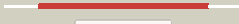



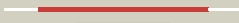




























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1341 (-) _1507579_1508193
Date	Wed Jul 31 22:05:44 BST 2019
Unique Job ID	7ab29eaec18504b5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3tquD_</a>	 Alignment		100.0	43	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> non-canonical purine ntp pyrophosphatase; <b>PDBTitle:</b> structure of a ham1 protein from coxiella burnetii
2	<a href="#">d1k7ka_</a>	 Alignment		100.0	46	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> ITPase-like <b>Family:</b> ITPase (Ham1)
3	<a href="#">c4bnqA_</a>	 Alignment		100.0	37	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> non-canonical purine ntp pyrophosphatase; <b>PDBTitle:</b> the structure of the staphylococcus aureus ham1 protein
4	<a href="#">d1vp2a_</a>	 Alignment		100.0	34	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> ITPase-like <b>Family:</b> ITPase (Ham1)
5	<a href="#">d2cara1</a>	 Alignment		100.0	31	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> ITPase-like <b>Family:</b> ITPase (Ham1)
6	<a href="#">d1v7ra_</a>	 Alignment		100.0	29	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> ITPase-like <b>Family:</b> ITPase (Ham1)
7	<a href="#">d1b78a_</a>	 Alignment		100.0	28	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> ITPase-like <b>Family:</b> ITPase (Ham1)
8	<a href="#">c4oo0B_</a>	 Alignment		96.9	28	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> maf-like protein bcal2394; <b>PDBTitle:</b> crystal structure of maf-like protein bcej2315_23540 from burkholderia2 cenocepacia
9	<a href="#">d2amha1</a>	 Alignment		96.2	16	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> ITPase-like <b>Family:</b> Maf-like
10	<a href="#">d1ex2a_</a>	 Alignment		95.4	17	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> ITPase-like <b>Family:</b> Maf-like
11	<a href="#">c4jhcA_</a>	 Alignment		92.1	21	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> maf-like protein ycef; <b>PDBTitle:</b> crystal structure of the uncharacterized maf protein ycef from e. coli

12	<a href="#">c4hebA</a>	Alignment		91.8	18	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> septum formation protein maf; <b>PDBTitle:</b> the crystal structure of maf protein of bacillus subtilis
13	<a href="#">c6mu0A</a>	Alignment		90.1	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> probable ribose-5-phosphate isomerase b; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase b from mycoplasma2 genitalium with bound ribulose-5-phosphate
14	<a href="#">c2p5xB</a>	Alignment		86.0	19	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> n-acetylserotonin o-methyltransferase-like protein; <b>PDBTitle:</b> crystal structure of maf domain of human n-acetylserotonin o-2 methyltransferase-like protein
15	<a href="#">d1u5wa1</a>	Alignment		85.4	15	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> TPase-like <b>Family:</b> YjxX-like
16	<a href="#">c4p0eB</a>	Alignment		84.3	19	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> maf-like protein yhde; <b>PDBTitle:</b> yhde e33a (p212121 space group)
17	<a href="#">c4em8A</a>	Alignment		83.4	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose 5-phosphate isomerase b; <b>PDBTitle:</b> the structure of ribose 5-phosphate isomerase b from anaplasma2 phagocytophilum
18	<a href="#">c5d5pC</a>	Alignment		78.6	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> hcgb; <b>PDBTitle:</b> hcgb from methanococcus maripaludis
19	<a href="#">c6fxsA</a>	Alignment		77.8	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose 5-phosphate isomerase, putative; <b>PDBTitle:</b> structure of trypanosoma brucei type b ribose 5-phosphate isomerase
20	<a href="#">c6fxwA</a>	Alignment		76.7	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative ribose 5-phosphate isomerase; <b>PDBTitle:</b> structure of leishmania infantum type b ribose 5-phosphate isomerase
21	<a href="#">d2vvpA1</a>	Alignment	not modelled	76.3	16	<b>Fold:</b> Ribose/Galactose isomerase RpiB/AlsB <b>Superfamily:</b> Ribose/Galactose isomerase RpiB/AlsB <b>Family:</b> Ribose/Galactose isomerase RpiB/AlsB
22	<a href="#">d1nn4a</a>	Alignment	not modelled	67.7	12	<b>Fold:</b> Ribose/Galactose isomerase RpiB/AlsB <b>Superfamily:</b> Ribose/Galactose isomerase RpiB/AlsB <b>Family:</b> Ribose/Galactose isomerase RpiB/AlsB
23	<a href="#">c3m1pA</a>	Alignment	not modelled	61.5	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose 5-phosphate isomerase; <b>PDBTitle:</b> structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with allose-6-phosphate
24	<a href="#">c3k7pA</a>	Alignment	not modelled	61.5	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose 5-phosphate isomerase; <b>PDBTitle:</b> structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.
25	<a href="#">c3c5yD</a>	Alignment	not modelled	56.5	18	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> ribose/galactose isomerase; <b>PDBTitle:</b> crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
26	<a href="#">d1o1xa</a>	Alignment	not modelled	54.3	23	<b>Fold:</b> Ribose/Galactose isomerase RpiB/AlsB <b>Superfamily:</b> Ribose/Galactose isomerase RpiB/AlsB <b>Family:</b> Ribose/Galactose isomerase RpiB/AlsB
27	<a href="#">c3he8A</a>	Alignment	not modelled	53.3	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase; <b>PDBTitle:</b> structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
28	<a href="#">c4lfmA</a>	Alignment	not modelled	51.7	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> galactose-6-phosphate isomerase subunit a; <b>PDBTitle:</b> crystal structure of d-galactose-6-phosphate isomerase in

						complex with2 d-psicose
29	<a href="#">c3brcA_</a>	Alignment	not modelled	48.6	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved protein of unknown function; <b>PDBTitle:</b> crystal structure of a conserved protein of unknown function from2 methanobacterium thermoautotrophicum
30	<a href="#">d1zwyw1</a>	Alignment	not modelled	47.4	19	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> ITPase-like <b>Family:</b> YjyX-like
31	<a href="#">c4fnD_</a>	Alignment	not modelled	43.3	15	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> galactose-6-phosphate isomerase subunit b; <b>PDBTitle:</b> crystal structure of d-galactose-6-phosphate isomerase in complex with2 d-ribulose
32	<a href="#">c3crqA_</a>	Alignment	not modelled	34.6	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna delta(2)-isopentenylpyrophosphate <b>PDBTitle:</b> structure of trna dimethylallyltransferase: rna2 modification through a channel
33	<a href="#">c5t3yA_</a>	Alignment	not modelled	28.4	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> two-component system response regulator; <b>PDBTitle:</b> solution structure of response regulator protein from burkholderia2 multivorans
34	<a href="#">c2ppwA_</a>	Alignment	not modelled	28.0	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> conserved domain protein; <b>PDBTitle:</b> the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
35	<a href="#">c3s5pA_</a>	Alignment	not modelled	27.8	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose 5-phosphate isomerase; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia
36	<a href="#">c3qd5B_</a>	Alignment	not modelled	26.3	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative ribose-5-phosphate isomerase; <b>PDBTitle:</b> crystal structure of a putative ribose-5-phosphate isomerase from2 coccidioides immitis solved by combined iodide ion sad and mr
37	<a href="#">c5zkeA_</a>	Alignment	not modelled	26.1	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> aminoacyl trna synthetase complex-interacting <b>PDBTitle:</b> crystal structure of n-terminal domain of plasmodium vivax p43 in2 space group p212121
38	<a href="#">c5vveA_</a>	Alignment	not modelled	25.5	33	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate mutase; <b>PDBTitle:</b> crystal structure of phosphoglycerate mutase from naegleria fowleri
39	<a href="#">d1vbva1</a>	Alignment	not modelled	23.0	44	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> YccV-like <b>Family:</b> YccV-like
40	<a href="#">c3a8tA_</a>	Alignment	not modelled	21.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate isopentenyltransferase; <b>PDBTitle:</b> plant adenylate isopentenyltransferase in complex with atp
41	<a href="#">d1l8na1</a>	Alignment	not modelled	20.1	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> alpha-D-glucuronidase/Hyaluronidase catalytic domain
42	<a href="#">d2nn6h3</a>	Alignment	not modelled	19.5	18	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
43	<a href="#">d2pc6a1</a>	Alignment	not modelled	19.4	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> llvH-like
44	<a href="#">d2fgca1</a>	Alignment	not modelled	19.3	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> llvH-like
45	<a href="#">c4pzuF_</a>	Alignment	not modelled	18.9	17	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> uncharacterized protein rv3404c/mt3512; <b>PDBTitle:</b> crystal structure of a putative uncharacterize protein rv3404c and2 likely sugar n-formyltransferase from mycobacterium tuberculosis
46	<a href="#">c1mqrA_</a>	Alignment	not modelled	17.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-d-glucuronidase; <b>PDBTitle:</b> the crystal structure of alpha-d-glucuronidase (e386q) from bacillus2 stearothermophilus t-6
47	<a href="#">d1u14a_</a>	Alignment	not modelled	15.9	19	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> ITPase-like <b>Family:</b> YjyX-like
48	<a href="#">d1c01a_</a>	Alignment	not modelled	15.9	30	<b>Fold:</b> gamma-Crystallin-like <b>Superfamily:</b> gamma-Crystallin-like <b>Family:</b> Plant antimicrobial protein MIAMP1
49	<a href="#">c2gx5B_</a>	Alignment	not modelled	15.3	9	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> gtp-sensing transcriptional pleiotropic repressor cody; <b>PDBTitle:</b> n-terminal gaf domain of transcriptional pleiotropic repressor cody
50	<a href="#">c1nm3B_</a>	Alignment	not modelled	15.1	24	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> protein hi0572; <b>PDBTitle:</b> crystal structure of heamophilus influenza hybrid-prx5
51	<a href="#">d2f1fa2</a>	Alignment	not modelled	14.4	9	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> llvH-like
52	<a href="#">c6jij8_</a>	Alignment	not modelled	13.6	28	<b>PDB header:</b> membrane protein <b>Chain:</b> 8: <b>PDB Molecule:</b> lhca8; <b>PDBTitle:</b> photosystem i of chlamydomonas reinhardtii
53	<a href="#">d2eyqa2</a>	Alignment	not modelled	13.6	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain

54	<a href="#">d1ixra2</a>	Alignment	not modelled	13.0	23	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> DNA helicase RuvA subunit, N-terminal domain
55	<a href="#">d3ehwa1</a>	Alignment	not modelled	12.6	60	<b>Fold:</b> beta-clip <b>Superfamily:</b> dUTPase-like <b>Family:</b> dUTPase-like
56	<a href="#">c3rh0A_</a>	Alignment	not modelled	12.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> arsenate reductase; <b>PDBTitle:</b> corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
57	<a href="#">c4an5F_</a>	Alignment	not modelled	11.5	19	<b>PDB header:</b> virus <b>Chain:</b> F: <b>PDB Molecule:</b> coat protein; <b>PDBTitle:</b> capsid structure and its stability at the late stages of bacteriophage2 spp1 assembly
58	<a href="#">c3onoA_</a>	Alignment	not modelled	11.5	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose/galactose isomerase; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase lacab_rpib from2 vibrio parahaemolyticus
59	<a href="#">c4hwgA_</a>	Alignment	not modelled	11.4	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine 2-epimerase; <b>PDBTitle:</b> structure of udp-n-acetylglucosamine 2-epimerase from rickettsia2 bellii
60	<a href="#">c4csqA_</a>	Alignment	not modelled	11.1	31	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr solution structure of pa3793 from pseudomonas aeruginosa
61	<a href="#">c2auaB_</a>	Alignment	not modelled	10.7	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> structure of bc2332: a protein of unknown function from bacillus2 cereus
62	<a href="#">c4w7gA_</a>	Alignment	not modelled	10.4	40	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> dynein light intermediate chain; <b>PDBTitle:</b> crystal structure of the dynein light intermediate chain's conserved2 domain
63	<a href="#">c2ymbB_</a>	Alignment	not modelled	9.9	27	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> mit domain-containing protein 1; <b>PDBTitle:</b> structures of mitd1
64	<a href="#">c2wmpB_</a>	Alignment	not modelled	9.6	33	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> papg protein; <b>PDBTitle:</b> structure of the e. coli chaperone papd in complex with the pilin2 domain of the paggii adhesin
65	<a href="#">c3fozB_</a>	Alignment	not modelled	8.9	23	<b>PDB header:</b> transferase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> trna delta(2)-isopentenylpyrophosphate transferase; <b>PDBTitle:</b> structure of e. coli isopentenyl-trna transferase in complex with e.2 coli trna(phe)
66	<a href="#">c3vhiA_</a>	Alignment	not modelled	8.8	21	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> bfpc; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of bfpc
67	<a href="#">c2wfbA_</a>	Alignment	not modelled	8.5	8	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein orp; <b>PDBTitle:</b> high resolution structure of the apo form of the orange2 protein (orp) from desulfovibrio gigas
68	<a href="#">c5wurB_</a>	Alignment	not modelled	8.3	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigw; <b>PDBTitle:</b> crystal structure of sigw in complex with its anti-sigma rsiw, an2 oxidized form
69	<a href="#">c1yd2A_</a>	Alignment	not modelled	8.2	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uvrabc system protein c; <b>PDBTitle:</b> crystal structure of the giy-yig n-terminal endonuclease domain of2 uvrC from thermotoga maritima: point mutant y19f bound to the3 catalytic divalent cation
70	<a href="#">c3exaD_</a>	Alignment	not modelled	8.1	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> trna delta(2)-isopentenylpyrophosphate transferase; <b>PDBTitle:</b> crystal structure of the full-length trna isopentenylpyrophosphate2 transferase (bh2366) from bacillus halodurans, northeast structural3 genomics consortium target bhr41.
71	<a href="#">c5y5pB_</a>	Alignment	not modelled	8.0	70	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> wsv112; <b>PDBTitle:</b> crystal structure of the dtpase of white spot syndrome virus in2 complex with du,ppi and mg2+
72	<a href="#">d1rdua_</a>	Alignment	not modelled	8.0	8	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Nitrogenase accessory factor-like <b>Family:</b> MTH1175-like
73	<a href="#">c3d3qB_</a>	Alignment	not modelled	8.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> trna delta(2)-isopentenylpyrophosphate transferase; <b>PDBTitle:</b> crystal structure of trna delta(2)-isopentenylpyrophosphate2 transferase (se0981) from staphylococcus epidermidis. northeast3 structural genomics consortium target ser100
74	<a href="#">c3f4fB_</a>	Alignment	not modelled	7.9	60	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> deoxyuridine 5'-triphosphate nucleotidohydrolase; <b>PDBTitle:</b> crystal structure of dut1p, a dtpase from saccharomyces cerevisiae
75	<a href="#">c3aerB_</a>	Alignment	not modelled	7.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit b; <b>PDBTitle:</b> structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
76	<a href="#">c4j05A_</a>	Alignment	not modelled	7.7	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphate transporter; <b>PDBTitle:</b> crystal structure of a eukaryotic phosphate transporter
77	<a href="#">c6jo52_</a>	Alignment	not modelled	7.6	50	<b>PDB header:</b> photosynthesis <b>Chain:</b> 2: <b>PDB Molecule:</b> chlorophyll a-b binding protein, chloroplastic;

						<b>PDBTitle:</b> structure of the green algal photosystem i supercomplex with light-2 harvesting complex i
78	<a href="#">c3h0dB_</a>	Alignment	not modelled	7.5	46	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> ctsr; <b>PDBTitle:</b> crystal structure of ctsr in complex with a 26bp dna duplex
79	<a href="#">c6ifhA_</a>	Alignment	not modelled	7.4	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sporulation initiation phosphotransferase f; <b>PDBTitle:</b> unphosphorylated spo0f from paenisporosarcina sp. tg-14
80	<a href="#">c4gmnA_</a>	Alignment	not modelled	7.4	26	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structural basis of rpl5 recognition by syo1
81	<a href="#">c2ymbC_</a>	Alignment	not modelled	7.4	27	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> mit domain-containing protein 1; <b>PDBTitle:</b> structures of mitd1
82	<a href="#">c1y7xA_</a>	Alignment	not modelled	7.3	20	<b>PDB header:</b> structural protein, protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> major vault protein; <b>PDBTitle:</b> solution structure of a two-repeat fragment of major vault2 protein
83	<a href="#">c6f1yj_</a>	Alignment	not modelled	6.9	55	<b>PDB header:</b> motor protein <b>Chain:</b> J: <b>PDB Molecule:</b> <b>PDBTitle:</b> dynein light intermediate chain region of the dynein2 tail/dynactin/bicdr1 complex
84	<a href="#">c6in7B_</a>	Alignment	not modelled	6.9	21	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> rna polymerase sigma-h factor; <b>PDBTitle:</b> crystal structure of algu in complex with muca(cyto)
85	<a href="#">c2jrlA_</a>	Alignment	not modelled	6.8	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
86	<a href="#">c5mvrA_</a>	Alignment	not modelled	6.8	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna threonylcarbamoyladenosine biosynthesis protein tsae; <b>PDBTitle:</b> crystal structure of bacillus subtilus ydib
87	<a href="#">c3so2A_</a>	Alignment	not modelled	6.7	50	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> chlorella dutpase
88	<a href="#">d1muma_</a>	Alignment	not modelled	6.6	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/isocitrate lyase-like
89	<a href="#">d1dq3a4</a>	Alignment	not modelled	6.5	10	<b>Fold:</b> Homing endonuclease-like <b>Superfamily:</b> Homing endonucleases <b>Family:</b> Intein endonuclease
90	<a href="#">c5zx3F_</a>	Alignment	not modelled	6.5	17	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigh; <b>PDBTitle:</b> mycobacterium tuberculosis rna polymerase holoenzyme with ecf sigma2 factor sigma h
91	<a href="#">c2gidP_</a>	Alignment	not modelled	6.4	36	<b>PDB header:</b> translation <b>Chain:</b> P: <b>PDB Molecule:</b> mitochondrial rna-binding protein 2; <b>PDBTitle:</b> crystal structures of trypanosoma brucei mrp1/mrp2
92	<a href="#">c1yd6A_</a>	Alignment	not modelled	6.4	36	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uvrc; <b>PDBTitle:</b> crystal structure of the giy-yig n-terminal endonuclease2 domain of uvrc from bacillus caldotenax
93	<a href="#">c3zf6A_</a>	Alignment	not modelled	6.4	50	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dutpase; <b>PDBTitle:</b> phage dutpases control transfer of virulence genes by a proto-2 oncogenic g protein-like mechanism. (staphylococcus bacteriophage3 80alpha dutpase d81a d110c s168c mutant with dupnhpp).
94	<a href="#">c6igz0_</a>	Alignment	not modelled	6.3	18	<b>PDB header:</b> plant protein <b>Chain:</b> 0: <b>PDB Molecule:</b> lhca-j; <b>PDBTitle:</b> structure of psi-lhci
95	<a href="#">c4lxuB_</a>	Alignment	not modelled	6.1	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> wlward, a sugar 3n-formyl transferase; <b>PDBTitle:</b> dtdp-fuc3n and 5-n-formyl-thf
96	<a href="#">c4p7dA_</a>	Alignment	not modelled	6.0	10	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> antitoxin hicb3; <b>PDBTitle:</b> antitoxin hicb3 crystal structure
97	<a href="#">d1rw1a_</a>	Alignment	not modelled	5.9	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> ArsC-like
98	<a href="#">c3dlmA_</a>	Alignment	not modelled	5.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histone-lysine n-methyltransferase setdb1; <b>PDBTitle:</b> crystal structure of tudor domain of human histone-lysine n-2 methyltransferase setdb1
99	<a href="#">c4etmB_</a>	Alignment	not modelled	5.7	9	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> low molecular weight protein-tyrosine-phosphatase yfkj; <b>PDBTitle:</b> crystal structure of yfkj from bacillus subtilis