



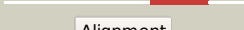

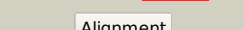

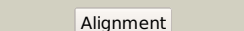





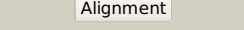

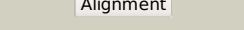
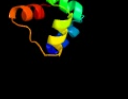
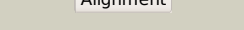

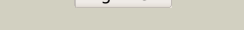



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0201c (-) _237892_238395
Date	Tue Jul 23 14:50:25 BST 2019
Unique Job ID	a5a3b86cf76f6eef

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1y9qA_</a>	 Alignment		95.8	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, hth_3 family; <b>PDBTitle:</b> crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
2	<a href="#">c2xcjB_</a>	 Alignment		95.3	25	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> c protein; <b>PDBTitle:</b> crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2
3	<a href="#">c3trbA_</a>	 Alignment		94.5	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> virulence-associated protein i; <b>PDBTitle:</b> structure of an adduction module antidote protein of a higa (higa)2 family from coxiella burnetii
4	<a href="#">c3cecA_</a>	 Alignment		94.4	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative antidote protein of plasmid maintenance system; <b>PDBTitle:</b> crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
5	<a href="#">c4mcxE_</a>	 Alignment		94.4	27	<b>PDB header:</b> toxin <b>Chain:</b> E: <b>PDB Molecule:</b> antidote protein; <b>PDBTitle:</b> p. vulgaris higba structure, crystal form 2
6	<a href="#">c6f8sA_</a>	 Alignment		94.1	18	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> xre family transcriptional regulator; <b>PDBTitle:</b> toxin-antitoxin complex grata
7	<a href="#">d1y9qa1</a>	 Alignment		94.0	22	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Probable transcriptional regulator VC1968, N-terminal domain
8	<a href="#">d1x57a1</a>	 Alignment		93.5	21	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> EDF1-like
9	<a href="#">d1adra_</a>	 Alignment		93.4	6	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
10	<a href="#">c3vk0B_</a>	 Alignment		93.2	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of hypothetical transcription factor nhf from2 neisseria
11	<a href="#">c3dnvB_</a>	 Alignment		93.1	14	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator hipb; <b>PDBTitle:</b> mdt protein

12	<a href="#">c6b9rD_</a>	Alignment		93.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> hydroxyethylphosphonate dioxygenase; <b>PDBTitle:</b> streptomyces albus hepd with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
13	<a href="#">c2o38A_</a>	Alignment		93.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> putative xre family transcriptional regulator
14	<a href="#">d2o38a1</a>	Alignment		93.0	16	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE1354
15	<a href="#">c5j9iH_</a>	Alignment		92.9	12	<b>PDB header:</b> antitoxin <b>Chain:</b> H: <b>PDB Molecule:</b> antitoxin iga-2; <b>PDBTitle:</b> crystal structure of the higa2 antitoxin c-terminal domain
16	<a href="#">c2jvIA_</a>	Alignment		92.8	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> trmbf1; <b>PDBTitle:</b> nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
17	<a href="#">d1rioa_</a>	Alignment		92.8	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
18	<a href="#">d1y7ya1</a>	Alignment		92.3	13	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
19	<a href="#">d2b5aa1</a>	Alignment		92.3	13	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
20	<a href="#">c2kpiA_</a>	Alignment		92.3	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> sos-response transcriptional repressor, lexa; <b>PDBTitle:</b> solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
21	<a href="#">d2icta1</a>	Alignment	not modelled	91.8	16	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
22	<a href="#">c3clcC_</a>	Alignment	not modelled	91.6	6	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> C: <b>PDB Molecule:</b> regulatory protein; <b>PDBTitle:</b> crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
23	<a href="#">d2a6ca1</a>	Alignment	not modelled	91.5	24	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE1354
24	<a href="#">c3f52A_</a>	Alignment	not modelled	91.3	17	<b>PDB header:</b> transcription activator <b>Chain:</b> A: <b>PDB Molecule:</b> clp gene regulator (clgr); <b>PDBTitle:</b> crystal structure of the clp gene regulator clgr from c. glutamicum
25	<a href="#">c2ebyA_</a>	Alignment	not modelled	91.3	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ybaq; <b>PDBTitle:</b> crystal structure of a hypothetical protein from e. coli
26	<a href="#">c3omtA_</a>	Alignment	not modelled	91.0	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
27	<a href="#">d2r1jl1</a>	Alignment	not modelled	90.7	6	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
28	<a href="#">c2ewtA_</a>	Alignment	not modelled	90.7	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> crystal structure of the dna-binding domain of bldd

29	<a href="#">c3eusB</a>	Alignment	not modelled	90.5	9	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna-binding protein; <b>PDBTitle:</b> the crystal structure of the dna binding protein from silicibacter2 pomeroyi
30	<a href="#">c2ppxA</a>	Alignment	not modelled	90.2	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein atu1735; <b>PDBTitle:</b> crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
31	<a href="#">d2ppxA1</a>	Alignment	not modelled	90.2	14	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
32	<a href="#">c5d50I</a>	Alignment	not modelled	90.2	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> I: <b>PDB Molecule:</b> repressor; <b>PDBTitle:</b> crystal structure of rep-ant complex from salmonella-temperate phage
33	<a href="#">d2ofya1</a>	Alignment	not modelled	90.0	21	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
34	<a href="#">c3zhiA</a>	Alignment	not modelled	89.9	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> ci; <b>PDBTitle:</b> n-terminal domain of the ci repressor from bacteriophage tp901-1
35	<a href="#">d1b0na2</a>	Alignment	not modelled	89.8	16	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
36	<a href="#">c3f6wE</a>	Alignment	not modelled	89.7	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> xre-family like protein; <b>PDBTitle:</b> xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
37	<a href="#">d1utxA</a>	Alignment	not modelled	89.6	18	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
38	<a href="#">c2mezA</a>	Alignment	not modelled	89.5	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> multi-protein bridging factor (mbp-like); <b>PDBTitle:</b> flexible anchoring of archaean mbf1 on ribosomes suggests role as2 recruitment factor
39	<a href="#">c5woqA</a>	Alignment	not modelled	89.1	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator clgr; <b>PDBTitle:</b> crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis
40	<a href="#">c3bs3A</a>	Alignment	not modelled	88.9	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> crystal structure of a putative dna-binding protein from bacteroides2 fragilis
41	<a href="#">c5jaaB</a>	Alignment	not modelled	88.6	12	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin iga-2; <b>PDBTitle:</b> crystal structure of the higba2 toxin-antitoxin complex
42	<a href="#">c3bdnB</a>	Alignment	not modelled	88.6	17	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> lambda repressor; <b>PDBTitle:</b> crystal structure of the lambda repressor
43	<a href="#">c5d4zF</a>	Alignment	not modelled	88.5	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> repressor; <b>PDBTitle:</b> crystal structure of repressor from salmonella-temperate phage
44	<a href="#">c3fmyA</a>	Alignment	not modelled	88.0	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator mqsa <b>PDBTitle:</b> structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
45	<a href="#">d1lmb3</a>	Alignment	not modelled	87.1	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
46	<a href="#">c1b0nA</a>	Alignment	not modelled	86.0	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> protein (sinr protein); <b>PDBTitle:</b> sinr protein/sini protein complex
47	<a href="#">d1sq8a</a>	Alignment	not modelled	86.0	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
48	<a href="#">c3op9A</a>	Alignment	not modelled	85.7	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> pli0006 protein; <b>PDBTitle:</b> crystal structure of transcriptional regulator from listeria innocua
49	<a href="#">c3b7hA</a>	Alignment	not modelled	84.0	17	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> prophage lp1 protein 11; <b>PDBTitle:</b> crystal structure of the prophage lp1 protein 11
50	<a href="#">c3gn5B</a>	Alignment	not modelled	84.0	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator mqsa (ygit/b3021); <b>PDBTitle:</b> structure of the e. coli protein mqsa (ygit/b3021)
51	<a href="#">c2mqkA</a>	Alignment	not modelled	83.8	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent target dna activator b; <b>PDBTitle:</b> solution structure of n terminal domain of the nub aaa+ atpase
52	<a href="#">c3pxpA</a>	Alignment	not modelled	83.6	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> helix-turn-helix domain protein; <b>PDBTitle:</b> crystal structure of a pas and dna binding domain containing protein2 (caur_2278) from chloroflexus aurantiacus j-10-fl at 2.30 a3 resolution
53	<a href="#">c5uk3J</a>	Alignment	not modelled	83.4	24	<b>PDB header:</b> lyase <b>Chain:</b> J: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of cyanase from t. urticae
54	<a href="#">d1r69a</a>	Alignment	not modelled	83.0	19	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
						<b>PDB header:</b> toxin/antitoxin/dna <b>Chain:</b> C: <b>PDB Molecule:</b> toxin-antitoxin system antidote

55	<a href="#">c4pu4C_</a>	Alignment	not modelled	82.8	16	transcriptional repressor <b>PDBTitle:</b> shewanella oneidensis mr-1 toxin antitoxin system hipa, hipb and its2 operator dna complex (space group p21)
56	<a href="#">c3kxaD_</a>	Alignment	not modelled	82.7	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of ngo0477 from neisseria gonorrhoeae
57	<a href="#">c4ybaA_</a>	Alignment	not modelled	82.7	11	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein c; <b>PDBTitle:</b> the structure of the c.kpn2i controller protein
58	<a href="#">c2bnoA_</a>	Alignment	not modelled	81.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxidase; <b>PDBTitle:</b> the structure of hydroxypropylphosphonic acid epoxidase from s.2 wedmorenis.
59	<a href="#">c3ivpD_</a>	Alignment	not modelled	81.2	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> putative transposon-related dna-binding protein; <b>PDBTitle:</b> the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
60	<a href="#">c3mfc_</a>	Alignment	not modelled	79.7	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> putative transcriptional regulator from staphylococcus aureus.
61	<a href="#">c6b9tH_</a>	Alignment	not modelled	79.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> methylphosphonate synthase; <b>PDBTitle:</b> crystal structure of mpns with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
62	<a href="#">d2croa_</a>	Alignment	not modelled	78.7	14	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
63	<a href="#">c4ghjA_</a>	Alignment	not modelled	78.6	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> 1.75 angstrom crystal structure of transcriptional regulator ftom2 vibrio vulnificus.
64	<a href="#">d1lib_</a>	Alignment	not modelled	78.2	22	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
65	<a href="#">c3lisB_</a>	Alignment	not modelled	78.0	21	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> csp231i c protein; <b>PDBTitle:</b> crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
66	<a href="#">c6fkgC_</a>	Alignment	not modelled	76.7	19	<b>PDB header:</b> toxin <b>Chain:</b> C: <b>PDB Molecule:</b> rv1990c (mbca); <b>PDBTitle:</b> crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
67	<a href="#">c2ef8A_</a>	Alignment	not modelled	72.8	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcription factor; <b>PDBTitle:</b> crystal structure of c.ecot38is
68	<a href="#">c5j2vA_</a>	Alignment	not modelled	72.5	17	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein; <b>PDBTitle:</b> molecular insight into the regulatory mechanism of the quorum-sensing2 repressor rsal in pseudomonas aeruginosa
69	<a href="#">c4o8bA_</a>	Alignment	not modelled	69.8	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of transcriptional regulator bswr
70	<a href="#">c3t76A_</a>	Alignment	not modelled	68.1	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator vanug; <b>PDBTitle:</b> crystal structure of transcriptional regulator vanug, form ii
71	<a href="#">c2fjrB_</a>	Alignment	not modelled	63.3	9	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> repressor protein ci; <b>PDBTitle:</b> crystal structure of bacteriophage 186
72	<a href="#">c4d10H_</a>	Alignment	not modelled	59.8	17	<b>PDB header:</b> signaling protein <b>Chain:</b> H: <b>PDB Molecule:</b> cop9 signalosome complex subunit 8; <b>PDBTitle:</b> crystal structure of the cop9 signalosome
73	<a href="#">d1zs4a1</a>	Alignment	not modelled	49.0	25	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Bacteriophage CII protein
74	<a href="#">c3qyxD_</a>	Alignment	not modelled	45.5	28	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> esx-1 secretion-associated regulator espr; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis espr in complex with a2 small dna fragment
75	<a href="#">c2ebiA_</a>	Alignment	not modelled	38.2	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna binding protein gt-1; <b>PDBTitle:</b> arabidopsis gt-1 dna-binding domain with t133d phosphomimetic mutation
76	<a href="#">c2ksnA_</a>	Alignment	not modelled	37.2	38	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin domain-containing protein 2; <b>PDBTitle:</b> solution structure of the n-terminal domain of dc-ubp/ubtd2
77	<a href="#">c4itqA_</a>	Alignment	not modelled	31.3	17	<b>PDB header:</b> gene regulation, structural protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein sco1480; <b>PDBTitle:</b> crystal structure of hypothetical protein sco1480 bound to dna
78	<a href="#">d1x41a1</a>	Alignment	not modelled	24.5	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
79	<a href="#">c2vgeA_</a>	Alignment	not modelled	20.9	26	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rela-associated inhibitor; <b>PDBTitle:</b> crystal structure of the c-terminal region of human iaspp
80	<a href="#">d2a0ba_</a>	Alignment	not modelled	20.6	17	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Histidine-containing phosphotransfer domain, HPT domain <b>Family:</b> Aerobic respiration control sensor protein, ArcB
81	<a href="#">c2elkA_</a>	Alignment	not modelled	20.5	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> spcc24b10.08c protein;

81	<a href="#">c2c1nA_</a>	Alignment	not modelled	20.3	42	<b>PDBTitle:</b> solution structure of the sant domain of fission yeast2 spcc24b10.08c protein <b>PDB header:</b> metal transport
82	<a href="#">c2hu9B_</a>	Alignment	not modelled	20.3	24	<b>Chain:</b> B: <b>PDB Molecule:</b> mercuric transport protein periplasmic component; <b>PDBTitle:</b> x-ray structure of the archaeoglobus fulgidus copz n-2 terminal domain
83	<a href="#">d2cqqa1</a>	Alignment	not modelled	20.1	47	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Myb/SANT domain
84	<a href="#">c2kwhA_</a>	Alignment	not modelled	19.9	78	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> rala-binding protein 1; <b>PDBTitle:</b> ral binding domain of rlip76 (ralbp1)
85	<a href="#">c3myfB_</a>	Alignment	not modelled	19.5	32	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> the crystal structure of the hpt domain from the hpt sensor hybrid2 histidine kinase from shewanella to 1.80a
86	<a href="#">c2ym0B_</a>	Alignment	not modelled	19.2	16	<b>PDB header:</b> cell invasion <b>Chain:</b> B: <b>PDB Molecule:</b> cell invasion protein sipd; <b>PDBTitle:</b> truncated sipd from salmonella typhimurium
87	<a href="#">c3iqta_</a>	Alignment	not modelled	17.3	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> signal transduction histidine-protein kinase bara; <b>PDBTitle:</b> structure of the hpt domain of sensor protein bara from escherichia2 coli cft073.
88	<a href="#">c3nzza_</a>	Alignment	not modelled	16.6	16	<b>PDB header:</b> cell invasion <b>Chain:</b> A: <b>PDB Molecule:</b> cell invasion protein sipd; <b>PDBTitle:</b> crystal structure of the salmonella type iii secretion system tip2 protein sipd
89	<a href="#">c1zgwA_</a>	Alignment	not modelled	16.1	9	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> ada polyprotein; <b>PDBTitle:</b> nmr structure of e. coli ada protein in complex with dna
90	<a href="#">d1sr2a_</a>	Alignment	not modelled	16.0	17	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Histidine-containing phosphotransfer domain, HPT domain <b>Family:</b> Sensor-like histidine kinase YojN, C-terminal domain
91	<a href="#">c1x41A_</a>	Alignment	not modelled	15.5	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional adaptor 2-like, isoform b; <b>PDBTitle:</b> solution structure of the myb-like dna binding domain of2 human transcriptional adaptor 2-like, isoform b
92	<a href="#">d2gnxa2</a>	Alignment	not modelled	15.2	32	<b>Fold:</b> Gelsolin-like <b>Superfamily:</b> FLJ32549 C-terminal domain-like <b>Family:</b> FLJ32549 C-terminal domain-like
93	<a href="#">c3l32B_</a>	Alignment	not modelled	14.3	28	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoprotein; <b>PDBTitle:</b> structure of the dimerisation domain of the rabies virus2 phosphoprotein
94	<a href="#">c4zp0A_</a>	Alignment	not modelled	13.6	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug transporter mdfa; <b>PDBTitle:</b> crystal structure of e. coli multidrug transporter mdfa in complex2 with deoxycholate
95	<a href="#">c4eefl_</a>	Alignment	not modelled	12.3	33	<b>PDB header:</b> immune system/inhibitor <b>Chain:</b> I: <b>PDB Molecule:</b> f-hb80.4, designed hemagglutinin binding protein; <b>PDBTitle:</b> crystal structure of the designed inhibitor protein f-hb80.4 in2 complex with the 1918 influenza virus hemagglutinin.
96	<a href="#">d1wn0a1</a>	Alignment	not modelled	11.7	17	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Histidine-containing phosphotransfer domain, HPT domain <b>Family:</b> Phosphorelay protein-like
97	<a href="#">c3hugl_</a>	Alignment	not modelled	11.5	22	<b>PDB header:</b> transcription/membrane protein <b>Chain:</b> J: <b>PDB Molecule:</b> probable conserved membrane protein; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
98	<a href="#">c2mpnA_</a>	Alignment	not modelled	11.3	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> inner membrane protein ygap; <b>PDBTitle:</b> 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli
99	<a href="#">c2mpnB_</a>	Alignment	not modelled	11.3	20	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> inner membrane protein ygap; <b>PDBTitle:</b> 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli