




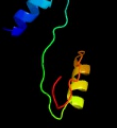

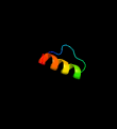


















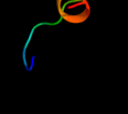



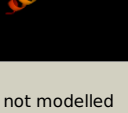


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3395A (-)_3811899_3812525
Date	Fri Aug 9 18:20:06 BST 2019
Unique Job ID	84fa96f13b4ef73f

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3aqoD_	 Alignment		32.9	17	PDB header: membrane protein Chain: D; PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: structure and function of a membrane component secdf that enhances2 protein export
2	d2f1da2	 Alignment		21.4	22	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Imidazole glycerol phosphate dehydratase
3	c4i0wA_	 Alignment		20.0	10	PDB header: hydrolase Chain: A; PDB Molecule: protease cspb; PDBTitle: structure of the clostridium perfringens cspb protease
4	d2ae8a2	 Alignment		15.6	22	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Imidazole glycerol phosphate dehydratase
5	d1rhya2	 Alignment		15.2	18	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Imidazole glycerol phosphate dehydratase
6	c3izcS_	 Alignment		14.6	18	PDB header: ribosome Chain: S; PDB Molecule: :60s ribosomal protein rpl20 (l18ae); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
7	d2nefa_	 Alignment		14.6	38	Fold: Regulatory factor Nef Superfamily: Regulatory factor Nef Family: Regulatory factor Nef
8	d1efnb_	 Alignment		14.0	38	Fold: Regulatory factor Nef Superfamily: Regulatory factor Nef Family: Regulatory factor Nef
9	c2xi1A_	 Alignment		12.6	23	PDB header: viral protein Chain: A; PDB Molecule: nef; PDBTitle: crystal structure of the hiv-1 nef sequenced from a patient's sample
10	c2na8A_	 Alignment		12.3	47	PDB header: membrane protein Chain: A; PDB Molecule: cytokine receptor common subunit beta; PDBTitle: transmembrane structure of the cytokine receptor common subunit beta
11	c2na9A_	 Alignment		12.2	47	PDB header: signaling protein Chain: A; PDB Molecule: cytokine receptor common subunit beta; PDBTitle: transmembrane structure of the p441a mutant of the cytokine receptor2 common subunit beta

12	c4fz1D_	Alignment		12.1	40	PDB header: transport protein Chain: D: PDB Molecule: pi-theraphotoxin-pc1a; PDBTitle: crystal structure of acid-sensing ion channel in complex with2 psalmotoxin 1 at high ph
13	c2f1dP_	Alignment		11.8	22	PDB header: lyase Chain: P: PDB Molecule: imidazoleglycerol-phosphate dehydratase 1; PDBTitle: x-ray structure of imidazoleglycerol-phosphate dehydratase
14	d1lmma_	Alignment		11.4	40	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Spider toxins
15	c3ik5A_	Alignment		11.4	31	PDB header: viral protein/signaling protein Chain: A: PDB Molecule: protein nef; PDBTitle: sivmac239 nef in complex with tcr zeta itam 1 polypeptide (a63-r80)
16	c3rbba_	Alignment		10.9	46	PDB header: viral protein, protein binding Chain: A: PDB Molecule: protein nef; PDBTitle: hiv-1 nef protein in complex with engineered hck sh3 domain
17	c4a19X_	Alignment		10.7	19	PDB header: ribosome Chain: X: PDB Molecule: rpl18a; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 2.
18	d1k1sa1	Alignment		9.4	18	Fold: Lesion bypass DNA polymerase (Y-family), little finger domain Superfamily: Lesion bypass DNA polymerase (Y-family), little finger domain Family: Lesion bypass DNA polymerase (Y-family), little finger domain
19	c2ae8C_	Alignment		9.0	22	PDB header: lyase Chain: C: PDB Molecule: imidazoleglycerol-phosphate dehydratase; PDBTitle: crystal structure of imidazoleglycerol-phosphate dehydratase from2 staphylococcus aureus subsp. aureus n315
20	c3kdqB_	Alignment		8.7	23	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of a functionally unknown conserved2 protein from corynebacterium diphtheriae.
21	c5dn1A_	Alignment	not modelled	8.4	17	PDB header: lyase Chain: A: PDB Molecule: imidazoleglycerol-phosphate dehydratase; PDBTitle: crystal structure of igpd from pyrococcus furiosus in complex with2 (s)-c348
22	c3zf7S_	Alignment	not modelled	8.3	26	PDB header: ribosome Chain: S: PDB Molecule: 60s ribosomal protein l18a; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
23	c2n8fA_	Alignment	not modelled	8.3	36	PDB header: toxin Chain: A: PDB Molecule: spider toxin pi-hexatoxin-hi1a; PDBTitle: chemical shift assignments and structure calculation of spider toxin2 pi-hexatoxin-hi1a
24	c3tb8A_	Alignment	not modelled	8.3	38	PDB header: apoptosis Chain: A: PDB Molecule: protein nef; PDBTitle: crystal structure of full-length myristoylated hiv-1 nef
25	c1rhyB_	Alignment	not modelled	8.2	18	PDB header: lyase Chain: B: PDB Molecule: imidazole glycerol phosphate dehydratase; PDBTitle: crystal structure of imidazole glycerol phosphate dehydratase
26	c4npgA_	Alignment	not modelled	7.7	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative lipoprotein; PDBTitle: crystal structure of a hypothetical protein (bt1938) from bacteroides2 thetaiotaomicron vpi-5482 at 2.50 a resolution
27	d2hmfa2	Alignment	not modelled	7.5	32	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
28	c5owuB_	Alignment	not modelled	7.4	28	PDB header: transport protein Chain: B: PDB Molecule: nucleoporin nup1; PDBTitle: kap95:nup1 complex
						PDB header: lyase

29	c6fwhH	Alignment	not modelled	6.6	23	Chain: H: PDB Molecule: imidazoglycerol-phosphate dehydratase; PDBTitle: acanthamoeba igpd in complex with r-c348 to 1.7a resolution
30	c3eujB	Alignment	not modelled	6.5	36	PDB header: cell cycle Chain: B: PDB Molecule: chromosome partition protein mukf; PDBTitle: crystal structure of muke-mukf(residues 292-443)-mukb(head domain)-2 atpgammas complex, symmetric dimer
31	c3u5eS	Alignment	not modelled	6.3	24	PDB header: ribosome Chain: S: PDB Molecule: 60s ribosomal protein l20-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome a
32	c3tumA	Alignment	not modelled	6.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase family protein; PDBTitle: 2.15 angstrom resolution crystal structure of a shikimate2 dehydrogenase family protein from pseudomonas putida kt2440 in3 complex with nad+
33	c2lxnA	Alignment	not modelled	6.0	6	PDB header: ligase Chain: A: PDB Molecule: gmp synthase [glutamine-hydrolyzing] subunit a; PDBTitle: solution nmr structure of glutamine amido transferase subunit of2 gaunosine monophosphate synthetase from methanocaldococcus jannaschii
34	d1vyua2	Alignment	not modelled	5.8	32	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
35	c4gkrA	Alignment	not modelled	5.8	19	PDB header: structural protein Chain: A: PDB Molecule: neck and c-terminal motor domain of kar3; PDBTitle: structure of the c-terminal motor domain of kar3 from candida glabrata
36	c2eggA	Alignment	not modelled	5.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate 5-dehydrogenase (aroe) from geobacillus2 kaustophilus
37	c3j3bS	Alignment	not modelled	5.7	23	PDB header: ribosome Chain: S: PDB Molecule: 60s ribosomal protein l18a; PDBTitle: structure of the human 60s ribosomal proteins
38	c5m5iC	Alignment	not modelled	5.7	33	PDB header: motor protein Chain: C: PDB Molecule: kinesin-like protein cut7; PDBTitle: pseudo-atomic model of microtubule-bound s.pombe kinesin-5 motor2 domain in the amppnp state (based on cryo-electron microscopy3 experiment): the n-terminus conformation allows formation of a cover4 neck bundle.
39	c2o61A	Alignment	not modelled	5.6	46	PDB header: transcription/dna Chain: A: PDB Molecule: transcription factor p65/interferon regulatory factor PDBTitle: crystal structure of nfkb, irf7, irf3 bound to the interferon-b2 enhancer
40	c6ezmL	Alignment	not modelled	5.6	14	PDB header: lyase Chain: L: PDB Molecule: imidazoglycerol-phosphate dehydratase; PDBTitle: imidazoglycerol-phosphate dehydratase from saccharomyces cerevisiae
41	c1ujjA	Alignment	not modelled	5.6	31	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h PDBTitle: solution structure of the herg k+ channel s5-p2 extracellular linker
42	c3j39S	Alignment	not modelled	5.6	23	PDB header: ribosome Chain: S: PDB Molecule: 60s ribosomal protein l18a; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
43	c4lomA	Alignment	not modelled	5.5	23	PDB header: lyase Chain: A: PDB Molecule: imidazoglycerol-phosphate dehydratase; PDBTitle: crystal structure of mycobacterium tuberculosis hisb in complex with2 its substrate
44	c3c65A	Alignment	not modelled	5.5	19	PDB header: hydrolase Chain: A: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of bacillus stearothermophilus uvr5' endonuclease2 domain
45	c3lreA	Alignment	not modelled	5.4	29	PDB header: motor protein Chain: A: PDB Molecule: kinesin-like protein kif18a; PDBTitle: crystal structure analysis of human kinesin-8 motor domain