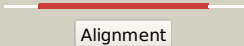

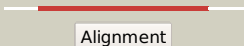

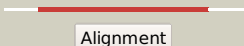







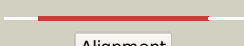











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2585c (- )_2911014_2912687
Date	Wed Aug 7 12:50:22 BST 2019
Unique Job ID	9ba2916c2018a872

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4onyB_</a>	 Alignment		100.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> extracellular solute-binding protein family 5; <b>PDBTitle:</b> crystal structure of a abc transporter, periplasmic substrate-binding2 protein from brucella melitensis
2	<a href="#">c4oetA_</a>	 Alignment		100.0	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative peptide abc-transport system periplasmic peptide- <b>PDBTitle:</b> crystal structure of nikz from campylobacter jejuni, unliganded form
3	<a href="#">c5isuA_</a>	 Alignment		100.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0135 protein; <b>PDBTitle:</b> 2.2 angstrom crystal structure of abc transporter substrate binding2 protein ctap (lmo0135) from listeria monocytogenes.
4	<a href="#">d1xoca1</a>	 Alignment		100.0	14	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
5	<a href="#">c5icqA_</a>	 Alignment		100.0	16	<b>PDB header:</b> periplasmic binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> methylocystis parvus obbp mbne; <b>PDBTitle:</b> methanobactin periplasmic binding protein
6	<a href="#">c3tpaA_</a>	 Alignment		100.0	15	<b>PDB header:</b> heme binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> heme-binding protein a; <b>PDBTitle:</b> structure of hbpa2 from haemophilus parasuis
7	<a href="#">c4qfkG_</a>	 Alignment		100.0	14	<b>PDB header:</b> peptide binding protein <b>Chain:</b> G: <b>PDB Molecule:</b> abc transporter periplasmic peptide-binding protein; <b>PDBTitle:</b> crystal structure of dipeptide binding protein from pseudoalteromonas2 sp. sm9913
8	<a href="#">c4oerA_</a>	 Alignment		100.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nika protein; <b>PDBTitle:</b> crystal structure of nika from brucella suis, unliganded form
9	<a href="#">c6hlxA_</a>	 Alignment		100.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> agaa; <b>PDBTitle:</b> structure of the pbp agaa in complex with agropinic acid from2 a.tumefacien r10
10	<a href="#">d1dpea_</a>	 Alignment		100.0	16	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
11	<a href="#">c3m8uA_</a>	 Alignment		100.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> heme-binding protein a; <b>PDBTitle:</b> crystal structure of glutathione-binding protein a (gbpa) from2 haemophilus parasuis sh0165 in complex with glutathione disulfide3 (gssg)

12	<a href="#">c2grvC_</a>	Alignment		100.0	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> lpqw; <b>PDBTitle:</b> crystal structure of lpqw
13	<a href="#">c2wokA_</a>	Alignment		100.0	16	<b>PDB header:</b> peptide binding protein/peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> clavulanic acid biosynthesis oligopeptide binding protein <b>PDBTitle:</b> clavulanic acid biosynthesis oligopeptide binding protein 2 complexed2 with bradykinin
14	<a href="#">d1zlqa1</a>	Alignment		100.0	14	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
15	<a href="#">c6i3gA_</a>	Alignment		100.0	13	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter, substrate-binding protein, family 5; <b>PDBTitle:</b> crystal structure of a putative peptide binding protein appa from2 clostridium difficile
16	<a href="#">d1jeta_</a>	Alignment		100.0	16	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
17	<a href="#">c3t66A_</a>	Alignment		100.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nickel abc transporter (nickel-binding protein); <b>PDBTitle:</b> crystal structure of nickel abc transporter from bacillus halodurans
18	<a href="#">c5u4oA_</a>	Alignment		100.0	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter substrate-binding protein; <b>PDBTitle:</b> a 2.05a x-ray structure of a bacterial extracellular solute-binding2 protein, family 5 for bacillus anthracis str. ames
19	<a href="#">c6npaA_</a>	Alignment		100.0	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> oligopeptide abc transporter, oligopeptide-binding protein; <b>PDBTitle:</b> crystal structure of oligopeptide abc transporter from bacillus2 anthracis str. ames (substrate-binding domain)
20	<a href="#">c6dtfA_</a>	Alignment		100.0	14	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic oligopeptide-binding protein; <b>PDBTitle:</b> crystal structure of haemophilus influenzae oppa complex with kkk
21	<a href="#">c1ztyA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> sugar binding protein, signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> chitin oligosaccharide binding protein; <b>PDBTitle:</b> crystal structure of the chitin oligasaccharide binding2 protein
22	<a href="#">c2d5wA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> peptide abc transporter, peptide-binding protein; <b>PDBTitle:</b> the crystal structure of oligopeptide binding protein from thermus2 thermophilus hb8 complexed with pentapeptide
23	<a href="#">c5yheA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nickel abc transporter substrate-binding protein; <b>PDBTitle:</b> the crystal structure of staphylococcus aureus cnta in complex with2 staphylopine and cobalt
24	<a href="#">c3zs6A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic oligopeptide-binding protein; <b>PDBTitle:</b> the structural characterization of burkholderia pseudomallei oppa.
25	<a href="#">c3o9pA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> peptide binding protein/peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic murein peptide-binding protein; <b>PDBTitle:</b> the structure of the escherichia coli murein tripeptide binding2 protein mppa
26	<a href="#">c3ry3B_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative solute-binding protein; <b>PDBTitle:</b> putative solute-binding protein from yersinia pestis.
27	<a href="#">c2o7jA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> oligopeptide abc transporter, periplasmic <b>PDBTitle:</b> the x-ray crystal structure of a thermophilic cellobiose2 binding protein bound with cellopentaose
						<b>PDB header:</b> peptide binding protein

28	<a href="#">c3ftoA</a>	Alignment	not modelled	100.0	14	<b>Chain:</b> A: <b>PDB Molecule:</b> oligopeptide-binding protein oppa; <b>PDBTitle:</b> crystal structure of oppa in a open conformation
29	<a href="#">d1uqwa</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
30	<a href="#">c6epzA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic alpha-galactoside-binding protein; <b>PDBTitle:</b> structure of the periplasmic binding protein melb (atu4661) in complex2 with melibiose from agrobacterium fabrum c58
31	<a href="#">c3rqtA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> 1.5 angstrom crystal structure of the complex of ligand binding2 component of abc-type import system from staphylococcus aureus with3 nickel and two histidines
32	<a href="#">c4zebA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter, substrate binding protein (agrocinopines a <b>PDBTitle:</b> pbp acca from a. tumefaciens c58 in complex with agrocinopine a
33	<a href="#">d1vr5a1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
34	<a href="#">c4pfwA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter substrate-binding protein; <b>PDBTitle:</b> crystal structure of mannohexaose bound oligopeptide abc transporter,2 periplasmic oligopeptide-binding protein (tm1226) from thermotoga3 maritima at 2.2 a resolution
35	<a href="#">c4fajA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> prgz; <b>PDBTitle:</b> structure and mode of peptide binding of pheromone receptor prgz
36	<a href="#">c4wedA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter, periplasmic solute-binding protein; <b>PDBTitle:</b> crystal structure of abc transporter substrate-binding protein from2 sinorhizobium mellioli
37	<a href="#">c4gl8B</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> oligopeptide abc transporter oppaiv; <b>PDBTitle:</b> x-ray crystal structure of a periplasmic oligopeptide-binding2 protein/oligopeptide abc transporter(oppaiv) from borrelia3 burgdorferi
38	<a href="#">c5yybA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative abc transporter periplasmic binding protein; <b>PDBTitle:</b> crystal structure of sialic acid binding protein from haemophilus2 ducreyi with neu5gc
39	<a href="#">c5kztB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> peptide binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> peptide/nickel transport system substrate-binding protein; <b>PDBTitle:</b> listeria monocytogenes oppa bound to peptide
40	<a href="#">c5ipwA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> oligopeptide abc transporter, periplasmic oligopeptide- <b>PDBTitle:</b> oligopeptide-binding protein oppa
41	<a href="#">c3lvuB</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, periplasmic substrate-binding protein; <b>PDBTitle:</b> crystal structure of abc transporter, periplasmic substrate-binding2 protein spo2066 from silicibacter pomeroyi
42	<a href="#">c3pamB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> transmembrane protein; <b>PDBTitle:</b> crystal structure of a domain of transmembrane protein of abc-type2 oligopeptide transport system from bartonella henselae str. houston-1
43	<a href="#">c3o6pA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> peptide abc transporter, peptide-binding protein; <b>PDBTitle:</b> crystal structure of peptide abc transporter, peptide-binding protein
44	<a href="#">c3l6gA</a>	Alignment	not modelled	84.3	19	<b>PDB header:</b> glycine betaine-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> betaine abc transporter permease and substrate binding <b>PDBTitle:</b> crystal structure of lactococcal opuac in its open conformation
45	<a href="#">c3tmgA</a>	Alignment	not modelled	80.0	23	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycine betaine, l-proline abc transporter, <b>PDBTitle:</b> crystal structure of glycine betaine, l-proline abc transporter,2 glycine/betaine/l-proline-binding protein (prox) from borrelia3 burgdorferi
46	<a href="#">c3chgB</a>	Alignment	not modelled	77.4	19	<b>PDB header:</b> ligand binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> glycine betaine-binding protein; <b>PDBTitle:</b> the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
47	<a href="#">c6jf1A</a>	Alignment	not modelled	69.5	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipoprotein; <b>PDBTitle:</b> crystal structure of the substrate binding protein of a methionine2 transporter from streptococcus pneumoniae
48	<a href="#">c5b3kA</a>	Alignment	not modelled	66.2	13	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pa3435; <b>PDBTitle:</b> c101a mutant of flavodoxin from pseudomonas aeruginosa
49	<a href="#">c4q0cA</a>	Alignment	not modelled	65.6	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> virulence sensor protein bvgs; <b>PDBTitle:</b> 3.1 a resolution crystal structure of the b. pertussis bvgs2 periplasmic domain
50	<a href="#">d1r9la</a>	Alignment	not modelled	63.3	20	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like

51	<a href="#">c2m6rA</a>	Alignment	not modelled	59.9	11	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> flavodoxin; <b>PDBTitle:</b> apo_yqca
52	<a href="#">c3nohA</a>	Alignment	not modelled	59.5	16	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative peptide binding protein; <b>PDBTitle:</b> crystal structure of a putative peptide binding protein (rumgna_00914)2 from ruminococcus gnavus atcc 29149 at 1.60 a resolution
53	<a href="#">c4h2dB</a>	Alignment	not modelled	57.3	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadh-dependent diflavin oxidoreductase 1; <b>PDBTitle:</b> crystal structure of ndor1
54	<a href="#">c2rejA</a>	Alignment	not modelled	57.2	16	<b>PDB header:</b> choline-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative glycine betaine abc transporter protein; <b>PDBTitle:</b> abc-transporter choline binding protein in unliganded semi-2 closed conformation
55	<a href="#">c4xz6A</a>	Alignment	not modelled	46.4	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycine betaine/proline abc transporter, periplasmic <b>PDBTitle:</b> tmox in complex with tmao
56	<a href="#">d1ykga1</a>	Alignment	not modelled	45.2	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Cytochrome p450 reductase N-terminal domain-like
57	<a href="#">c3f6sl</a>	Alignment	not modelled	44.8	14	<b>PDB header:</b> electron transport <b>Chain:</b> I: <b>PDB Molecule:</b> flavodoxin; <b>PDBTitle:</b> desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin alternate2 conformers
58	<a href="#">c4heqB</a>	Alignment	not modelled	38.6	19	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> flavodoxin; <b>PDBTitle:</b> the crystal structure of flavodoxin from desulfovibrio gigas
59	<a href="#">c2v25B</a>	Alignment	not modelled	37.1	13	<b>PDB header:</b> receptor <b>Chain:</b> B: <b>PDB Molecule:</b> major cell-binding factor; <b>PDBTitle:</b> structure of the campylobacter jejuni antigen peb1a, an2 aspartate and glutamate receptor with bound aspartate
60	<a href="#">d5nula</a>	Alignment	not modelled	36.4	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
61	<a href="#">d2fz5a1</a>	Alignment	not modelled	34.4	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
62	<a href="#">d1e5da1</a>	Alignment	not modelled	33.4	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
63	<a href="#">c4yo3G</a>	Alignment	not modelled	33.3	24	<b>PDB header:</b> transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> tssa; <b>PDBTitle:</b> enteroaggregative escherichia coli tssa n-terminal fragment
64	<a href="#">c5vegC</a>	Alignment	not modelled	32.4	13	<b>PDB header:</b> electron transport <b>Chain:</b> C: <b>PDB Molecule:</b> flavodoxin; <b>PDBTitle:</b> structure of a short-chain flavodoxin associated with a non-canonical2 pdu bacterial microcompartment
65	<a href="#">c5gzsa</a>	Alignment	not modelled	31.5	8	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ggdef family protein; <b>PDBTitle:</b> structure of vc protein
66	<a href="#">c3woaA</a>	Alignment	not modelled	30.7	12	<b>PDB header:</b> dna binding protein, sugar binding prote <b>Chain:</b> A: <b>PDB Molecule:</b> repressor protein ci, maltose-binding periplasmic protein; <b>PDBTitle:</b> crystal structure of lambda repressor (1-45) fused with maltose-2 binding protein
67	<a href="#">d1f4pa</a>	Alignment	not modelled	30.2	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
68	<a href="#">c6g7cF</a>	Alignment	not modelled	29.7	24	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> impa-related domain protein; <b>PDBTitle:</b> nt2-ctd domains of the tssa component from the type vi secretion2 system of aeromonas hydrophila.
69	<a href="#">c6fsiA</a>	Alignment	not modelled	29.7	6	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> flavodoxin; <b>PDBTitle:</b> crystal structure of semiquinone flavodoxin 1 from bacillus cereus2 (1.32 a resolution)
70	<a href="#">c3r6uA</a>	Alignment	not modelled	29.0	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> choline-binding protein; <b>PDBTitle:</b> crystal structure of choline binding protein opubc from bacillus2 subtilis
71	<a href="#">c3hr4C</a>	Alignment	not modelled	26.8	14	<b>PDB header:</b> oxidoreductase/metal binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> nitric oxide synthase, inducible; <b>PDBTitle:</b> human inos reductase and calmodulin complex
72	<a href="#">c3hlyA</a>	Alignment	not modelled	26.3	17	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> flavodoxin-like domain; <b>PDBTitle:</b> crystal structure of the flavodoxin-like domain from synechococcus sp2 q5mzp6_synp6 protein. northeast structural genomics consortium target3 snr135d.
73	<a href="#">d1ycga1</a>	Alignment	not modelled	25.2	8	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
74	<a href="#">c3gxaA</a>	Alignment	not modelled	24.4	20	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane lipoprotein gna1946; <b>PDBTitle:</b> crystal structure of gna1946
75	<a href="#">c3ir1F</a>	Alignment	not modelled	23.9	20	<b>PDB header:</b> protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> outer membrane lipoprotein gna1946; <b>PDBTitle:</b> crystal structure of lipoprotein gna1946 from neisseria meningitidis
76	<a href="#">c1n5tA</a>	Alignment	not modelled	23.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipoprotein;

76	<a href="#">c4q3a</a>	Alignment	not modelled	23.0	17	<b>PDBTitle:</b> crystal structure of an atmb (putative membrane lipoprotein) from2 streptococcus mutans ua159 at 1.91 a resolution <b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> lipoprotein;
77	<a href="#">c4oteA</a>	Alignment	not modelled	22.6	21	<b>PDBTitle:</b> crystal structure of a putative lipoprotein (cd630_1653) from2 clostridium difficile 630 at 2.20 a resolution
78	<a href="#">d1qcrd2</a>	Alignment	not modelled	21.2	29	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Cytochrome bc1 domain
79	<a href="#">d1g7da</a>	Alignment	not modelled	21.2	13	<b>Fold:</b> ERP29 C domain-like <b>Superfamily:</b> ERP29 C domain-like <b>Family:</b> ERP29 C domain-like
80	<a href="#">d1ja1a2</a>	Alignment	not modelled	20.2	9	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Cytochrome p450 reductase N-terminal domain-like
81	<a href="#">c2hnbA</a>	Alignment	not modelled	20.1	14	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> protein mioc; <b>PDBTitle:</b> solution structure of a bacterial holo-flavodoxin
82	<a href="#">c4kysA</a>	Alignment	not modelled	20.1	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiamine pyridinylase i; <b>PDBTitle:</b> clostridium botulinum thiaminase i in complex with thiamin
83	<a href="#">d1sw5a</a>	Alignment	not modelled	19.8	17	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
84	<a href="#">c5iiaH</a>	Alignment	not modelled	19.6	21	<b>PDB header:</b> cell adhesion <b>Chain:</b> H: <b>PDB Molecule:</b> vitelline envelope sperm lysin receptor; <b>PDBTitle:</b> crystal structure of putative formyltetrahydrofolate synthetase2 (tm1766) from thermotoga maritima at 1.85 a resolution (crystal form i)
85	<a href="#">c5a4jC</a>	Alignment	not modelled	18.9	31	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> formate--tetrahydrofolate ligase; <b>PDBTitle:</b> crystal structure of fthfs1 from t.acetoxydans re1
86	<a href="#">c3do6B</a>	Alignment	not modelled	18.4	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> formate--tetrahydrofolate ligase; <b>PDBTitle:</b> crystal structure of formyltetrahydrofolate synthetase2 (tm1766) from thermotoga maritima at 1.85 a resolution
87	<a href="#">d1b1ca</a>	Alignment	not modelled	17.2	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Cytochrome p450 reductase N-terminal domain-like
88	<a href="#">d2vv5a2</a>	Alignment	not modelled	17.2	21	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Mechanosensitive channel protein MscS (YggB), C-terminal domain <b>Family:</b> Mechanosensitive channel protein MscS (YggB), C-terminal domain
89	<a href="#">c4n82B</a>	Alignment	not modelled	17.1	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ribonucleotide reductase; <b>PDBTitle:</b> x-ray crystal structure of streptococcus sanguinis nrdox
90	<a href="#">d1ydga</a>	Alignment	not modelled	16.0	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> WrbA-like
91	<a href="#">c4ne4A</a>	Alignment	not modelled	15.9	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter, substrate binding protein <b>PDBTitle:</b> crystal structure of abc transporter substrate binding protein prox2 from agrobacterium tumefaciens cocrystalized with btb
92	<a href="#">c6onpA</a>	Alignment	not modelled	15.8	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic binding protein xoxj; <b>PDBTitle:</b> crystal structure of periplasmic binding protein xoxj from2 methylobacterium extorquens am1
93	<a href="#">c6j7aB</a>	Alignment	not modelled	15.2	11	<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)
94	<a href="#">c1bvyf</a>	Alignment	not modelled	14.6	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> protein (cytochrome p450 bm-3); <b>PDBTitle:</b> complex of the heme and fmn-binding domains of the2 cytochrome p450(bm-3)
95	<a href="#">d1bvyf</a>	Alignment	not modelled	14.6	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
96	<a href="#">c5widB</a>	Alignment	not modelled	14.6	11	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> flavodoxin; <b>PDBTitle:</b> structure of a flavodoxin from the domain archaea
97	<a href="#">d2f06a2</a>	Alignment	not modelled	14.6	37	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> BT0572-like
98	<a href="#">d1vmea1</a>	Alignment	not modelled	14.4	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
99	<a href="#">c6detA</a>	Alignment	not modelled	14.4	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> tv2483; <b>PDBTitle:</b> the crystal structure of tv2483 bound to l-arginine