























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0065 (-) _71818_72219
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1v8pa_	 Alignment		99.9	23	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
2	c1v8pK_	 Alignment		99.9	23	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
3	d2fe1a1	 Alignment		99.9	28	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
4	c2fe1A_	 Alignment		99.9	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
5	c4xgrG_	 Alignment		99.8	14	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addiction module from mycobacterial species
6	c3tndC_	 Alignment		99.6	13	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
7	c3zvkc_	 Alignment		99.6	16	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
8	c5l6mC_	 Alignment		99.6	15	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
9	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
10	c3h87B_	 Alignment		99.5	15	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
11	c5x3tD_	 Alignment		99.5	15	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis

12	c6nkIA_	Alignment		99.5	14	PDB header: antitoxin Chain: A; PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
13	c5sv2A_	Alignment		99.5	18	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
14	c6a7vG_	Alignment		99.5	18	PDB header: toxin/antitoxin Chain: G; PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
15	d2h1ca1	Alignment		99.5	12	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
16	c4chgC_	Alignment		99.4	22	PDB header: toxin/antitoxin Chain: C; PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
17	c3dboB_	Alignment		99.4	17	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
18	d1y82a1	Alignment		99.4	11	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
19	d1v96a1	Alignment		99.4	11	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
20	c3i8oA_	Alignment		99.0	15	PDB header: rna binding protein Chain: A; PDB Molecule: kh domain-containing protein mj1533; PDBTitle: a domain of a functionally unknown protein from2 methanocaldococcus jannaschii dsm 2661.
21	c5ywwA_	Alignment	not modelled	99.0	13	PDB header: hydrolase Chain: A; PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
22	c5f4hF_	Alignment	not modelled	98.9	13	PDB header: hydrolase Chain: F; PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
23	c3ix7A_	Alignment	not modelled	98.9	20	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
24	d1w8ja_	Alignment	not modelled	98.6	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
25	d1o4wa_	Alignment	not modelled	98.6	20	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
26	c2lcqA_	Alignment	not modelled	98.1	12	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	97.2	18	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	97.0	22	PDB header: hydrolase Chain: A; PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
29	c5jpd_	Alignment	not modelled	96.5	14	PDB header: ribosome Chain: D; PDB Molecule: wd40 domain proteins;

						PDBTitle: cryo-em structure of the 90s pre-ribosome
30	c6g5iy	Alignment	not modelled	93.2	28	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	c2hwyB	Alignment	not modelled	86.8	20	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
32	c4mj7B	Alignment	not modelled	86.1	12	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	c2mdtA	Alignment	not modelled	85.1	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
34	c3v33A	Alignment	not modelled	79.7	26	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 conserved domain with zinc-finger motif
35	c3v32B	Alignment	not modelled	74.6	26	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 n-terminal conserved domain
36	d1cmwa2	Alignment	not modelled	33.9	27	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
37	d1xo1a2	Alignment	not modelled	20.0	9	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
38	d1hi9a	Alignment	not modelled	19.7	31	Fold: Dipeptide transport protein Superfamily: Dipeptide transport protein Family: Dipeptide transport protein
39	d1vjla	Alignment	not modelled	18.0	22	Fold: Hypothetical protein TM0160 Superfamily: Hypothetical protein TM0160 Family: Hypothetical protein TM0160
40	c3zddA	Alignment	not modelled	11.4	19	PDB header: hydrolase/dna Chain: A: PDB Molecule: protein xni; PDBTitle: structure of e. coli exoix in complex with the palindromic 5ov62 oligonucleotide and potassium
41	c3j21P	Alignment	not modelled	10.0	8	PDB header: ribosome Chain: P: PDB Molecule: 50s ribosomal protein l18e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
42	c3izcR	Alignment	not modelled	9.6	19	PDB header: ribosome Chain: R: PDB Molecule: 60s ribosomal protein rpl18 (l18e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
43	c3t8iC	Alignment	not modelled	8.5	25	PDB header: hydrolase Chain: C: PDB Molecule: purine nucleosidase, (iunh-2); PDBTitle: structural analysis of thermostable s. solfataricus purine-specific2 nucleoside hydrolase
44	c3zf7I	Alignment	not modelled	8.2	30	PDB header: ribosome Chain: I: PDB Molecule: 60s ribosomal protein l18; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
45	d3eeqa1	Alignment	not modelled	7.9	14	Fold: CobE/GbiG C-terminal domain-like Superfamily: CobE/GbiG C-terminal domain-like Family: CobE/GbiG C-terminal domain-like
46	c3t8jA	Alignment	not modelled	7.4	13	PDB header: hydrolase Chain: A: PDB Molecule: purine nucleosidase, (iunh-1); PDBTitle: structural analysis of thermostable s. solfataricus pyrimidine-2 specific nucleoside hydrolase
47	c3j39Q	Alignment	not modelled	7.4	19	PDB header: ribosome Chain: Q: PDB Molecule: 60s ribosomal protein l18; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
48	c3iz5R	Alignment	not modelled	7.2	26	PDB header: ribosome Chain: R: PDB Molecule: 60s ribosomal protein l18 (l18e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
49	c6ba0D	Alignment	not modelled	7.0	13	PDB header: hydrolase Chain: D: PDB Molecule: cytidine/uridine-specific hydrolase; PDBTitle: pyrimidine-specific ribonucleoside hydrolase from gardnerella2 vaginalis
50	c2c40B	Alignment	not modelled	7.0	0	PDB header: hydrolase Chain: B: PDB Molecule: inosine-uridine preferring nucleoside hydrolase family PDBTitle: crystal structure of inosine-uridine preferring nucleoside2 hydrolase from bacillus anthracis at 2.2a resolution
51	c3j3bQ	Alignment	not modelled	6.9	22	PDB header: ribosome Chain: Q: PDB Molecule: 60s ribosomal protein l18; PDBTitle: structure of the human 60s ribosomal proteins
52	c2pb7A	Alignment	not modelled	6.6	22	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase uhrf1; PDBTitle: crystal structure of the sra domain of the human uhrf12 protein
53	c1s1iO	Alignment	not modelled	6.1	21	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l18; 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.
54	c4a1aN	Alignment	not modelled	5.7	30	PDB header: ribosome Chain: N: PDB Molecule: rpl18; 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 3.
55 c4nzpA_	Alignment not modelled	5.2
	27	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: the crystal structure of argininosuccinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168