
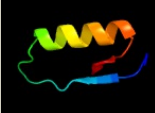



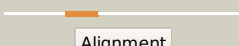
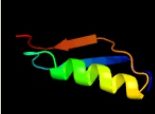
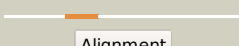

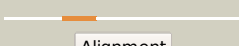

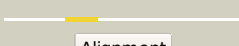
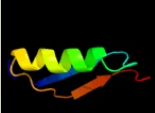



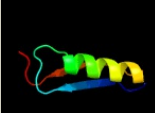

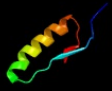

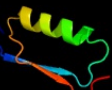
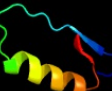
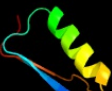



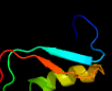


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1698 (-) _1922752_1923696
Date	Fri Aug 2 13:30:29 BST 2019
Unique Job ID	c9a736473e3d8e5f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1sy7B_	 Alignment		92.9	9	PDB header: oxidoreductase Chain: B; PDB Molecule: catalase 1; PDBTitle: crystal structure of the catalase-1 from neurospora crassa, native2 structure at 1.75a resolution.
2	d1p80a1	 Alignment		88.9	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
3	c1p81A_	 Alignment		88.3	19	PDB header: oxidoreductase Chain: A; PDB Molecule: catalase hpii; PDBTitle: crystal structure of the d181e variant of catalase hpii2 from e. coli
4	d1sy7a1	 Alignment		86.9	9	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
5	d1o57a2	 Alignment		82.0	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
6	d1mzva_	 Alignment		81.2	21	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
7	d1vcha1	 Alignment		80.4	31	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
8	c1o57A_	 Alignment		79.6	15	PDB header: dna binding protein Chain: A; PDB Molecule: pur operon repressor; PDBTitle: crystal structure of the purine operon repressor of2 bacillus subtilis
9	c4lzaB_	 Alignment		79.5	36	PDB header: transferase Chain: B; PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of adenine phosphoribosyltransferase from2 thermoanaerobacter pseudethanolicus atcc 33223, nysgrc target 029700.
10	d1y0ba1	 Alignment		78.5	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
11	c2dy0A_	 Alignment		77.7	21	PDB header: transferase Chain: A; PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of project jw0458 from escherichia coli

12	c3ej6D_	Alignment		77.6	19	PDB header: oxidoreductase Chain: D: PDB Molecule: catalase-3; PDBTitle: neurospora crassa catalase-3 crystal structure
13	d1g2qa_	Alignment		77.3	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
14	c4m0kD_	Alignment		76.8	26	PDB header: transferase Chain: D: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of adenine phosphoribosyltransferase from2 rhodothermus marinus dsm 4252, nysgrc target 029775.
15	c2vrnA_	Alignment		76.3	21	PDB header: hydrolase Chain: A: PDB Molecule: protease i; PDBTitle: the structure of the stress response protein dr1199 from deinococcus2 radiodurans: a member of the dj-1 superfamily
16	c5zgoB_	Alignment		75.4	24	PDB header: transferase Chain: B: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of apt2 from thermus thermophilus hb8
17	d1zn7a1	Alignment		73.0	24	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
18	c5fv8B_	Alignment		72.7	23	PDB header: structural protein Chain: B: PDB Molecule: fosw; PDBTitle: structure of cjun-fosw coiled coil complex.
19	c5fv8A_	Alignment		72.7	23	PDB header: structural protein Chain: A: PDB Molecule: fosw; PDBTitle: structure of cjun-fosw coiled coil complex.
20	d1lh0a_	Alignment		71.5	9	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
21	d1vmea1	Alignment	not modelled	68.4	10	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
22	c2wnsB_	Alignment	not modelled	66.9	14	PDB header: transferase Chain: B: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: human orotate phosphoribosyltransferase (oprtae) domain of2 uridine 5'-monophosphate synthase (umps) in complex with3 its substrate orotidine 5'-monophosphate (omp)
23	c5hkiD_	Alignment	not modelled	64.2	14	PDB header: transferase Chain: D: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of mycobacterium tuberculosis h37rv orotate2 phosphoribosyltransferase in complex with fe(iii) dicitrate
24	d2fz5a1	Alignment	not modelled	64.1	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
25	c5yw2D_	Alignment	not modelled	60.7	12	PDB header: transferase Chain: D: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of adenine phosphoribosyltransferase from2 francisella tularensis.
26	c2ywtA_	Alignment	not modelled	59.9	9	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: crystal structure of hypoxanthine-guanine2 phosphoribosyltransferase with gmp from thermus3 thermophilus hb8
27	c3mjda_	Alignment	not modelled	59.4	7	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 1.9 angstrom crystal structure of orotate phosphoribosyltransferase2 (pyre) francisella tularensis.
						PDB header: transferase Chain: A: PDB Molecule: adenine phosphoribosyltransferase,

28	c5vn4A	Alignment	not modelled	59.3	12	putative; PDBTitle: crystal structure of adenine phosphoribosyl transferase from <i>Trypanosoma brucei</i> in complex with amp, pyrophosphate, and ribose-5-phosphate
29	c5eswB	Alignment	not modelled	58.9	19	PDB header: transferase Chain: B: PDB Molecule: purine/pyrimidine phosphoribosyltransferase; PDBTitle: crystal structure of apo hypoxanthine-guanine phosphoribosyltransferase from <i>Legionella pneumophila</i>
30	c2p1zA	Alignment	not modelled	56.8	20	PDB header: transferase Chain: A: PDB Molecule: phosphoribosyltransferase; PDBTitle: crystal structure of phosphoribosyltransferase from <i>Corynebacterium diphtheriae</i>
31	c6apsA	Alignment	not modelled	56.2	14	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: <i>Trypanosoma brucei</i> hypoxanthine-guanine phosphoribosyltransferase in complex with [(2-((guanine-9H-yl)methyl)propane-1,3-diy)bis(oxy)3]bis(methylene)diphosphonic acid
32	c6fkip	Alignment	not modelled	55.6	13	PDB header: membrane protein Chain: P: PDB Molecule: atp synthase subunit c, chloroplastic; PDBTitle: chloroplast <i>f1fo</i> conformation 3
33	c1ychD	Alignment	not modelled	54.4	10	PDB header: oxidoreductase Chain: D: PDB Molecule: nitric oxide reductase; PDBTitle: x-ray crystal structures of <i>Moraxella thermoacetica</i> <i>fprA</i> : novel diiron site structure and mechanistic insights into a scavenging nitric oxide reductase
34	c3dezA	Alignment	not modelled	54.1	15	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of orotate phosphoribosyltransferase from <i>Streptococcus mutans</i>
35	c3o7mD	Alignment	not modelled	53.0	9	PDB header: transferase Chain: D: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: 1.98 angstrom resolution crystal structure of a hypoxanthine-guanine phosphoribosyltransferase (<i>hpt-2</i>) from <i>Bacillus anthracis</i> str. 'Ames3 ancestor'
36	c2yzkC	Alignment	not modelled	52.9	17	PDB header: transferase Chain: C: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of orotate phosphoribosyltransferase from <i>Aeropyrum pernix</i>
37	c4pawA	Alignment	not modelled	52.9	10	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: structure of hypothetical protein <i>hp1257</i> .
38	d1vdma1	Alignment	not modelled	52.3	22	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
39	d1p17b	Alignment	not modelled	49.7	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
40	d1yfa1	Alignment	not modelled	49.2	12	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
41	c1yfaA	Alignment	not modelled	49.2	12	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: novel imp binding in feedback inhibition of hypoxanthine-guanine phosphoribosyltransferase from <i>Thermoanaerobacter tengcongensis</i>
42	c2przB	Alignment	not modelled	46.3	19	PDB header: transferase Chain: B: PDB Molecule: orotate phosphoribosyltransferase 1; PDBTitle: <i>S. cerevisiae</i> orotate phosphoribosyltransferase complexed with <i>omp</i>
43	d1ecfa1	Alignment	not modelled	44.5	11	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
44	c1vmeB	Alignment	not modelled	44.4	10	PDB header: electron transport Chain: B: PDB Molecule: flavoprotein; PDBTitle: crystal structure of flavoprotein (<i>tm0755</i>) from <i>Thermotoga maritima</i> at 2.180 Å resolution
45	c3m3hA	Alignment	not modelled	44.0	20	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 1.75 angstrom resolution crystal structure of an orotate phosphoribosyltransferase from <i>Bacillus anthracis</i> str. 'Ames3 ancestor'
46	d1qo0d	Alignment	not modelled	43.1	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: Positive regulator of the amidase operon <i>AmiR</i>
47	d2aeaa1	Alignment	not modelled	41.7	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
48	d1hqxa	Alignment	not modelled	41.4	9	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
49	d1z7ga1	Alignment	not modelled	41.3	21	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
50	d1yoba1	Alignment	not modelled	41.0	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
51	d1tc1a	Alignment	not modelled	40.5	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
						PDB header: transferase Chain: A: PDB Molecule: hypoxanthine phosphoribosyltransferase;

52	c3kb8A_	Alignment	not modelled	40.2	9	PDBTitle: 2.09 angstrom resolution structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-1) from bacillus anthracis str. 'ames3 ancestor' in complex with gmp
53	c5vogA_	Alignment	not modelled	40.1	17	PDB header: transferase Chain: A: PDB Molecule: putative phosphoribosyltransferase; PDBTitle: crystal structure of a hypothetical protein from neisseria gonorrhoeae2 with bound ppppp
54	c1pzmB_	Alignment	not modelled	39.9	13	PDB header: transferase Chain: B: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: crystal structure of hgprt-ase from leishmania tarentolae in complex2 with gmp
55	d1l1qa_	Alignment	not modelled	38.9	14	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
56	c2iufA_	Alignment	not modelled	38.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: catalase; PDBTitle: the structures of penicillium vitale catalase: resting2 state, oxidised state (compound i) and complex with3 aminotriazole
57	c3hlyA_	Alignment	not modelled	38.1	11	PDB header: flavoprotein Chain: A: PDB Molecule: flavodoxin-like domain; PDBTitle: crystal structure of the flavodoxin-like domain from synechococcus sp2 q5mzp6_syp6 protein. northeast structural genomics consortium target3 snr135d.
58	c4zu3D_	Alignment	not modelled	37.7	24	PDB header: lyase Chain: D: PDB Molecule: halohydrin epoxidase b; PDBTitle: halohydrin hydrogen-halide-lyases, hheb
59	c5ipfA_	Alignment	not modelled	37.1	12	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase (hgprt); PDBTitle: crystal structure of hypoxanthine-guanine phosphoribosyltransferase2 from schistosoma mansoni in complex with imp
60	c1gph1_	Alignment	not modelled	37.0	19	PDB header: transferase Chain: 1: PDB Molecule: glutamine phosphoribosyl-pyrophosphate amidotransferase; PDBTitle: structure of the allosteric regulatory enzyme of purine biosynthesis
61	c4rhyC_	Alignment	not modelled	35.9	11	PDB header: transferase/transferase inhibitor Chain: C: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: crystal structures of mycobacterium tuberculosis 6-oxopurine2 phosphoribosyltransferase which is a potential target for drug3 development against this disease
62	d1sqsa_	Alignment	not modelled	35.3	23	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Hypothetical protein SP1951
63	d1g9sa_	Alignment	not modelled	35.3	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
64	c3mudA_	Alignment	not modelled	34.9	11	PDB header: contractile protein Chain: A: PDB Molecule: dna repair protein xrcc4,tropomyosin alpha-1 chain; PDBTitle: structure of the tropomyosin overlap complex from chicken smooth2 muscle
65	c3cneD_	Alignment	not modelled	34.5	9	PDB header: hydrolase Chain: D: PDB Molecule: putative protease i; PDBTitle: crystal structure of the putative protease i from bacteroides2 thetaiotaomicron
66	d1gph11	Alignment	not modelled	34.0	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
67	d1j7ja_	Alignment	not modelled	33.4	21	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
68	c4rqbB_	Alignment	not modelled	33.3	12	PDB header: transferase Chain: B: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: crystal structure of a hypoxanthine phosphoribosyltransferase (target2 id nysgrc-029686) from staphylococcus aureus (tetragonal space group)
69	c3n2IA_	Alignment	not modelled	33.1	5	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 2.1 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase (pyre) from vibrio cholerae o1 biovar eltor3 str. n16961
70	c4e08B_	Alignment	not modelled	32.4	23	PDB header: motor protein Chain: B: PDB Molecule: dj-1 beta; PDBTitle: crystal structure of drosophila melanogaster dj-1beta
71	d1ufra_	Alignment	not modelled	32.0	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
72	c2gd7B_	Alignment	not modelled	31.8	21	PDB header: transcription Chain: B: PDB Molecule: hexim1 protein; PDBTitle: the structure of the cyclin t-binding domain of hexim12 reveals the molecular basis for regulation of3 transcription elongation
73	c1go4F_	Alignment	not modelled	31.8	22	PDB header: cell cycle Chain: F: PDB Molecule: mitotic spindle assembly checkpoint protein mad1; PDBTitle: crystal structure of mad1-mad2 reveals a conserved mad2 binding motif2 in mad1 and cdc20.
74	d1pzma_	Alignment	not modelled	31.7	13	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
75	d1qb7a_	Alignment	not modelled	31.3	20	Fold: PRTase-like Superfamily: PRTase-like

						Family:Phosphoribosyltransferases (PRTases)
76	c6h9mA	Alignment	not modelled	31.1	12	PDB header: membrane protein Chain: A: PDB Molecule: coiled-coil domain-containing protein 90b, mitochondrial, PDBTitle: coiled-coil domain-containing protein 90b residues 43-125 from homo2 sapiens fused to a gcn4 adaptor
77	c4lyyA	Alignment	not modelled	30.3	14	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: crystal structure of hypoxanthine phosphoribosyltransferase from2 shewanella pealeana atcc 700345, nysgrc target 029677.
78	c1ecjB	Alignment	not modelled	30.0	11	PDB header: transferase Chain: B: PDB Molecule: glutamine phosphoribosylpyrophosphate PDBTitle: escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
79	c4z1oB	Alignment	not modelled	29.4	24	PDB header: transferase Chain: B: PDB Molecule: phosphoribosyltransferase; PDBTitle: hypoxanthine-guanine-xanthine phosphoribosyltransferase (hgxpirt) from2 sulfobolus solfataricus in complex with alpha-3 phosphoribosylpyrophosphoric acid (prpp) and magnesium
80	d2axte1	Alignment	not modelled	27.7	40	Fold: Single transmembrane helix Superfamily: Cytochrome b559 subunits Family: Cytochrome b559 subunits
81	c3jcue	Alignment	not modelled	27.2	33	PDB header: membrane protein Chain: E: PDB Molecule: cytochrome b559 subunit alpha; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
82	c2wc1A	Alignment	not modelled	27.1	17	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin; PDBTitle: three-dimensional structure of the nitrogen fixation2 flavodoxin (niff) from rhodobacter capsulatus at 2.2 a
83	c3kziE	Alignment	not modelled	26.9	40	PDB header: electron transport Chain: E: PDB Molecule: cytochrome b559 subunit alpha; PDBTitle: crystal structure of monomeric form of cyanobacterial photosystem ii
84	c2j5dA	Alignment	not modelled	26.9	33	PDB header: membrane protein Chain: A: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting protein 3; PDBTitle: nmr structure of bnip3 transmembrane domain in lipid bicelles
85	d1p5fa	Alignment	not modelled	26.8	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
86	c3d4oA	Alignment	not modelled	26.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase subunit a; PDBTitle: crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
87	c4ug1A	Alignment	not modelled	26.6	19	PDB header: cell cycle Chain: A: PDB Molecule: cell cycle protein gpsb; PDBTitle: gpsb n-terminal domain
88	c5t4oj	Alignment	not modelled	25.4	8	PDB header: hydrolase Chain: J: PDB Molecule: atp synthase subunit b; PDBTitle: autoinhibited e. coli atp synthase state 1
89	d2a4ka1	Alignment	not modelled	25.3	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
90	c3qw4B	Alignment	not modelled	25.1	22	PDB header: transferase, lyase Chain: B: PDB Molecule: ump synthase; PDBTitle: structure of leishmania donovani ump synthase
91	c3fseB	Alignment	not modelled	24.9	26	PDB header: hydrolase Chain: B: PDB Molecule: two-domain protein containing dj-1/thij/pfpi-like and PDBTitle: crystal structure of a two-domain protein containing dj-1/thij/pfpi-2 like and ferritin-like domains (ava_4496) from anaerobaculum variabilis3 atcc 29413 at 1.90 a resolution
92	c4pfqF	Alignment	not modelled	24.7	10	PDB header: transferase Chain: F: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: crystal structure of hypoxanthine phosphoribosyltransferase from2 brachy bacterium faecium dsm 4810, nysgrc target 029763.
93	c5cdjA	Alignment	not modelled	24.4	18	PDB header: chaperone Chain: A: PDB Molecule: rubisco large subunit-binding protein subunit alpha, PDBTitle: apical domain of chloroplast chaperonin 60a
94	c2e76E	Alignment	not modelled	24.0	26	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
95	c2e75E	Alignment	not modelled	24.0	26	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
96	c1vf5R	Alignment	not modelled	24.0	26	PDB header: photosynthesis Chain: R: PDB Molecule: protein pet I; PDBTitle: crystal structure of cytochrome b6f complex from m.laminosus
97	c2e74E	Alignment	not modelled	24.0	26	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex from m.laminosus
98	c1vf5E	Alignment	not modelled	24.0	26	PDB header: photosynthesis Chain: E: PDB Molecule: protein pet I; PDBTitle: crystal structure of cytochrome b6f complex from m.laminosus
99	c4h0IE	Alignment	not modelled	24.0	26	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: cytochrome b6f complex crystal structure from

						mastigocladus laminosus2 with n-side inhibitor nqno
100	d2e74e1	Alignment	not modelled	24.0	26	Fold: Single transmembrane helix Superfamily: PetL subunit of the cytochrome b6f complex Family: PetL subunit of the cytochrome b6f complex
101	c4h13E	Alignment	not modelled	24.0	26	PDB header: photosynthesis Chain: E; PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex from mastigocladus2 laminosus with tds
102	c6c4jA	Alignment	not modelled	23.0	16	PDB header: oxidoreductase Chain: A; PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: ligand bound full length hugdh with a104l substitution
103	c2ka1B	Alignment	not modelled	22.9	33	PDB header: membrane protein Chain: B; PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
104	c2ka1A	Alignment	not modelled	22.9	33	PDB header: membrane protein Chain: A; PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
105	c2ka2A	Alignment	not modelled	22.9	33	PDB header: membrane protein Chain: A; PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
106	c2ka2B	Alignment	not modelled	22.9	33	PDB header: membrane protein Chain: B; PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
107	d1srva	Alignment	not modelled	22.8	24	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
108	c2ebuA	Alignment	not modelled	22.0	24	PDB header: replication Chain: A; PDB Molecule: replication factor c subunit 1; PDBTitle: solution structure of the brct domain from human2 replication factor c large subunit 1
109	d1uklc	Alignment	not modelled	21.9	11	Fold: HLH-like Superfamily: HLH, helix-loop-helix DNA-binding domain Family: HLH, helix-loop-helix DNA-binding domain
110	c4pv1E	Alignment	not modelled	21.7	24	PDB header: electron transport/inhibitor Chain: E; PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: cytochrome b6f structure from m. laminosus with the quinone analog2 inhibitor stigmatellin
111	c4i7zE	Alignment	not modelled	21.7	24	PDB header: photosynthesis Chain: E; PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of cytochrome b6f in dogp, with disordered rieske2 iron-sulfur protein soluble domain
112	d1sjpa2	Alignment	not modelled	21.5	22	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
113	d1oi4a1	Alignment	not modelled	21.4	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
114	c2yy0D	Alignment	not modelled	21.2	20	PDB header: transcription Chain: D; PDB Molecule: c-myc-binding protein; PDBTitle: crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
115	c2jbhA	Alignment	not modelled	21.0	19	PDB header: transferase Chain: A; PDB Molecule: phosphoribosyltransferase domain-containing protein 1; PDBTitle: human phosphoribosyl transferase domain containing 1
116	c2e43A	Alignment	not modelled	20.5	21	PDB header: transcription/dna Chain: A; PDB Molecule: ccaat/enhancer-binding protein beta; PDBTitle: crystal structure of c/ebpbeta bzip homodimer k269a mutant2 bound to a high affinity dna fragment
117	c4d02A	Alignment	not modelled	20.3	8	PDB header: electron transport Chain: A; PDB Molecule: anaerobic nitric oxide reductase flavorubredoxin; PDBTitle: the crystallographic structure of flavorubredoxin from escherichia2 coli