





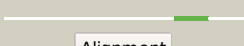




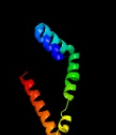



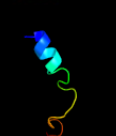
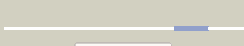





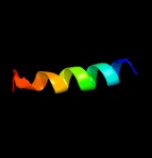
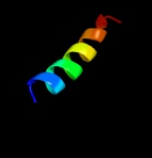


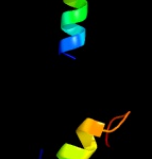
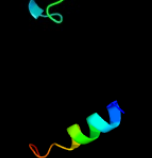


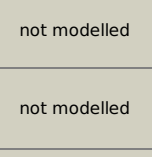


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3238c (-)_3613661_3614395
Date	Thu Aug 8 16:20:44 BST 2019
Unique Job ID	22eade944475f732

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4a2nB_	 Alignment		99.9	11	PDB header: transferase Chain: B: PDB Molecule: isoprenylcysteine carboxyl methyltransferase; PDBTitle: crystal structure of ma-icmt
2	c5v7pA_	 Alignment		99.9	19	PDB header: transferase Chain: A: PDB Molecule: protein-s-isoprenylcysteine o-methyltransferase; PDBTitle: atomic structure of the eukaryotic intramembrane ras methyltransferase2 icmt (isoprenylcysteine carboxyl methyltransferase), in complex with3 a monobody
3	c4quvB_	 Alignment		99.9	12	PDB header: oxidoreductase, membrane protein Chain: B: PDB Molecule: delta(14)-sterol reductase; PDBTitle: structure of an integral membrane delta(14)-sterol reductase
4	c4y9iA_	 Alignment		57.6	33	PDB header: oxidoreductase Chain: A: PDB Molecule: mycobacterium tuberculosis paralougous family 11; PDBTitle: structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
5	c3r5yC_	 Alignment		37.7	23	PDB header: unknown function Chain: C: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of a deazaflavin-dependent nitroreductase from nocardia2 farcinica, with co-factor f420
6	d1kf6c_	 Alignment		36.2	17	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
7	c3r5wO_	 Alignment		25.6	23	PDB header: oxidoreductase Chain: O: PDB Molecule: deazaflavin-dependent nitroreductase; PDBTitle: structure of ddn, the deazaflavin-dependent nitroreductase from2 mycobacterium tuberculosis involved in bioreductive activation of pa-3 824, with co-factor f420
8	c5e8jC_	 Alignment		23.8	20	PDB header: translation Chain: C: PDB Molecule: rnmt-activating mini protein; PDBTitle: crystal structure of mrna cap guanine-n7 methyltransferase in complex2 with ram
9	c3h96B_	 Alignment		21.7	14	PDB header: flavoprotein Chain: B: PDB Molecule: f420-h2 dependent reductase a; PDBTitle: msmeg_3358 f420 reductase
10	c5c6hN_	 Alignment		20.3	47	PDB header: apoptosis/apoptosis regulator Chain: N: PDB Molecule: mule bh3 peptide from e3 ubiquitin-protein ligase huwe1; PDBTitle: mcl-1 complexed with mule
11	c5c6hT_	 Alignment		20.3	47	PDB header: apoptosis/apoptosis regulator Chain: T: PDB Molecule: mule bh3 peptide from e3 ubiquitin-protein ligase huwe1; PDBTitle: mcl-1 complexed with mule

12	c5c6hH_	Alignment		20.3	47	PDB header: apoptosis/apoptosis regulator Chain: H: PDB Molecule: mule bh3 peptide from e3 ubiquitin-protein ligase huwe1; PDBTitle: mcl-1 complexed with mule
13	c5c6hD_	Alignment		20.3	47	PDB header: apoptosis/apoptosis regulator Chain: D: PDB Molecule: mule bh3 peptide from e3 ubiquitin-protein ligase huwe1; PDBTitle: mcl-1 complexed with mule
14	c5c6hP_	Alignment		20.3	47	PDB header: apoptosis/apoptosis regulator Chain: P: PDB Molecule: mule bh3 peptide from e3 ubiquitin-protein ligase huwe1; PDBTitle: mcl-1 complexed with mule
15	c5c6hB_	Alignment		19.9	47	PDB header: apoptosis/apoptosis regulator Chain: B: PDB Molecule: mule bh3 peptide from e3 ubiquitin-protein ligase huwe1; PDBTitle: mcl-1 complexed with mule
16	c5c6hX_	Alignment		19.6	47	PDB header: apoptosis/apoptosis regulator Chain: X: PDB Molecule: mule bh3 peptide from e3 ubiquitin-protein ligase huwe1; PDBTitle: mcl-1 complexed with mule
17	c3r5zB_	Alignment		18.8	14	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of a deazaflavin-dependent reductase from nocardia2 farcinica, with co-factor f420
18	c5c6hR_	Alignment		18.1	42	PDB header: apoptosis/apoptosis regulator Chain: R: PDB Molecule: mule bh3 peptide from e3 ubiquitin-protein ligase huwe1; PDBTitle: mcl-1 complexed with mule
19	c5c6hL_	Alignment		16.5	47	PDB header: apoptosis/apoptosis regulator Chain: L: PDB Molecule: mule bh3 peptide from e3 ubiquitin-protein ligase huwe1; PDBTitle: mcl-1 complexed with mule
20	c5c6hF_	Alignment		15.8	47	PDB header: apoptosis/apoptosis regulator Chain: F: PDB Molecule: mule bh3 peptide from e3 ubiquitin-protein ligase huwe1; PDBTitle: mcl-1 complexed with mule
21	d1k99a_	Alignment	not modelled	13.4	7	Fold: HMG-box Superfamily: HMG-box Family: HMG-box
22	c5c6hV_	Alignment	not modelled	13.1	40	PDB header: apoptosis/apoptosis regulator Chain: V: PDB Molecule: mule bh3 peptide from e3 ubiquitin-protein ligase huwe1; PDBTitle: mcl-1 complexed with mule
23	c5c6hJ_	Alignment	not modelled	10.3	42	PDB header: apoptosis/apoptosis regulator Chain: J: PDB Molecule: mule bh3 peptide from e3 ubiquitin-protein ligase huwe1; PDBTitle: mcl-1 complexed with mule
24	c1p58F_	Alignment	not modelled	9.7	23	PDB header: virus Chain: F: PDB Molecule: envelope protein m; PDBTitle: complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
25	c6dftE_	Alignment	not modelled	9.6	29	PDB header: transferase Chain: E: PDB Molecule: deoxyhypusine synthase; PDBTitle: trypanosoma brucei deoxyhypusine synthase
26	c5ht7A_	Alignment	not modelled	9.5	14	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a transition-metal-ion-binding betagamma-2 crystallin from methanosaeta thermophila
27	c1p58E_	Alignment	not modelled	9.1	19	PDB header: virus Chain: E: PDB Molecule: envelope protein m; PDBTitle: complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
28	c4lqdH_	Alignment	not modelled	9.0	26	PDB header: signaling protein Chain: H: PDB Molecule: ras association domain family member 5, rassf5; PDBTitle: structural basis for autoactivation of human mst2 kinase and its2 regulation by rassf5

29	c5o60g	Alignment	not modelled	8.2	50	PDB header: ribosome Chain: G; PDB Molecule: 50s ribosomal protein l6; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
30	c6em5v	Alignment	not modelled	8.0	31	PDB header: ribosome Chain: V; PDB Molecule: 60s ribosomal protein l23-a; PDBTitle: state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
31	c6dftj	Alignment	not modelled	7.8	31	PDB header: transferase Chain: J; PDB Molecule: deoxyhypusine synthase regulatory subunit; PDBTitle: trypanosoma brucei deoxyhypusine synthase
32	d2i5ha1	Alignment	not modelled	7.8	22	Fold: AF1531-like Superfamily: AF1531-like Family: AF1531-like
33	c2i5ha	Alignment	not modelled	7.8	22	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein af1531; PDBTitle: crystal structure of af1531 from archaeoglobus fulgidus,2 pfam duf655
34	c1geaA	Alignment	not modelled	7.6	36	PDB header: neuropeptide Chain: A; PDB Molecule: pituitary adenylate cyclase activating PDBTitle: receptor-bound conformation of pacap21
35	c1ckxA	Alignment	not modelled	7.6	36	PDB header: metal transport Chain: A; PDB Molecule: cystic fibrosis transmembrane conductance PDBTitle: cystic fibrosis transmembrane conductance regulator:2 solution structures of peptides based on the phe508 region,3 the most common site of disease-causing delta-f508 mutation
36	c4p63A	Alignment	not modelled	6.7	23	PDB header: transferase Chain: A; PDB Molecule: probable deoxyhypusine synthase; PDBTitle: crystal structure of deoxyhypusine synthase from pyrococcus horikoshii
37	d2e74g1	Alignment	not modelled	6.6	29	Fold: Single transmembrane helix Superfamily: PetG subunit of the cytochrome b6f complex Family: PetG subunit of the cytochrome b6f complex
38	c1vf5G	Alignment	not modelled	6.4	24	PDB header: photosynthesis Chain: G; PDB Molecule: protein pet g; PDBTitle: crystal structure of cytochrome b6f complex from m.laminosus
39	d1vf5g	Alignment	not modelled	6.4	24	Fold: Single transmembrane helix Superfamily: PetG subunit of the cytochrome b6f complex Family: PetG subunit of the cytochrome b6f complex
40	d1e7la1	Alignment	not modelled	6.3	38	Fold: LEM/SAP HeH motif Superfamily: Recombination endonuclease VII, C-terminal and dimerization domains Family: Recombination endonuclease VII, C-terminal and dimerization domains
41	c4bqqB	Alignment	not modelled	6.3	19	PDB header: hydrolase Chain: B; PDB Molecule: integrase; PDBTitle: protein crystal structure of the n-terminal and recombinase domains of2 the streptomyces temperate phage serine recombinase, fc31 integrase.
42	c2mc0A	Alignment	not modelled	6.2	23	PDB header: transcription activator/antibiotic Chain: A; PDB Molecule: hth-type transcriptional activator tipa; PDBTitle: structural basis of a thiopeptide antibiotic multidrug resistance2 system from streptomyces lividans:nosiheptide in complex with tipas
43	c4hxC	Alignment	not modelled	5.8	22	PDB header: rna/rna binding protein/hydrolase Chain: C; PDB Molecule: histone rna hairpin-binding protein; PDBTitle: structure of mrna stem-loop, human stem-loop binding protein and2 3'hexo ternary complex
44	d1dhsa	Alignment	not modelled	5.8	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Deoxyhypusine synthase, DHS
45	c2yqrA	Alignment	not modelled	5.6	20	PDB header: rna binding protein Chain: A; PDB Molecule: kiaa0907 protein; PDBTitle: solution structure of the kh domain in kiaa0907 protein
46	c3j2pD	Alignment	not modelled	5.5	21	PDB header: viral protein Chain: D; PDB Molecule: small envelope protein m; PDBTitle: cryoem structure of dengue virus envelope protein heterotetramer
47	d2oy9a1	Alignment	not modelled	5.5	11	Fold: BH2638-like Superfamily: BH2638-like Family: BH2638-like
48	c5n7kD	Alignment	not modelled	5.4	32	PDB header: cell adhesion Chain: D; PDB Molecule: marvel domain-containing protein 2; PDBTitle: crystal structure of the coiled-coil domain of human tricellulin
49	c2na6C	Alignment	not modelled	5.4	56	PDB header: apoptosis Chain: C; PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
50	c2na6A	Alignment	not modelled	5.4	56	PDB header: apoptosis Chain: A; PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
51	d1hhsa	Alignment	not modelled	5.4	44	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: dsRNA phage RNA-dependent RNA-polymerase
52	c2na6B	Alignment	not modelled	5.4	56	PDB header: apoptosis Chain: B; PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor