


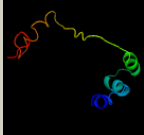

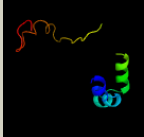

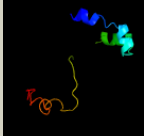

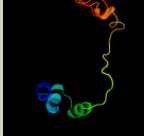

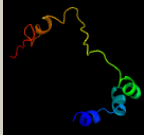

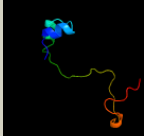



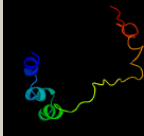

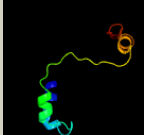


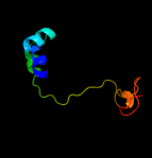
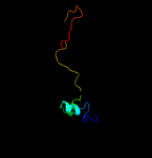

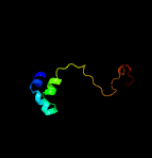

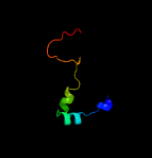
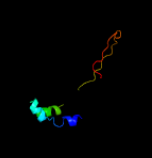
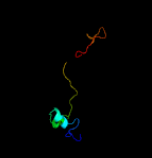
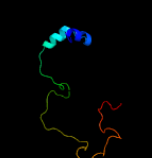


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2331_(-)_2604307_2604693
Date	Mon Aug 5 13:25:48 BST 2019
Unique Job ID	e4c70823d45cf04b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1kqfa2</a>	 Alignment		99.2	29	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
2	<a href="#">c1kqgA</a>	 Alignment		99.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> formate dehydrogenase, nitrate-inducible, major subunit; <b>PDBTitle:</b> formate dehydrogenase n from e. coli
3	<a href="#">c1h0hA</a>	 Alignment		98.8	27	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> formate dehydrogenase subunit alpha; <b>PDBTitle:</b> tungsten containing formate dehydrogenase from desulfovibrio gigas
4	<a href="#">d1h0ha2</a>	 Alignment		98.8	25	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
5	<a href="#">d1ogya2</a>	 Alignment		98.8	29	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
6	<a href="#">d2jioa2</a>	 Alignment		98.7	35	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
7	<a href="#">c4aayE</a>	 Alignment		98.6	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> aroa; <b>PDBTitle:</b> crystal structure of the arsenite oxidase protein complex2 from rhizobium species strain nt-26
8	<a href="#">c2nyaF</a>	 Alignment		98.5	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> periplasmic nitrate reductase; <b>PDBTitle:</b> crystal structure of the periplasmic nitrate reductase2 (nap) from escherichia coli
9	<a href="#">c2v45A</a>	 Alignment		98.5	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic nitrate reductase; <b>PDBTitle:</b> a new catalytic mechanism of periplasmic nitrate reductase2 from desulfovibrio desulfuricans atcc 27774 from3 crystallographic and epr data and based on detailed4 analysis of the sixth ligand
10	<a href="#">d2iv2x2</a>	 Alignment		98.4	29	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
11	<a href="#">c2iv2X</a>	 Alignment		98.3	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> formate dehydrogenase h; <b>PDBTitle:</b> reinterpretation of reduced form of formate dehydrogenase h from e.2 coli

12	<a href="#">c1ogyA</a>	Alignment		98.3	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic nitrate reductase; <b>PDBTitle:</b> crystal structure of the heterodimeric nitrate reductase2 from rhodobacter sphaeroides
13	<a href="#">d1y5ia2</a>	Alignment		98.2	23	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
14	<a href="#">c2ivfA</a>	Alignment		98.2	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ethylbenzene dehydrogenase alpha-subunit; <b>PDBTitle:</b> ethylbenzene dehydrogenase from aromatoleum aromaticum
15	<a href="#">c5ch7E</a>	Alignment		98.1	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> dmsio reductase family type ii enzyme, molybdopterin <b>PDBTitle:</b> crystal structure of the perchlorate reductase pcrab - phe164 gate2 switch intermediate - from azospira suillum ps
16	<a href="#">d1g8ka2</a>	Alignment		97.8	34	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
17	<a href="#">c1g8jC</a>	Alignment		97.8	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> arsenite oxidase; <b>PDBTitle:</b> crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
18	<a href="#">c2vpyE</a>	Alignment		97.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> thiosulfate reductase; <b>PDBTitle:</b> polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
19	<a href="#">c1y5iA</a>	Alignment		97.8	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> respiratory nitrate reductase 1 alpha chain; <b>PDBTitle:</b> the crystal structure of the narghi mutant nari-k86a
20	<a href="#">d1dmra2</a>	Alignment		97.7	21	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
21	<a href="#">c1tmoA</a>	Alignment	not modelled	97.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trimethylamine n-oxide reductase; <b>PDBTitle:</b> trimethylamine n-oxide reductase from shewanella massilia
22	<a href="#">c1eu1A</a>	Alignment	not modelled	97.4	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dimethyl sulfoxide reductase; <b>PDBTitle:</b> the crystal structure of rhodobacter sphaeroides dimethylsulfoxide2 reductase reveals two distinct molybdenum coordination environments.
23	<a href="#">d1tmoa2</a>	Alignment	not modelled	97.3	17	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
24	<a href="#">d1eu1a2</a>	Alignment	not modelled	97.2	26	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
25	<a href="#">c1vlfO</a>	Alignment	not modelled	97.1	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Q: <b>PDB Molecule:</b> pyrogallol hydroxytransferase large subunit; <b>PDBTitle:</b> crystal structure of pyrogallol-phloroglucinol transhydroxylase from2 pelobacter acidigallici complexed with inhibitor 1,2,4,5-3 tetrahydroxy-benzene
26	<a href="#">c6cz7C</a>	Alignment	not modelled	97.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> arra; <b>PDBTitle:</b> the arsenate respiratory reductase (arr) complex from shewanella sp.2 ana-3
27	<a href="#">c1h5nC</a>	Alignment	not modelled	96.7	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dmsio reductase; <b>PDBTitle:</b> dmsio reductase modified by the presence of dms and air
						<b>PDB header:</b> lyase

28	<a href="#">c2e7zA_</a>	Alignment	not modelled	96.3	25	<b>Chain:</b> A: <b>PDB Molecule:</b> acetylene hydratase ahv; <b>PDBTitle:</b> acetylene hydratase from pelobacter acetylenicus
29	<a href="#">d1vlfm2</a>	Alignment	not modelled	95.9	17	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
30	<a href="#">c5t5mB_</a>	Alignment	not modelled	88.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> tungsten formylmethanofuran dehydrogenase subunit fwdb; <b>PDBTitle:</b> tungsten-containing formylmethanofuran dehydrogenase from 2 methanothermobacter wolfeii, trigonal form at 2.5 a.
31	<a href="#">d1ja1a1</a>	Alignment	not modelled	58.5	20	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> NADPH-cytochrome p450 reductase FAD-binding domain-like
32	<a href="#">c2ev2B_</a>	Alignment	not modelled	48.6	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein rv1264/mt1302; <b>PDBTitle:</b> structure of rv1264n, the regulatory domain of the mycobacterial2 adenyllyl cylcase rv1264, at ph 8.5
33	<a href="#">d1jb9a1</a>	Alignment	not modelled	43.8	23	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
34	<a href="#">d1ddga1</a>	Alignment	not modelled	42.6	31	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> NADPH-cytochrome p450 reductase FAD-binding domain-like
35	<a href="#">c1l0oC_</a>	Alignment	not modelled	39.2	26	<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 sigma f
36	<a href="#">d1l0oc_</a>	Alignment	not modelled	39.2	26	<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
37	<a href="#">c2kvtA_</a>	Alignment	not modelled	34.7	54	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yaia; <b>PDBTitle:</b> solution nmr structure of yaia from escherichia eoli. northeast2 structural genomics target er244
38	<a href="#">d1f20a1</a>	Alignment	not modelled	32.4	33	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> NADPH-cytochrome p450 reductase FAD-binding domain-like
39	<a href="#">d1ku2a1</a>	Alignment	not modelled	26.8	31	<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
40	<a href="#">d1r8da_</a>	Alignment	not modelled	26.1	15	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
41	<a href="#">d2fug32</a>	Alignment	not modelled	23.0	15	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
42	<a href="#">c6j7aB_</a>	Alignment	not modelled	21.2	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> heme oxygenase 1,nadph--cytochrome p450 reductase; <b>PDBTitle:</b> fusion protein of heme oxygenase-1 and nadph cytochrome p450 reductase2 (17aa)
43	<a href="#">c6nu9A_</a>	Alignment	not modelled	20.7	32	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> zinc-binding non-structural protein; <b>PDBTitle:</b> crystal structure of a zinc-binding non-structural protein from the2 hepatitis e virus
44	<a href="#">c2bpoA_</a>	Alignment	not modelled	19.7	23	<b>PDB header:</b> reductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph-cytochrom p450 reductase; <b>PDBTitle:</b> crystal structure of the yeast cpr triple mutant: d74g, y75f, k78a.
45	<a href="#">c3qftA_</a>	Alignment	not modelled	18.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph--cytochrome p450 reductase; <b>PDBTitle:</b> crystal structure of nadph-cytochrome p450 reductase (fad/nadph domain2 and r457h mutant)
46	<a href="#">c2qtzA_</a>	Alignment	not modelled	17.7	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> smethionine synthase reductase; <b>PDBTitle:</b> crystal structure of the nadp+-bound fad-containing fnr-like module of2 human methionine synthase reductase
47	<a href="#">c3hh0C_</a>	Alignment	not modelled	17.4	0	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, merr family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, merr family from2 bacillus cereus
48	<a href="#">d2bw3a1</a>	Alignment	not modelled	16.3	33	<b>Fold:</b> Hermes dimerisation domain <b>Superfamily:</b> Hermes dimerisation domain <b>Family:</b> Hermes dimerisation domain
49	<a href="#">c6amaO_</a>	Alignment	not modelled	15.1	21	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> O: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> structure of s. coelicolor/s. venezuelae bldc-smea-sffa complex to2 3.09 angstrom
50	<a href="#">c3mqjA_</a>	Alignment	not modelled	14.1	26	<b>PDB header:</b> transcription activator <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor coe1; <b>PDBTitle:</b> human early b-cell factor 1 (ebf1) ipt/tig domain
51	<a href="#">c1y6uA_</a>	Alignment	not modelled	14.0	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> excisionase from transposon tn916; <b>PDBTitle:</b> the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases
52	<a href="#">c1f20A_</a>	Alignment	not modelled	13.6	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitric-oxide synthase; <b>PDBTitle:</b> crystal structure of rat neuronal nitric-oxide synthase fad/nadp+2 domain at 1.9a resolution.
53	<a href="#">c6efvA_</a>	Alignment	not modelled	13.0	31	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase [nadph] flavoprotein alpha-component; <b>PDBTitle:</b> the nadph-dependent sulfite reductase flavoprotein

						adopts an extended2 conformation that is unique to this diflavin reductase
54	<a href="#">c4ediC_</a>	Alignment	not modelled	12.0	18	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> ethanolamine utilization protein; <b>PDBTitle:</b> disulfide bonded eutl from clostridium perfringens
55	<a href="#">d1qfza1</a>	Alignment	not modelled	11.8	42	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
56	<a href="#">c5o5jE_</a>	Alignment	not modelled	11.8	22	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> 30s ribosomal protein s5; <b>PDBTitle:</b> structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
57	<a href="#">c1ifpA_</a>	Alignment	not modelled	11.1	39	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> major coat protein assembly; <b>PDBTitle:</b> inovirus (filamentous bacteriophage) strain pf3 major coat2 protein assembly
58	<a href="#">c1tliA_</a>	Alignment	not modelled	10.7	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitric-oxide synthase, brain; <b>PDBTitle:</b> crystal structure of rat neuronal nitric-oxide synthase2 reductase module at 2.3 a resolution.
59	<a href="#">c3t0vA_</a>	Alignment	not modelled	10.1	12	<b>PDB header:</b> transcription regulator/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr
60	<a href="#">c3ezfA_</a>	Alignment	not modelled	9.7	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> para; <b>PDBTitle:</b> partition protein
61	<a href="#">c1ddiA_</a>	Alignment	not modelled	9.6	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase [nadph] flavoprotein alpha-component; <b>PDBTitle:</b> crystal structure of sir-fp60
62	<a href="#">c2jmlA_</a>	Alignment	not modelled	9.3	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> dna binding domain/transcriptional regulator; <b>PDBTitle:</b> solution structure of the n-terminal domain of cara repressor
63	<a href="#">c4l4qA_</a>	Alignment	not modelled	8.9	67	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosylmethionine synthase; <b>PDBTitle:</b> methionine adenosyltransferase
64	<a href="#">c2dqdB_</a>	Alignment	not modelled	8.6	26	<b>PDB header:</b> hydrolase, dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> deoxyguanosinetriphosphate triphosphohydrolase, putative; <b>PDBTitle:</b> crystal structure of dntp triphosphohydrolase from thermus2 thermophilus hb8, which is homologous to dgtp triphosphohydrolase
65	<a href="#">c3dupB_</a>	Alignment	not modelled	8.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of mutt/nudix family hydrolase from rhodospirillum2 rubrum atcc 11170
66	<a href="#">c2fugC_</a>	Alignment	not modelled	8.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh-quinone oxidoreductase chain 3; <b>PDBTitle:</b> crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
67	<a href="#">c4dqkA_</a>	Alignment	not modelled	8.1	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional p-450/nadph-p450 reductase; <b>PDBTitle:</b> crystal structure of the fad binding domain of cytochrome p450 bm3
68	<a href="#">c3io0A_</a>	Alignment	not modelled	8.0	36	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> etub protein; <b>PDBTitle:</b> crystal structure of etub from clostridium kluveri
69	<a href="#">d2p7vb1</a>	Alignment	not modelled	7.9	15	<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
70	<a href="#">c1dpuA_</a>	Alignment	not modelled	7.3	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> replication protein a (rpa32) c-terminal domain; <b>PDBTitle:</b> solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
71	<a href="#">d1dpua_</a>	Alignment	not modelled	7.3	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> C-terminal domain of RPA32
72	<a href="#">c4cc9B_</a>	Alignment	not modelled	7.3	20	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> protein vpx; <b>PDBTitle:</b> crystal structure of human samhd1 (amino acid residues 582-626) bound2 to vpx isolated from sooty mangabey and human dcaf1 (amino acid3 residues 1058-1396)
73	<a href="#">c4hpvA_</a>	Alignment	not modelled	7.1	67	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosylmethionine synthase; <b>PDBTitle:</b> crystal structure of s-adenosylmethionine synthetase from sulfolobus2 solfataricus
74	<a href="#">c4fayC_</a>	Alignment	not modelled	7.0	24	<b>PDB header:</b> glycerol-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> microcompartments protein; <b>PDBTitle:</b> crystal structure of a trimeric bacterial microcompartment shell2 protein pdub with glycerol metabolites
75	<a href="#">c1j9zB_</a>	Alignment	not modelled	7.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadph-cytochrome p450 reductase; <b>PDBTitle:</b> cypor-w677g
76	<a href="#">c4r4eA_</a>	Alignment	not modelled	6.8	17	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator glnr; <b>PDBTitle:</b> structure of glnr-dna complex
77	<a href="#">c2lfwA_</a>	Alignment	not modelled	6.7	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> phyr sigma-like domain; <b>PDBTitle:</b> nmr structure of the phyrsl-nepr complex from sphingomonas sp. fr1
78	<a href="#">c2vz4A_</a>	Alignment	not modelled	6.6	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional activator tipa;

78	<a href="#">c4vz4A_</a>	Alignment	not modelled	6.6	11	<b>PDBTitle:</b> the n-terminal domain of merr-like protein tipal bound to promoter dna <b>PDB header:</b> dna binding
79	<a href="#">c5af3A_</a>	Alignment	not modelled	6.5	6	<b>Chain:</b> A; <b>PDB Molecule:</b> vapbc49; <b>PDBTitle:</b> x-ray crystal structure of rv2018 from mycobacterium tuberculosis
80	<a href="#">c5c8eC_</a>	Alignment	not modelled	6.4	25	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> C; <b>PDB Molecule:</b> light-dependent transcriptional regulator carh; <b>PDBTitle:</b> crystal structure of thermus thermophilus carh bound to2 adenosylcobalamin and a 26-bp dna segment
81	<a href="#">c5u4nA_</a>	Alignment	not modelled	6.1	25	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> fructose-1; <b>PDBTitle:</b> crystal structure of a fructose-bisphosphate aldolase from neisseria2 gonorrhoeae
82	<a href="#">c3u27D_</a>	Alignment	not modelled	6.1	19	<b>PDB header:</b> structural protein <b>Chain:</b> D; <b>PDB Molecule:</b> microcompartments protein; <b>PDBTitle:</b> crystal structure of ethanolamine utilization protein eutl from2 leptotrichia buccalis c-1013-b
83	<a href="#">c5z9aB_</a>	Alignment	not modelled	6.0	31	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> chorismate synthase; <b>PDBTitle:</b> crystal structure of chorismate synthase from pseudomonas aeruginosa
84	<a href="#">c3iwfA_</a>	Alignment	not modelled	5.7	6	<b>PDB header:</b> transcription regulator <b>Chain:</b> A; <b>PDB Molecule:</b> transcription regulator rpir family; <b>PDBTitle:</b> the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
85	<a href="#">c5i44E_</a>	Alignment	not modelled	5.4	17	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> E; <b>PDB Molecule:</b> chromosome-anchoring protein raca; <b>PDBTitle:</b> structure of raca-dna complex; p21 form