

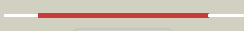




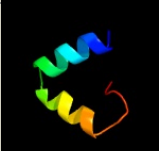

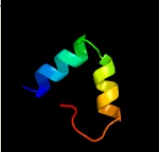

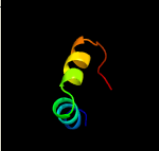

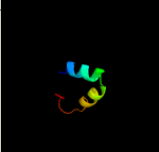

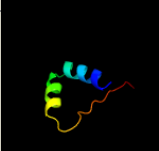

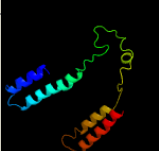

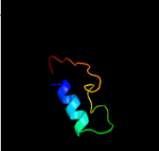







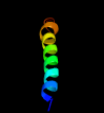

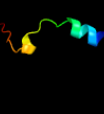
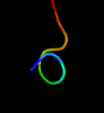


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0446c (-)_534448_535218
Date	Tue Jul 23 14:50:52 BST 2019
Unique Job ID	fe31a972d308597f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4a2nB_	 Alignment		99.9	12	PDB header: transferase Chain: B: PDB Molecule: isoprenylcysteine carboxyl methyltransferase; PDBTitle: crystal structure of ma-icmt
2	c4quvB_	 Alignment		99.9	17	PDB header: oxidoreductase, membrane protein Chain: B: PDB Molecule: delta(14)-sterol reductase; PDBTitle: structure of an integral membrane delta(14)-sterol reductase
3	c5v7pA_	 Alignment		99.9	17	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
4	c4y9iA_	 Alignment		72.1	25	PDB header: oxidoreductase Chain: A: PDB Molecule: mycobacterium tuberculosis paralogous family 11; PDBTitle: structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
5	c3r5yC_	 Alignment		68.0	32	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	c3r5wO_	 Alignment		60.5	21	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
7	c3h96B_	 Alignment		56.2	32	PDB header: flavoprotein Chain: B: PDB Molecule: f420-h2 dependent reductase a; PDBTitle: msmeg_3358 f420 reductase
8	c3r5zB_	 Alignment		54.6	29	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
9	c6hwhX_	 Alignment		46.7	23	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
10	c4p63A_	 Alignment		35.8	18	PDB header: transferase Chain: A: PDB Molecule: probable deoxyhypusine synthase; PDBTitle: crystal structure of deoxyhypusine synthase from pyrococcus horikoshii
11	d1e7la1	 Alignment		32.9	56	Fold: LEM/SAP HeH motif Superfamily: Recombination endonuclease VII, C-terminal and dimerization domains Family: Recombination endonuclease VII, C-terminal and dimerization domains

12	c6dftj_	Alignment		26.6	18	PDB header: transferase Chain: J: PDB Molecule: deoxyhypusine synthase regulatory subunit; PDBTitle: trypanosoma brucei deoxyhypusine synthase
13	c5ht7A_	Alignment		24.1	27	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
14	c4hxcC_	Alignment		23.5	17	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
15	c5e8jC_	Alignment		22.1	19	PDB header: translation Chain: C: PDB Molecule: rrnmt-activating mini protein; PDBTitle: crystal structure of mrna cap guanine-n7 methyltransferase in complex2 with ram
16	c4q2eA_	Alignment		16.0	11	PDB header: transferase Chain: A: PDB Molecule: phosphatidate cytidyltransferase; PDBTitle: crystal structure of an intramembrane cdp-dag synthetase central for2 phospholipid biosynthesis (s200c/s258c, active mutant)
17	c6cebP_	Alignment		14.6	30	PDB header: signaling protein Chain: P: PDB Molecule: insulin receptor; PDBTitle: insulin receptor ectodomain in complex with two insulin molecules - c12 symmetry
18	d1rgoa2	Alignment		14.5	83	Fold: CCCH zinc finger Superfamily: CCCH zinc finger Family: CCCH zinc finger
19	c6dftE_	Alignment		12.7	12	PDB header: transferase Chain: E: PDB Molecule: deoxyhypusine synthase; PDBTitle: trypanosoma brucei deoxyhypusine synthase
20	d1x9na1	Alignment		12.0	13	Fold: ATP-dependent DNA ligase DNA-binding domain Superfamily: ATP-dependent DNA ligase DNA-binding domain Family: ATP-dependent DNA ligase DNA-binding domain
21	d1p3ie_	Alignment	not modelled	9.4	27	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
22	d1ld3a_	Alignment	not modelled	9.3	20	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
23	d2pxyd2	Alignment	not modelled	9.0	44	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
24	d1d5mb2	Alignment	not modelled	8.9	57	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
25	c5mquA_	Alignment	not modelled	8.7	33	PDB header: virus Chain: A: PDB Molecule: vp1; PDBTitle: crystal structure of bovine enterovirus 2 determined with serial2 femtosecond x-ray crystallography
26	d1klub2	Alignment	not modelled	8.6	57	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
27	c2klqA_	Alignment	not modelled	8.6	75	PDB header: replication Chain: A: PDB Molecule: dna replication licensing factor mcm6; PDBTitle: the solution structure of cbd of human mcm6
28	c4wm8A_	Alignment	not modelled	8.3	42	PDB header: virus Chain: A: PDB Molecule: vp1; PDBTitle: crystal structure of human enterovirus d68
						PDB header: transferase Chain: D: PDB Molecule: ribosomal rna large subunit

29	c5zyoD_	Alignment	not modelled	8.3	44	PDB header: crystal structure of domain-swapped circular-permuted ybea (cp74) from <i>Escherichia coli</i>
30	c6ijjA_	Alignment	not modelled	8.0	40	PDB header: viral protein Chain: A; PDB Molecule: vp1; PDB Title: cryo-em structure of cv-a10 mature virion
31	d1hxs1_	Alignment	not modelled	7.8	42	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
32	d1pvc1_	Alignment	not modelled	7.8	42	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
33	d2fmme1	Alignment	not modelled	7.6	21	Fold: ENT-like Superfamily: ENT-like Family: Emsy N terminal (ENT) domain-like
34	d1h8ta_	Alignment	not modelled	7.6	50	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
35	c5lc5m_	Alignment	not modelled	7.4	13	PDB header: oxidoreductase Chain: M; PDB Molecule: nadh-ubiquinone oxidoreductase chain 4; PDB Title: structure of mammalian respiratory complex I, class 2
36	d1bx2b2	Alignment	not modelled	7.4	57	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
37	d1bev1_	Alignment	not modelled	7.3	38	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
38	d1d4m1_	Alignment	not modelled	7.2	58	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
39	d1cov1_	Alignment	not modelled	7.0	42	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
40	d1dhsa_	Alignment	not modelled	6.9	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Deoxyhypusine synthase, DHS
41	c2fmmE_	Alignment	not modelled	6.8	21	PDB header: transcription Chain: E; PDB Molecule: protein emsy; PDB Title: crystal structure of emsy-hp1 complex
42	d1eqzg_	Alignment	not modelled	6.8	27	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
43	d1eah1_	Alignment	not modelled	6.7	42	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
44	c3mp7B_	Alignment	not modelled	6.6	40	PDB header: protein transport Chain: B; PDB Molecule: preprotein translocase subunit SecE; PDB Title: lateral opening of a translocon upon entry of protein suggests the 2 mechanism of insertion into membranes
45	c1z7s1_	Alignment	not modelled	6.4	42	PDB header: virus Chain: 1; PDB Molecule: human coxsackievirus A21; PDB Fragment: viral protein 1; PDB Title: the crystal structure of coxsackievirus A21
46	d1y14b2	Alignment	not modelled	6.3	67	Fold: Dodecin subunit-like Superfamily: N-terminal, heterodimerisation domain of RBP7 (RpoE) Family: N-terminal, heterodimerisation domain of RBP7 (RpoE)
47	d2fdbm1	Alignment	not modelled	6.3	42	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
48	d1ev11_	Alignment	not modelled	6.2	50	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
49	c4bipA_	Alignment	not modelled	6.2	46	PDB header: virus Chain: A; PDB Molecule: vp1; PDB Title: homology model of coxsackievirus A7 (cav7) full capsid proteins.
50	d1aym1_	Alignment	not modelled	6.1	50	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
51	c1p58F_	Alignment	not modelled	5.9	36	PDB header: virus Chain: F; PDB Molecule: envelope protein M; PDB Title: complex organization of dengue virus membrane proteins as revealed by 2.95 angstrom cryo-em reconstruction
52	d1kx5a_	Alignment	not modelled	5.9	24	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
53	d1r1a1_	Alignment	not modelled	5.9	50	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
54	c2xp1A_	Alignment	not modelled	5.8	25	PDB header: transcription Chain: A; PDB Molecule: spt6; PDB Title: structure of the tandem sh2 domains from <i>Antonospora locustae</i> 2 transcription elongation factor spt6
55	c3vbuA_	Alignment	not modelled	5.7	27	PDB header: virus Chain: A; PDB Molecule: genome polyprotein, capsid protein vp1; PDB Title: crystal structure of empty human enterovirus 71 particle
56	c3vbuA_	Alignment	not modelled	5.6	27	PDB header: virus Chain: A; PDB Molecule: genome polyprotein, capsid protein vp1;

56	c5vblA_	Alignment	not modelled	5.0	49	PDBTitle: crystal structure of formaldehyde treated human enterovirus 71 (space2 group i23)
57	d1pov1_	Alignment	not modelled	5.6	42	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
58	c5k0uA_	Alignment	not modelled	5.6	40	PDB header: virus Chain: A: PDB Molecule: capsid protein vp1; PDBTitle: cryoem structure of the full virion of a human rhinovirus c
59	c5xtdo_	Alignment	not modelled	5.6	16	PDB header: oxidoreductase/electron transport Chain: O: PDB Molecule: nadh dehydrogenase [ubiquinone] flavoprotein 2, PDBTitle: cryo-em structure of human respiratory complex i
60	c4q2gA_	Alignment	not modelled	5.5	10	PDB header: transferase Chain: A: PDB Molecule: phosphatidate cytidyltransferase; PDBTitle: crystal structure of an intramembrane cdp-dag synthetase central for2 phospholipid biosynthesis (s200c/s223c, inactive mutant)
61	c5xs5A_	Alignment	not modelled	5.3	46	PDB header: virus Chain: A: PDB Molecule: genome polyprotein; PDBTitle: structure of coxsackievirus a6 (cva6) virus procapsid particle
62	d1rhl1_	Alignment	not modelled	5.3	27	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
63	d1mqta_	Alignment	not modelled	5.2	50	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
64	d1loopa_	Alignment	not modelled	5.1	50	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
65	d1ncqa_	Alignment	not modelled	5.1	27	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
66	c5jzgA_	Alignment	not modelled	5.0	40	PDB header: virus Chain: A: PDB Molecule: capsid protein vp1; PDBTitle: cryoem structure of the native empty particle of a human rhinovirus c