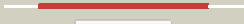



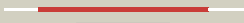








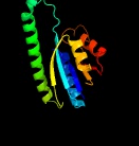
















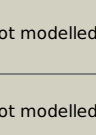


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2026c (-) _2271871_2272755
Date	Mon Aug 5 13:25:13 BST 2019
Unique Job ID	5cc779369edbb8c5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jaxA_	 Alignment		100.0	55	PDB header: protein binding Chain: A: PDB Molecule: hypothetical protein tb31.7; PDBTitle: universal stress protein rv2623 from mycobaterium2 tuberculosis
2	c3olqA_	 Alignment		100.0	13	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
3	c3loqA_	 Alignment		100.0	21	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
4	c3mt0A_	 Alignment		100.0	19	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
5	c3ab8B_	 Alignment		100.0	20	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.
6	c4r2jA_	 Alignment		100.0	12	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
7	c3s3tD_	 Alignment		99.9	35	PDB header: chaperone Chain: D: PDB Molecule: nucleotide-binding protein, universal stress protein uspa PDBTitle: universal stress protein uspa from lactobacillus plantarum
8	c3hgmD_	 Alignment		99.9	37	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
9	d1tq8a_	 Alignment		99.8	34	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
10	c3fh0A_	 Alignment		99.8	41	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_	 Alignment		99.8	22	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: universal stress protein; PDBTitle: structure of universal stress protein from archaeoglobus fulgidus

12	d2z3va1	Alignment		99.8	25	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
13	c4wnyA	Alignment		99.8	26	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
14	c5ahwC	Alignment		99.8	24	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	d1mjha	Alignment		99.7	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
16	c4r2lB	Alignment		99.7	24	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	d2gm3a1	Alignment		99.7	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
18	c3fg9B	Alignment		99.7	22	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
19	d1q77a	Alignment		99.6	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
20	d1jmva	Alignment		99.6	21	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
21	c2pfsA	Alignment	not modelled	99.6	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of universal stress protein from nitrosomonas2 europaea
22	c2dumD	Alignment	not modelled	99.6	17	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein ph0823; PDBTitle: crystal structure of hypothetical protein, ph0823
23	c3idfA	Alignment	not modelled	99.5	18	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
24	c3g40A	Alignment	not modelled	87.0	14	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
25	c3a2kB	Alignment	not modelled	80.4	21	PDB header: ligase/rna Chain: B: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils complexed with trna
26	c6eoaA	Alignment	not modelled	79.3	11	PDB header: flavoprotein Chain: A: PDB Molecule: phosphopantothenoilcysteine decarboxylase; PDBTitle: crystal structure of hal3 from cryptococcus neoformans
27	c4kpuB	Alignment	not modelled	70.0	11	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
28	c6qlgD	Alignment	not modelled	69.1	12	PDB header: transferase Chain: D: PDB Molecule: flavin prenyltransferase pad1, mitochondrial;

						PDBTitle: crystal structure of anubix (pada1) in complex with fmn and2 dimethylallyl pyrophosphate PDB header: electron transport Chain: B: PDB Molecule: electron transfer flavoprotein, beta subunit; PDBTitle: crystal structure of an electron transfer flavoprotein from2 geobacillus metallireducens
29	c5ow0B_	Alignment	not modelled	68.7	18	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
30	d1sbza_	Alignment	not modelled	65.4	18	PDB header: flavoprotein Chain: E: PDB Molecule: electron transfer flavoprotein small subunit; PDBTitle: the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
31	c5ol2E_	Alignment	not modelled	63.2	13	PDB header: lyase Chain: B: PDB Molecule: 3-octaprenyl-4-hydroxybenzoate carboxy-lyase; PDBTitle: crystal structure of ubix, an aromatic acid decarboxylase from the2 colwellia psychrerythraea 34h
32	c4rheB_	Alignment	not modelled	62.2	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative flavoprotein decarboxylase; PDBTitle: crystal structure of fmn-dependent cysteine decarboxylases tvaf from2 thioviridamide biosynthesis
33	c6jlsA_	Alignment	not modelled	61.4	17	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: structure of a probable aromatic acid decarboxylase
34	c3zquA_	Alignment	not modelled	61.0	14	PDB header: lyase Chain: A: PDB Molecule: ppc decarboxylase athal3a; PDBTitle: ppc decarboxylase mutant c175s
35	c1mv1A_	Alignment	not modelled	59.9	12	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
36	d1mv1a_	Alignment	not modelled	59.9	12	PDB header: ligase Chain: A: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
37	c2e21A_	Alignment	not modelled	59.9	15	PDB header: transferase Chain: A: PDB Molecule: nhej polymerase; PDBTitle: structure of the nhej polymerase from methanocella paludicola
38	c5dmuA_	Alignment	not modelled	57.6	21	PDB header: lyase Chain: B: PDB Molecule: mersacidin decarboxylase,immunoglobulin g-binding protein PDBTitle: crystal structure of the mrsd-protein a fusion protein
39	c5h75B_	Alignment	not modelled	57.1	18	PDB header: hydrolase/transferase Chain: B: PDB Molecule: probable atp-dependent dna ligase; PDBTitle: crystal structure of pseudomonas aeruginosa ligd polymerase2 domain
40	c2faoB_	Alignment	not modelled	56.2	9	PDB header: cell cycle Chain: A: PDB Molecule: putative cell cycle protein mesj; PDBTitle: structure of the mesj pp-atpase from escherichia coli
41	c1ni5A_	Alignment	not modelled	55.0	16	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
42	c2p0yA_	Alignment	not modelled	49.6	18	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
43	d1p3y1_	Alignment	not modelled	47.6	21	PDB header: transferase Chain: A: PDB Molecule: putative dna ligase-like protein rv0938/mt0965; PDBTitle: crystal structure of the polymerase domain from mycobacterium2 tuberculosis ligase d
44	c2iruA_	Alignment	not modelled	46.9	18	PDB header: transferase Chain: B: PDB Molecule: dna polymerase ligd, polymerase domain; PDBTitle: structure of prim-polc from mycobacterium smegmatis
45	c5op0B_	Alignment	not modelled	45.7	3	PDB header: ligase Chain: C: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
46	c1vl2C_	Alignment	not modelled	44.9	9	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	d1qzua_	Alignment	not modelled	44.4	24	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
48	c2ppvA_	Alignment	not modelled	43.4	30	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
49	d1p5dx1	Alignment	not modelled	41.2	17	PDB header: isomerase Chain: A: PDB Molecule: phosphoglucomutase; PDBTitle: crystal structure of phosphoglucomutase from xanthomonas citri2 complexed with glucose-1-phosphate
50	c5bmpA_	Alignment	not modelled	39.5	10	PDB header: isomerase Chain: A: PDB Molecule: phosphomannomutase/phosphoglucomutase; PDBTitle: structure of the p368g mutant of pmm/pgm from p. aeruginosa
51	c3c04A_	Alignment	not modelled	35.9	17	

52	d2hzba1	Alignment	not modelled	35.5	24	Fold: CofD-like Superfamily: CofD-like Family: CofD-like
53	d1g5qa	Alignment	not modelled	35.4	9	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
54	c3vrhA	Alignment	not modelled	35.0	31	PDB header: rna binding protein Chain: A: PDB Molecule: putative uncharacterized protein ph0300; PDBTitle: crystal structure of ph0300
55	c3mcf	Alignment	not modelled	31.2	14	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.
56	c6fahB	Alignment	not modelled	31.2	10	PDB header: flavoprotein Chain: B: PDB Molecule: cafeoyl-coa reductase-etf complex subunit card; PDBTitle: molecular basis of the flavin-based electron-bifurcating cafeoyl-coa2 reductase reaction
57	c6jddA	Alignment	not modelled	29.2	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: cypemycin cysteine dehydrogenase (decarboxylating); PDBTitle: crystal structure of the cypemycin decarboxylase cypd.
58	c5ghaC	Alignment	not modelled	29.1	29	PDB header: transferase/transport protein Chain: C: PDB Molecule: sulfur transferase ttua; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
59	c4hjhA	Alignment	not modelled	28.5	12	PDB header: isomerase Chain: A: PDB Molecule: phosphomannomutase; PDBTitle: iodide sad phased crystal structure of a phosphoglucomutase from2 brucella melitensis complexed with glucose-6-phosphate
60	d1to6a	Alignment	not modelled	27.6	27	Fold: Glycerate kinase I Superfamily: Glycerate kinase I Family: Glycerate kinase I
61	c3jqgD	Alignment	not modelled	27.2	12	PDB header: oxidoreductase Chain: D: PDB Molecule: epidermin biosynthesis protein epid; PDBTitle: epidermin biosynthesis protein epid from staphylococcus aureus
62	c2nz2A	Alignment	not modelled	26.9	9	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
63	c1kh2D	Alignment	not modelled	25.8	9	PDB header: ligase Chain: D: PDB Molecule: argininosuccinate synthetase; PDBTitle: crystal structure of thermus thermophilus hb8 argininosuccinate2 synthetase in complex with atp
64	c1wqaB	Alignment	not modelled	25.2	15	PDB header: isomerase Chain: B: PDB Molecule: phospho-sugar mutase; PDBTitle: crystal structure of pyrococcus horikoshii2 phosphomannomutase/phosphoglucomutase complexed with mg2+
65	c3uw2A	Alignment	not modelled	25.1	14	PDB header: isomerase Chain: A: PDB Molecule: phosphoglucomutase/phosphomannomutase family protein; PDBTitle: x-ray crystal structure of phosphoglucomutase/phosphomannomutase2 family protein (bth_i1489)from burkholderia thailandensis
66	c1qzuB	Alignment	not modelled	24.1	25	PDB header: lyase Chain: B: PDB Molecule: hypothetical protein mds018; PDBTitle: crystal structure of human phosphopantothenoylcysteine decarboxylase
67	d2g0ta1	Alignment	not modelled	22.7	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
68	d1m7ja3	Alignment	not modelled	22.7	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: D-aminoacylase, catalytic domain
69	c4i2iA	Alignment	not modelled	21.9	13	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	d1ni5a1	Alignment	not modelled	21.6	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
71	c2yxba	Alignment	not modelled	20.5	17	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
72	c4kr7A	Alignment	not modelled	20.5	14	PDB header: transferase/rna Chain: A: PDB Molecule: probable trna sulfurtransferase; PDBTitle: crystal structure of a 4-thiouridine synthetase - rna complex with2 bound atp
73	d1xrsa	Alignment	not modelled	20.4	10	Fold: TIM beta/alpha-barrel Superfamily: Cobalamin (vitamin B12)-dependent enzymes Family: D-lysine 5,6-aminomutase alpha subunit, KamD
74	c2f7iA	Alignment	not modelled	19.9	16	PDB header: isomerase Chain: A: PDB Molecule: 455aa long hypothetical phospho-sugar mutase; PDBTitle: crystal structure of sulfobolus tokodaii2 phosphomannomutase/phosphoglucomutase
75	c3pdkB	Alignment	not modelled	19.8	9	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: crystal structure of phosphoglucosamine mutase from b. anthracis

76	c2ejbA	Alignment	not modelled	19.7	9	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
77	c2j4dA	Alignment	not modelled	19.4	12	PDB header: dna binding protein Chain: A: PDB Molecule: cryptochrome dash; PDBTitle: cryptochrome 3 from arabidopsis thaliana
78	c3i3wB	Alignment	not modelled	19.0	15	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: structure of a phosphoglucosamine mutase from francisella tularensis
79	d1o94c	Alignment	not modelled	18.9	6	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
80	c4nzpA	Alignment	not modelled	18.0	6	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: the crystal structure of argininosuccinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
81	d1wy5a1	Alignment	not modelled	18.0	11	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
82	c3lqkA	Alignment	not modelled	17.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase subunit b; PDBTitle: crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
83	d3clsc1	Alignment	not modelled	17.3	3	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
84	d1j20a1	Alignment	not modelled	17.2	9	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
85	d3clsd1	Alignment	not modelled	17.1	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
86	d1ylqa1	Alignment	not modelled	17.0	33	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Catalytic subunit of bi-partite nucleotidyltransferase
87	c6gyzB	Alignment	not modelled	16.6	14	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: crystal structure of glmm from staphylococcus aureus
88	c3cwcB	Alignment	not modelled	16.5	34	PDB header: transferase Chain: B: PDB Molecule: putative glycerate kinase 2; PDBTitle: crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
89	d2iela1	Alignment	not modelled	16.3	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
90	d1vl2a1	Alignment	not modelled	16.0	9	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
91	c5hn6A	Alignment	not modelled	15.6	24	PDB header: oxidoreductase Chain: A: PDB Molecule: homoisocitrate dehydrogenase; PDBTitle: crystal structure of beta-decarboxylating dehydrogenase (tk0280) from2 thermococcus kodakarensis complexed with mn and 3-isopropylmalate
92	c3r8wC	Alignment	not modelled	15.5	12	PDB header: oxidoreductase Chain: C: PDB Molecule: 3-isopropylmalate dehydrogenase 2, chloroplastic; PDBTitle: structure of 3-isopropylmalate dehydrogenase isoform 2 from2 arabidopsis thaliana at 2.2 angstrom resolution
93	c6j4nD	Alignment	not modelled	15.3	20	PDB header: hydrolase Chain: D: PDB Molecule: metallo-beta-lactamases pngm-1; PDBTitle: structure of papua new guinea mbl-1(pngm-1) native
94	c1tuoA	Alignment	not modelled	15.2	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative phosphomannomutase; PDBTitle: crystal structure of putative phosphomannomutase from2 thermus thermophilus hb8
95	c4hqnb	Alignment	not modelled	15.2	18	PDB header: cell adhesion Chain: B: PDB Molecule: sporozoite surface protein 2; PDBTitle: crystal structure of manganese-loaded plasmodium vivax trap protein
96	d1rvga	Alignment	not modelled	15.1	28	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
97	c1o94D	Alignment	not modelled	15.1	17	PDB header: electron transport Chain: D: PDB Molecule: electron transfer flavoprotein alpha-subunit; PDBTitle: ternary complex between trimethylamine dehydrogenase and2 electron transferring flavoprotein
98	d3pmgal	Alignment	not modelled	14.9	19	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
99	d1cnza	Alignment	not modelled	14.6	16	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases