

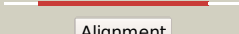

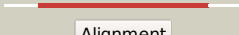



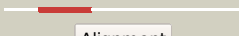















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0803_(purL)_895823_898087
Date	Fri Jul 26 01:50:38 BST 2019
Unique Job ID	fd3215139c9c7c53

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1t3tA_</a>	 Alignment		100.0	27	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphoribosylformylglycinamide synthase; <b>PDBTitle:</b> structure of formylglycinamide synthetase
2	<a href="#">c3ac6A_</a>	 Alignment		100.0	43	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphoribosylformylglycinamide synthase 2; <b>PDBTitle:</b> crystal structure of purl from thermus thermophilus
3	<a href="#">c3d54I_</a>	 Alignment		100.0	39	<b>PDB header:</b> ligase <b>Chain:</b> I; <b>PDB Molecule:</b> phosphoribosylformylglycinamide synthase ii; <b>PDBTitle:</b> structure of purlqs from thermotoga maritima
4	<a href="#">c2hs0A_</a>	 Alignment		100.0	40	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphoribosylformylglycinamide synthase ii; <b>PDBTitle:</b> t. maritima purl complexed with atp
5	<a href="#">d1vk3a1</a>	 Alignment		100.0	51	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
6	<a href="#">c2btuB_</a>	 Alignment		100.0	19	<b>PDB header:</b> synthase <b>Chain:</b> B; <b>PDB Molecule:</b> phosphoribosyl-aminoimidazole synthetase; <b>PDBTitle:</b> crystal structure of phosphoribosylformylglycinamide cyclo-ligase2 from bacillus anthracis at 2.3a resolution.
7	<a href="#">c3vysC_</a>	 Alignment		100.0	20	<b>PDB header:</b> metal binding protein/transferase <b>Chain:</b> C; <b>PDB Molecule:</b> hydrogenase expression/formation protein htype; <b>PDBTitle:</b> crystal structure of the hypc-hypd-hype complex (form i)
8	<a href="#">c3mcqA_</a>	 Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> thiamine-monophosphate kinase; <b>PDBTitle:</b> crystal structure of thiamine-monophosphate kinase (mfla_0573) from2 methylobacillus flagellatus kt at 1.91 a resolution
9	<a href="#">c5cm7A_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> thiamine-monophosphate kinase; <b>PDBTitle:</b> structure of thiamine-monophosphate kinase from acinetobacter2 baumannii in complex with adenosine diphosphate (adp) and thiamine3 diphosphate (tpp)
10	<a href="#">c5vk4B_</a>	 Alignment		100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> phosphoribosylformylglycinamide cyclo-ligase; <b>PDBTitle:</b> crystal structure of a phosphoribosylformylglycinamide cyclo-ligase2 from neisseria gonorrhoeae bound to amppnp and magnesium
11	<a href="#">c3fd5B_</a>	 Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> selenide, water dikinase 1; <b>PDBTitle:</b> crystal structure of human selenophosphate synthetase 12 complex with amppc

12	<a href="#">c1cliD_</a>	Alignment		100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> protein (phosphoribosyl-aminoimidazole synthetase); <b>PDBTitle:</b> x-ray crystal structure of aminoimidazole ribonucleotide synthetase2 (purm), from the e. coli purine biosynthetic pathway, at 2.5 a3 resolution
13	<a href="#">c3u0oA_</a>	Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> selenide, water dikinase; <b>PDBTitle:</b> the crystal structure of selenophosphate synthetase from e. coli
14	<a href="#">c2z1eA_</a>	Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase expression/formation protein hype; <b>PDBTitle:</b> crystal structure of hype from thermococcus kodakaraensis (outward2 form)
15	<a href="#">c2zodB_</a>	Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> selenide, water dikinase; <b>PDBTitle:</b> crystal structure of selenophosphate synthetase from aquifex aeolicus
16	<a href="#">c2zauB_</a>	Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> selenide, water dikinase; <b>PDBTitle:</b> crystal structure of an n-terminally truncated2 selenophosphate synthetase from aquifex aeolicus
17	<a href="#">c3vtiD_</a>	Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> hydrogenase maturation factor; <b>PDBTitle:</b> crystal structure of hype-hypf complex
18	<a href="#">c2z1tA_</a>	Alignment		100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase expression/formation protein hype; <b>PDBTitle:</b> crystal structure of hydrogenase maturation protein hype
19	<a href="#">c2rb9D_</a>	Alignment		100.0	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hype protein; <b>PDBTitle:</b> crystal structure of e.coli hype
20	<a href="#">d1t3ta5</a>	Alignment		100.0	22	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
21	<a href="#">c3m84A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylformylglycinamide cyclo-ligase; <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole synthetase from2 francisella tularensis
22	<a href="#">c2yxzA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiamin-monophosphate kinase; <b>PDBTitle:</b> crystal structure of tt0281 from thermus thermophilus hb8
23	<a href="#">c2z01A_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylformylglycinamide cyclo-ligase; <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole synthetase from2 geobacillus kaustophilus
24	<a href="#">c3c9uB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thiamine monophosphate kinase; <b>PDBTitle:</b> aathil complexed with adp and tpp
25	<a href="#">c2v9yA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylformylglycinamide cyclo-ligase; <b>PDBTitle:</b> human aminoimidazole ribonucleotide synthetase
26	<a href="#">d1vk3a2</a>	Alignment	not modelled	100.0	32	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
27	<a href="#">c5i16A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative selenophosphate synthetase; <b>PDBTitle:</b> crystal structure of n-terminus truncated selenophosphate synthetase2 from leishmania major
28	<a href="#">c1vqvB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thiamine monophosphate kinase; <b>PDBTitle:</b> crystal structure of thiamine monophosphate kinase

					(thil)2 from aquifex aeolicus
29	<a href="#">c5avmE_</a>	Alignment	not modelled	100.0	18 <b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> phosphoribosylformylglycinamide cyclo-ligase; <b>PDBTitle:</b> crystal structures of 5-aminoimidazole ribonucleotide (air)2 synthetase, purm, from thermus thermophilus
30	<a href="#">d1t3ta6</a>	Alignment	not modelled	100.0	31 <b>Fold:</b> PurM C-terminal domain-like <b>Superfamily:</b> PurM C-terminal domain-like <b>Family:</b> PurM C-terminal domain-like
31	<a href="#">d1t3ta4</a>	Alignment	not modelled	100.0	29 <b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
32	<a href="#">d1vk3a3</a>	Alignment	not modelled	100.0	44 <b>Fold:</b> PurM C-terminal domain-like <b>Superfamily:</b> PurM C-terminal domain-like <b>Family:</b> PurM C-terminal domain-like
33	<a href="#">c3mdoB_</a>	Alignment	not modelled	100.0	16 <b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphoribosylformylglycinamide cyclo-ligase; <b>PDBTitle:</b> crystal structure of a putative phosphoribosylformylglycinamide2 cyclo-ligase (bdi_2101) from parabacteroides distasonis atcc 8503 at3 1.91 a resolution
34	<a href="#">d1t3ta7</a>	Alignment	not modelled	100.0	24 <b>Fold:</b> PurM C-terminal domain-like <b>Superfamily:</b> PurM C-terminal domain-like <b>Family:</b> PurM C-terminal domain-like
35	<a href="#">c3kizA_</a>	Alignment	not modelled	100.0	19 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylformylglycinamide cyclo-ligase; <b>PDBTitle:</b> crystal structure of putative phosphoribosylformylglycinamide cyclo-2 ligase (yp_676759.1) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution
36	<a href="#">d2z1ea2</a>	Alignment	not modelled	99.9	19 <b>Fold:</b> PurM C-terminal domain-like <b>Superfamily:</b> PurM C-terminal domain-like <b>Family:</b> PurM C-terminal domain-like
37	<a href="#">d2zoda2</a>	Alignment	not modelled	99.9	16 <b>Fold:</b> PurM C-terminal domain-like <b>Superfamily:</b> PurM C-terminal domain-like <b>Family:</b> PurM C-terminal domain-like
38	<a href="#">d1clia2</a>	Alignment	not modelled	99.9	19 <b>Fold:</b> PurM C-terminal domain-like <b>Superfamily:</b> PurM C-terminal domain-like <b>Family:</b> PurM C-terminal domain-like
39	<a href="#">d1clia1</a>	Alignment	not modelled	99.9	21 <b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
40	<a href="#">d1clib1</a>	Alignment	not modelled	99.9	19 <b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
41	<a href="#">d3c9ua2</a>	Alignment	not modelled	99.9	17 <b>Fold:</b> PurM C-terminal domain-like <b>Superfamily:</b> PurM C-terminal domain-like <b>Family:</b> PurM C-terminal domain-like
42	<a href="#">d2zaua1</a>	Alignment	not modelled	99.8	23 <b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
43	<a href="#">d2zoda1</a>	Alignment	not modelled	99.8	23 <b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
44	<a href="#">d3c9ua1</a>	Alignment	not modelled	99.8	16 <b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
45	<a href="#">d1t3ta1</a>	Alignment	not modelled	99.7	32 <b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> FGAM synthase PurL, linker domain <b>Family:</b> FGAM synthase PurL, linker domain
46	<a href="#">d2z1ea1</a>	Alignment	not modelled	99.7	21 <b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
47	<a href="#">c5kdmD_</a>	Alignment	not modelled	96.9	16 <b>PDB header:</b> chaperone / dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> major tegument protein; <b>PDBTitle:</b> crystal structure of ebv tegument protein bnr1 in complex with2 histone chaperone daxx and histones h3.3-h4
48	<a href="#">d3dhxa1</a>	Alignment	not modelled	60.1	12 <b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> NIL domain-like
49	<a href="#">c4zc0A_</a>	Alignment	not modelled	53.6	20 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> structure of a dodecameric bacterial helicase
50	<a href="#">d1rp3a1</a>	Alignment	not modelled	52.5	44 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma3 domain
51	<a href="#">d1ku2a1</a>	Alignment	not modelled	50.2	47 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma3 domain
52	<a href="#">c1l0oC_</a>	Alignment	not modelled	49.7	39 <b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> sigma factor; <b>PDBTitle:</b> crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf
53	<a href="#">d1l0oc_</a>	Alignment	not modelled	49.7	39 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
54	<a href="#">c2zc2A</a>	Alignment	not modelled	46.5	21 <b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dnad-like replication protein;

54	<a href="#">c2c2a</a>	Alignment	not modelled	48.5	21	<b>PDBTitle:</b> crystal structure of dnad-like replication protein from streptococcus2 mutans ua159, gi 24377835, residues 127-199
55	<a href="#">d1to3a</a>	Alignment	not modelled	46.2	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
56	<a href="#">c3jrkG</a>	Alignment	not modelled	44.6	20	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> tagatose 1,6-diphosphate aldolase 2; <b>PDBTitle:</b> a putative tagatose 1,6-diphosphate aldolase from streptococcus2 pyogenes
57	<a href="#">d1llua2</a>	Alignment	not modelled	39.9	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
58	<a href="#">c1yvlB</a>	Alignment	not modelled	39.0	18	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> signal transducer and activator of transcription <b>PDBTitle:</b> structure of unphosphorylated stat1
59	<a href="#">d2csua1</a>	Alignment	not modelled	38.7	9	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
60	<a href="#">d2qrra1</a>	Alignment	not modelled	38.1	10	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> NIL domain-like
61	<a href="#">c1szpC</a>	Alignment	not modelled	35.7	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> dna repair protein rad51; <b>PDBTitle:</b> a crystal structure of the rad51 filament
62	<a href="#">c3bkhA</a>	Alignment	not modelled	35.2	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lytic transglycosylase; <b>PDBTitle:</b> crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
63	<a href="#">d1pyta</a>	Alignment	not modelled	34.3	8	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Protease propeptides/inhibitors <b>Family:</b> Pancreatic carboxypeptidase, activation domain
64	<a href="#">c4nmnA</a>	Alignment	not modelled	33.7	18	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> aquifex aeolicus replicative helicase (dnab) complexed with adp, at2 3.3 resolution
65	<a href="#">d1o6xa</a>	Alignment	not modelled	33.7	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Protease propeptides/inhibitors <b>Family:</b> Pancreatic carboxypeptidase, activation domain
66	<a href="#">d1pcaa1</a>	Alignment	not modelled	33.4	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Protease propeptides/inhibitors <b>Family:</b> Pancreatic carboxypeptidase, activation domain
67	<a href="#">d1ayea2</a>	Alignment	not modelled	32.7	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Protease propeptides/inhibitors <b>Family:</b> Pancreatic carboxypeptidase, activation domain
68	<a href="#">d1kwma2</a>	Alignment	not modelled	32.2	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Protease propeptides/inhibitors <b>Family:</b> Pancreatic carboxypeptidase, activation domain
69	<a href="#">d2boaa2</a>	Alignment	not modelled	31.8	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Protease propeptides/inhibitors <b>Family:</b> Pancreatic carboxypeptidase, activation domain
70	<a href="#">d1rjwa2</a>	Alignment	not modelled	30.5	10	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
71	<a href="#">d1uufa2</a>	Alignment	not modelled	30.4	11	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
72	<a href="#">d1piwa2</a>	Alignment	not modelled	30.4	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
73	<a href="#">c4y5wD</a>	Alignment	not modelled	30.2	15	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> signal transducer and activator of transcription 6; <b>PDBTitle:</b> transcription factor-dna complex
74	<a href="#">c5l37E</a>	Alignment	not modelled	29.8	16	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> mism0273; <b>PDBTitle:</b> the structure of the pentameric shell protein mism0273 from the rmm2 microcompartment
75	<a href="#">d1nsaa2</a>	Alignment	not modelled	29.6	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Protease propeptides/inhibitors <b>Family:</b> Pancreatic carboxypeptidase, activation domain
76	<a href="#">c5vt9A</a>	Alignment	not modelled	29.3	11	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin light chain tgmlc1; <b>PDBTitle:</b> myosin light chain 1 and myoa complex
77	<a href="#">d1pbaa</a>	Alignment	not modelled	29.0	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Protease propeptides/inhibitors <b>Family:</b> Pancreatic carboxypeptidase, activation domain
78	<a href="#">c4rgwB</a>	Alignment	not modelled	26.7	15	<b>PDB header:</b> transferase/transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription initiation factor tfiid subunit 7; <b>PDBTitle:</b> crystal structure of a taf1-taf7 complex in human transcription factor2 iid
79	<a href="#">d1jqga2</a>	Alignment	not modelled	26.6	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Protease propeptides/inhibitors <b>Family:</b> Pancreatic carboxypeptidase, activation domain
80	<a href="#">c1uusa</a>	Alignment	not modelled	24.3	11	<b>PDB header:</b> signal transduction <b>Chain:</b> A: <b>PDB Molecule:</b> stat protein; <b>PDBTitle:</b> structure of an activated dictyostelium stat in its2 dna-unbound form
						<b>PDB header:</b> replication

81	<a href="#">c3bgwD_</a>	Alignment	not modelled	24.1	18	<b>Chain:</b> D: <b>PDB Molecule:</b> dnab-like replicative helicase; <b>PDBTitle:</b> the structure of a dnab-like replicative helicase and its interactions2 with primase
82	<a href="#">d2rcfa1</a>	Alignment	not modelled	22.3	14	<b>Fold:</b> OB-fold <b>Superfamily:</b> EutN/CcmL-like <b>Family:</b> EutN/CcmL-like
83	<a href="#">c5h29A_</a>	Alignment	not modelled	22.1	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase/glutathione-related protein; <b>PDBTitle:</b> crystal structure of the ntd_n/c domain of alkylhydroperoxide2 reductase ahpf from enterococcus faecalis (v583)
84	<a href="#">d2pifa1</a>	Alignment	not modelled	21.7	19	<b>Fold:</b> PSTPO5379-like <b>Superfamily:</b> PSTPO5379-like <b>Family:</b> PSTPO5379-like
85	<a href="#">d2qswa1</a>	Alignment	not modelled	20.1	10	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> NIL domain-like
86	<a href="#">c2q6tB_</a>	Alignment	not modelled	19.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dnab replication fork helicase; <b>PDBTitle:</b> crystal structure of the thermus aquaticus dnab monomer
87	<a href="#">d2guka1</a>	Alignment	not modelled	19.7	7	<b>Fold:</b> PG1857-like <b>Superfamily:</b> PG1857-like <b>Family:</b> PG1857-like
88	<a href="#">c1vjqB_</a>	Alignment	not modelled	19.6	23	<b>PDB header:</b> structural genomics, de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> designed protein; <b>PDBTitle:</b> designed protein based on backbone conformation of2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal3 predicted stability.
89	<a href="#">c2bmaA_</a>	Alignment	not modelled	18.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase (nadp+); <b>PDBTitle:</b> the crystal structure of plasmodium falciparum glutamate2 dehydrogenase, a putative target for novel antimalarial3 drugs
90	<a href="#">c2vznA_</a>	Alignment	not modelled	17.9	33	<b>PDB header:</b> allergen <b>Chain:</b> A: <b>PDB Molecule:</b> venom allergen 3; <b>PDBTitle:</b> crystal structure of the major allergen from fire ant venom, sol i 3
91	<a href="#">c4ex8A_</a>	Alignment	not modelled	17.8	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> alna; <b>PDBTitle:</b> crystal structure of the prealnumycin c-glycosynthase alna
92	<a href="#">c6bbmA_</a>	Alignment	not modelled	17.4	15	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> mechanisms of opening and closing of the bacterial replicative2 helicase: the dnab helicase and lambda p helicase loader complex
93	<a href="#">c3gndC_</a>	Alignment	not modelled	16.9	20	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> aldolase lsrf; <b>PDBTitle:</b> crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
94	<a href="#">c5firH_</a>	Alignment	not modelled	16.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> paxt-1; <b>PDBTitle:</b> crystal structure of c. elegans xrn2 in complex with the2 xrn2-binding domain of paxt-1
95	<a href="#">d1qnxA_</a>	Alignment	not modelled	16.9	30	<b>Fold:</b> PR-1-like <b>Superfamily:</b> PR-1-like <b>Family:</b> PR-1-like
96	<a href="#">d1pbya1</a>	Alignment	not modelled	16.8	23	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
97	<a href="#">c5weeD_</a>	Alignment	not modelled	16.7	20	<b>PDB header:</b> lipid binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> venom allergen like protein 4; <b>PDBTitle:</b> crystal structure of hpva14
98	<a href="#">c3if8A_</a>	Alignment	not modelled	16.4	13	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> protein zwilch homolog; <b>PDBTitle:</b> crystal structure of zwilch, a member of the rzz kinetochore complex
99	<a href="#">c2vyeA_</a>	Alignment	not modelled	15.8	15	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> crystal structure of the dnac-ssdna complex