




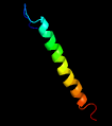

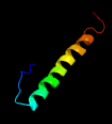















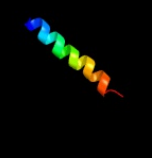

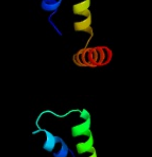
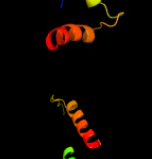


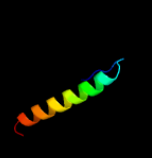
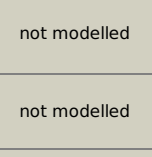


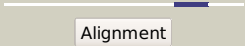

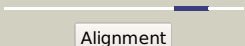

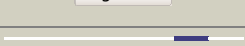


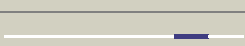

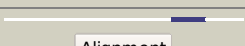
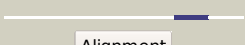
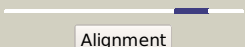

Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3166c (-)_3534389_3535348
Date	Thu Aug 8 16:20:35 BST 2019
Unique Job ID	d5bb85bf3a300f09

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1wo1A_	 Alignment		68.3	11	PDB header: unknown function Chain: A: PDB Molecule: 122aa long conserved hypothetical protein; PDBTitle: crystal structure of st0689, an archaeal hepn homologue
2	c2hsbA_	 Alignment		46.8	12	PDB header: unknown function Chain: A: PDB Molecule: hypothetical upf0332 protein af0298; PDBTitle: crystal structure of a hepn domain containing protein (af_0298) from2 archaeoglobus fulgidus at 1.95 a resolution
3	c2k9yB_	 Alignment		32.9	21	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
4	c2k9yA_	 Alignment		32.9	21	PDB header: transferase Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
5	c4nqfB_	 Alignment		32.4	14	PDB header: transferase Chain: B: PDB Molecule: nucleotidyltransferase; PDBTitle: crystal structure of hepn domain protein
6	c2n7iA_	 Alignment		29.3	38	PDB header: hormone receptor Chain: A: PDB Molecule: prolactin receptor; PDBTitle: nmr structure of the prolactin receptor transmembrane domain
7	c2dr1A_	 Alignment		23.7	28	PDB header: transferase Chain: A: PDB Molecule: 386aa long hypothetical serine aminotransferase; PDBTitle: crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
8	c2hdyA_	 Alignment		19.0	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: selenocysteine lyase; PDBTitle: structure of human selenocysteine lyase
9	d1jqoa_	 Alignment		18.8	15	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate carboxylase
10	c1jqoA_	 Alignment		18.8	15	PDB header: lyase Chain: A: PDB Molecule: phosphoenolpyruvate carboxylase; PDBTitle: crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
11	c3o10D_	 Alignment		17.1	12	PDB header: chaperone Chain: D: PDB Molecule: sacsin; PDBTitle: crystal structure of the hepn domain from human sacsin

12	d1ufba_	Alignment		15.0	19	Fold: Four-helical up-and-down bundle Superfamily: Nucleotidyltransferase substrate binding subunit/domain Family: HEPN domain
13	c4xtrG_	Alignment		14.5	27	PDB header: hydrolase/transport protein Chain: G; PDB Molecule: pep12p; PDBTitle: structure of get3 bound to the transmembrane domain of pep12
14	d1utga_	Alignment		13.6	19	Fold: Uteroglobin-like Superfamily: Uteroglobin-like Family: Uteroglobin-like
15	c1puoA_	Alignment		13.0	25	PDB header: allergen Chain: A; PDB Molecule: major allergen i polypeptide, fused chain 2, chain 1; PDBTitle: crystal structure of fel d 1- the major cat allergen
16	d1utra_	Alignment		12.5	12	Fold: Uteroglobin-like Superfamily: Uteroglobin-like Family: Uteroglobin-like
17	c3geiB_	Alignment		11.7	19	PDB header: hydrolase Chain: B; PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from chlorobium tepidum in complex2 with gcp
18	d2ejna1	Alignment		11.5	27	Fold: Uteroglobin-like Superfamily: Uteroglobin-like Family: Uteroglobin-like
19	c2xa0C_	Alignment		10.3	42	PDB header: apoptosis Chain: C; PDB Molecule: apoptosis regulator bax; PDBTitle: crystal structure of bcl-2 in complex with a bax bh32 peptide
20	c5usrG_	Alignment		10.0	16	PDB header: transferase Chain: G; PDB Molecule: cysteine desulfurase, mitochondrial; PDBTitle: crystal structure of human nfs1-isd11 in complex with e. coli acyl-2 carrier protein at 3.09 angstroms
21	c5zsqA_	Alignment	not modelled	9.8	18	PDB header: biosynthetic protein Chain: A; PDB Molecule: cysteine desulfurase; PDBTitle: nifs from hydrogenimonas thermophila, soaked with l-cysteine for 4 min
22	d1ccda_	Alignment	not modelled	9.7	12	Fold: Uteroglobin-like Superfamily: Uteroglobin-like Family: Uteroglobin-like
23	c2ks1A_	Alignment	not modelled	9.2	22	PDB header: transferase Chain: A; PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: heterodimeric association of transmembrane domains of erbb1 and erbb2 receptors enabling kinase activation
24	c2jwaA_	Alignment	not modelled	9.2	22	PDB header: transferase Chain: A; PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: erbb2 transmembrane segment dimer spatial structure
25	c1xzqA_	Alignment	not modelled	9.1	27	PDB header: hydrolase Chain: A; PDB Molecule: probable trna modification gtpase trme; PDBTitle: structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf
26	c2v75A_	Alignment	not modelled	8.5	20	PDB header: nuclear protein Chain: A; PDB Molecule: nuclear polyadenylated rna-binding protein nab2; PDBTitle: n-terminal domain of nab2
27	c3wy7D_	Alignment	not modelled	8.1	18	PDB header: transferase Chain: D; PDB Molecule: 8-amino-7-oxononanoate synthase; PDBTitle: crystal structure of mycobacterium smegmatis 7-keto-8-aminopelargonic2 acid (kapa) synthase biof
28	c2m59A_	Alignment	not modelled	8.0	21	PDB header: transferase Chain: A; PDB Molecule: vascular endothelial growth factor receptor 2; PDBTitle: spatial structure of dimeric vegfr2 membrane domain in dpc micelles

29	c2m59B_		Alignment	not modelled	8.0	21	PDB header: transferase Chain: B: PDB Molecule: vascular endothelial growth factor receptor 2; PDBTitle: spatial structure of dimeric vegfr2 membrane domain in dpc micelles
30	c4eb5B_		Alignment	not modelled	7.9	14	PDB header: transferase/metal binding protein Chain: B: PDB Molecule: probable cysteine desulfurase 2; PDBTitle: a. fulgidus iscs-iscu complex structure
31	c4f40B_		Alignment	not modelled	7.8	13	PDB header: oxidoreductase Chain: B: PDB Molecule: prostaglandin f2-alpha synthase/d-arabinose dehydrogenase; PDBTitle: x-ray crystal structure of apo prostaglandin f synthase from2 leishmania major friedlin
32	c2momC_		Alignment	not modelled	7.6	19	PDB header: membrane protein Chain: C: PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles
33	c2momB_		Alignment	not modelled	7.6	19	PDB header: membrane protein Chain: B: PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles
34	c1zzaA_		Alignment	not modelled	7.4	50	PDB header: membrane protein Chain: A: PDB Molecule: stannin; PDBTitle: solution nmr structure of the membrane protein stannin
35	d2csba1		Alignment	not modelled	7.2	26	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Topoisomerase V repeat domain
36	d1p3wa_		Alignment	not modelled	6.7	29	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
37	d1nvja_		Alignment	not modelled	6.5	32	Fold: alpha/beta-Hammerhead Superfamily: Molybdopterin synthase subunit MoaE Family: Molybdopterin synthase subunit MoaE
38	c2wmmA_		Alignment	not modelled	6.3	13	PDB header: cell cycle Chain: A: PDB Molecule: chromosome partition protein mukb; PDBTitle: crystal structure of the hinge domain of mukb
39	c3lvmB_		Alignment	not modelled	6.3	29	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of e.coli iscs
40	c4q76B_		Alignment	not modelled	6.1	10	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase 2, chloroplastic; PDBTitle: crystal structure of nfs2 c384s mutant, the plastidial cysteine2 desulfurase from arabidopsis thaliana
41	c6jbcC_		Alignment	not modelled	5.9	18	PDB header: transferase Chain: C: PDB Molecule: molybdenum cofactor biosynthesis protein e; PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
42	c6jbc0D_		Alignment	not modelled	5.8	26	PDB header: transferase Chain: D: PDB Molecule: putative molybdenum cofactor biosynthesis protein; PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
43	c5usrC_		Alignment	not modelled	5.8	18	PDB header: transferase Chain: C: PDB Molecule: cysteine desulfurase, mitochondrial; PDBTitle: crystal structure of human nfs1-isd11 in complex with e. coli acyl-2 carrier protein at 3.09 angstroms
44	c4bk8A_		Alignment	not modelled	5.8	33	PDB header: oxidoreductase Chain: A: PDB Molecule: desulfoferrodoxin, ferrous iron-binding region; PDBTitle: superoxide reductase (neelaredoxin) from ignicoccus2 hospitalis
45	c6hwhX_		Alignment	not modelled	5.8	14	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
46	c3exmA_		Alignment	not modelled	5.7	20	PDB header: hydrolase Chain: A: PDB Molecule: phosphatase sc4828; PDBTitle: crystal structure of the phosphatase sc4828 with the non-hydrolyzable2 nucleotide gpcp
47	c5b87B_		Alignment	not modelled	5.7	21	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of a cysteine desulfurase from thermococcus2 onnurineus na1 in complex with alanine at 2.3 angstrom resolution
48	c2lowA_		Alignment	not modelled	5.7	11	PDB header: membrane protein Chain: A: PDB Molecule: apelin receptor; PDBTitle: solution structure of ar55 in 50% hfp
49	c3c0uA_		Alignment	not modelled	5.6	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yaeq; PDBTitle: crystal structure of e.coli yaeq protein
50	c1bm4A_		Alignment	not modelled	5.4	25	PDB header: viral protein Chain: A: PDB Molecule: protein (moloney murine leukemia virus capsid); PDBTitle: momlv capsid protein major homology region peptide analog
51	c1w7pD_		Alignment	not modelled	5.4	9	PDB header: protein transport Chain: D: PDB Molecule: vps36p, ylr417w; PDBTitle: the crystal structure of endosomal complex escrt-ii2 (vps22/vps25/vps36)
52	c2qieA_		Alignment	not modelled	5.4	23	PDB header: transferase Chain: A: PDB Molecule: molybdopterin-converting factor subunit 2; PDBTitle: staphylococcus aureus molybdopterin synthase in complex with precursor 2 z

53	c5o4uK_	Alignment	not modelled	5.3	25	PDB header: cell adhesion Chain: K: PDB Molecule: flagellin; PDBTitle: the flagellin of pyrococcus furiosus
54	c2k59B_	Alignment	not modelled	5.3	21	PDB header: transport protein Chain: B: PDB Molecule: neuronal acetylcholine receptor subunit beta-2; PDBTitle: nmr structures of the second transmembrane domain of the2 neuronal acetylcholine receptor beta 2 subunit
55	c2wp4A_	Alignment	not modelled	5.3	27	PDB header: transferase Chain: A: PDB Molecule: molybdopterin-converting factor subunit 2 1; PDBTitle: crystal structure of rv3119 from mycobacterium tuberculosis
56	c3rpfB_	Alignment	not modelled	5.3	18	PDB header: transferase Chain: B: PDB Molecule: molybdopterin synthase catalytic subunit; PDBTitle: protein-protein complex of subunit 1 and 2 of molybdopterin-converting2 factor from helicobacter pylori 26695
57	d2ot9a1	Alignment	not modelled	5.3	18	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: YaeQ-like
58	c4l3uA_	Alignment	not modelled	5.2	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf3571 family protein (abaye3784) from2 acinetobacter baumannii aye at 1.95 a resolution
59	c2omdB_	Alignment	not modelled	5.2	36	PDB header: lyase Chain: B: PDB Molecule: molybdopterin-converting factor subunit 2; PDBTitle: crystal structure of molybdopterin converting factor subunit 22 (aq_2181) from aquifex aeolicus vf5
60	c3gehA_	Alignment	not modelled	5.1	26	PDB header: hydrolase Chain: A: PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from nostoc in complex with gdp, folinic2 acid and zn
61	d1y76a1	Alignment	not modelled	5.1	10	Fold: L27 domain Superfamily: L27 domain Family: L27 domain
62	c2gl7C_	Alignment	not modelled	5.1	41	PDB header: transcription Chain: C: PDB Molecule: b-cell lymphoma 9 protein; PDBTitle: crystal structure of a beta-catenin/bcl9/tcf4 complex
63	c3sl9D_	Alignment	not modelled	5.1	41	PDB header: signaling protein, protein binding Chain: D: PDB Molecule: b-cell cll/lymphoma 9 protein; PDBTitle: x-ray structure of beta catenin in complex with bcl9