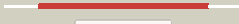



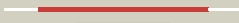



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3180c (-) _3549251_3549685
Date	Thu Aug 8 16:20:37 BST 2019
Unique Job ID	771910bb8ac91c4d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2fe1a1	 Alignment		99.8	29	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
2	c2fe1A_	 Alignment		99.8	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
3	d1v8pa_	 Alignment		99.7	20	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
4	c1v8pK_	 Alignment		99.7	20	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
5	c5wzfB_	 Alignment		99.6	20	PDB header: hydrolase Chain: B: PDB Molecule: 23s rrna-specific endonuclease vapc20; PDBTitle: crystal structure of mycobacterium tuberculosis vapc20 (rv2549c),2 sarcin-ricin loop cleaving toxin
6	c4xgrG_	 Alignment		99.6	24	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addiction module from mycobacterial species
7	c5x3tD_	 Alignment		99.4	22	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
8	d2h1ca1	 Alignment		99.4	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
9	c3zvkc_	 Alignment		99.3	9	PDB header: antitoxin/toxin/dna Chain: C: PDB Molecule: toxin of toxin-antitoxin system; PDBTitle: crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
10	c6a7vG_	 Alignment		99.3	14	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
11	d1y82a1	 Alignment		99.3	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain

12	c6nklA_	Alignment		99.2	12	PDB header: antitoxin Chain: A: PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
13	c3h87B_	Alignment		99.2	19	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
14	d1v96a1	Alignment		99.2	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
15	c4chgC_	Alignment		99.1	17	PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
16	c3tndC_	Alignment		99.1	14	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
17	c5sv2A_	Alignment		99.1	16	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
18	c5l6mC_	Alignment		99.1	11	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
19	c3dboB_	Alignment		99.0	19	PDB header: toxin/antitoxin Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a member of the vapbc family of toxin-antitoxin2 systems, vapbc-5, from mycobacterium tuberculosis
20	d1w8ia_	Alignment		98.6	12	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
21	c3i8oA_	Alignment	not modelled	98.6	12	PDB header: rna binding protein Chain: A: PDB Molecule: kh domain-containing protein mj1533; PDBTitle: a domain of a functionally unknown protein from methanocaldococcus2 jannaschii dsm 2661.
22	c3ix7A_	Alignment	not modelled	98.4	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ttha0540; PDBTitle: crystal structure of a domain of functionally unknown protein from2 thermus thermophilus hb8
23	c5ywwA_	Alignment	not modelled	98.3	16	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
24	c5f4hF_	Alignment	not modelled	98.2	16	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
25	d1o4wa_	Alignment	not modelled	98.2	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
26	c2lcqA_	Alignment	not modelled	98.2	16	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
27	c2hwwC_	Alignment	not modelled	97.7	14	PDB header: rna binding protein Chain: C: PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
28	c5yz4A_	Alignment	not modelled	96.5	16	PDB header: hydrolase Chain: A: PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
						PDB header: ribosome

29	c5jppd_	Alignment	not modelled	96.2	16	Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
30	c6g5iy_	Alignment	not modelled	96.2	23	PDB header: ribosome Chain: Y: PDB Molecule: 40s ribosomal protein s24; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state r
31	c2mdtA_	Alignment	not modelled	95.6	14	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: a pilt n-terminus domain protein sso1118 from hyperthermophilic2 archaeon sulfobolus solfataricus p2
32	c4mj7B_	Alignment	not modelled	93.8	10	PDB header: rna binding protein Chain: B: PDB Molecule: rrna-processing protein utp23; PDBTitle: crystal structure of the pin domain of saccharomyces cerevisiae utp23
33	c2hwyB_	Alignment	not modelled	76.0	14	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
34	d1wbha1	Alignment	not modelled	41.6	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
35	c6oviA_	Alignment	not modelled	31.0	13	PDB header: lyase Chain: A: PDB Molecule: keto-deoxy-phosphogluconate aldolase; PDBTitle: crystal structure of kdpq aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate
36	d1vhca_	Alignment	not modelled	26.5	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
37	c2yw3E_	Alignment	not modelled	22.8	23	PDB header: lyase Chain: E: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3- PDBTitle: crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 dehydro-3-deoxyphosphogluconate aldolase from tthb1
38	c4yakD_	Alignment	not modelled	21.0	14	PDB header: ligase Chain: D: PDB Molecule: beta subunit of acyl-coa synthetase (ndp forming); PDBTitle: ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 in complex with coenzyme a, acetyl-coenzyme a and with3 phosphorylated phosphohistidine segment (site i orientation)
39	d2ebfx2	Alignment	not modelled	17.2	15	Fold: EreA/ChaN-like Superfamily: EreA/ChaN-like Family: PMT domain-like
40	d1mxsa_	Alignment	not modelled	16.0	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
41	d1hx0a2	Alignment	not modelled	16.0	25	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
42	c4fxeB_	Alignment	not modelled	13.6	7	PDB header: toxin/toxin inhibitor Chain: B: PDB Molecule: antitoxin relb; PDBTitle: crystal structure of the intact e. coli relbe toxin-antitoxin complex
43	c4e38A_	Alignment	not modelled	13.5	14	PDB header: lyase Chain: A: PDB Molecule: keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate PDBTitle: crystal structure of probable keto-hydroxyglutarate-aldolase from2 vibionales bacterium swat-3 (target efi-502156)
44	c1jqsB_	Alignment	not modelled	13.0	28	PDB header: ribosome Chain: B: PDB Molecule: elongation factor g; PDBTitle: fitting of l11 protein and elongation factor g (domain g'2 and v) in the cryo-em map of e. coli 70s ribosome bound3 with ef-g and gmpccp, a nonhydrolysable gtp analog
45	c4qcca_	Alignment	not modelled	12.9	14	PDB header: structural protein, lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase, peptidyl- PDBTitle: structure of a cube-shaped, highly porous protein cage designed by2 fusing symmetric oligomeric domains
46	c4bk9B_	Alignment	not modelled	12.6	13	PDB header: lyase Chain: B: PDB Molecule: 2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxo PDBTitle: crystal structure of 2-keto-3-deoxy-6-phospho-gluconate aldolase from2 zymomonas mobilis atcc 29191
47	c2k29A_	Alignment	not modelled	12.2	7	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb
48	d1hi9a_	Alignment	not modelled	11.7	17	Fold: Dipeptide transport protein Superfamily: Dipeptide transport protein Family: Dipeptide transport protein
49	d2gja2	Alignment	not modelled	11.3	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
50	c2zkr9_	Alignment	not modelled	10.9	25	PDB header: ribosomal protein/rna Chain: 9: PDB Molecule: 60s ribosomal protein l32; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
51	d3dhpa2	Alignment	not modelled	10.8	25	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
52	d1v32a_	Alignment	not modelled	10.8	16	Fold: SWIB/MDM2 domain Superfamily: SWIB/MDM2 domain Family: SWIB/MDM2 domain
53	d1g94a2	Alignment	not modelled	10.7	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases

						Family: Amylase, catalytic domain
54	c3v33A	Alignment	not modelled	10.2	23	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 conserved domain with zinc-finger motif
55	d1piia2	Alignment	not modelled	10.2	23	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
56	c3fesB	Alignment	not modelled	10.1	13	PDB header: atp binding protein Chain: B: PDB Molecule: atp-dependent clp endopeptidase; PDBTitle: crystal structure of the atp-dependent clp protease clpc from2 clostridium difficile
57	d1jaea2	Alignment	not modelled	9.8	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
58	d1y81a1	Alignment	not modelled	9.7	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
59	c1bplA	Alignment	not modelled	9.7	10	PDB header: glycosyltransferase Chain: A: PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: glycosyltransferase
60	c1mwoA	Alignment	not modelled	9.4	40	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase; PDBTitle: crystal structure analysis of the hyperthermostable2 pyrococcus woesei alpha-amylase
61	d1mxga2	Alignment	not modelled	9.2	40	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
62	c1jdaA	Alignment	not modelled	9.0	20	PDB header: hydrolase Chain: A: PDB Molecule: 1,4-alpha maltotetrahydrolase; PDBTitle: maltotetraose-forming exo-amylase
63	d1vc4a	Alignment	not modelled	9.0	22	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
64	c4hecB	Alignment	not modelled	9.0	13	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium tuberculosis
65	c3labA	Alignment	not modelled	8.7	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative kdpg (2-keto-3-deoxy-6-phosphogluconate) aldolase; PDBTitle: crystal structure of a putative kdpg (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
66	d1nowa1	Alignment	not modelled	8.5	33	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
67	c1ud8A	Alignment	not modelled	8.4	10	PDB header: hydrolase Chain: A: PDB Molecule: amylase; PDBTitle: crystal structure of amyk38 with lithium ion
68	d1hvx2	Alignment	not modelled	8.2	40	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
69	c5guiA	Alignment	not modelled	8.2	16	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein clpc1, chloroplastic; PDBTitle: crystal structure of the n-terminal domain of caseinolytic protease2 associated chaperone clpc1 from arabidopsis thaliana
70	d1yhta1	Alignment	not modelled	8.1	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
71	d1qvra1	Alignment	not modelled	8.0	21	Fold: Double Clp-N motif Superfamily: Double Clp-N motif Family: Double Clp-N motif
72	c1j1hA	Alignment	not modelled	7.9	26	PDB header: rna binding protein Chain: A: PDB Molecule: small protein b; PDBTitle: solution structure of a tmrna-binding protein, smpb, from2 thermus thermophilus
73	c3v32B	Alignment	not modelled	7.9	26	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 n-terminal conserved domain
74	c1p6vC	Alignment	not modelled	7.8	26	PDB header: rna binding protein/rna Chain: C: PDB Molecule: ssra-binding protein; PDBTitle: crystal structure of the trna domain of transfer-messenger2 rna in complex with smpb
75	d1p6va	Alignment	not modelled	7.8	26	Fold: Small protein B (SmpB) Superfamily: Small protein B (SmpB) Family: Small protein B (SmpB)
76	c2h9aA	Alignment	not modelled	7.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: carbon monoxide dehydrogenase corrinoid/iron-sulfur PDBTitle: corrinoid iron-sulfur protein
77	d1a53a	Alignment	not modelled	7.7	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
78	c3ff4A	Alignment	not modelled	7.5	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein chu_1412
79	c2qpuB	Alignment	not modelled	7.4	20	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amylase type a isozyme; PDBTitle: sugar tongs mutant s378p in complex with acarbose
						Fold: Retrovirus capsid protein, N-terminal core domain

80	d1em9a_	Alignment	not modelled	7.4	13	Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
81	c2duwA_	Alignment	not modelled	7.3	26	PDB header: ligand binding protein Chain: A: PDB Molecule: putative coa-binding protein; PDBTitle: solution structure of putative coa-binding protein of2 klebsiella pneumoniae
82	c4y0bA_	Alignment	not modelled	7.2	7	PDB header: protein binding Chain: A: PDB Molecule: double clp-n motif protein; PDBTitle: the structure of arabidopsis clp1
83	c1gcyA_	Alignment	not modelled	7.2	20	PDB header: hydrolase Chain: A: PDB Molecule: glucan 1,4-alpha-maltotetrahydrolase; PDBTitle: high resolution crystal structure of maltotetraose-forming2 exo-amylase
84	c3cceY_	Alignment	not modelled	7.2	35	PDB header: ribosome Chain: Y: PDB Molecule: 50s ribosomal protein l32e; PDBTitle: structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation u2535a
85	d1vqoy1	Alignment	not modelled	7.2	35	Fold: Barstar-like Superfamily: Ribosomal protein L32e Family: Ribosomal protein L32e
86	c4hh5A_	Alignment	not modelled	7.2	18	PDB header: protein binding Chain: A: PDB Molecule: putative type vi secretion protein; PDBTitle: n-terminal domain (1-163) of clp1 atpase from e.coli eaec sc1l t6ss.
87	c5u2lA_	Alignment	not modelled	7.2	20	PDB header: protein binding Chain: A: PDB Molecule: heat shock protein 104; PDBTitle: crystal structure of the hsp104 n-terminal domain from candida 2 albicans
88	d2d3na2	Alignment	not modelled	7.1	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
89	c4uqwA_	Alignment	not modelled	6.9	15	PDB header: chaperone Chain: A: PDB Molecule: protein clpv1; PDBTitle: coevolution of the atpase clpv, the tssb-tssc sheath and2 the accessory hsie protein distinguishes two type vi3 secretion classes
90	c2v82A_	Alignment	not modelled	6.9	13	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
91	d1jaka1	Alignment	not modelled	6.9	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
92	c6emwD_	Alignment	not modelled	6.9	10	PDB header: chaperone Chain: D: PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: structure of s.aureus clpc in complex with meca
93	c1jd7A_	Alignment	not modelled	6.9	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplanctis alpha-amylase
94	d2f2ab1	Alignment	not modelled	6.9	20	Fold: GatB/YqeY motif Superfamily: GatB/YqeY motif Family: GatB/GatE C-terminal domain-like
95	c6gyaA_	Alignment	not modelled	6.8	20	PDB header: hydrolase Chain: A: PDB Molecule: a-amylase; PDBTitle: amylase in complex with branched ligand
96	d1ud2a2	Alignment	not modelled	6.5	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
97	d1gcyA2	Alignment	not modelled	6.5	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
98	d1tfra2	Alignment	not modelled	6.5	8	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
99	c3blpX_	Alignment	not modelled	6.4	25	PDB header: hydrolase Chain: X: PDB Molecule: alpha-amylase 1; PDBTitle: role of aromatic residues in human salivary alpha-amylase