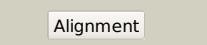
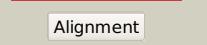
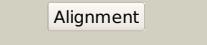


Phyre²

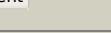
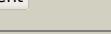
Email	mdejesus@rockefeller.edu
Description	RVBD1962c_(-)_2204873_2205280
Date	Mon Aug 5 13:25:06 BST 2019
Unique Job ID	beac800aeb7052db

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1v8pa_			99.7	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
2	c1v8pK_			99.7	21	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
3	d2fe1a1			99.7	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
4	c2fe1A_			99.7	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
5	c5wzfB_			99.6	16	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_			99.5	21	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addiction module from mycobacterial species
7	d2h1ca1			99.5	26	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
8	c6a7vG_			99.4	17	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
9	c3h87B_			99.4	17	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
10	c3zvkC_			99.4	17	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
11	d1y82a1			99.3	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain

12	c6nkIA			99.2	14	PDB header: antitoxin Chain: A: PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 Å resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
13	c5x3tD			99.2	18	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
14	c4chgC			99.2	13	PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
15	d1v96a1			99.2	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
16	c5l6mC			99.1	16	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deletac:vapc1 form)
17	c3tndC			99.1	17	PDB header: translation, toxin Chain: C: PDB Molecule: tRNA(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
18	c5sv2A			99.0	15	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
19	c3dboB			98.9	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	c3i8oA			98.7	16	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.
21	c3ix7A		not modelled	98.5	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein thta0540; PDBTitle: crystal structure of a domain of functionally unknown protein from thermus thermophilus hb8
22	d1w8ia		not modelled	98.3	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
23	d1o4wa		not modelled	97.9	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
24	c5ywwA		not modelled	97.9	20	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
25	c2hwwC		not modelled	97.9	16	PDB header: RNA binding protein Chain: C: PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
26	c5f4hf		not modelled	97.8	16	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
27	c2lcqA		not modelled	97.8	16	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
28	c5jpqd		not modelled	96.3	15	PDB header: ribosome Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
29	c6nafiv		not modelled	95.5	17	PDB header: ribosome Chain: Y: PDB Molecule: 40S ribosomal protein s24;

29	cog01y	Alignment	not modelled	95.5	17	PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state r
30	c5yz4A	Alignment	not modelled	95.0	14	PDB header: hydrolase Chain: A: PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
31	c2mdtA	Alignment	not modelled	93.0	18	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: a pilt n-terminus domain protein sso118 from hyperthermophilic2 archaeon sulfobolus softaricus p2
32	c4mj7B	Alignment	not modelled	92.5	9	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	72.2	17	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
34	d1tfra2	Alignment	not modelled	69.2	7	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
35	c4mwaA	Alignment	not modelled	46.4	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
36	c2zkr9	Alignment	not modelled	41.2	29	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 an8 3.8 a cryo-em map
37	c4a1cX	Alignment	not modelled	39.3	16	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.
38	c3j3be	Alignment	not modelled	38.6	26	PDB header: ribosome Chain: E: PDB Molecule: 60s ribosomal protein l6; PDBTitle: structure of the human 60s ribosomal proteins
39	c3zf7i	Alignment	not modelled	34.4	11	PDB header: ribosome Chain: I: PDB Molecule: 60s ribosomal protein l18; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
40	c3cceY	Alignment	not modelled	34.2	33	PDB header: ribosome Chain: Y: PDB Molecule: 50s ribosomal protein l32e; PDBTitle: structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation u2535a
41	d1vgoy1	Alignment	not modelled	34.2	33	Fold: Barstar-like Superfamily: Ribosomal protein L32e Family: Ribosomal protein L32e
42	c5mq9A	Alignment	not modelled	32.4	16	PDB header: translation Chain: A: PDB Molecule: uncharacterized protein yacp; PDBTitle: crystal structure of rae1 (yacp) from bacillus subtilis (w164l mutant)
43	d3eeqa1	Alignment	not modelled	32.0	10	Fold: CobE/GbiG C-terminal domain-like Superfamily: CobE/GbiG C-terminal domain-like Family: CobE/GbiG C-terminal domain-like
44	d1y81a1	Alignment	not modelled	26.8	5	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
45	c3j21b	Alignment	not modelled	24.5	29	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)
46	c3lotC	Alignment	not modelled	23.6	14	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	c3c6cA	Alignment	not modelled	23.2	33	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
48	c2duwA	Alignment	not modelled	22.9	20	PDB header: ligand binding protein Chain: A: PDB Molecule: putative coa-binding protein; PDBTitle: solution structure of putative coa-binding protein of2 klebsiella pneumoniae
49	c3no5C	Alignment	not modelled	22.6	29	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
50	d1ulza2	Alignment	not modelled	22.4	13	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
51	c3e02A	Alignment	not modelled	21.5	33	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849; PDBTitle: crystal structure of a duf849 family protein (bxe_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution
52	c3iz5h	Alignment	not modelled	21.4	21	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
53	d2j9ga2	Alignment	not modelled	20.9	18	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like

54	d1iuka_		not modelled	20.6	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
55	c5zmyF_		not modelled	20.5	14	PDB header: hydrolase Chain: F: PDB Molecule: cis-epoxysuccinate hydrolase; PDBTitle: crystal structure of a cis-epoxysuccinate hydrolase producing d(-)-2 tartaric acids
56	c3e49A_		not modelled	18.5	38	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 (bxe_c0966) from burholderia xenovorans lb4003 at 1.75 a resolution
57	c3chvA_		not modelled	18.1	29	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
58	c2ihnA_		not modelled	17.8	5	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
59	c2y7eA_		not modelled	17.7	33	PDB header: lyase Chain: A: PDB Molecule: 3-keto-5-aminohexanoate cleavage enzyme; PDBTitle: crystal structure of the 3-keto-5-aminohexanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form)
60	c4nnca_		not modelled	17.0	14	PDB header: lyase Chain: A: PDB Molecule: obca, oxalate biosynthetic component a; PDBTitle: ternary complex of obca with c4-coa adduct and oxalate
61	d2w6ka1		not modelled	14.8	27	Fold: CobE/GbiG C-terminal domain-like Superfamily: CobE/GbiG C-terminal domain-like Family: CobE/GbiG C-terminal domain-like
62	d1xo1a2		not modelled	14.5	11	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
63	d1cmwa2		not modelled	13.6	20	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
64	c3v33A_		not modelled	13.3	20	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcpip1 conserved domain with zinc-finger motif
65	c3v32B_		not modelled	13.0	20	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcpip1 n-terminal conserved domain
66	c1s1i0_		not modelled	11.8	45	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.
67	d1kzyc2		not modelled	9.9	33	Fold: BRCT domain Superfamily: BRCT domain Family: 53BP1
68	d2csua1		not modelled	9.2	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
69	d1w96a2		not modelled	8.4	16	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
70	c2cokA_		not modelled	7.7	20	PDB header: transferase Chain: A: PDB Molecule: poly [adp-ribose] polymerase-1; PDBTitle: solution structure of brct domain of poly(adp-ribose)2 polymerase-1
71	c3eeqB_		not modelled	6.7	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative cobalamin biosynthesis protein g homolog; PDBTitle: crystal structure of a putative cobalamin biosynthesis protein g2 homolog from sulfolobus solfataricus
72	c3ghfA_		not modelled	6.7	16	PDB header: cell cycle Chain: A: PDB Molecule: septum site-determining protein minc; PDBTitle: crystal structure of the septum site-determining protein minc from2 salmonella typhimurium
73	c1gr0A_		not modelled	6.6	13	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.
74	d1j6ua1		not modelled	6.5	20	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
75	d1xmxa_		not modelled	5.5	24	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hypothetical protein VC1899
76	c3ff4A_		not modelled	5.4	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein chu_1412
77	c1uliC_		not modelled	5.3	21	PDB header: isomerase Chain: C: PDB Molecule: myo-inositol-1-phosphate synthase; PDBTitle: myo-inositol phosphate synthase mips from a. fulgidus