

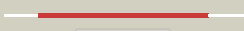
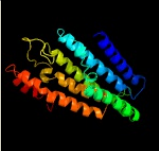



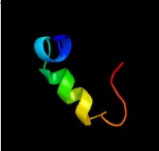



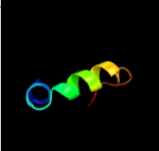

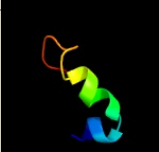

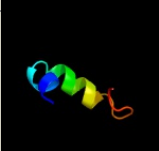

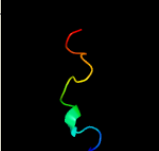

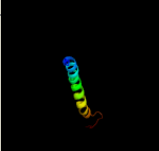




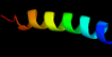




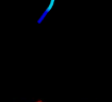
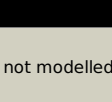


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1216c_(-)_1359478_1360152
Date	Wed Jul 31 22:05:30 BST 2019
Unique Job ID	7c3688e1798028c3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4quvB_</a>	 Alignment		100.0	18	<b>PDB header:</b> oxidoreductase, membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> delta(14)-sterol reductase; <b>PDBTitle:</b> structure of an integral membrane delta(14)-sterol reductase
2	<a href="#">c5v7pA_</a>	 Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-s-isoprenylcysteine o-methyltransferase; <b>PDBTitle:</b> atomic structure of the eukaryotic intramembrane ras methyltransferase2 icmt (isoprenylcysteine carboxyl methyltransferase), in complex with3 a monobody
3	<a href="#">c4a2nB_</a>	 Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> isoprenylcysteine carboxyl methyltransferase; <b>PDBTitle:</b> crystal structure of ma-icmt
4	<a href="#">c4y9iA_</a>	 Alignment		78.7	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mycobacterium tuberculosis paralougous family 11; <b>PDBTitle:</b> structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
5	<a href="#">c3r5yC_</a>	 Alignment		72.7	32	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structure of a deazaflavin-dependent nitroreductase from nocardia2 farcinica, with co-factor f420
6	<a href="#">c3r5wO_</a>	 Alignment		70.3	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> deazaflavin-dependent nitroreductase; <b>PDBTitle:</b> structure of ddn, the deazaflavin-dependent nitroreductase from2 mycobacterium tuberculosis involved in bioreductive activation of pa-3 824, with co-factor f420
7	<a href="#">c3r5zB_</a>	 Alignment		64.7	23	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structure of a deazaflavin-dependent reductase from nocardia2 farcinica, with co-factor f420
8	<a href="#">c3h96B_</a>	 Alignment		61.9	17	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> f420-h2 dependent reductase a; <b>PDBTitle:</b> msmeg_3358 f420 reductase
9	<a href="#">c5e8jC_</a>	 Alignment		48.8	24	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> rnmt-activating mini protein; <b>PDBTitle:</b> crystal structure of mrna cap guanine-n7 methyltransferase in complex2 with ram
10	<a href="#">c2kncA_</a>	 Alignment		32.2	12	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiib; <b>PDBTitle:</b> platelet integrin alfa-iib-beta3 transmembrane-cytoplasmic2 heterocomplex
11	<a href="#">d1e7la1</a>	 Alignment		26.6	38	<b>Fold:</b> LEM/SAP HeH motif <b>Superfamily:</b> Recombination endonuclease VII, C-terminal and dimerization domains <b>Family:</b> Recombination endonuclease VII, C-terminal and dimerization domains

12	<a href="#">c2l8sA_</a>	Alignment		18.7	12	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> integrin alpha-1; <b>PDBTitle:</b> solution nmr structure of transmembrane and cytosolic regions of f2 integrin alpha1 in detergent micelles
13	<a href="#">c5ht7A_</a>	Alignment		16.6	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a transition-metal-ion-binding betagamma-2 crystallin from methanosaeta thermophila
14	<a href="#">d1nu9c1</a>	Alignment		15.2	38	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Staphylocoagulase <b>Family:</b> Staphylocoagulase
15	<a href="#">c6hlwB_</a>	Alignment		13.9	20	<b>PDB header:</b> viral protein <b>Chain:</b> B; <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> crystal structure of human acbd3 gold domain in complex with 3a2 protein of enterovirus-a71 (fusion protein)
16	<a href="#">d1uc8a1</a>	Alignment		13.5	27	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> Lysine biosynthesis enzyme LysX, N-terminal domain
17	<a href="#">c5vhxE_</a>	Alignment		12.3	12	<b>PDB header:</b> transport protein <b>Chain:</b> E; <b>PDB Molecule:</b> glutamate receptor 2, germ cell-specific gene 1-like <b>PDBTitle:</b> glua2-1xgsg1l bound to zk
18	<a href="#">c6hltD_</a>	Alignment		12.0	27	<b>PDB header:</b> viral protein <b>Chain:</b> D; <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> crystal structure of human acbd3 gold domain in complex with 3a2 protein of rhinovirus-14 (hrv14)
19	<a href="#">d1rgoa2</a>	Alignment		11.3	67	<b>Fold:</b> CCCH zinc finger <b>Superfamily:</b> CCCH zinc finger <b>Family:</b> CCCH zinc finger
20	<a href="#">c6hmvB_</a>	Alignment		10.5	20	<b>PDB header:</b> viral protein <b>Chain:</b> B; <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> crystal structure of human acbd3 gold domain in complex with 3a2 protein of enterovirus-d68 (fusion protein, lvvy mutant)
21	<a href="#">c1p58F_</a>	Alignment	not modelled	10.4	25	<b>PDB header:</b> virus <b>Chain:</b> F; <b>PDB Molecule:</b> envelope protein m; <b>PDBTitle:</b> complex organization of dengue virus membrane proteins as revealed by 2.9.5 angstrom cryo-em reconstruction
22	<a href="#">c6hwhX_</a>	Alignment	not modelled	9.0	15	<b>PDB header:</b> electron transport <b>Chain:</b> X; <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 4; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from 2 mycobacterium smegmatis
23	<a href="#">c4tz7A_</a>	Alignment	not modelled	9.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphatidylinositol-4-phosphate 5-kinase, type i, alpha; <b>PDBTitle:</b> crystal structure of type i phosphatidylinositol 4-phosphate 5-kinase2 alpha from zebrafish
24	<a href="#">c4b1pJ_</a>	Alignment	not modelled	8.8	21	<b>PDB header:</b> transferase/dna <b>Chain:</b> J; <b>PDB Molecule:</b> rna polymerase subunit 13; <b>PDBTitle:</b> archaeal rnap-dna binary complex at 4.32ang
25	<a href="#">c3x29A_</a>	Alignment	not modelled	8.6	14	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> claudin-19; <b>PDBTitle:</b> crystal structure of mouse claudin-19 in complex with c-terminal2 fragment of clostridium perfringens enterotoxin
26	<a href="#">d1xyqa_</a>	Alignment	not modelled	8.5	24	<b>Fold:</b> Prion-like <b>Superfamily:</b> Prion-like <b>Family:</b> Prion-like
27	<a href="#">c4aybQ_</a>	Alignment	not modelled	8.1	21	<b>PDB header:</b> transferase <b>Chain:</b> Q; <b>PDB Molecule:</b> dna-directed rna polymerase; <b>PDBTitle:</b> rnap at 3.2ang
28	<a href="#">c2klqA_</a>	Alignment	not modelled	7.5	50	<b>PDB header:</b> replication <b>Chain:</b> A; <b>PDB Molecule:</b> dna replication licensing factor mcm6; <b>PDBTitle:</b> the solution structure of cbd of human mcm6

29	<a href="#">d2oy9a1</a>	Alignment	not modelled	7.0	23	<b>Fold:</b> BH2638-like <b>Superfamily:</b> BH2638-like <b>Family:</b> BH2638-like
30	<a href="#">d1s7ia_</a>	Alignment	not modelled	6.9	29	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> DGPF domain (Pfam 04946)
31	<a href="#">c1p58E_</a>	Alignment	not modelled	6.8	17	<b>PDB header:</b> virus <b>Chain:</b> E: <b>PDB Molecule:</b> envelope protein m; <b>PDBTitle:</b> complex organization of dengue virus membrane proteins as revealed by 2 9.5 angstrom cryo-em reconstruction
32	<a href="#">c5x7rB_</a>	Alignment	not modelled	6.6	31	<b>PDB header:</b> hydrolase, transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycoside hydrolase family 31 alpha-glucosidase; <b>PDBTitle:</b> crystal structure of paenibacillus sp. 598k alpha-1,6-2 glucosyltransferase complexed with isomaltotetraose
33	<a href="#">c3hhcD_</a>	Alignment	not modelled	6.6	43	<b>PDB header:</b> cytokine <b>Chain:</b> D: <b>PDB Molecule:</b> interleukin-28b; <b>PDBTitle:</b> interferon-lambda is functionally an interferon but structurally2 related to the il-10 family
34	<a href="#">c5lnks_</a>	Alignment	not modelled	6.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> S: <b>PDB Molecule:</b> <b>PDBTitle:</b> entire ovine respiratory complex i
35	<a href="#">c2k1aA_</a>	Alignment	not modelled	6.1	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> bicelle-embedded integrin alpha(iiB) transmembrane segment
36	<a href="#">d1y14b2</a>	Alignment	not modelled	6.1	50	<b>Fold:</b> Dodecin subunit-like <b>Superfamily:</b> N-terminal, heterodimerisation domain of RBP7 (RpoE) <b>Family:</b> N-terminal, heterodimerisation domain of RBP7 (RpoE)
37	<a href="#">c2a1sC_</a>	Alignment	not modelled	5.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> poly(a)-specific ribonuclease parn; <b>PDBTitle:</b> crystal structure of native parn nuclease domain
38	<a href="#">c5kk2E_</a>	Alignment	not modelled	5.7	14	<b>PDB header:</b> membrane protein, transport protein, sig <b>Chain:</b> E: <b>PDB Molecule:</b> voltage-dependent calcium channel gamma-2 subunit; <b>PDBTitle:</b> architecture of fully occupied glua2 ampa receptor - tarp complex2 elucidated by single particle cryo-electron microscopy
39	<a href="#">c2p51A_</a>	Alignment	not modelled	5.7	24	<b>PDB header:</b> hydrolase, gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> sppc18.06c protein; <b>PDBTitle:</b> crystal structure of the s. pombe pop2p deadenylation subunit
40	<a href="#">c5x51X_</a>	Alignment	not modelled	5.6	17	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> rna polymerase subunit, found in rna polymerase complexes <b>PDBTitle:</b> rna polymerase ii from komagataella pastoris (type-3 crystal)
41	<a href="#">c2xp1A_</a>	Alignment	not modelled	5.5	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> spt6; <b>PDBTitle:</b> structure of the tandem sh2 domains from antonospora locustae2 transcription elongation factor spt6
42	<a href="#">c2e0cA_</a>	Alignment	not modelled	5.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 409aa long hypothetical nadp-dependent isocitrate <b>PDBTitle:</b> crystal structure of isocitrate dehydrogenase from sulfobolbus tokodaii2 strain7 at 2.0 a resolution
43	<a href="#">c5lnko_</a>	Alignment	not modelled	5.3	5	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> <b>PDBTitle:</b> entire ovine respiratory complex i
44	<a href="#">c6cebP_</a>	Alignment	not modelled	5.1	23	<b>PDB header:</b> signaling protein <b>Chain:</b> P: <b>PDB Molecule:</b> insulin receptor; <b>PDBTitle:</b> insulin receptor ectodomain in complex with two insulin molecules - c12 symmetry