
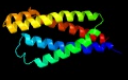






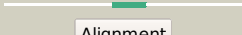

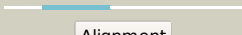


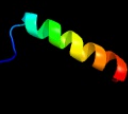

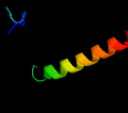


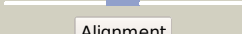
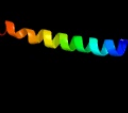
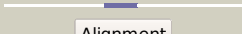


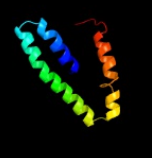


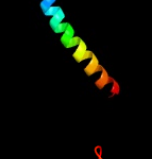



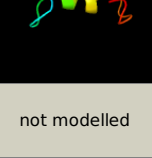


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0412c (-) _498303_499622
Date	Tue Jul 23 14:50:48 BST 2019
Unique Job ID	7542c0a10a34133f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xuaB_	 Alignment		91.1	12	PDB header: signaling protein Chain: B: PDB Molecule: methyl-accepting chemotaxis sensory transducer; PDBTitle: the ligand-free dimer of chemoreceptor mcp2201 ligand binding domain
2	c4z9hA_	 Alignment		67.3	13	PDB header: protein binding Chain: A: PDB Molecule: methyl-accepting chemotaxis protein ii; PDBTitle: asp-tar from e. coli
3	c5awwG_	 Alignment		60.5	39	PDB header: protein transport/immune system Chain: G: PDB Molecule: putative preprotein translocase, secg subunit; PDBTitle: precise resting state of thermus thermophilus secyeg
4	c2d4uA_	 Alignment		50.2	10	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein i; PDBTitle: crystal structure of the ligand binding domain of the bacterial serine2 chemoreceptor tsr
5	c5nf8A_	 Alignment		43.7	16	PDB header: membrane protein Chain: A: PDB Molecule: respiratory supercomplex factor 1, mitochondrial; PDBTitle: solution structure of detergent-solubilized rcf1, a yeast2 mitochondrial inner membrane protein involved in respiratory complex3 iii/iv supercomplex formation
6	c3va9A_	 Alignment		38.3	11	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase; PDBTitle: crystal structure of the rhodopseudomonas palustris histidine kinase2 hk9 sensor domain
7	c6f46A_	 Alignment		27.9	23	PDB header: apoptosis Chain: A: PDB Molecule: bcl-2-like protein 1; PDBTitle: structure of the transmembrane helix of bclxl in phospholipid2 nanodiscs
8	c2mkvA_	 Alignment		26.3	22	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
9	d2liga_	 Alignment		26.1	17	Fold: Four-helical up-and-down bundle Superfamily: Aspartate receptor, ligand-binding domain Family: Aspartate receptor, ligand-binding domain
10	c2kncA_	 Alignment		20.1	10	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiib; PDBTitle: platelet integrin alfaiiib-beta3 transmembrane-cytoplasmic2 heterocomplex
11	c6hwhX_	 Alignment		19.9	15	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis

12	c2lonA_	Alignment		15.2	15	PDB header: membrane protein Chain: A: PDB Molecule: hig1 domain family member 1b; PDBTitle: backbone structure of human membrane protein higd1b
13	d2itba1	Alignment		14.8	13	Fold: Ferritin-like Superfamily: Ferritin-like Family: MiaE-like
14	c6h9cD_	Alignment		14.5	63	PDB header: virus Chain: D: PDB Molecule: vp7; PDBTitle: cryo-em structure of archaeal extremophilic internal membrane-2 containing haloarcula californiae icosahedral virus 1 (hciv-1) at 3 3.74 angstroms resolution.
15	c6f87C_	Alignment		14.2	23	PDB header: transferase Chain: C: PDB Molecule: threonylcarbamoyl-amp synthase; PDBTitle: crystal structure of p. abyssi sua5 complexed with l-threonine and ppi
16	c1n7sA_	Alignment		12.7	25	PDB header: transport protein Chain: A: PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: high resolution structure of a truncated neuronal snare complex
17	c5ireD_	Alignment		10.5	27	PDB header: virus Chain: D: PDB Molecule: m protein; PDBTitle: the cryo-em structure of zika virus
18	c4xypA_	Alignment		9.8	44	PDB header: viral protein Chain: A: PDB Molecule: fusion protein; PDBTitle: crystal structure of a piscine viral fusion protein
19	c6jimA_	Alignment		9.7	20	PDB header: viral protein/rna Chain: A: PDB Molecule: helicase; PDBTitle: viral helicase protein
20	c5wsnD_	Alignment		9.5	23	PDB header: virus Chain: D: PDB Molecule: m protein; PDBTitle: structure of japanese encephalitis virus
21	c4qr8B_	Alignment	not modelled	9.5	12	PDB header: hydrolase Chain: B: PDB Molecule: xaa-pro dipeptidase; PDBTitle: crystal structure of e coli pepq
22	c6adqP_	Alignment	not modelled	9.0	28	PDB header: electron transport Chain: P: PDB Molecule: prokaryotic respiratory supercomplex associate factor 1 PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
23	c2mgxA_	Alignment	not modelled	9.0	18	PDB header: unknown function Chain: A: PDB Molecule: steroid receptor rna activator 1; PDBTitle: nmr structure of sra1p c-terminal domain
24	c6an7D_	Alignment	not modelled	8.7	7	PDB header: transport protein Chain: D: PDB Molecule: transport permease protein; PDBTitle: crystal structure of o-antigen polysaccharide abc-transporter
25	c6cc4A_	Alignment	not modelled	8.4	19	PDB header: transport protein Chain: A: PDB Molecule: soluble cytochrome b562, lipid ii flippase murj chimera; PDBTitle: structure of murj from escherichia coli
26	c3j2pD_	Alignment	not modelled	8.4	9	PDB header: viral protein Chain: D: PDB Molecule: small envelope protein m; PDBTitle: cryoem structure of dengue virus envelope protein heterotetramer
27	c3mzIH_	Alignment	not modelled	7.9	19	PDB header: protein transport Chain: H: PDB Molecule: protein transport protein sec31; PDBTitle: sec13/sec31 edge element, loop deletion mutant
28	c4wfaU_	Alignment	not modelled	7.7	44	PDB header: ribosome Chain: U: PDB Molecule: 50s ribosomal protein l28; PDBTitle: the crystal structure of the large ribosomal subunit of staphylococcus2 aureus in complex with linezolid

29	c1qw1A	Alignment	not modelled	7.4	31	PDB header: gene regulation Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: solution structure of the c-terminal domain of dtxr2 residues 110-226
30	c3mb2J	Alignment	not modelled	7.3	50	PDB header: isomerase Chain: J: PDB Molecule: 4-oxalocrotonate tautomerase family enzyme - beta subunit; PDBTitle: kinetic and structural characterization of a heterohexameric 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the 4 tautomerase superfamily
31	c6hwhT	Alignment	not modelled	7.3	12	PDB header: electron transport Chain: T: PDB Molecule: uncharacterized protein msmeg_4692/msmei_4575; PDBTitle: structure of a functional obligate respiratory supercomplex from <i>Mycobacterium smegmatis</i>
32	c1gl2A	Alignment	not modelled	7.0	29	PDB header: membrane protein Chain: A: PDB Molecule: endobrevin; PDBTitle: crystal structure of an endosomal snare core complex
33	c4cbfB	Alignment	not modelled	6.9	23	PDB header: virus Chain: B: PDB Molecule: m protein; PDBTitle: near-atomic resolution cryo-em structure of dengue serotype 4 virus
34	c2pm7A	Alignment	not modelled	6.7	19	PDB header: protein transport Chain: A: PDB Molecule: protein transport protein sec31; PDBTitle: crystal structure of yeast sec13/31 edge element of the copii2 vesicular coat, selenomethionine version
35	c2yruA	Alignment	not modelled	6.6	12	PDB header: apoptosis Chain: A: PDB Molecule: steroid receptor rna activator 1; PDBTitle: solution structure of mouse steroid receptor rna activator2 1 (sra1) protein
36	c1sfcl	Alignment	not modelled	6.5	25	PDB header: transport protein Chain: I: PDB Molecule: protein (synaptobrevin 2); PDBTitle: neuronal synaptic fusion complex
37	c1p58E	Alignment	not modelled	6.5	9	PDB header: virus Chain: E: PDB Molecule: envelope protein m; PDBTitle: complex organization of dengue virus membrane proteins as revealed by 2.9.5 angstrom cryo-em reconstruction
38	c2lomA	Alignment	not modelled	6.5	6	PDB header: membrane protein Chain: A: PDB Molecule: hig1 domain family member 1a; PDBTitle: backbone structure of human membrane protein higd1a
39	c5ux1D	Alignment	not modelled	6.4	14	PDB header: lyase Chain: D: PDB Molecule: trna-(ms2)io(6)a)-hydroxylase-like; PDBTitle: protein 43 with aldehyde deformylating oxygenase activity from <i>Synechococcus</i>
40	d1hw1a2	Alignment	not modelled	6.4	7	Fold: GntR ligand-binding domain-like Superfamily: GntR ligand-binding domain-like Family: GntR ligand-binding domain-like
41	c1urgA	Alignment	not modelled	6.2	18	PDB header: transport protein Chain: A: PDB Molecule: m-tomosyn isoform; PDBTitle: crystal structure of neuronal q-snares in complex with r-snare motif2 of tomosyn
42	c6an7C	Alignment	not modelled	6.2	7	PDB header: transport protein Chain: C: PDB Molecule: transport permease protein; PDBTitle: crystal structure of o-antigen polysaccharide abc-transporter
43	c3hd7A	Alignment	not modelled	6.1	25	PDB header: exocytosis Chain: A: PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: helical extension of the neuronal snare complex into the membrane, 2 spacegroup c 1 2 1
44	d2hs5a2	Alignment	not modelled	6.1	24	Fold: GntR ligand-binding domain-like Superfamily: GntR ligand-binding domain-like Family: GntR ligand-binding domain-like
45	c3dwIG	Alignment	not modelled	6.0	21	PDB header: structural protein Chain: G: PDB Molecule: actin-related protein 2/3 complex subunit 5; PDBTitle: crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
46	d1jr1a4	Alignment	not modelled	5.6	43	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
47	c5j12A	Alignment	not modelled	5.4	36	PDB header: signaling protein Chain: A: PDB Molecule: thymic stromal lymphopoietin; PDBTitle: structure of human tslp:tslr in complex with mouse il-7ralpha
48	c3gw4B	Alignment	not modelled	5.3	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein from deinococcus2 radiodurans. northeast structural genomics consortium target drr162b.
49	c6gv9K	Alignment	not modelled	5.3	17	PDB header: protein fibril Chain: K: PDB Molecule: prepilin peptidase-dependent protein d; PDBTitle: structure of the type iv pilus from enterohemorrhagic escherichia coli2 (ehc)
50	c3b5nE	Alignment	not modelled	5.3	21	PDB header: membrane protein Chain: E: PDB Molecule: synaptobrevin homolog 1; PDBTitle: structure of the yeast plasma membrane snare complex
51	c2eqaA	Alignment	not modelled	5.2	18	PDB header: rna binding protein Chain: A: PDB Molecule: hypothetical protein st1526; PDBTitle: crystal structure of the hypothetical sua5 protein from <i>Sulfolobus tokodaii</i>
52	d2axth1	Alignment	not modelled	5.2	10	Fold: Single transmembrane helix Superfamily: Photosystem II 10 kDa phosphoprotein PsbH Family: PsbH-like
53	c2axth	Alignment	not modelled	5.2	10	PDB header: electron transport Chain: H: PDB Molecule: photosystem ii reaction center h protein; PDBTitle: crystal structure of photosystem ii from

				thermosynechococcus elongatus		
54	d1ff3c_	Alignment	not modelled	5.1	45	Fold: Ferredoxin-like Superfamily: Peptide methionine sulfoxide reductase Family: Peptide methionine sulfoxide reductase
55	c2vxgB_	Alignment	not modelled	5.1	24	PDB header: gene regulation Chain: B: PDB Molecule: cg6181-pa, isoform a; PDBTitle: crystal structure of the conserved c-terminal region of ge-2 1
56	c3csxA_	Alignment	not modelled	5.0	35	PDB header: metal binding protein,unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structural characterization of a protein in the duf6832 family- crystal structure of cce_0567 from the3 cyanobacterium cyanothece 51142.