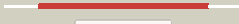



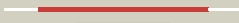


















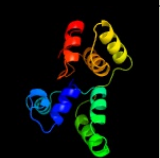
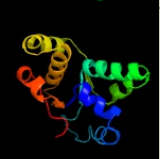

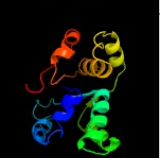
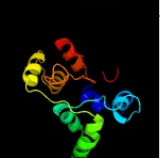
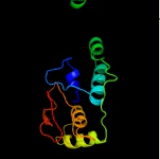
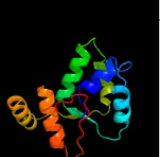


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3408 (-)_3826728_3827138
Date	Fri Aug 9 18:20:08 BST 2019
Unique Job ID	98a02cec91f225c5

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2fe1a1	 Alignment		99.6	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
2	c2fe1A_	 Alignment		99.6	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
3	c5wzfB_	 Alignment		99.6	19	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
4	d1v8pa_	 Alignment		99.6	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
5	c1v8pK_	 Alignment		99.5	18	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
6	c4xqrG_	 Alignment		99.5	17	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addiction module from mycobacterial species
7	d2h1ca1	 Alignment		99.4	23	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
8	c6a7vG_	 Alignment		99.4	16	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
9	c3zvkc_	 Alignment		99.3	12	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	c5x3tD_	 Alignment		99.3	19	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
11	c6nklA_	 Alignment		99.2	11	PDB header: antitoxin Chain: A: PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae

12	c5l6mC_	Alignment		99.1	22	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
13	c4chgC_	Alignment		99.1	16	PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
14	d1y82a1	Alignment		99.0	23	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
15	c3tndC_	Alignment		99.0	12	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
16	c3h87B_	Alignment		99.0	21	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
17	d1v96a1	Alignment		99.0	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
18	c5sv2A_	Alignment		98.9	17	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
19	c3dboB_	Alignment		98.8	16	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	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
21	c3i8oA_	Alignment	not modelled	98.6	13	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	22	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	c5f4hF_	Alignment	not modelled	97.9	16	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
24	d1o4wa_	Alignment	not modelled	97.9	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
25	c2hwwC_	Alignment	not modelled	97.9	12	PDB header: rna binding protein Chain: C: PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
26	c5ywwA_	Alignment	not modelled	97.9	16	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
27	c2lqA_	Alignment	not modelled	97.8	17	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
28	c5yz4A_	Alignment	not modelled	96.7	20	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	96.7	12	Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
30	c6g5iy_	Alignment	not modelled	95.0	16	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	c4mj7B_	Alignment	not modelled	91.3	13	PDB header: rna binding protein Chain: B: PDB Molecule: rrna-processing protein utp23; PDBTitle: crystal structure of the pin domain of saccharomyces cerevisiae utp23
32	c2mdtA_	Alignment	not modelled	85.6	15	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: a pilt n-terminus domain protein sso1118 from hyperthermophilic2 archaeon sulfolobus solfataricus p2
33	c2hwyB_	Alignment	not modelled	80.0	12	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
34	d1tfra2	Alignment	not modelled	53.2	10	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
35	c2zkr9_	Alignment	not modelled	38.8	6	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
36	d1ulza2	Alignment	not modelled	36.4	17	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
37	d1y81a1	Alignment	not modelled	35.7	5	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
38	c2duwA_	Alignment	not modelled	33.9	15	PDB header: ligand binding protein Chain: A: PDB Molecule: putative coa-binding protein; PDBTitle: solution structure of putative coa-binding protein of2 klebsiella pneumoniae
39	c4mwaA_	Alignment	not modelled	33.7	30	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: 1.85 angstrom crystal structure of gcpe protein from bacillus2 anthracis
40	c3j3be_	Alignment	not modelled	33.0	11	PDB header: ribosome Chain: E: PDB Molecule: 60s ribosomal protein l6; PDBTitle: structure of the human 60s ribosomal proteins
41	c4a1cX_	Alignment	not modelled	32.6	21	PDB header: ribosome Chain: X: PDB Molecule: 60s ribosomal protein l32; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
42	d2j9ga2	Alignment	not modelled	32.2	17	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
43	c3zf7i_	Alignment	not modelled	30.9	11	PDB header: ribosome Chain: I: PDB Molecule: 60s ribosomal protein l18; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
44	c3cceY_	Alignment	not modelled	30.5	18	PDB header: ribosome Chain: Y: PDB Molecule: 50s ribosomal protein l32e; PDBTitle: structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation u2535a
45	d1vqoy1	Alignment	not modelled	30.5	18	Fold: Barstar-like Superfamily: Ribosomal protein L32e Family: Ribosomal protein L32e
46	c3lotC_	Alignment	not modelled	29.9	29	PDB header: structure genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function (np_070038.1) from2 archaeoglobus fulgidus at 1.89 a resolution
47	c3no5C_	Alignment	not modelled	28.8	24	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a pfam duf849 domain containing protein2 (reut_a1631) from ralstonia eutropha jmp134 at 1.90 a resolution
48	c3c6cA_	Alignment	not modelled	28.5	24	PDB header: hydrolase Chain: A: PDB Molecule: 3-keto-5-aminohexanoate cleavage enzyme; PDBTitle: crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution
49	c3e02A_	Alignment	not modelled	27.1	19	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849; PDBTitle: crystal structure of a duf849 family protein (bx_e_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution
50	d1iuka_	Alignment	not modelled	26.9	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
51	d2csua1	Alignment	not modelled	24.5	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
52	c5zmyF_	Alignment	not modelled	24.3	19	PDB header: hydrolase Chain: F: PDB Molecule: cis-epoxysuccinate hydrolase; PDBTitle: crystal structure of a cis-epoxysuccinate hydrolase producing d(-)-2 tartaric acids
53	c3e49A_	Alignment	not modelled	23.9	19	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849 with a tim barrel fold; PDBTitle: crystal structure of a prokaryotic domain of unknown function (duf849)2 with a tim barrel fold (bx_e_c0966) from

						burkholderia xenovorans lb4003 at 1.75 a resolution PDB header: metal binding protein Chain: A: PDB Molecule: prokaryotic domain of unknown function (duf849) with a tim PDBTitle: crystal structure of a prokaryotic domain of unknown function (duf849)2 member (spoa0042) from silicibacter pomeroyi dss-3 at 1.45 a3 resolution
54	c3chvA_	Alignment	not modelled	23.8	24	PDB header: ribosome Chain: H: PDB Molecule: 60s ribosomal protein l7a (l7ae); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
55	c3iz5h_	Alignment	not modelled	23.6	11	PDB header: ribosome Chain: B: PDB Molecule: 50s ribosomal protein l2p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
56	c3j21b_	Alignment	not modelled	22.9	18	PDB header: lyase Chain: A: PDB Molecule: 3-keto-5-amino-hexanoate cleavage enzyme; PDBTitle: crystal structure of the 3-keto-5-amino-hexanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form)
57	c2y7eA_	Alignment	not modelled	22.3	33	PDB header: lyase Chain: A: PDB Molecule: obca, oxalate biosynthetic component a; PDBTitle: ternary complex of obca with c4-coa adduct and oxalate
58	c4nncA_	Alignment	not modelled	20.5	14	PDB header: translation Chain: A: PDB Molecule: uncharacterized protein yacp; PDBTitle: crystal structure of rae1 (yacp) from bacillus subtilis (w164l mutant)
59	c5mq9A_	Alignment	not modelled	17.3	14	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
60	c2ihnA_	Alignment	not modelled	15.7	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein fdra; PDBTitle: crystal structure of a predicated acyl-coa synthetase from e.coli
61	c3dmyA_	Alignment	not modelled	15.5	29	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 n-terminal conserved domain
62	c3v32B_	Alignment	not modelled	15.3	20	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 gmppcp, a nonhydrolysable gtp analog
63	c1jqsB_	Alignment	not modelled	15.3	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein chu_1412
64	c3ff4A_	Alignment	not modelled	14.4	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
65	d1gr0a1	Alignment	not modelled	14.0	10	PDB header: transferase Chain: B: PDB Molecule: atp-citrate synthase; PDBTitle: truncated human atp-citrate lyase with citrate bound
66	c3mwdB_	Alignment	not modelled	14.0	18	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 conserved domain with zinc-finger motif
67	c3v33A_	Alignment	not modelled	13.7	20	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
68	d1w96a2	Alignment	not modelled	13.4	8	PDB header: ribosome Chain: 0: PDB Molecule: 60s ribosomal protein l32; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
69	c1s1i0_	Alignment	not modelled	13.2	18	PDB header: isomerase Chain: A: PDB Molecule: inositol-3-phosphate synthase; PDBTitle: myo-inositol 1-phosphate synthase from mycobacterium2 tuberculosis in complex with nad and zinc.
70	c1gr0A_	Alignment	not modelled	11.9	12	PDB header: dna binding protein Chain: B: PDB Molecule: orf067; PDBTitle: g1 orf67 / staphylococcus aureus sigmaa domain 4 complex
71	c4g94B_	Alignment	not modelled	11.4	6	PDB header: isomerase Chain: C: PDB Molecule: myo-inositol-1-phosphate synthase; PDBTitle: myo-inositol phosphate synthase mips from a. fulgidus
72	c1u1iC_	Alignment	not modelled	11.2	16	Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
73	d2fywa1	Alignment	not modelled	10.3	18	PDB header: lyase Chain: A: PDB Molecule: citryl-coa synthetase small subunit; PDBTitle: structure of citryl-coa synthetase from hydrogenobacter thermophilus
74	c6hxqA_	Alignment	not modelled	10.3	18	PDB header: ligase Chain: A: PDB Molecule: alanine-anticapsin ligase bacd; PDBTitle: crystal structure of bacd, an l-amino acid dipeptide ligase from2 bacillus subtilis
75	c3vmmA_	Alignment	not modelled	9.9	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: 457aa long hypothetical protein; PDBTitle: crystal structure of ph0766 from pyrococcus horikoshii ot3
76	c2csuB_	Alignment	not modelled	9.8	18	Fold: BRCT domain Superfamily: BRCT domain Family: 53BP1
77	d1kzyc2	Alignment	not modelled	9.5	10	

78	d1pia2	Alignment	not modelled	9.2	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
79	c1z7eC	Alignment	not modelled	9.1	21	PDB header: hydrolase Chain: C: PDB Molecule: protein arna; PDBTitle: crystal structure of full length arna
80	d1j6ua1	Alignment	not modelled	9.0	15	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
81	d1nmpa	Alignment	not modelled	9.0	26	Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
82	d1a53a	Alignment	not modelled	8.9	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
83	d1xo1a2	Alignment	not modelled	8.8	8	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
84	d2gx8a1	Alignment	not modelled	8.6	20	Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
85	c6melA	Alignment	not modelled	8.4	12	PDB header: ligase Chain: A: PDB Molecule: succinate--coa ligase subunit alpha; PDBTitle: succinyl-coa synthase from campylobacter jejuni
86	c3qvjB	Alignment	not modelled	8.4	12	PDB header: isomerase Chain: B: PDB Molecule: putative hydantoin racemase; PDBTitle: allantoin racemase from klebsiella pneumoniae
87	c2gx8B	Alignment	not modelled	8.2	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: nif3-related protein; PDBTitle: the crystal structure of bacillus cereus protein related to nif3
88	d1wbha1	Alignment	not modelled	7.9	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
89	c2nydB	Alignment	not modelled	7.6	24	PDB header: unknown function Chain: B: PDB Molecule: upf0135 protein sa1388; PDBTitle: crystal structure of staphylococcus aureus hypothetical protein sa1388
90	d1i4na	Alignment	not modelled	7.5	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
91	c2yv1A	Alignment	not modelled	7.5	22	PDB header: ligase Chain: A: PDB Molecule: succinyl-coa ligase [adp-forming] subunit alpha; PDBTitle: crystal structure of succinyl-coa synthetase alpha chain from2 methanocaldococcus jannaschii dsm 2661
92	c6oviA	Alignment	not modelled	7.5	5	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
93	d2jfga1	Alignment	not modelled	7.2	20	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
94	c2yv2A	Alignment	not modelled	7.2	22	PDB header: ligase Chain: A: PDB Molecule: succinyl-coa synthetase alpha chain; PDBTitle: crystal structure of succinyl-coa synthetase alpha chain from2 aeropyrum pernix k1
95	c2kpiA	Alignment	not modelled	6.9	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein sco3027; PDBTitle: solution nmr structure of streptomyces coelicolor sco30272 modeled with zn+2 bound, northeast structural genomics3 consortium target rr58
96	d1gsoa2	Alignment	not modelled	6.8	22	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
97	c3va7A	Alignment	not modelled	6.7	17	PDB header: ligase Chain: A: PDB Molecule: klla0e08119p; PDBTitle: crystal structure of the kluyveromyces lactis urea carboxylase
98	d1mxsa	Alignment	not modelled	6.5	9	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
99	c4yakD	Alignment	not modelled	6.5	16	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)