

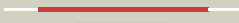










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2704 (-)_3019468_3019896
Date	Wed Aug 7 12:50:35 BST 2019
Unique Job ID	ba8686f32574d490

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3i7tA_	 Alignment		100.0	100	PDB header: unknown function Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of rv2704, a member of highly conserved2 yjgf/yer057c/uk114 family, from mycobacterium tuberculosis
2	d2b33a1	 Alignment		100.0	30	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
3	d1nq3a_	 Alignment		100.0	29	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
4	d1onia_	 Alignment		100.0	29	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
5	d1qaha_	 Alignment		100.0	29	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
6	c3r0pB_	 Alignment		100.0	23	PDB header: hydrolase Chain: B; PDB Molecule: l- <i>psp</i> putative endoribonuclease; PDBTitle: crystal structure of l- <i>psp</i> putative endoribonuclease from uncultured2 organism
7	c2ig8C_	 Alignment		100.0	29	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
8	c3k0tA_	 Alignment		100.0	25	PDB header: sugar binding protein Chain: A; PDB Molecule: endoribonuclease l- <i>psp</i> , putative; PDBTitle: crystal structure of pspto - <i>psp</i> protein in complex with d-beta-glucose2 from pseudomonas syringae pv. tomato str. dc3000
9	c6izhE_	 Alignment		100.0	33	PDB header: hydrolase Chain: E; PDB Molecule: 2-aminomuconate deaminase; PDBTitle: crystal structure of deaminase amne from pseudomonas sp. ap-3
10	c3quwA_	 Alignment		100.0	24	PDB header: protein binding Chain: A; PDB Molecule: protein mmf1; PDBTitle: crystal structure of yeast mmf1
11	c1xrgB_	 Alignment		100.0	32	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: putative translation initiation inhibitor, yjgf family; PDBTitle: conserved hypothetical protein from clostridium thermocellum cth-2968

12	d2ewca1	Alignment		100.0	23	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
13	c3m4sC	Alignment		100.0	30	PDB header: unknown function Chain: C: PDB Molecule: putative endoribonuclease I- <i>psp</i> ; PDBTitle: crystal structure of a putative endoribonuclease I- <i>psp</i> from <i>entamoeba2</i> histolytica, orthorhombic form
14	d2cvla1	Alignment		100.0	29	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
15	d1pf5a	Alignment		100.0	30	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
16	d1jd1a	Alignment		100.0	29	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
17	c3l7qD	Alignment		100.0	30	PDB header: translation Chain: D: PDB Molecule: putative translation initiation inhibitor, <i>ald</i> r regulator- PDBTitle: crystal structure of <i>ald</i> r from <i>streptococcus mutans</i>
18	c5v4dE	Alignment		100.0	35	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 <i>yyfa</i> from <i>yersinia pestis</i>
19	c5yu2D	Alignment		100.0	28	PDB header: gene regulation Chain: D: PDB Molecule: translation initiation inhibitor homologue; PDBTitle: structure of ribonuclease <i>yabj</i>
20	d1x25a1	Alignment		100.0	27	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
21	c3gtzA	Alignment	not modelled	100.0	18	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>2 salmonella typhimurium</i>
22	c3lmeE	Alignment	not modelled	100.0	28	PDB header: translation Chain: E: PDB Molecule: possible translation initiation inhibitor; PDBTitle: structure of probable translation initiation inhibitor from (<i>rpa2473</i>) ² from <i>rhodopseudomonas palustris</i>
23	d1qd9a	Alignment	not modelled	100.0	30	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
24	d1xrqa	Alignment	not modelled	100.0	33	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
25	c2dyyG	Alignment	not modelled	100.0	34	PDB header: structural genomics, unknown function Chain: G: PDB Molecule: <i>upf0076</i> protein <i>ph0854</i> ; PDBTitle: crystal structure of putative translation initiation ² inhibitor <i>ph0854</i> from <i>pyrococcus horikoshii</i>
26	d1j7ha	Alignment	not modelled	100.0	31	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
27	c3v4dC	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: C: PDB Molecule: aminoacrylate peracid reductase <i>rutc</i> ; PDBTitle: crystal structure of <i>rutc</i> protein a member of the <i>yjg</i> f family from <i>2 e.coli</i>
28	c5v4fA	Alignment	not modelled	100.0	36	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 conserved2 rid protein family <i>yyfb</i> from <i>yersinia pestis</i>
						PDB header: structural genomics, unknown function

29	c3k12F_	Alignment	not modelled	100.0	26	Chain: F; PDB Molecule: uncharacterized protein a6v7t0; PDBTitle: crystal structure of an uncharacterized protein a6v7t0 from <i>2 pseudomonas aeruginosa</i>
30	c3kjl_	Alignment	not modelled	100.0	27	PDB header: unknown function Chain: L; PDB Molecule: nmb1025 protein; PDBTitle: crystal structure of nmb1025, a member of yjgf protein family, from <i>2 neisseria meningitidis</i> (hexagonal crystal form)
31	d2cwja1	Alignment	not modelled	100.0	32	Fold: Bacillus chorismate mutase-like Superfamily: Yjgf-like Family: Yjgf/L-PSP
32	c5hp8C_	Alignment	not modelled	100.0	30	PDB header: hydrolase Chain: C; PDB Molecule: reactive intermediate deaminase a, chloroplastic; PDBTitle: crystal structures of rida in complex with pyruvate
33	d1qu9a_	Alignment	not modelled	100.0	25	Fold: Bacillus chorismate mutase-like Superfamily: Yjgf-like Family: Yjgf/L-PSP
34	c3lybC_	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: C; PDB Molecule: putative endoribonuclease; PDBTitle: structure of putative endoribonuclease (kp1_3112) from <i>klebsiella2 pneumoniae</i>
35	d2otma1	Alignment	not modelled	99.9	15	Fold: Bacillus chorismate mutase-like Superfamily: Yjgf-like Family: Yjgf/L-PSP
36	c3d01G_	Alignment	not modelled	99.9	21	PDB header: structural genomics, unknown function Chain: G; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the protein atu1372 with unknown function from <i>2 agrobacterium tumefaciens</i>
37	c3i3fB_	Alignment	not modelled	99.9	22	PDB header: unknown function Chain: B; PDB Molecule: hypothetical protein; PDBTitle: hypothetical protein from <i>giardia lamblia</i> gl50803_14299
38	c4bpsA_	Alignment	not modelled	99.9	28	PDB header: hydrolase Chain: A; PDB Molecule: ftkbo; PDBTitle: crystal structure of chorismatase at 1.08 angstrom resolution.
39	c5a3kA_	Alignment	not modelled	99.9	33	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	c2p18A_	Alignment	not modelled	34.1	14	PDB header: hydrolase Chain: A; PDB Molecule: glyoxalase ii; PDBTitle: crystal structure of the leishmania infantum glyoxalase ii
41	d1qnaa1	Alignment	not modelled	21.9	19	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
42	c2x47A_	Alignment	not modelled	19.8	13	PDB header: signaling protein Chain: A; PDB Molecule: macro domain-containing protein 1; PDBTitle: crystal structure of human macrod1
43	c6gjeB_	Alignment	not modelled	17.6	26	PDB header: protein transport Chain: B; PDB Molecule: cubilin; PDBTitle: structure of the amnionless(20-357)-cubilin(36-135) complex
44	c2ii1A_	Alignment	not modelled	16.7	16	PDB header: hydrolase Chain: A; PDB Molecule: acetamidase; PDBTitle: crystal structure of acetamidase (10172637) from <i>bacillus halodurans2</i> at 1.95 a resolution
45	c5zr1A_	Alignment	not modelled	16.1	15	PDB header: dna binding protein/dna Chain: A; PDB Molecule: origin recognition complex subunit 1; PDBTitle: <i>saccharomyces cerevisiae</i> origin recognition complex bound to a 72-bp2 origin dna containing acs and b1 element
46	c5subuC_	Alignment	not modelled	15.0	28	PDB header: hydrolase Chain: C; PDB Molecule: putative acetamidase/formamidase; PDBTitle: 2.75 angstrom resolution crystal structure of acetamidase from <i>2 yersinia enterocolitica</i> .
47	c3mlcC_	Alignment	not modelled	14.6	24	PDB header: isomerase Chain: C; PDB Molecule: fg41 malonate semialdehyde decarboxylase; PDBTitle: crystal structure of fg41msad inactivated by 3-chloropropiolate
48	c2qbbF_	Alignment	not modelled	14.6	17	PDB header: ribosome Chain: F; PDB Molecule: 30s ribosomal protein s6; PDBTitle: crystal structure of the bacterial ribosome from <i>escherichia coli</i> in2 complex with gentamicin. this file contains the 30s subunit of the3 second 70s ribosome, with gentamicin bound. the entire crystal4 structure contains two 70s ribosomes and is described in remark 400.
49	d2qalf1	Alignment	not modelled	14.6	17	Fold: Ferredoxin-like Superfamily: Ribosomal protein S6 Family: Ribosomal protein S6
50	d1nh2a1	Alignment	not modelled	14.4	14	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
51	d1mp9a1	Alignment	not modelled	14.3	21	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
52	c5fszA_	Alignment	not modelled	14.0	13	PDB header: hydrolase Chain: A; PDB Molecule: macrodomain; PDBTitle: crystal structure of <i>trypanosoma cruzi</i> macrodomain
53	c3r2uC_	Alignment	not modelled	14.0	8	PDB header: hydrolase Chain: C; PDB Molecule: metallo-beta-lactamase family protein; PDBTitle: 2.1 angstrom resolution crystal structure of metallo-beta-lactamase2 from <i>staphylococcus aureus</i> subsp. <i>aureus</i> col
54	c2wknE_	Alignment	not modelled	13.9	18	PDB header: hydrolase Chain: E; PDB Molecule: formamidase; PDBTitle: gamma lactamase from <i>delftia acidovorans</i>

55	d1xm8a_	Alignment	not modelled	13.4	16	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)
56	d1cdwa1	Alignment	not modelled	12.8	19	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
57	d2f4la1	Alignment	not modelled	12.5	16	Fold: CUB-like Superfamily: Acetamidase/Formamidase-like Family: Acetamidase/Formamidase-like
58	c1mp9B_	Alignment	not modelled	12.3	20	PDB header: dna binding protein Chain: B: PDB Molecule: tata-binding protein; PDBTitle: tbp from a mesothermophilic archaeon, sulfobolus acidocaldarius
59	d1r5pa_	Alignment	not modelled	12.1	33	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: KaiB-like
60	c1d3uA_	Alignment	not modelled	12.1	11	PDB header: gene regulation/dna Chain: A: PDB Molecule: tata-binding protein; PDBTitle: tata-binding protein/transcription factor (ii)b/bre+tata-2 box complex from pyrococcus woesei
61	c3mjjD_	Alignment	not modelled	12.0	9	PDB header: hydrolase Chain: D: PDB Molecule: predicted acetamidase/formamidase; PDBTitle: crystal structure analysis of a recombinant predicted2 acetamidase/formamidase from the thermophile thermoanaerobacter3 tengcongensis
62	c2z8uQ_	Alignment	not modelled	11.9	20	PDB header: transcription Chain: Q: PDB Molecule: tata-box-binding protein; PDBTitle: methanococcus jannaschii tbp
63	d2a6aa1	Alignment	not modelled	10.5	7	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
64	d1xhja_	Alignment	not modelled	10.4	18	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like
65	c2kjaA_	Alignment	not modelled	9.3	28	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s6; PDBTitle: solution structure and backbone dynamics of the permutant p54-55
66	c5e84B_	Alignment	not modelled	9.2	12	PDB header: chaperone Chain: B: PDB Molecule: 78 kda glucose-regulated protein; PDBTitle: atp-bound state of bip
67	c2f6aj_	Alignment	not modelled	9.1	24	PDB header: cell adhesion/structural protein Chain: J: PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure
68	c4kunB_	Alignment	not modelled	9.1	14	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein lpp1115; PDBTitle: crystal structure of legionella pneumophila lpp1115 / kaib
69	d1g0wa1	Alignment	not modelled	8.8	16	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
70	c6fcgB_	Alignment	not modelled	8.8	10	PDB header: hydrolase Chain: B: PDB Molecule: glycoside hydrolase, gh17 family; PDBTitle: crystal structure of an endo-laminarinase from formosa hel1_33_131
71	d1qh4a1	Alignment	not modelled	8.6	22	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
72	d1mzja2	Alignment	not modelled	8.3	17	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
73	c4j8fA_	Alignment	not modelled	7.9	21	PDB header: chaperone Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein; PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip
74	c2f6aF_	Alignment	not modelled	7.8	24	PDB header: cell adhesion/structural protein Chain: F: PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure
75	c2f6aE_	Alignment	not modelled	7.8	24	PDB header: cell adhesion/structural protein Chain: E: PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure
76	c2f6aI_	Alignment	not modelled	7.8	24	PDB header: cell adhesion/structural protein Chain: I: PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure
77	c2f6aG_	Alignment	not modelled	7.8	24	PDB header: cell adhesion/structural protein Chain: G: PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure
78	c2f6aH_	Alignment	not modelled	7.8	24	PDB header: cell adhesion/structural protein Chain: H: PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure
79	d2qeda1	Alignment	not modelled	7.7	15	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)
80	c5mb9B_	Alignment	not modelled	7.6	19	PDB header: chaperone Chain: B: PDB Molecule: putative heat shock protein; PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair
81	c1okjB_	Alignment	not modelled	7.6	20	PDB header: hydrolase Chain: B: PDB Molecule: trna threonylcarbamoyladenine biosynthesis protein tsab;

						PDBTitle: crystal structure of the essential e. coli yeaz2 protein by mad method using the gadolinium complex3 "dotma"
82	c2d3mA_	Alignment	not modelled	7.5	8	PDB header: transferase Chain: A: PDB Molecule: pentaketide chromone synthase; PDBTitle: pentaketide chromone synthase complexed with coenzyme a
83	c4gs5A_	Alignment	not modelled	7.4	10	PDB header: ligase Chain: A: PDB Molecule: acyl-coa synthetase (amp-forming)/amp-acid ligase ii-like PDBTitle: the crystal structure of acyl-coa synthetase (amp-forming)/amp-acid2 ligase ii-like protein from dyadobacter fermentans dsm 18053
84	c3j0xl_	Alignment	not modelled	7.2	17	PDB header: ribosome Chain: I: PDB Molecule: 30s ribosomal protein s6; PDBTitle: structural characterization of mrna-trna translocation intermediates2 (30s ribosome of class 4b of the six classes)
85	d1qh5a_	Alignment	not modelled	7.2	25	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)
86	c6n9aB_	Alignment	not modelled	7.1	7	PDB header: biosynthetic protein Chain: B: PDB Molecule: trna threonylcarbamoyladenine biosynthesis protein tsab; PDBTitle: crystal structure of thermotoga maritima threonylcarbamoyladenine2 biosynthesis complex tsab2d2e2 bound to atp and carboxy-amp
87	c3oqhB_	Alignment	not modelled	7.1	19	PDB header: ligase Chain: B: PDB Molecule: putative uncharacterized protein yvmc; PDBTitle: crystal structure of b. licheniformis cdps yvmc-blic
88	d2ix4a2	Alignment	not modelled	7.1	21	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
89	d1mp9a2	Alignment	not modelled	7.0	18	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
90	c5br9C_	Alignment	not modelled	7.0	21	PDB header: unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein with similarity to2 peptidase yeaz from pseudomonas aeruginosa
91	d1veha_	Alignment	not modelled	7.0	15	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like
92	d1sxc1	Alignment	not modelled	7.0	17	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: DNA polymerase III clamp loader subunits, C-terminal domain
93	d1cdwa2	Alignment	not modelled	6.9	22	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
94	c1cagA_	Alignment	not modelled	6.8	29	PDB header: collagen Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution
95	c1cagC_	Alignment	not modelled	6.8	29	PDB header: collagen Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution
96	d1sfla_	Alignment	not modelled	6.8	5	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
97	d1qm4a1	Alignment	not modelled	6.4	20	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
98	c3r6mD_	Alignment	not modelled	6.3	29	PDB header: hydrolase Chain: D: PDB Molecule: yeaz, resuscitation promoting factor; PDBTitle: crystal structure of vibrio parahaemolyticus yeaz
99	c5obuA_	Alignment	not modelled	6.2	12	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein dnak; PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.