment	not modelled	15.8	19	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
40	d1prtb1	Alignment	not modelled	15.5	19	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
41	c2fyuE_	Alignment	not modelled	15.5	43	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit, **PDBTitle:** crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
42	d1sy6a1	Alignment	not modelled	15.5	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
43	c3l7oB_	Alignment	not modelled	15.4	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
44	c2g5iB_	Alignment	not modelled	14.9	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase **PDBTitle:** structure of trna-dependent amidotransferase gatcab2 complexed with adp-alf4
45	d1xmwa2	Alignment	not modelled	14.8	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
46	c1bcpH_	Alignment	not modelled	13.7	19	**PDB header:**toxin **Chain:** H: **PDB Molecule:**pertussis toxin; **PDBTitle:** binary complex of pertussis toxin and atp
47	c3bxzA_	Alignment	not modelled	13.2	33	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**preprotein translocase subunit seca; **PDBTitle:** crystal structure of the isolated dead motor domains from2 escherichia coli seca
48	d1m5ha1	Alignment	not modelled	12.4	42	**Fold:**Ferredoxin-like **Superfamily:**Formylmethanofuran:tetrahydromethanopterin formyltransferase **Family:**Formylmethanofuran:tetrahydromethanopterin formyltransferase
49	d1tf5a4	Alignment	not modelled	12.2	33	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
50	d1m0sa2	Alignment	not modelled	12.2	19	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
51	d1m5sa1	Alignment	not modelled	12.1	42	**Fold:**Ferredoxin-like **Superfamily:**Formylmethanofuran:tetrahydromethanopterin formyltransferase **Family:**Formylmethanofuran:tetrahydromethanopterin formyltransferase
52	d1ftra1	Alignment	not modelled	12.1	46	**Fold:**Ferredoxin-like **Superfamily:**Formylmethanofuran:tetrahydromethanopterin formyltransferase **Family:**Formylmethanofuran:tetrahydromethanopterin formyltransferase
53	c2uv0G_	Alignment	not modelled	12.0	25	**PDB header:**transcription **Chain:** G: **PDB Molecule:**transcriptional activator protein lasr; **PDBTitle:** structure of the p. aeruginosa lasr ligand-binding domain2 bound to its autoinducer

54	d2d6fc2	Alignment	not modelled	11.8	46	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
55	c3c4iA_	Alignment	not modelled	11.8	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding protein hu homolog; **PDBTitle:** crystal structure analysis of n terminal region containing the2 dimerization domain and dna binding domain of hu protein(histone like3 protein-dna binding) from mycobacterium tuberculosis [h37rv]
56	c1gjjA_	Alignment	not modelled	11.6	33	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lap2; **PDBTitle:** n-terminal constant region of the nuclear envelope protein2 lap2
57	d1dcza_	Alignment	not modelled	11.5	33	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
58	c3u5cl_	Alignment	not modelled	11.3	22	**PDB header:**ribosome **Chain:** l: **PDB Molecule:**40s ribosomal protein s8-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
59	c1pd7B_	Alignment	not modelled	11.0	60	**PDB header:**transcription **Chain:** B: **PDB Molecule:**mad1; **PDBTitle:** extended sid of mad1 bound to the pah2 domain of msin3b
60	d2gtia2	Alignment	not modelled	10.8	10	**Fold:**EndoU-like **Superfamily:**EndoU-like **Family:**Nsp15 C-terminal domain-like
61	c3dlaD_	Alignment	not modelled	10.5	14	**PDB header:**ligase **Chain:** D: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don
62	c1jbjA_	Alignment	not modelled	10.4	18	**PDB header:**immune system **Chain:** A: **PDB Molecule:**cd3 epsilon and gamma ectodomain fragment **PDBTitle:** cd3 epsilon and gamma ectodomain fragment complex in single-2 chain construct
63	c6paxA_	Alignment	not modelled	10.4	22	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**homeobox protein pax-6; **PDBTitle:** crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
64	c2vb0A_	Alignment	not modelled	10.1	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**polyprotein 3bcd; **PDBTitle:** crystal structure of coxsackievirus b3 proteinase 3c
65	d1flja_	Alignment	not modelled	9.8	25	**Fold:**Carbonic anhydrase **Superfamily:**Carbonic anhydrase **Family:**Carbonic anhydrase
66	c1lk5C_	Alignment	not modelled	9.8	14	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-ribose-5-phosphate isomerase; **PDBTitle:** structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
67	c3qp1A_	Alignment	not modelled	9.7	30	**PDB header:**transcription **Chain:** A: **PDB Molecule:**cvir transcriptional regulator; **PDBTitle:** crystal structure of cvir ligand-binding domain bound to the native2 ligand c6-hsl
68	d1aola_	Alignment	not modelled	9.7	23	**Fold:**ENV polyprotein, receptor-binding domain **Superfamily:**ENV polyprotein, receptor-binding domain **Family:**ENV polyprotein, receptor-binding domain
69	c1m1jA_	Alignment	not modelled	9.7	50	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**fibrinogen alpha subunit; **PDBTitle:** crystal structure of native chicken fibrinogen with two different2 bound ligands
70	d1o8ba2	Alignment	not modelled	9.5	19	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
71	c2f1mA_	Alignment	not modelled	9.4	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein a; **PDBTitle:** conformational flexibility in the multidrug efflux system protein acra
72	c2nu9E_	Alignment	not modelled	9.3	21	**PDB header:**ligase **Chain:** E: **PDB Molecule:**succinyl-coa synthetase beta chain; **PDBTitle:** c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form
73	d1wgma_	Alignment	not modelled	9.2	11	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
74	d1px5a1	Alignment	not modelled	9.1	28	**Fold:**PAP/OAS1 substrate-binding domain **Superfamily:**PAP/OAS1 substrate-binding domain **Family:**2'-5'-oligoadenylate synthetase 1, OAS1, second domain
75	d2f3na1	Alignment	not modelled	9.1	13	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
76	d1b7go2	Alignment	not modelled	9.0	23	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
77	c2p5zX_	Alignment	not modelled	8.9	17	**PDB header:**structural genomics, unknown function **Chain:** X: **PDB Molecule:**type vi secretion system component; **PDBTitle:** the e. coli c3393 protein is a component of the type vi secretion2 system and exhibits structural similarity to t4 bacteriophage tail3 proteins gp27 and gp5
78	d1y5ic1	Alignment	not modelled	8.9	15	**Fold:**Heme-binding four-helical bundle **Superfamily:**Respiratory nitrate reductase 1 gamma chain **Family:**Respiratory nitrate reductase 1 gamma chain

79	c2oy7A_	Alignment	not modelled	8.8	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer surface protein a; **PDBTitle:** the crystal structure of ospa mutant
80	d2hz5a1	Alignment	not modelled	8.8	47	**Fold:**Profilin-like **Superfamily:**Roadblock/LC7 domain **Family:**Roadblock/LC7 domain
81	d1jqna_	Alignment	not modelled	8.7	44	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate carboxylase
82	d2p5zx2	Alignment	not modelled	8.6	17	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
83	d2pxyd2	Alignment	not modelled	8.6	44	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
84	d1h59b_	Alignment	not modelled	8.5	38	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Growth factor receptor domain **Family:**Growth factor receptor domain
85	d2guja1	Alignment	not modelled	8.5	25	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**XkdM-like
86	c1m0sA_	Alignment	not modelled	8.5	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** northeast structural genomics consortium (nesg id ir21)
87	c2j8qB_	Alignment	not modelled	8.5	40	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**cleavage and polyadenylation specificity factor 5; **PDBTitle:** crystal structure of human cleavage and polyadenylation2 specificity factor 5 (cpsf5) in complex with a sulphate3 ion.
88	c1lkzB_	Alignment	not modelled	8.3	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase a; **PDBTitle:** crystal structure of d-ribose-5-phosphate isomerase (rpia)2 from escherichia coli.
89	c3ghgD_	Alignment	not modelled	8.3	33	**PDB header:**blood clotting **Chain:** D: **PDB Molecule:**fibrinogen alpha chain; **PDBTitle:** crystal structure of human fibrinogen
90	d2pwwa1	Alignment	not modelled	8.3	8	**Fold:**TBP-like **Superfamily:**YugN-like **Family:**YugN-like
91	d1m6ia3	Alignment	not modelled	8.2	43	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
92	c2aujD_	Alignment	not modelled	8.1	33	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of thermus aquaticus rna polymerase beta'-subunit2 insert
93	d1ooha_	Alignment	not modelled	8.1	33	**Fold:**EF Hand-like **Superfamily:**Insect pheromone/odorant-binding proteins **Family:**Insect pheromone/odorant-binding proteins
94	d1pfva2	Alignment	not modelled	8.0	40	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
95	d1u1ia1	Alignment	not modelled	8.0	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
96	d1k8ba_	Alignment	not modelled	8.0	36	**Fold:**Ribosome binding domain-like **Superfamily:**Translation initiation factor 2 beta, aIF2beta, N-terminal domain **Family:**Translation initiation factor 2 beta, aIF2beta, N-terminal domain
97	c1p84E_	Alignment	not modelled	8.0	43	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
98	c2kkpA_	Alignment	not modelled	8.0	36	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** solution nmr structure of the phage integrase sam-like2 domain from moth 1796 from moorella thermoacetica.3 northeast structural genomics consortium target mtr39k4 (residues 64-171).
99	d1uoua3	Alignment	not modelled	7.9	16	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain