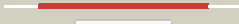



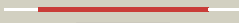




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3678c_(-)_4118237_4118692
Date	Fri Aug 9 18:20:37 BST 2019
Unique Job ID	766e0de4d5b2c260

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2otma1	 Alignment		100.0	34	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
2	c3d01G	 Alignment		100.0	51	PDB header: structural genomics, unknown function Chain: G: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the protein atu1372 with unknown function from2 agrobacterium tumefaciens
3	c3k0tA	 Alignment		100.0	26	PDB header: sugar binding protein Chain: A: PDB Molecule: endoribonuclease I-psp, putative; PDBTitle: crystal structure of pspto -psp protein in complex with d-beta-glucose2 from pseudomonas syringae pv. tomato str. dc3000
4	c5v4dE	 Alignment		100.0	25	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: putative translational inhibitor protein; PDBTitle: crystal structure of the protein of unknown function of the conserved2 rid protein family yyfa from yersinia pestis
5	c3l7qD	 Alignment		100.0	30	PDB header: translation Chain: D: PDB Molecule: putative translation initiation inhibitor, aldr regulator- PDBTitle: crystal structure of aldr from streptococcus mutans
6	d1nq3a	 Alignment		100.0	25	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
7	c3r0pB	 Alignment		100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: l-psp putative endoribonuclease; PDBTitle: crystal structure of l-psp putative endoribonuclease from uncultured2 organism
8	d1onia	 Alignment		100.0	21	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
9	d2cvla1	 Alignment		100.0	28	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
10	c5yu2D	 Alignment		100.0	25	PDB header: gene regulation Chain: D: PDB Molecule: translation initiation inhibitor homologue; PDBTitle: structure of ribonuclease yabj
11	d1qaha	 Alignment		100.0	24	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP

12	d2b33a1	Alignment		100.0	26	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
13	c1xrgB_	Alignment		100.0	28	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative translation initiation inhibitor, yjg family; PDBTitle: conserved hypothetical protein from clostridium thermocellum cth-2968
14	d1j7ha_	Alignment		100.0	28	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
15	c3m4sC_	Alignment		100.0	27	PDB header: unknown function Chain: C: PDB Molecule: putative endoribonuclease l-pp; PDBTitle: crystal structure of a putative endoribonuclease l-pp from entamoeba2 histolytica, orthorhombic form
16	d1qd9a_	Alignment		100.0	30	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
17	c3quwA_	Alignment		100.0	30	PDB header: protein binding Chain: A: PDB Molecule: protein mmf1; PDBTitle: crystal structure of yeast mmf1
18	d1x25a1	Alignment		100.0	29	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
19	d1jd1a_	Alignment		100.0	31	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
20	d1xrga_	Alignment		100.0	28	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
21	c3lmeE_	Alignment	not modelled	100.0	17	PDB header: translation Chain: E: PDB Molecule: possible translation initiation inhibitor; PDBTitle: structure of probable translation initiation inhibitor from (rpa2473)2 from rhodospseudomonas palustris
22	c3v4dC_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: C: PDB Molecule: aminoacrylate peracid reductase rutc; PDBTitle: crystal structure of rutc protein a member of the yjgf family from2 e.coli
23	c2dyyG_	Alignment	not modelled	100.0	29	PDB header: structural genomics, unknown function Chain: G: PDB Molecule: upf0076 protein ph0854; PDBTitle: crystal structure of putative translation initiation2 inhibitor ph0854 from pyrococcus horikoshii
24	d2cwja1	Alignment	not modelled	100.0	29	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
25	d1qu9a_	Alignment	not modelled	100.0	27	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
26	c2ig8C_	Alignment	not modelled	100.0	19	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein pa3499; PDBTitle: crystal structure of a protein of unknown function pa3499 from2 pseudomonas aeruginosa
27	d1pf5a_	Alignment	not modelled	100.0	22	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
28	c6izhE_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: E: PDB Molecule: 2-aminomuconate deaminase; PDBTitle: crystal structure of deaminase amne from pseudomonas sp. ap-3
						PDB header: hydrolase

29	c5hp8C	Alignment	not modelled	100.0	27	Chain: C: PDB Molecule: reactive intermediate deaminase a, chloroplastic; PDBTitle: crystal structures of rida in complex with pyruvate
30	c3gtzA	Alignment	not modelled	100.0	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative translation initiation inhibitor; PDBTitle: crystal structure of a putative translation initiation inhibitor from <i>Salmonella typhimurium</i>
31	c5v4fA	Alignment	not modelled	100.0	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative translational inhibitor protein; PDBTitle: crystal structure of the protein of unknown function of the conserved <i>Yjfb</i> protein family <i>Yjfb</i> from <i>Yersinia pestis</i>
32	c3i7tA	Alignment	not modelled	100.0	25	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of rv2704, a member of highly conserved <i>Yjgf/yer057c/uk114</i> family, from <i>Mycobacterium tuberculosis</i>
33	c3kjlL	Alignment	not modelled	100.0	14	PDB header: unknown function Chain: L: PDB Molecule: nmb1025 protein; PDBTitle: crystal structure of nmb1025, a member of <i>Yjgf</i> protein family, from <i>Neisseria meningitidis</i> (hexagonal crystal form)
34	d2ewca1	Alignment	not modelled	100.0	12	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
35	c3k12F	Alignment	not modelled	100.0	20	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: uncharacterized protein a6v7t0; PDBTitle: crystal structure of an uncharacterized protein a6v7t0 from <i>Pseudomonas aeruginosa</i>
36	c3i3fB	Alignment	not modelled	100.0	16	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: hypothetical protein from <i>Giardia lamblia</i> gl50803_14299
37	c3lybC	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: C: PDB Molecule: putative endoribonuclease; PDBTitle: structure of putative endoribonuclease (kp1_3112) from <i>Klebsiella pneumoniae</i>
38	c4bpsA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: fkb0; PDBTitle: crystal structure of chorismatase at 1.08 angstrom resolution.
39	c5a3kA	Alignment	not modelled	99.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: putative pteridine-dependent dioxygenase; PDBTitle: chorismatase mechanisms reveal fundamentally different types of 2 reaction in a single conserved protein fold
40	c2uvkB	Alignment	not modelled	50.8	24	PDB header: unknown function Chain: B: PDB Molecule: yjht; PDBTitle: structure of yjht
41	c2iyjA	Alignment	not modelled	47.2	15	PDB header: isomerase Chain: A: PDB Molecule: thiol disulfide interchange protein dsbc; PDBTitle: crystal structure of the n-terminal dimer domain of <i>E. coli</i> dsbc
42	c5yy8A	Alignment	not modelled	43.3	17	PDB header: protein binding Chain: A: PDB Molecule: influenza virus ns1a-binding protein; PDBTitle: crystal structure of the kelch domain of human ns1-bp
43	d1t3ba2	Alignment	not modelled	40.5	16	Fold: Cystatin-like Superfamily: DsbC/DsbG N-terminal domain-like Family: DsbC/DsbG N-terminal domain-like
44	d1eeja2	Alignment	not modelled	26.4	17	Fold: Cystatin-like Superfamily: DsbC/DsbG N-terminal domain-like Family: DsbC/DsbG N-terminal domain-like
45	c3pw1A	Alignment	not modelled	21.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: phenylacetic acid degradation protein paaa; PDBTitle: the phenylacetyl-coa monoxygenase paaac subcomplex with phenylacetyl-2 coa
46	c1t3bA	Alignment	not modelled	19.6	20	PDB header: isomerase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbc; PDBTitle: x-ray structure of dsbc from <i>Haemophilus influenzae</i>
47	c3fqmA	Alignment	not modelled	11.5	38	PDB header: metal binding protein Chain: A: PDB Molecule: non-structural protein 5a; PDBTitle: crystal structure of a novel dimeric form of hcv ns5a domain i protein
48	c1ox3A	Alignment	not modelled	9.1	20	PDB header: chaperone Chain: A: PDB Molecule: fibritin; PDBTitle: crystal structure of mini-fibritin
49	c2dc1B	Alignment	not modelled	9.1	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical upf0166 protein ph1503; PDBTitle: structure of ph1503 protein from <i>Pyrococcus horikoshii</i> ot3
50	c1jzdA	Alignment	not modelled	7.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbc; PDBTitle: dsbc-dsbdalpha complex
51	c4htgA	Alignment	not modelled	7.9	15	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: porphobilinogen deaminase, chloroplastic; PDBTitle: porphobilinogen deaminase from <i>Arabidopsis thaliana</i>
52	c4npbA	Alignment	not modelled	7.7	12	PDB header: isomerase Chain: A: PDB Molecule: protein disulfide isomerase ii; PDBTitle: the crystal structure of thiol:disulfide interchange protein dsbc from <i>Yersinia pestis</i> co92
53	d1gtk2	Alignment	not modelled	7.2	13	Fold: dsRBD-like Superfamily: Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain Family: Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
54	d2fug31	Alignment	not modelled	6.8	50	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain

55	d1obba2	Alignment	not modelled	6.7	31	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: AglA-like glucosidase
56	d1vjta2	Alignment	not modelled	6.7	25	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: AglA-like glucosidase
57	d1r5pa_	Alignment	not modelled	6.5	21	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: KaiB-like
58	c2j5uB_	Alignment	not modelled	6.5	17	PDB header: cell shape regulation Chain: B: PDB Molecule: mrec protein; PDBTitle: mrec lysteria monocytogenes
59	d1twfc2	Alignment	not modelled	6.2	14	Fold: Insert subdomain of RNA polymerase alpha subunit Superfamily: Insert subdomain of RNA polymerase alpha subunit Family: Insert subdomain of RNA polymerase alpha subunit
60	c4kunB_	Alignment	not modelled	6.1	8	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein lpp1115; PDBTitle: crystal structure of legionella pneumophila lpp1115 / kaib
61	c2xn4A_	Alignment	not modelled	5.8	17	PDB header: structural protein Chain: A: PDB Molecule: kelch-like protein 2; PDBTitle: crystal structure of the kelch domain of human klh2 (mayven)
62	d1up7a2	Alignment	not modelled	5.3	31	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: AglA-like glucosidase
63	d1s6ya2	Alignment	not modelled	5.3	19	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: AglA-like glucosidase