

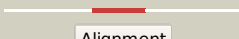
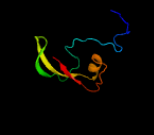

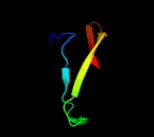









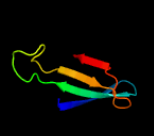



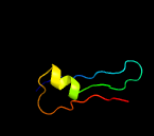

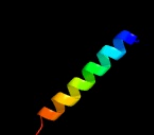
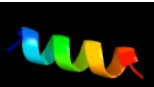


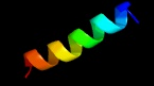
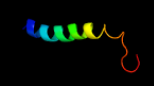






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0227c (-)_271574_272839
Date	Tue Jul 23 14:50:28 BST 2019
Unique Job ID	52dc5cb7e1c529ed

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4qa8A_	 Alignment		97.1	16	PDB header: lipid transport Chain: A: PDB Molecule: putative lipoprotein lprf; PDBTitle: crystal structure of lprf from mycobacterium bovis
2	c3mhaB_	 Alignment		95.6	21	PDB header: lipid binding protein Chain: B: PDB Molecule: lipoprotein lprg; PDBTitle: crystal structure of lprg from mycobacterium tuberculosis bound to pim
3	c4f7bA_	 Alignment		94.8	21	PDB header: cell adhesion Chain: A: PDB Molecule: lysosome membrane protein 2; PDBTitle: structure of the lysosomal domain of limp-2
4	d2byoa1	 Alignment		94.3	23	Fold: LoLA-like prokaryotic lipoproteins and lipoprotein localization factors Superfamily: Prokaryotic lipoproteins and lipoprotein localization factors Family: LppX-like
5	c5lqdA_	 Alignment		93.9	27	PDB header: cell adhesion Chain: A: PDB Molecule: platelet glycoprotein 4; PDBTitle: the cidra domain from mcvar1 pfemp1 bound to cd36
6	c2v43A_	 Alignment		90.3	20	PDB header: regulator Chain: A: PDB Molecule: sigma-e factor regulatory protein rseb; PDBTitle: crystal structure of rseb: a sensor for periplasmic stress2 response in e. coli
7	c3bk5A_	 Alignment		90.0	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative outer membrane lipoprotein-sorting protein; PDBTitle: crystal structure of putative outer membrane lipoprotein-sorting2 protein domain from vibrio parahaemolyticus
8	c3buuB_	 Alignment		89.8	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized lola superfamily protein ne2245; PDBTitle: crystal structure of lola superfamily protein ne2245 from2 nitrosomonas europaea
9	c4z48B_	 Alignment		86.7	22	PDB header: structural biology, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf1329 family protein (despig_00262) from2 desulfovibrio piger atcc 29098 at 1.75 a resolution
10	d2in5a1	 Alignment		76.1	28	Fold: YmcC-like Superfamily: YmcC-like Family: YmcC-like
11	c6et5b_	 Alignment		59.3	24	PDB header: photosynthesis Chain: B: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis

12	c1xrdA_	Alignment		57.6	38	PDB header: membrane protein Chain: A: PDB Molecule: light-harvesting protein b-880, alpha chain; PDBTitle: light-harvesting complex 1 alfa subunit from wild-type2 rhodospirillum rubrum
13	d1xrda1	Alignment		57.6	38	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
14	c3wmmY_	Alignment		57.6	19	PDB header: photosynthesis Chain: Y: PDB Molecule: lh1 alpha polypeptide; PDBTitle: crystal structure of the lh1-rc complex from thermochromatium tepidum2 in c2 form
15	c2kncB_	Alignment		52.6	21	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaIb-beta3 transmembrane-cytoplasmic2 heterocomplex
16	c2kluA_	Alignment		43.4	13	PDB header: immune system, membrane protein Chain: A: PDB Molecule: t-cell surface glycoprotein cd4; PDBTitle: nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
17	c2n2aA_	Alignment		41.8	25	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erb2-2; PDBTitle: spatial structure of her2/erb2 dimeric transmembrane domain in the2 presence of cytoplasmic jxtamembrane domains
18	c6cfwE_	Alignment		37.4	25	PDB header: membrane protein Chain: E: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
19	c6f0kA_	Alignment		28.0	18	PDB header: membrane protein Chain: A: PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii
20	c5yanE_	Alignment		27.8	28	PDB header: structural protein Chain: E: PDB Molecule: collagen; PDBTitle: deconstructing the salt-bridge network of a computationally designed2 collagen heterotrimer
21	c5yanB_	Alignment	not modelled	25.7	28	PDB header: structural protein Chain: B: PDB Molecule: collagen; PDBTitle: deconstructing the salt-bridge network of a computationally designed2 collagen heterotrimer
22	c2rmzA_	Alignment	not modelled	23.7	20	PDB header: cell adhesion Chain: A: PDB Molecule: integrin beta-3; PDBTitle: bicelle-embedded integrin beta3 transmembrane segment
23	c5zazA_	Alignment	not modelled	22.3	21	PDB header: cell adhesion Chain: A: PDB Molecule: integrin beta-2; PDBTitle: solution structure of integrin b2 monomer tranmembrane domain in2 bicelle
24	c2l9uA_	Alignment	not modelled	21.3	14	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erb2-3; PDBTitle: spatial structure of dimeric erb23 transmembrane domain
25	c2l9uB_	Alignment	not modelled	21.3	14	PDB header: membrane protein Chain: B: PDB Molecule: receptor tyrosine-protein kinase erb2-3; PDBTitle: spatial structure of dimeric erb23 transmembrane domain
26	c1w8xP_	Alignment	not modelled	20.3	23	PDB header: virus Chain: P: PDB Molecule: protein p16; PDBTitle: structural analysis of prd1
27	c2k59B_	Alignment	not modelled	16.7	18	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
28	d2hi6a1	Alignment	not modelled	16.1	55	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IlvD-like Family: AF0055-like
						PDB header: transferase

29	c2jwaA_	Alignment	not modelled	15.8	23	Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: erbb2 transmembrane segment dimer spatial structure
30	c6hwhX_	Alignment	not modelled	15.8	24	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
31	c6btmD_	Alignment	not modelled	15.7	21	PDB header: membrane protein Chain: D: PDB Molecule: alternative complex iii subunit d; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
32	c2k9yA_	Alignment	not modelled	15.3	27	PDB header: transferase Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
33	c2k9yB_	Alignment	not modelled	15.3	27	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
34	c2m20B_	Alignment	not modelled	14.8	15	PDB header: signaling protein Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: egfr transmembrane - juxtamembrane (tm-jm) segment in bicelles: md2 guided nmr refined structure.
35	c3monE_	Alignment	not modelled	14.5	22	PDB header: sweet-tasting protein Chain: E: PDB Molecule: monellin; PDBTitle: crystal structures of two intensely sweet proteins
36	c2ks1A_	Alignment	not modelled	14.3	28	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation
37	c3eh4A_	Alignment	not modelled	13.5	26	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c oxidase subunit 1; PDBTitle: structure of the reduced form of cytochrome ba3 oxidase from thermus2 thermophilus
38	c1dxzA_	Alignment	not modelled	13.2	24	PDB header: transmembrane protein Chain: A: PDB Molecule: acetylcholine receptor protein, alpha chain; PDBTitle: m2 transmembrane segment of alpha-subunit of nicotinic2 acetylcholine receptor from torpedo californica, nmr, 203 structures
39	d1xmea1	Alignment	not modelled	13.1	26	Fold: Cytochrome c oxidase subunit I-like Superfamily: Cytochrome c oxidase subunit I-like Family: Cytochrome c oxidase subunit I-like
40	c3uc9A_	Alignment	not modelled	12.0	31	PDB header: recombination Chain: A: PDB Molecule: increased recombination centers protein 6; PDBTitle: crystal structure of yeast irc6p - a novel type of conserved clathrin2 accessory protein
41	d3e9va1	Alignment	not modelled	10.8	83	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
42	c5h3wa_	Alignment	not modelled	10.7	40	PDB header: cell adhesion Chain: A: PDB Molecule: fibronectin/fibrinogen binding protein; PDBTitle: the structure of the c-terminal of the fibronectin/fibrinogen-binding2 protein from streptococcus suis (fbps)
43	c3jbrE_	Alignment	not modelled	10.6	18	PDB header: membrane protein Chain: E: PDB Molecule: voltage-dependent calcium channel gamma-1 subunit; PDBTitle: cryo-em structure of the rabbit voltage-gated calcium channel cav1.12 complex at 4.2 angstrom
44	c3c5mC_	Alignment	not modelled	10.1	18	PDB header: lyase Chain: C: PDB Molecule: oligogalacturonate lyase; PDBTitle: crystal structure of oligogalacturonate lyase (vpa0088)2 from vibrio parahaemolyticus. northeast structural3 genomics consortium target vpr199
45	c1hgza_	Alignment	not modelled	10.0	32	PDB header: virus Chain: A: PDB Molecule: ph75 inovirus major coat protein; PDBTitle: filamentous bacteriophage ph75
46	c1hgvA_	Alignment	not modelled	10.0	32	PDB header: virus Chain: A: PDB Molecule: ph75 inovirus major coat protein; PDBTitle: filamentous bacteriophage ph75
47	c2zxeG_	Alignment	not modelled	9.7	21	PDB header: hydrolase/transport protein Chain: G: PDB Molecule: phospholemman-like protein; PDBTitle: crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
48	c2ysfA_	Alignment	not modelled	9.7	24	PDB header: protein binding Chain: A: PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: solution structure of the fourth ww domain from the human2 e3 ubiquitin-protein ligase itchy homolog, itch
49	c6n3qD_	Alignment	not modelled	9.6	11	PDB header: transport protein Chain: D: PDB Molecule: protein translocation protein sec63; PDBTitle: cryo-em structure of the yeast sec complex
50	d2z15a1	Alignment	not modelled	9.6	50	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
51	d3proc2	Alignment	not modelled	9.2	31	Fold: Alpha-lytic protease prodomain-like Superfamily: Alpha-lytic protease prodomain Family: Alpha-lytic protease prodomain
52	d2i9aa1	Alignment	not modelled	9.2	20	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: EGF-type module
53	c5lqfA_	Alignment	not modelled	9.1	31	PDB header: transcription Chain: A: PDB Molecule: telomerase reverse transcriptase; PDBTitle: solution structure of the n-terminal domain of ogataea polymorpha2 telomerase reverse transcriptase
						PDB header: transmembrane protein

54	c1ciA_	Alignment	not modelled	9.0	14	Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
55	c1iziC_	Alignment	not modelled	8.8	37	PDB header: photosynthesis Chain: C: PDB Molecule: photosystem ii: subunit psbc; PDBTitle: crystal structure of photosystem ii
56	c6b15A_	Alignment	not modelled	8.7	21	PDB header: sugar binding protein Chain: A: PDB Molecule: amy13k; PDBTitle: crystal structure of cbmbc (family cbm26) from eubacterium rectale2 amy13k
57	c3be3A_	Alignment	not modelled	8.7	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein belonging to pfam duf16532 from bordetella bronchiseptica
58	c5uxmA_	Alignment	not modelled	8.5	23	PDB header: transferase Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: type ii dah7ps from pseudomonas aeruginosa with trp bound
59	c2mltA_	Alignment	not modelled	8.4	29	PDB header: toxin (hemolytic polypeptide) Chain: A: PDB Molecule: melittin; PDBTitle: melittin
60	c2mltB_	Alignment	not modelled	8.4	29	PDB header: toxin (hemolytic polypeptide) Chain: B: PDB Molecule: melittin; PDBTitle: melittin
61	c6o4mA_	Alignment	not modelled	8.4	29	PDB header: toxin Chain: A: PDB Molecule: melittin; PDBTitle: racemic melittin
62	c6o4mB_	Alignment	not modelled	8.4	29	PDB header: toxin Chain: B: PDB Molecule: melittin; PDBTitle: racemic melittin
63	c6dstA_	Alignment	not modelled	8.4	29	PDB header: toxin Chain: A: PDB Molecule: melittin; PDBTitle: recombinant melittin
64	c5kk2E_	Alignment	not modelled	8.2	15	PDB header: membrane protein, transport protein, sig Chain: E: PDB Molecule: voltage-dependent calcium channel gamma-2 subunit; PDBTitle: architecture of fully occupied glua2 ampa receptor - tarp complex2 elucidated by single particle cryo-electron microscopy
65	c3h4rA_	Alignment	not modelled	8.2	25	PDB header: hydrolase Chain: A: PDB Molecule: exodeoxyribonuclease 8; PDBTitle: crystal structure of e. coli rece exonuclease
66	c3rg9A_	Alignment	not modelled	8.2	14	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: bifunctional dihydrofolate reductase-thymidylate synthase; PDBTitle: trypanosoma brucei dihydrofolate reductase (tbdhfr) in complex with2 wr99210
67	c2m3eA_	Alignment	not modelled	8.0	19	PDB header: membrane protein Chain: A: PDB Molecule: integrin alpha-1; PDBTitle: the integrin alpha 1 transmembrane domain in bicelles: structure and2 interaction with integrin beta 2
68	c2hg5D_	Alignment	not modelled	7.9	24	PDB header: membrane protein Chain: D: PDB Molecule: kcsa channel; PDBTitle: cs+ complex of a k channel with an amide to ester substitution in the2 selectivity filter
69	c4jcbD_	Alignment	not modelled	7.8	16	PDB header: photosynthesis Chain: D: PDB Molecule: light-harvesting protein b-875 alpha chain; PDBTitle: rc-lh1-pufx dimer complex from rhodobacter sphaeroides
70	c6nd1A_	Alignment	not modelled	7.8	11	PDB header: protein transport Chain: A: PDB Molecule: protein translocation protein sec63; PDBTitle: cryoem structure of the sec complex from yeast
71	d1ttza_	Alignment	not modelled	7.8	23	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
72	c4twmA_	Alignment	not modelled	7.7	23	PDB header: plant protein Chain: A: PDB Molecule: dioscorin 5; PDBTitle: crystal structure of dioscorin from dioscorea japonica
73	c5k31E_	Alignment	not modelled	7.3	22	PDB header: structural protein Chain: E: PDB Molecule: collagen alpha-1(i) chain; PDBTitle: crystal structure of human fibrillar procollagen type i c-propeptide2 homo-trimer
74	c6cfwC_	Alignment	not modelled	7.3	5	PDB header: membrane protein Chain: C: PDB Molecule: monovalent cation/h+ antiporter subunit g; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
75	c2xueB_	Alignment	not modelled	7.3	36	PDB header: oxidoreductase Chain: B: PDB Molecule: lysine-specific demethylase 6b; PDBTitle: crystal structure of jmj3
76	c4proD_	Alignment	not modelled	7.3	45	PDB header: serine protease Chain: D: PDB Molecule: alpha-lytic protease; PDBTitle: alpha-lytic protease complexed with pro region
77	d2p7tc1	Alignment	not modelled	7.2	24	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
78	c5lnkv_	Alignment	not modelled	7.2	10	PDB header: oxidoreductase Chain: V: PDB Molecule: mitochondrial complex i, b14.7 subunit; PDBTitle: entire ovine respiratory complex i
79	c5z08D_	Alignment	not modelled	7.1	29	PDB header: cell cycle Chain: D: PDB Molecule: cenp-h; PDBTitle: the crystal structure of kinetochore subunits cenp-h/i/k triple2 complex PDB header: transcription

80	c4by6B_	Alignment	not modelled	7.1	24	Chain: B: PDB Molecule: general negative regulator of transcription subunit 2; PDBTitle: yeast not1-not2-not5 complex
81	c2ap7A_	Alignment	not modelled	7.1	41	PDB header: antibiotic Chain: A: PDB Molecule: bombinin h2; PDBTitle: solution structure of bombinin h2 in dpc micelles
82	c2jp3A_	Alignment	not modelled	7.1	17	PDB header: transcription Chain: A: PDB Molecule: fyxd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles
83	c4c0fC_	Alignment	not modelled	7.1	24	PDB header: gene regulation Chain: C: PDB Molecule: ccr4-not transcription complex subunit 2; PDBTitle: structure of the not-box domain of human cnot2
84	c5td6A_	Alignment	not modelled	7.0	17	PDB header: rna binding protein Chain: A: PDB Molecule: fog-3 protein; PDBTitle: c. elegans fog-3 btg/tob domain - h47n, c117a
85	c4c0dB_	Alignment	not modelled	6.8	24	PDB header: gene regulation Chain: B: PDB Molecule: ccr4-not transcription complex subunit 2; PDBTitle: structure of the not module of the human ccr4-not complex2 (cnot1-cnot2-cnot3)
86	c2ks1B_	Alignment	not modelled	6.8	18	PDB header: transferase Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: heterodimeric association of transmembrane domains of erb1 and erbb22 receptors enabling kinase activation
87	c6fzvA_	Alignment	not modelled	6.8	31	PDB header: structural protein Chain: A: PDB Molecule: collagen alpha-1(iii) chain; PDBTitle: crystal structure of the metalloproteinase enhancer pcpe-1 bound to2 the procollagen c propeptide trimer (short)
88	c6mjpC_	Alignment	not modelled	6.8	10	PDB header: lipid transport Chain: C: PDB Molecule: lipopolysaccharide export system protein lptc; PDBTitle: lptb(e163q)fgc from vibrio cholerae
89	c2c11A_	Alignment	not modelled	6.7	21	PDB header: hydrolase Chain: A: PDB Molecule: restriction endonuclease; PDBTitle: structure of the bfii restriction endonuclease
90	c2n28A_	Alignment	not modelled	6.7	14	PDB header: viral protein Chain: A: PDB Molecule: protein vpu; PDBTitle: solid-state nmr structure of vpu
91	d2pila_	Alignment	not modelled	6.7	26	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
92	d2o9ux1	Alignment	not modelled	6.6	22	Fold: Cystatin-like Superfamily: Cystatin/monellin Family: Monellin
93	d1zaka2	Alignment	not modelled	6.6	63	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
94	c4ezhA_	Alignment	not modelled	6.6	40	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase 6b; PDBTitle: the crystal structure of kdm6b bound with h3k27me3 peptide
95	d1lgha_	Alignment	not modelled	6.6	30	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
96	d1m1ca_	Alignment	not modelled	6.4	13	Fold: L-A virus major coat protein Superfamily: L-A virus major coat protein Family: L-A virus major coat protein
97	c1m1cB_	Alignment	not modelled	6.4	13	PDB header: virus Chain: B: PDB Molecule: major coat protein; PDBTitle: structure of the l-a virus
98	c3avsA_	Alignment	not modelled	6.4	36	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase 6a; PDBTitle: catalytic fragment of utx/kdm6a bound with n-oxyalylglycine, and2 ni(ii)
99	c6cfwl_	Alignment	not modelled	6.4	16	PDB header: membrane protein Chain: I: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase