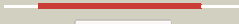

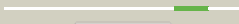








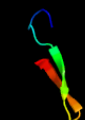





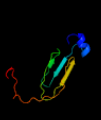

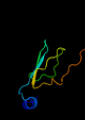




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2171_(lppM)_2432959_2433642
Date	Mon Aug 5 13:25:29 BST 2019
Unique Job ID	ad1da7844e8b399a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2nc8A_	 Alignment		100.0	100	PDB header: protein binding Chain: A: PDB Molecule: lipoprotein lppm; PDBTitle: nmr structure of the mycobacterium tuberculosis lppm (rv2171) protein2 folded domain
2	c2momB_	 Alignment		50.8	23	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
3	c2momC_	 Alignment		50.8	23	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
4	c2kncA_	 Alignment		47.3	17	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
5	c6agfB_	 Alignment		36.3	8	PDB header: membrane protein Chain: B: PDB Molecule: sodium channel subunit beta-1; PDBTitle: structure of the human voltage-gated sodium channel nav1.4 in complex2 with beta1
6	c3ol0C_	 Alignment		30.0	28	PDB header: de novo protein Chain: C: PDB Molecule: de novo designed monomer trefoil-fold sub-domain which PDBTitle: crystal structure of monofoil-4p homo-trimer: de novo designed monomer2 trefoil-fold sub-domain which forms homo-trimer assembly
7	d1mqma_	 Alignment		25.8	18	Fold: Viral protein domain Superfamily: Viral protein domain Family: Influenza hemagglutinin headpiece
8	c5zlgA_	 Alignment		25.2	18	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome b reductase 1; PDBTitle: human duodenal cytochrome b (dcbt) in zinc ion and ascorbate bound2 form
9	d2visc_	 Alignment		24.9	20	Fold: Viral protein domain Superfamily: Viral protein domain Family: Influenza hemagglutinin headpiece
10	d2viua_	 Alignment		24.8	20	Fold: Viral protein domain Superfamily: Viral protein domain Family: Influenza hemagglutinin headpiece
11	c2k1IB_	 Alignment		20.4	19	PDB header: signaling protein Chain: B: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3

12	c2k1kA_	Alignment		20.4	19	PDB header: signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
13	c2k1kB_	Alignment		20.4	19	PDB header: signaling protein Chain: B: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
14	c2k1IA_	Alignment		20.4	19	PDB header: signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
15	c3a0hj_	Alignment		20.1	8	PDB header: electron transport Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: crystal structure of i-substituted photosystem ii complex
16	d2axtj1	Alignment		20.1	8	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein J, Psbj Family: Psbj-like
17	c1ha0A_	Alignment		19.0	20	PDB header: viral protein Chain: A: PDB Molecule: protein (hemagglutinin precursor); PDBTitle: hemagglutinin precursor ha0
18	c3lhnB_	Alignment		17.5	18	PDB header: lipid binding protein Chain: B: PDB Molecule: lipoprotein; PDBTitle: crystal structure of putative lipoprotein (np_718719.1) from2 shewanella oneidensis at 1.42 a resolution
19	d1q1ua_	Alignment		16.3	17	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
20	c4ev6E_	Alignment		16.0	20	PDB header: metal transport Chain: E: PDB Molecule: magnesium transport protein cora; PDBTitle: the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
21	c6dlnB_	Alignment	not modelled	15.7	9	PDB header: membrane protein Chain: B: PDB Molecule: transmembrane protein gp41; PDBTitle: oligomeric structure of the hiv gp41 mper-tmd in phospholipid bilayers
22	c2bbjB_	Alignment	not modelled	15.5	14	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
23	d1qqla_	Alignment	not modelled	14.6	28	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
24	c5namA_	Alignment	not modelled	14.6	16	PDB header: signaling protein Chain: A: PDB Molecule: toll-like receptor 4; PDBTitle: nmr structure of tlr4 transmembrane domain (624-670) in dmpg/dhpc2 bicelles
25	c5v2sA_	Alignment	not modelled	14.5	21	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i
26	c6f7eA_	Alignment	not modelled	14.2	16	PDB header: carbohydrate Chain: A: PDB Molecule: putative secreted cellulose binding protein; PDBTitle: nmr solution structure of the cellulose-binding family 2 carbohydrate2 binding domain (cbm2) from sclpmo9c
27	d1h6ta1	Alignment	not modelled	14.0	23	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Internalin Ig-like domain
28	c3f1rA_	Alignment	not modelled	14.0	39	PDB header: hormone Chain: A: PDB Molecule: fibroblast growth factor 20; PDBTitle: crystal structure of fgf20 dimer

29	c3hbwA	Alignment	not modelled	13.6	17	PDB header: hormone Chain: A: PDB Molecule: fibroblast growth factor 13; PDBTitle: crystal structure of human fibroblast growth factor2 homologous factor 2a (fhf2a), also referred to as3 fibroblast growth factor 13a (fgf13a)
30	c4u3qA	Alignment	not modelled	13.1	24	PDB header: lipid binding protein Chain: A: PDB Molecule: 17 kda lipoprotein; PDBTitle: crystal structure of recombinant tp0435 from treponema pallidum
31	c5xnmj	Alignment	not modelled	12.7	13	PDB header: membrane protein Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: structure of unstacked c2s2m2-type psii-lhcii supercomplex from pism2 sativum
32	c6e8wC	Alignment	not modelled	12.7	8	PDB header: viral protein Chain: C: PDB Molecule: envelope glycoprotein gp160; PDBTitle: mper-tm domain of hiv-1 envelope glycoprotein (env)
33	d1hkna	Alignment	not modelled	12.6	33	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
34	c5xsyB	Alignment	not modelled	12.6	8	PDB header: membrane protein Chain: B: PDB Molecule: voltage-gated sodium channel beta subunit 1; PDBTitle: structure of the nav1.4-beta1 complex from electric eel
35	c5csaA	Alignment	not modelled	12.5	18	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of domains bt-bccp-ac1-ac5 of yeast acetyl-coa2 carboxylase
36	d1qqka	Alignment	not modelled	12.3	28	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
37	c3v42A	Alignment	not modelled	12.1	21	PDB header: protein binding Chain: A: PDB Molecule: folliculin; PDBTitle: crystal structure of renal tumor suppressor protein, folliculin
38	d1lhka	Alignment	not modelled	12.0	28	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
39	c2l8sA	Alignment	not modelled	11.7	20	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-1; PDBTitle: solution nmr structure of transmembrane and cytosolic regions of2 integrin alpha1 in detergent micelles
40	c6ntwA	Alignment	not modelled	11.6	57	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: probable l,d-transpeptidase yccb; PDBTitle: crystal structure of e. coli yccb
41	c3ogfA	Alignment	not modelled	11.4	36	PDB header: de novo protein Chain: A: PDB Molecule: de novo designed dimeric trefoil-fold sub-domain which PDBTitle: crystal structure of difoil-4p homo-trimer: de novo designed dimeric2 trefoil-fold sub-domain which forms homo-trimer assembly
42	c4uqzB	Alignment	not modelled	11.3	50	PDB header: protein transport Chain: B: PDB Molecule: hsib1; PDBTitle: coevolution of the atpase clpv, the tssb-tssc sheath and2 the accessory hsie protein distinguishes two type vi3 secretion classes
43	c3cfuA	Alignment	not modelled	11.2	10	PDB header: lipoprotein Chain: A: PDB Molecule: uncharacterized lipoprotein yjha; PDBTitle: crystal structure of the yjha protein from bacillus subtilis.2 northeast structural genomics consortium target sr562
44	d1nuna	Alignment	not modelled	11.0	22	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
45	d1ti8a1	Alignment	not modelled	10.6	25	Fold: Viral protein domain Superfamily: Viral protein domain Family: Influenza hemagglutinin headpiece
46	c3jcuJ	Alignment	not modelled	10.1	17	PDB header: membrane protein Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
47	c2mkvA	Alignment	not modelled	9.6	8	PDB header: transport protein Chain: A: PDB Molecule: sodium/potassium-transporting atpase subunit gamma; PDBTitle: structure of the na,k-atpase regulatory protein fxyd2b in micelles
48	c5fu5A	Alignment	not modelled	8.6	24	PDB header: sugar binding protein Chain: A: PDB Molecule: cbm77-rfpl; PDBTitle: the complexity of the ruminococcus flavefaciens cellulosome2 reflects an expansion in glycan recognition
49	c6c14A	Alignment	not modelled	8.5	13	PDB header: membrane protein, metal transport Chain: A: PDB Molecule: protocadherin-15; PDBTitle: cryoem structure of mouse pcdh15-1ec-lhfpl5 complex
50	d1bfga	Alignment	not modelled	8.4	33	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
51	d1fmms	Alignment	not modelled	7.9	33	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
52	d1i8na	Alignment	not modelled	7.8	40	Fold: Hairpin loop containing domain-like Superfamily: Hairpin loop containing domain-like Family: Anti-platelet protein
53	c1i8nA	Alignment	not modelled	7.8	40	PDB header: toxin Chain: A: PDB Molecule: anti-platelet protein; PDBTitle: crystal structure of leech anti-platelet protein
						Fold: beta-Trefoil

54	d3brda3	Alignment	not modelled	7.6	13	Superfamily: DNA-binding protein LAG-1 (CSL) Family: DNA-binding protein LAG-1 (CSL)
55	c3mlhA	Alignment	not modelled	7.3	19	PDB header: viral protein Chain: A: PDB Molecule: hemagglutinin; PDBTitle: crystal structure of the 2009 h1n1 influenza virus hemagglutinin2 receptor-binding domain
56	c2k9yA	Alignment	not modelled	7.0	20	PDB header: transferase Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
57	d1oisa	Alignment	not modelled	7.0	36	Fold: Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment Superfamily: Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment Family: Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment
58	c2pohA	Alignment	not modelled	6.6	14	PDB header: viral protein Chain: A: PDB Molecule: head completion protein; PDBTitle: structure of phage p22 tail needle gp26
59	c2z4hB	Alignment	not modelled	6.3	8	PDB header: signaling protein activator Chain: B: PDB Molecule: copper homeostasis protein cutf; PDBTitle: crystal structure of the cpx pathway activator nlpe from2 escherichia coli
60	d1h6ua1	Alignment	not modelled	6.2	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Internalin Ig-like domain
61	c3j0cH	Alignment	not modelled	6.2	8	PDB header: virus Chain: H: PDB Molecule: e2 envelope glycoprotein; PDBTitle: models of e1, e2 and cp of venezuelan equine encephalitis virus tc-832 strain restrained by a near atomic resolution cryo-em map
62	c2k3iA	Alignment	not modelled	6.1	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yii5; PDBTitle: solution nmr structure of protein yii5 from shigella flexneri.2 northeast structural genomics consortium target sfr90
63	c4dzgA	Alignment	not modelled	6.1	17	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: plig; PDBTitle: crystal structure of aeromonas hydrophila plig, a periplasmic lysozyme2 inhibitor of g-type lysozyme
64	d1ry7a	Alignment	not modelled	6.0	33	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
65	c4heaK	Alignment	not modelled	5.9	18	PDB header: oxidoreductase Chain: K: PDB Molecule: nadh-quinone oxidoreductase subunit 11; PDBTitle: crystal structure of the entire respiratory complex i from thermus2 thermophilus
66	c5k6iA	Alignment	not modelled	5.8	11	PDB header: hydrolase Chain: A: PDB Molecule: b-glucosidase; PDBTitle: structure of a gh3 b-glucosidase from cow rumen metagenome
67	c3rkoF	Alignment	not modelled	5.6	14	PDB header: oxidoreductase Chain: F: PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
68	d1k4ta3	Alignment	not modelled	5.5	18	Fold: Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment Superfamily: Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment Family: Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment
69	c4b19A	Alignment	not modelled	5.5	38	PDB header: toxin Chain: A: PDB Molecule: pepa1; PDBTitle: s. aureus pepa1 nmr structure
70	c2fyuE	Alignment	not modelled	5.3	12	PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit, PDBTitle: crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor