

Phyre2

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Description	RVBD0960_(-)_1073549_1073932
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Unique Job ID	a1cff4d2643b1e66

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1v8pa_	Alignment		99.9	25	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
2	c1v8pK_	Alignment		99.9	25	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
3	d2fe1a1	Alignment		99.7	31	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
4	c2fe1A_	Alignment		99.7	31	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		99.4	18	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addition module from mycobacterial species
6	c6a7vG_	Alignment		99.3	20	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
7	c3zvK_	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
8	c5x3tD_	Alignment		99.2	22	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
9	c5wzfB_	Alignment		99.2	26	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	c5l6mC_	Alignment		99.1	15	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
11	c3i8oA_	Alignment		99.0	17	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.

12	c4chgC_	Alignment		99.0	22	PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
13	c6nkIA_	Alignment		99.0	15	PDB header: antitoxin Chain: A: PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
14	c5sv2A_	Alignment		99.0	21	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
15	c3tndC_	Alignment		99.0	11	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
16	d2h1ca1	Alignment		99.0	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
17	c3ix7A_	Alignment		98.9	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
18	c3h87B_	Alignment		98.8	13	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
19	c3dboB_	Alignment		98.8	21	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	d1v96a1	Alignment		98.7	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
21	c5ywwA_	Alignment	not modelled	98.7	14	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
22	c5f4hF_	Alignment	not modelled	98.7	14	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
23	d1y82a1	Alignment	not modelled	98.6	11	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
24	c2lqA_	Alignment	not modelled	98.0	16	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
25	d1o4wa_	Alignment	not modelled	97.9	20	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
26	d1w8ia_	Alignment	not modelled	97.5	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
27	c2hwwC_	Alignment	not modelled	96.9	18	PDB header: rna binding protein Chain: C: PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
28	c2mdtA_	Alignment	not modelled	95.4	22	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: a pilt n-terminus domain protein sso1118 from hyperthermophilic2 archaean sulfolobus solfataricus p2
29	c5yz4A_	Alignment	not modelled	94.9	22	PDB header: hydrolase Chain: A: PDB Molecule: rrna-processing protein fcf1;

						PDBTitle: structure of the pin domain endonuclease utp24
30	c5jpd	Alignment	not modelled	94.5	19	PDB header: ribosome Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
31	c6g5iy	Alignment	not modelled	94.5	24	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
32	c2hwyB	Alignment	not modelled	69.5	21	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
33	c4mj7B	Alignment	not modelled	55.0	7	PDB header: rna binding protein Chain: B: PDB Molecule: rrna-processing protein utp23; PDBTitle: crystal structure of the pin domain of saccharomyces cerevisiae utp23
34	c3v33A	Alignment	not modelled	49.4	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	45.0	30	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 n-terminal conserved domain
36	c1ql1A	Alignment	not modelled	14.7	23	PDB header: virus Chain: A: PDB Molecule: pf1 bacteriophage coat protein b; PDBTitle: inovirus (filamentous bacteriophage) strain pf1 major coat2 protein assembly
37	c2ifmA	Alignment	not modelled	11.6	23	PDB header: virus Chain: A: PDB Molecule: pf1 filamentous bacteriophage; PDBTitle: pf1 filamentous bacteriophage: refinement of a molecular2 model by simulated annealing using 3.3 angstroms3 resolution x-ray fibre diffraction data
38	d1vjla	Alignment	not modelled	11.2	14	Fold: Hypothetical protein TM0160 Superfamily: Hypothetical protein TM0160 Family: Hypothetical protein TM0160
39	c3rmsA	Alignment	not modelled	9.3	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein svir_20580 from2 saccharomonospora viridis
40	d2gixa1	Alignment	not modelled	6.7	13	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
41	d1nowa1	Alignment	not modelled	6.3	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
42	d1q0qa2	Alignment	not modelled	6.3	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
43	d1qbaa3	Alignment	not modelled	6.0	31	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
44	c2zkr6	Alignment	not modelled	5.5	6	PDB header: ribosomal protein/rna Chain: 6: PDB Molecule: 60s ribosomal protein l30e; 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
45	c3rpmA	Alignment	not modelled	5.4	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetyl-hexosaminidase; PDBTitle: crystal structure of the first gh20 domain of a novel beta-n-acetyl-2 hexosaminidase strh from streptococcus pneumoniae r6
46	c4mcjC	Alignment	not modelled	5.3	11	PDB header: transferase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative nucleoside deoxyribosyltransferase2 (bdi_0649) from parabacteroides distasonis atcc 8503 at 2.40 a3 resolution
47	c2ylaA	Alignment	not modelled	5.3	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis