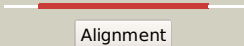

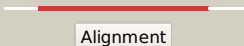

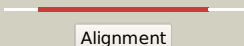







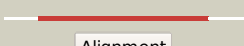









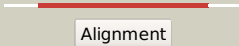

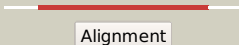

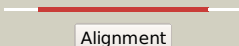



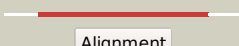

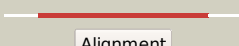

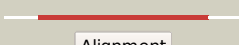







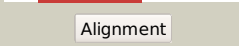




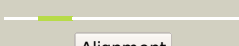


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2624c (-) _2950499_2951317
Date	Wed Aug 7 12:50:26 BST 2019
Unique Job ID	c9459937c8dc0308

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3loqA_			100.0	19	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: universal stress protein; PDBTitle: the crystal structure of a universal stress protein from archaeoglobus2 fulgidus dsm 4304
2	c2jaxA_			100.0	30	PDB header: protein binding Chain: A: PDB Molecule: hypothetical protein tb31.7; PDBTitle: universal stress protein rv2623 from mycobaterium2 tuberculosis
3	c3mt0A_			100.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pa1789; PDBTitle: the crystal structure of a functionally unknown protein pa1789 from2 pseudomonas aeruginosa pao1
4	c3ab8B_			100.0	16	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein ttha0350; PDBTitle: crystal structure of the hypothetical tandem-type universal stress2 protein ttha0350 complexed with atps.
5	c4r2jA_			100.0	16	PDB header: metal binding protein, unknown function Chain: A: PDB Molecule: universal stress protein e; PDBTitle: crystal structure of ydaa (universal stress protein e) from salmonella2 typhimurium
6	c3olqA_			100.0	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: universal stress protein e; PDBTitle: the crystal structure of a universal stress protein e from proteus2 mirabilis hi4320
7	c3s3tD_			99.9	34	PDB header: chaperone Chain: D: PDB Molecule: nucleotide-binding protein, universal stress protein uspa PDBTitle: universal stress protein uspa from lactobacillus plantarum
8	d2z3va1			99.8	24	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
9	c3hgmD_			99.8	29	PDB header: signaling protein Chain: D: PDB Molecule: universal stress protein tead; PDBTitle: universal stress protein tead from the trap transporter teaabc of2 halomonas elongata
10	c3fh0A_			99.8	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative universal stress protein kpn_01444; PDBTitle: crystal structure of putative universal stress protein kpn_01444 -2 atpase
11	c3dloC_			99.8	24	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: universal stress protein; PDBTitle: structure of universal stress protein from archaeoglobus fulgidus

12	c4wnyA_	 Alignment		99.8	23	PDB header: signaling protein Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of a protein from the universal stress protein2 family from burkholderia pseudomallei
13	d1mjha_	 Alignment		99.8	29	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
14	c5ahwC_	 Alignment		99.8	23	PDB header: signaling protein Chain: C: PDB Molecule: universal stress protein; PDBTitle: crystal structure of universal stress protein msmeg_3811 in2 complex with camp
15	d1tq8a_	 Alignment		99.8	32	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
16	c4r2lB_	 Alignment		99.8	29	PDB header: unknown function Chain: B: PDB Molecule: universal stress protein f; PDBTitle: crystal structure of ynaf (universal stress protein f) from salmonella2 typhimurium
17	c2pfsA_	 Alignment		99.7	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of universal stress protein from nitrosomonas2 europaea
18	d2gm3a1	 Alignment		99.7	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
19	d1jmva_	 Alignment		99.7	24	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
20	c3idfA_	 Alignment		99.7	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: usp-like protein; PDBTitle: the crystal structure of a usp-like protein from wolinnella2 succinogenes to 2.0a
21	c3fg9B_	 Alignment	not modelled	99.6	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein of universal stress protein uspa family; PDBTitle: the crystal structure of an universal stress protein uspa2 family protein from lactobacillus plantarum wcfs1
22	d1q77a_	 Alignment	not modelled	99.6	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
23	c2dumD_	 Alignment	not modelled	99.5	23	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein ph0823; PDBTitle: crystal structure of hypothetical protein, ph0823
24	c2ejbA_	 Alignment	not modelled	85.7	21	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
25	c3zquA_	 Alignment	not modelled	84.4	19	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: structure of a probable aromatic acid decarboxylase
26	c4nzpA_	 Alignment	not modelled	76.8	9	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: the crystal structure of argininosuccinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
27	c3a2kB_	 Alignment	not modelled	74.8	14	PDB header: ligase/rna Chain: B: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils complexed with trna
28	c6qlgD_	 Alignment	not modelled	62.0	21	PDB header: transferase Chain: D: PDB Molecule: flavin prenyltransferase pad1, mitochondrial; PDBTitle: crystal structure of anubix (pada1) in complex with fmn and2 dimethylallyl pyrophosphate

29	c3u7rB_	Alignment	not modelled	60.6	13	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-dependent frn reductase; PDBTitle: ferb - flavoenzyme nad(p)h:(acceptor) oxidoreductase (ferb) from2 paracoccus denitrificans
30	c6eoaA_	Alignment	not modelled	60.5	21	PDB header: flavoprotein Chain: A: PDB Molecule: phosphopantothenoylcysteine decarboxylase; PDBTitle: crystal structure of hal3 from cryptococcus neoformans
31	c5h75B_	Alignment	not modelled	58.5	24	PDB header: lyase Chain: B: PDB Molecule: mersacidin decarboxylase,immunoglobulin g-binding protein PDBTitle: crystal structure of the mrsd-protein a fusion protein
32	d1qzua_	Alignment	not modelled	57.1	26	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
33	d1g5qa_	Alignment	not modelled	54.0	17	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
34	c2p0yA_	Alignment	not modelled	52.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein lp_0780; PDBTitle: crystal structure of q88yi3_lacpl from lactobacillus plantarum.2 northeast structural genomics consortium target lpr6
35	c4kpuB_	Alignment	not modelled	52.3	4	PDB header: electron transport Chain: B: PDB Molecule: electron transfer flavoprotein alpha/beta-subunit; PDBTitle: electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
36	c3jqgD_	Alignment	not modelled	51.1	9	PDB header: oxidoreductase Chain: D: PDB Molecule: epidermin biosynthesis protein epid; PDBTitle: epidermin biosynthesis protein epid from staphylococcus aureus
37	c4rheB_	Alignment	not modelled	50.1	18	PDB header: lyase Chain: B: PDB Molecule: 3-octaprenyl-4-hydroxybenzoate carboxylase; PDBTitle: crystal structure of ubix, an aromatic acid decarboxylase from the2 colwellia psychrerythraea 34h
38	d2dbsa1	Alignment	not modelled	48.5	25	Fold: TTHC002-like Superfamily: TTHC002-like Family: TTHC002-like
39	c6jlsA_	Alignment	not modelled	46.3	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative flavoprotein decarboxylase; PDBTitle: crystal structure of fmn-dependent cysteine decarboxylases tvaf from2 thioviridamide biosynthesis
40	d1sbza_	Alignment	not modelled	44.0	24	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
41	c5ow0B_	Alignment	not modelled	42.9	20	PDB header: electron transport Chain: B: PDB Molecule: electron transfer flavoprotein, beta subunit; PDBTitle: crystal structure of an electron transfer flavoprotein from2 geobacillus metallireducens
42	c3s40C_	Alignment	not modelled	42.3	10	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. sterne
43	d1mvla_	Alignment	not modelled	42.1	22	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
44	c1mvIA_	Alignment	not modelled	42.1	22	PDB header: lyase Chain: A: PDB Molecule: ppc decarboxylase athal3a; PDBTitle: ppc decarboxylase mutant c175s
45	c5dldA_	Alignment	not modelled	41.6	19	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: crystal structure of a udp-n-acetylglucosamine 2-epimerase from2 burkholderia vietnamiensis complexed with udp-glcnac and udp
46	d1p3y1_	Alignment	not modelled	40.8	24	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
47	c5ol2E_	Alignment	not modelled	40.3	17	PDB header: flavoprotein Chain: E: PDB Molecule: electron transfer flavoprotein small subunit; PDBTitle: the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
48	c3g40A_	Alignment	not modelled	40.3	10	PDB header: transport protein Chain: A: PDB Molecule: na-k-cl cotransporter; PDBTitle: crystal structure of the cytoplasmic domain of a2 prokaryotic cation chloride cotransporter
49	c3mcuF_	Alignment	not modelled	40.1	26	PDB header: oxidoreductase Chain: F: PDB Molecule: dipicolinate synthase, b chain; PDBTitle: crystal structure of the dipicolinate synthase chain b from bacillus2 cereus. northeast structural genomics consortium target bcr215.
50	c3crqA_	Alignment	not modelled	38.9	19	PDB header: transferase Chain: A: PDB Molecule: trna delta(2)-isopentenylpyrophosphate PDBTitle: structure of trna dimethylallyltransferase: rna2 modification through a channel
51	c2ppvA_	Alianment	not modelled	38.7	19	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein belonging to the upf0052

						(se_0549) from2 staphylococcus epidermidis atcc 12228 at 2.00 a resolution
52	c2e21A	Alignment	not modelled	35.1	5	PDB header: ligase Chain: A: PDB Molecule: trna(ile)-lysidine synthase; PDBTitle: crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
53	c1ni5A	Alignment	not modelled	35.0	16	PDB header: cell cycle Chain: A: PDB Molecule: putative cell cycle protein mesj; PDBTitle: structure of the mesj pp-atpase from escherichia coli
54	c6jddA	Alignment	not modelled	34.6	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: cypemycin cysteine dehydrogenase (decarboxylating); PDBTitle: crystal structure of the cypemycin decarboxylase cypd.
55	c3fozB	Alignment	not modelled	34.1	19	PDB header: transferase/rna Chain: B: PDB Molecule: trna delta(2)-isopentenylpyrophosphate transferase; PDBTitle: structure of e. coli isopentenyl-trna transferase in complex with e.2 coli trna(phe)
56	c4iwmD	Alignment	not modelled	34.0	14	PDB header: unknown function Chain: D: PDB Molecule: upf0135 protein mj0927; PDBTitle: crystal structure of the conserved hypothetical protein mj0927 from2 methanocaldococcus jannaschii (in p21 form)
57	c3lqkA	Alignment	not modelled	33.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase subunit b; PDBTitle: crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
58	c1dd9A	Alignment	not modelled	32.9	17	PDB header: transferase Chain: A: PDB Molecule: dna primase; PDBTitle: structure of the dnag catalytic core
59	d1dd9a	Alignment	not modelled	32.9	17	Fold: DNA primase core Superfamily: DNA primase core Family: DNA primase DnaG catalytic core
60	d2hy5b1	Alignment	not modelled	32.1	8	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
61	d1p5dx1	Alignment	not modelled	32.1	13	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
62	c3umvB	Alignment	not modelled	32.0	21	PDB header: lyase Chain: B: PDB Molecule: deoxyribodipyrimidine photo-lyase; PDBTitle: eukaryotic class ii cpd photolyase structure reveals a basis for2 improved uv-tolerance in plants
63	c1vl2C	Alignment	not modelled	31.6	6	PDB header: ligase Chain: C: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
64	d2hzba1	Alignment	not modelled	31.2	17	Fold: CofD-like Superfamily: CofD-like Family: CofD-like
65	c3vrhA	Alignment	not modelled	31.0	7	PDB header: rna binding protein Chain: A: PDB Molecule: putative uncharacterized protein ph0300; PDBTitle: crystal structure of ph0300
66	c3c04A	Alignment	not modelled	28.4	13	PDB header: isomerase Chain: A: PDB Molecule: phosphomannomutase/phosphoglucomutase; PDBTitle: structure of the p368g mutant of pmm/pgm from p. aeruginosa
67	c5z6vA	Alignment	not modelled	28.3	13	PDB header: protein transport Chain: A: PDB Molecule: abc-type uncharacterized transport system periplasmic PDBTitle: crystal structure of a substrate-binding protein from rhodothermus2 marinus
68	d2j07a2	Alignment	not modelled	28.2	7	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
69	c4l2iA	Alignment	not modelled	27.5	19	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein alpha subunit; PDBTitle: electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
70	c4qg5D	Alignment	not modelled	26.9	21	PDB header: isomerase Chain: D: PDB Molecule: putative phosphoglucomutase; PDBTitle: crystal structure of phosphoglucomutase from leishmania major at 3.52 angstrom resolution
71	d1xrsa	Alignment	not modelled	26.8	13	Fold: TIM beta/alpha-barrel Superfamily: Cobalamin (vitamin B12)-dependent enzymes Family: D-lysine 5,6-aminomutase alpha subunit, KamD
72	c4hqnb	Alignment	not modelled	26.3	20	PDB header: cell adhesion Chain: B: PDB Molecule: sporozoite surface protein 2; PDBTitle: crystal structure of manganese-loaded plasmodium vivax trap protein
73	d2fywa1	Alignment	not modelled	25.9	29	Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
74	d1nmpa	Alignment	not modelled	24.5	39	Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
75	c5f4bB	Alignment	not modelled	24.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p)h dehydrogenase (quinone); PDBTitle: structure of b. abortus wrba-related protein a (wrpa)
76	c2yybA	Alignment	not modelled	23.6	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ttha1606; PDBTitle: crystal structure of ttha1606 from thermus thermophilus hb8

77	c2xrzA_	Alignment	not modelled	23.3	9	PDB header: lyase/dna Chain: A: PDB Molecule: deoxyribodipyrimidine photolyase; PDBTitle: x-ray structure of archaeal class ii cpd photolyase from2 methanosarcina mazeri in complex with intact cpd-lesion
78	d2d1pb1	Alignment	not modelled	22.7	22	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
79	c2nydB_	Alignment	not modelled	22.4	17	PDB header: unknown function Chain: B: PDB Molecule: upf0135 protein sa1388; PDBTitle: crystal structure of staphylococcus aureus hypothetical protein sa1388
80	c2gpwC_	Alignment	not modelled	21.8	14	PDB header: ligase Chain: C: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of the biotin carboxylase subunit, f363a2 mutant, of acetyl-coa carboxylase from escherichia coli.
81	c2c5sA_	Alignment	not modelled	21.6	17	PDB header: rna-binding protein Chain: A: PDB Molecule: probable thiamine biosynthesis protein thii; PDBTitle: crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain
82	c1kh2D_	Alignment	not modelled	21.4	9	PDB header: ligase Chain: D: PDB Molecule: argininosuccinate synthetase; PDBTitle: crystal structure of thermus thermophilus hb8 argininosuccinate2 synthetase in complex with atp
83	c5ol2D_	Alignment	not modelled	20.9	11	PDB header: flavoprotein Chain: D: PDB Molecule: electron transfer flavoprotein large subunit; PDBTitle: the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
84	c3i42A_	Alignment	not modelled	20.5	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: response regulator receiver domain protein (chey-like); PDBTitle: structure of response regulator receiver domain (chey-like) from2 methylobacillus flagellatus
85	c5bmpA_	Alignment	not modelled	20.3	8	PDB header: isomerase Chain: A: PDB Molecule: phosphoglucomutase; PDBTitle: crystal structure of phosphoglucomutase from xanthomonas citri2 complexed with glucose-1-phosphate
86	d1ni5a1	Alignment	not modelled	20.1	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
87	d1m7ja3	Alignment	not modelled	20.0	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: D-aminoacylase, catalytic domain
88	c5gafi_	Alignment	not modelled	19.9	6	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein I10; PDBTitle: rnc in complex with srp
89	d1t6t1_	Alignment	not modelled	19.8	10	Fold: Toprim domain Superfamily: Toprim domain Family: Toprim domain
90	c3g8rA_	Alignment	not modelled	19.7	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: probable spore coat polysaccharide biosynthesis protein e; PDBTitle: crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
91	c3dzcA_	Alignment	not modelled	19.7	14	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: 2.35 angstrom resolution structure of wecb (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
92	c3uw2A_	Alignment	not modelled	19.5	15	PDB header: isomerase Chain: A: PDB Molecule: phosphoglucomutase/phosphomannomutase family protein; PDBTitle: x-ray crystal structure of phosphoglucomutase/phosphomannomutase2 family protein (bth_11489)from burkholderia thailandensis
93	d1to6a_	Alignment	not modelled	19.4	19	Fold: Glycerate kinase I Superfamily: Glycerate kinase I Family: Glycerate kinase I
94	c5ghaC_	Alignment	not modelled	19.2	10	PDB header: transferase/transport protein Chain: C: PDB Molecule: sulfur transferase ttua; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
95	c2au3A_	Alignment	not modelled	19.2	24	PDB header: transferase Chain: A: PDB Molecule: dna primase; PDBTitle: crystal structure of the aquifex aeolicus primase (zinc binding and2 rna polymerase domains)
96	c1xuzA_	Alignment	not modelled	19.2	21	PDB header: biosynthetic protein Chain: A: PDB Molecule: polysialic acid capsule biosynthesis protein siac; PDBTitle: crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
97	c3i3wB_	Alignment	not modelled	18.1	18	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: structure of a phosphoglucosamine mutase from francisella tularensis
98	d2c5sa1	Alignment	not modelled	18.0	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Thil-like
99	c4okuA_	Alignment	not modelled	18.0	16	PDB header: cell adhesion Chain: A: PDB Molecule: micronemal protein mic2; PDBTitle: structure of toxoplasma gondii promic2