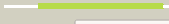

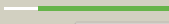

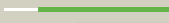



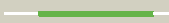















Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3749Ac_(RVBD3749Ac)_4198062_4198370
 Date Fri Aug 9 18:20:45 BST 2019
 Unique Job ID 4772e0ced2156890

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hwwC_	 Alignment		63.6	21	PDB header: rna binding protein Chain: C: PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
2	d2fe1a1	 Alignment		59.2	9	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
3	c2fe1A_	 Alignment		59.2	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
4	c6a7vG_	 Alignment		57.0	13	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
5	c3ix7A_	 Alignment		50.2	23	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
6	c5jppd_	 Alignment		45.0	19	PDB header: ribosome Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
7	c4ndkA_	 Alignment		40.6	39	PDB header: fluorescent protein, de novo protein Chain: A: PDB Molecule: e23p-yfp, gfp-like fluorescent chromoprotein fp506, PDBTitle: crystal structure of a computational designed engrailed homeodomain2 variant fused with yfp
8	c3tndC_	 Alignment		39.6	9	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapc toxin-antitoxin complex
9	d1v8pa_	 Alignment		38.2	8	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
10	c3i8oA_	 Alignment		37.7	14	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.
11	d1o4wa_	 Alignment		36.9	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain

12	c4ndlC_	Alignment		35.3	32	PDB header: de novo protein Chain: C: PDB Molecule: enh-c2b, computational designed homodimer; PDBTitle: computational design and experimental verification of a symmetric2 homodimer
13	c5yz4A_	Alignment		33.8	19	PDB header: hydrolase Chain: A: PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
14	c1v8pK_	Alignment		32.1	9	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
15	c5wzfB_	Alignment		25.1	17	PDB header: hydrolase Chain: B: PDB Molecule: 23s rrna-specific endonuclease vappc20; PDBTitle: crystal structure of mycobacterium tuberculosis vappc20 (rv2549c),2 sarcin-ricin loop cleaving toxin
16	c4mj7B_	Alignment		21.4	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
17	d1v96a1	Alignment		16.2	25	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
18	d1g3wa2	Alignment		16.0	12	Fold: Iron-dependent repressor protein, dimerization domain Superfamily: Iron-dependent repressor protein, dimerization domain Family: Iron-dependent repressor protein, dimerization domain
19	c5nvpB_	Alignment		11.9	43	PDB header: cell cycle Chain: B: PDB Molecule: autophagy-related protein 16-1; PDBTitle: structure of human atg5-atg16l1(atg5bd) complex (i4)
20	c5npwF_	Alignment		11.8	43	PDB header: cell cycle Chain: F: PDB Molecule: autophagy-related protein 16-1; PDBTitle: structure of human atg5-atg16l1(atg5bd) complex (c2)
21	c5nvpD_	Alignment	not modelled	11.8	43	PDB header: cell cycle Chain: D: PDB Molecule: autophagy-related protein 16-1; PDBTitle: structure of human atg5-atg16l1(atg5bd) complex (i4)
22	c3dboB_	Alignment	not modelled	9.2	45	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
23	d1w8ia_	Alignment	not modelled	8.8	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
24	c2rghA_	Alignment	not modelled	7.6	8	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
25	c2rgoA_	Alignment	not modelled	7.1	9	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
26	c5x3tD_	Alignment	not modelled	7.0	19	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vappc26; PDBTitle: vapbc from mycobacterium tuberculosis
27	d1h41a1	Alignment	not modelled	7.0	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: alpha-D-glucuronidase/Hyaluronidase catalytic domain
28	c6g4ww_	Alignment	not modelled	6.9	31	PDB header: ribosome Chain: W: PDB Molecule: 40s ribosomal protein s15a; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state a PDB header: oxidoreductase

29	c3da1A_	Alignment	not modelled	6.8	9	Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: x-ray structure of the glycerol-3-phosphate dehydrogenase2 from bacillus halodurans complexed with fad. northeast3 structural genomics consortium target bhr167.
30	c2hwyB_	Alignment	not modelled	6.8	23	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
31	c4tq0D_	Alignment	not modelled	6.6	38	PDB header: protein binding Chain: D: PDB Molecule: autophagy-related protein 16-1; PDBTitle: crystal structure of human atg5-atg16n69
32	d1u6za1	Alignment	not modelled	6.6	19	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: Ppx associated domain
33	c4tq0B_	Alignment	not modelled	6.3	38	PDB header: protein binding Chain: B: PDB Molecule: autophagy-related protein 16-1; PDBTitle: crystal structure of human atg5-atg16n69
34	c6nd1E_	Alignment	not modelled	6.2	8	PDB header: protein transport Chain: E: PDB Molecule: translocation protein sec66; PDBTitle: cryoem structure of the sec complex from yeast
35	c4m3lC_	Alignment	not modelled	6.1	23	PDB header: ligase Chain: C: PDB Molecule: e3 ubiquitin-protein ligase trim63; PDBTitle: crystal structure of the coiled coil domain of murf1
36	c1gqkB_	Alignment	not modelled	6.0	20	PDB header: hydrolase Chain: B: PDB Molecule: alpha-d-glucuronidase; PDBTitle: structure of pseudomonas cellulosa alpha-d-glucuronidase complexed2 with glucuronic acid
37	d1l8na1	Alignment	not modelled	5.5	30	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: alpha-D-glucuronidase/Hyaluronidase catalytic domain
38	c1mqrA_	Alignment	not modelled	5.3	30	PDB header: hydrolase Chain: A: PDB Molecule: alpha-d-glucuronidase; PDBTitle: the crystal structure of alpha-d-glucuronidase (e386q) from bacillus2 stearothermophilus t-6
39	c5mdxX_	Alignment	not modelled	5.3	29	PDB header: photosynthesis Chain: X: PDB Molecule: photosystem ii reaction center protein x; PDBTitle: cryo-em structure of the psii supercomplex from arabidopsis thaliana
40	c5mdxx_	Alignment	not modelled	5.3	29	PDB header: photosynthesis Chain: X: PDB Molecule: photosystem ii reaction center protein x; PDBTitle: cryo-em structure of the psii supercomplex from arabidopsis thaliana
41	c2g16A_	Alignment	not modelled	5.3	45	PDB header: luminescent protein Chain: A: PDB Molecule: green fluorescent protein; PDBTitle: structure of s65a y66s gfp variant after backbone2 fragmentation