
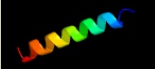
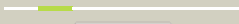




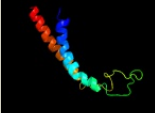




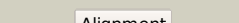
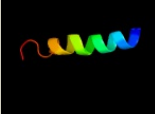






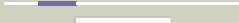



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0528 (-) _618308_619897
Date	Fri Jul 26 01:50:07 BST 2019
Unique Job ID	eccb70fd4daa25c8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1y5ic1</a>	 Alignment		68.9	25	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Respiratory nitrate reductase 1 gamma chain <b>Family:</b> Respiratory nitrate reductase 1 gamma chain
2	<a href="#">c5lm4A</a>	 Alignment		63.7	19	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> excitatory amino acid transporter 1,neutral amino acid <b>PDBTitle:</b> structure of the thermostabilized eaat1 cryst-ii mutant in complex2 with l-asg and the allosteric inhibitor ucph101
3	<a href="#">d1wjwa</a>	 Alignment		42.0	19	<b>Fold:</b> TBP-like <b>Superfamily:</b> Phosphoglucomutase, C-terminal domain <b>Family:</b> Phosphoglucomutase, C-terminal domain
4	<a href="#">c6oceB</a>	 Alignment		28.2	15	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> stress-gated cation channel 1.2; <b>PDBTitle:</b> structure of the rice hyperosmolality-gated ion channel osca1.2
5	<a href="#">c2k21A</a>	 Alignment		18.0	25	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> potassium voltage-gated channel subfamily e <b>PDBTitle:</b> nmr structure of human kcne1 in Impg micelles at ph 6.0 and2 40 degree c
6	<a href="#">c2ndjA</a>	 Alignment		15.8	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> potassium voltage-gated channel subfamily e member 3; <b>PDBTitle:</b> structural basis for kcne3 and estrogen modulation of the kcnq12 channel
7	<a href="#">c2k9yA</a>	 Alignment		15.6	27	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> ephrin type-a receptor 2; <b>PDBTitle:</b> epha2 dimeric structure in the lipidic bicelle at ph 5.0
8	<a href="#">c2k9yB</a>	 Alignment		15.6	27	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> ephrin type-a receptor 2; <b>PDBTitle:</b> epha2 dimeric structure in the lipidic bicelle at ph 5.0
9	<a href="#">c1f20A</a>	 Alignment		15.3	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> nitric-oxide synthase; <b>PDBTitle:</b> crystal structure of rat neuronal nitric-oxide synthase fad/nadp+2 domain at 1.9a resolution.
10	<a href="#">c1bhbA</a>	 Alignment		12.4	26	<b>PDB header:</b> photoreceptor <b>Chain:</b> A; <b>PDB Molecule:</b> bacteriorhodopsin; <b>PDBTitle:</b> three-dimensional structure of (1-71) bacterioopsin2 solubilized in methanol-chloroform and sds micelles3 determined by 15n-1h heteronuclear nmr spectroscopy
11	<a href="#">c5ochF</a>	 Alignment		11.8	22	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> atp-binding cassette sub-family b member 8, mitochondrial; <b>PDBTitle:</b> the crystal structure of human abcb8 in an outward-facing state

12	<a href="#">c2m0qA_</a>	Alignment		11.5	21	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> potassium voltage-gated channel subfamily e member 2; <b>PDBTitle:</b> solution nmr analysis of intact kcne2 in detergent micelles2 demonstrate a straight transmembrane helix
13	<a href="#">c6nd1E_</a>	Alignment		11.3	13	<b>PDB header:</b> protein transport <b>Chain:</b> E; <b>PDB Molecule:</b> translocation protein sec66; <b>PDBTitle:</b> cryoem structure of the sec complex from yeast
14	<a href="#">c5ws4A_</a>	Alignment		11.0	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> crystal structure of tripartite-type abc transporter macb from2 acinetobacter baumannii
15	<a href="#">c2kluA_</a>	Alignment		10.4	32	<b>PDB header:</b> immune system, membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> t-cell surface glycoprotein cd4; <b>PDBTitle:</b> nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
16	<a href="#">c2ks1B_</a>	Alignment		9.9	28	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> epidermal growth factor receptor; <b>PDBTitle:</b> heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation
17	<a href="#">c5a43B_</a>	Alignment		9.5	33	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> putative fluoride ion transporter crcb; <b>PDBTitle:</b> crystal structure of a dual topology fluoride ion channel.
18	<a href="#">c2m1jA_</a>	Alignment		9.4	23	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> prion-like protein doppel; <b>PDBTitle:</b> ovine doppel signal peptide (1-30)
19	<a href="#">c5gasN_</a>	Alignment		8.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> N; <b>PDB Molecule:</b> archaeal/vacuolar-type h+-atpase subunit i; <b>PDBTitle:</b> thermus thermophilus v/a-atpase, conformation 2
20	<a href="#">c6adqP_</a>	Alignment		8.3	30	<b>PDB header:</b> electron transport <b>Chain:</b> P; <b>PDB Molecule:</b> prokaryotic respiratory supercomplex associate factor 1 <b>PDBTitle:</b> respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
21	<a href="#">c6gctA_</a>	Alignment	not modelled	8.1	21	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> neutral amino acid transporter b(0); <b>PDBTitle:</b> cryo-em structure of the human neutral amino acid transporter asct2
22	<a href="#">c2m20B_</a>	Alignment	not modelled	8.0	28	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> epidermal growth factor receptor; <b>PDBTitle:</b> egfr transmembrane - juxtamembrane (tm-jm) segment in bicelles: md2 guided nmr refined structure.
23	<a href="#">c3j1rP_</a>	Alignment	not modelled	7.9	44	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> P; <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
24	<a href="#">c3j1rE_</a>	Alignment	not modelled	7.9	44	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> E; <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
25	<a href="#">c3j1rF_</a>	Alignment	not modelled	7.9	44	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> F; <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
26	<a href="#">c3j1rB_</a>	Alignment	not modelled	7.9	44	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
27	<a href="#">c3j1rS_</a>	Alignment	not modelled	7.9	44	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> S; <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
28	<a href="#">c3j1rO_</a>	Alignment	not modelled	7.9	44	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> O; <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
						<b>PDB header:</b> cell adhesion, structural protein

29	<a href="#">c3j1rM_</a>	Alignment	not modelled	7.9	44	<b>Chain:</b> M: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
30	<a href="#">c3j1rR_</a>	Alignment	not modelled	7.9	44	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> R: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
31	<a href="#">c3j1rH_</a>	Alignment	not modelled	7.9	44	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> H: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
32	<a href="#">c3j1rI_</a>	Alignment	not modelled	7.9	44	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> I: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
33	<a href="#">c3j1rG_</a>	Alignment	not modelled	7.9	44	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> G: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
34	<a href="#">c3j1rL_</a>	Alignment	not modelled	7.9	44	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> L: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
35	<a href="#">c3j1rN_</a>	Alignment	not modelled	7.9	44	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> N: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
36	<a href="#">c3j1rC_</a>	Alignment	not modelled	7.9	44	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
37	<a href="#">c3j1rO_</a>	Alignment	not modelled	7.9	44	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> Q: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
38	<a href="#">c3j1rU_</a>	Alignment	not modelled	7.9	44	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> U: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
39	<a href="#">c3j1rA_</a>	Alignment	not modelled	7.9	44	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
40	<a href="#">c3j1rD_</a>	Alignment	not modelled	7.9	44	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
41	<a href="#">c3j1rJ_</a>	Alignment	not modelled	7.9	44	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> J: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
42	<a href="#">c3j1rK_</a>	Alignment	not modelled	7.9	44	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> K: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
43	<a href="#">c3j1rT_</a>	Alignment	not modelled	7.9	44	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> T: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
44	<a href="#">d1xrda1</a>	Alignment	not modelled	7.7	27	<b>Fold:</b> Light-harvesting complex subunits <b>Superfamily:</b> Light-harvesting complex subunits <b>Family:</b> Light-harvesting complex subunits
45	<a href="#">c1xrdA_</a>	Alignment	not modelled	7.7	27	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> light-harvesting protein b-880, alpha chain; <b>PDBTitle:</b> light-harvesting complex 1 alfa subunit from wild-type2 rhodospirillum rubrum
46	<a href="#">d1qhda2</a>	Alignment	not modelled	7.5	39	<b>Fold:</b> Viral protein domain <b>Superfamily:</b> Viral protein domain <b>Family:</b> Top domain of virus capsid protein
47	<a href="#">c1afoB_</a>	Alignment	not modelled	7.4	22	<b>PDB header:</b> integral membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> glycophorin a; <b>PDBTitle:</b> dimeric transmembrane domain of human glycophorin a, nmr,2 20 structures
48	<a href="#">c2mpnB_</a>	Alignment	not modelled	7.3	15	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> inner membrane protein ygap; <b>PDBTitle:</b> 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli
49	<a href="#">c2mpnA_</a>	Alignment	not modelled	7.3	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> inner membrane protein ygap; <b>PDBTitle:</b> 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli
50	<a href="#">c6et5b_</a>	Alignment	not modelled	7.0	23	<b>PDB header:</b> photosynthesis <b>Chain:</b> B: <b>PDB Molecule:</b> ; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
51	<a href="#">c3wmmY_</a>	Alignment	not modelled	6.9	32	<b>PDB header:</b> photosynthesis <b>Chain:</b> Y: <b>PDB Molecule:</b> lh1 alpha polypeptide; <b>PDBTitle:</b> crystal structure of the lh1-rc complex from thermochromatium tepidum2 in c2 form
52	<a href="#">c5mkkB_</a>	Alignment	not modelled	5.9	16	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> multidrug resistance abc transporter atp-binding and ; <b>PDBTitle:</b> crystal structure of the heterodimeric abc transporter tmrab, a2 homolog of the antigen translocation complex tap
53	<a href="#">c5eh4C_</a>	Alignment	not modelled	5.9	24	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> glycophorin-a; <b>PDBTitle:</b> crystal structure of the glycophorin a transmembrane dimer in lipidic2 cubic phase
54	<a href="#">c5eh4A_</a>	Alignment	not modelled	5.9	24	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycophorin-a; <b>PDBTitle:</b> crystal structure of the glycophorin a transmembrane

						dimer in lipidic2 cubic phase
55	<a href="#">c5eh4B_</a>	Alignment	not modelled	5.9	24	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> glycophorin-a; <b>PDBTitle:</b> crystal structure of the glycophorin a transmembrane dimer in lipidic2 cubic phase
56	<a href="#">c5eh4D_</a>	Alignment	not modelled	5.9	24	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> glycophorin-a; <b>PDBTitle:</b> crystal structure of the glycophorin a transmembrane dimer in lipidic2 cubic phase
57	<a href="#">c5eh6A_</a>	Alignment	not modelled	5.9	24	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycophorin-a; <b>PDBTitle:</b> crystal structure of the glycophorin a transmembrane monomer in2 lipidic cubic phase
58	<a href="#">c2mc0A_</a>	Alignment	not modelled	5.7	27	<b>PDB header:</b> transcription activator/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional activator tipa; <b>PDBTitle:</b> structural basis of a thiopeptide antibiotic multidrug resistance2 system from streptomyces lividans:nosiheptide in complex with tipas
59	<a href="#">c2na9A_</a>	Alignment	not modelled	5.7	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytokine receptor common subunit beta; <b>PDBTitle:</b> transmembrane structure of the p441a mutant of the cytokine receptor2 common subunit beta
60	<a href="#">c2na8A_</a>	Alignment	not modelled	5.7	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytokine receptor common subunit beta; <b>PDBTitle:</b> transmembrane structure of the cytokine receptor common subunit beta
61	<a href="#">c3wvfA_</a>	Alignment	not modelled	5.6	15	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> membrane protein insertase yidc; <b>PDBTitle:</b> crystal structure of yidc from escherichia coli
62	<a href="#">c5sv1Y_</a>	Alignment	not modelled	5.5	30	<b>PDB header:</b> transport protein <b>Chain:</b> Y: <b>PDB Molecule:</b> biopolymer transport protein exbd; <b>PDBTitle:</b> structure of the exbb/exbd complex from e. coli at ph 4.5
63	<a href="#">c3iykA_</a>	Alignment	not modelled	5.5	43	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> vp5; <b>PDBTitle:</b> bluetongue virus structure reveals a sialic acid binding domain,2 amphipathic helices and a central coiled coil in the outer capsid3 proteins
64	<a href="#">c2n2aA_</a>	Alignment	not modelled	5.4	21	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbB-2; <b>PDBTitle:</b> spatial structure of her2/erbB2 dimeric transmembrane domain in the2 presence of cytoplasmic juxtamembrane domains
65	<a href="#">c5sv1Z_</a>	Alignment	not modelled	5.4	30	<b>PDB header:</b> transport protein <b>Chain:</b> Z: <b>PDB Molecule:</b> biopolymer transport protein exbd; <b>PDBTitle:</b> structure of the exbb/exbd complex from e. coli at ph 4.5
66	<a href="#">c5u1dA_</a>	Alignment	not modelled	5.3	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> antigen peptide transporter 1; <b>PDBTitle:</b> cryo-em structure of the human tap atp-binding cassette transporter
67	<a href="#">c6f2wA_</a>	Alignment	not modelled	5.3	4	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative amino acid/polyamine transport protein; <b>PDBTitle:</b> bacterial asc transporter crystal structure in open to in conformation
68	<a href="#">c4pe5A_</a>	Alignment	not modelled	5.2	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate receptor ionotropic, nmda 1; <b>PDBTitle:</b> crystal structure of glun1a/glun2b nmda receptor ion channel