


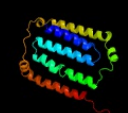
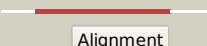

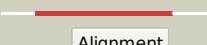
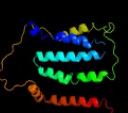
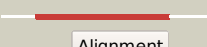

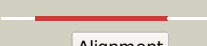








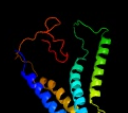


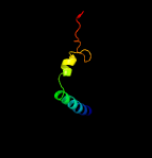

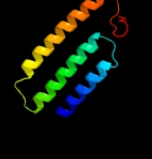

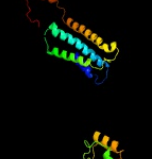
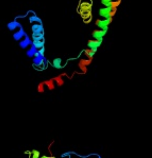
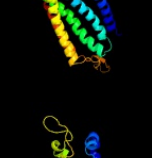

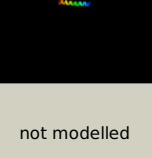


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD3154\_(nuo)\_3521136\_3521924  
 Date Thu Aug 8 16:20:34 BST 2019  
 Unique Job ID fbf1f40d998b3df1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6nbxG_</a>	 Alignment		100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G; <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit j; <b>PDBTitle:</b> t.elongatus ndh (data-set 2)
2	<a href="#">c3rkoF_</a>	 Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F; <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit j; <b>PDBTitle:</b> crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
3	<a href="#">c6humG_</a>	 Alignment		100.0	32	<b>PDB header:</b> proton transport <b>Chain:</b> G; <b>PDB Molecule:</b> nadh dehydrogenase subunit 6; <b>PDBTitle:</b> structure of the photosynthetic complex i from thermosynechococcus2 elongatus
4	<a href="#">c6gcs6_</a>	 Alignment		100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> 6; <b>PDB Molecule:</b> nd6 subunit (nu6m); <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
5	<a href="#">c4heaJ_</a>	 Alignment		100.0	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> J; <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit 10; <b>PDBTitle:</b> crystal structure of the entire respiratory complex i from thermus2 thermophilus
6	<a href="#">c5xtm_</a>	 Alignment		98.8	16	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> M; <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase 75 kda subunit, <b>PDBTitle:</b> cryo-em structure of human respiratory complex i
7	<a href="#">c6g2jJ_</a>	 Alignment		98.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> J; <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 6; <b>PDBTitle:</b> mouse mitochondrial complex i in the active state
8	<a href="#">c5ldwJ_</a>	 Alignment		98.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> J; <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 6; <b>PDBTitle:</b> structure of mammalian respiratory complex i, class1
9	<a href="#">c6cfwD_</a>	 Alignment		97.5	12	<b>PDB header:</b> membrane protein <b>Chain:</b> D; <b>PDB Molecule:</b> mbh subunit; <b>PDBTitle:</b> cryoem structure of a respiratory membrane-bound hydrogenase
10	<a href="#">c4djiA_</a>	 Alignment		52.6	13	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> probable glutamate/gamma-aminobutyrate antiporter; <b>PDBTitle:</b> structure of glutamate-gaba antiporter gadc
11	<a href="#">d2fd5a2</a>	 Alignment		42.8	16	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain

12	<a href="#">c2m20B_</a>	Alignment		41.4	38	<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.
13	<a href="#">c3rkoM_</a>	Alignment		39.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> M: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit m; <b>PDBTitle:</b> crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
14	<a href="#">c6cfwG_</a>	Alignment		37.2	9	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> monovalent cation/h+ antiporter subunit c; <b>PDBTitle:</b> cryoem structure of a respiratory membrane-bound hydrogenase
15	<a href="#">d1sgva1</a>	Alignment		36.0	30	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> PUA domain
16	<a href="#">c3kp9A_</a>	Alignment		33.6	12	<b>PDB header:</b> blood coagulation,oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> vkorc1/thioredoxin domain protein; <b>PDBTitle:</b> structure of a bacterial homolog of vitamin k epoxide reductase
17	<a href="#">c6e2fC_</a>	Alignment		31.8	10	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily v <b>PDBTitle:</b> cryo-em structure of human trpv6 in complex with calmodulin
18	<a href="#">c4or2A_</a>	Alignment		30.5	9	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> soluble cytochrome b562, metabotropic glutamate receptor 1; <b>PDBTitle:</b> human class c g protein-coupled metabotropic glutamate receptor 1 in2 complex with a negative allosteric modulator
19	<a href="#">c5ir6B_</a>	Alignment		24.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bd-type quinol oxidase subunit ii; <b>PDBTitle:</b> the structure of bd oxidase from geobacillus thermodenitrificans
20	<a href="#">c5gapG_</a>	Alignment		21.4	27	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> u4/u6 small nuclear ribonucleoprotein prp3; <b>PDBTitle:</b> body region of the u4/u6.u5 tri-snrnp
21	<a href="#">c5is0E_</a>	Alignment	not modelled	21.3	18	<b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily v <b>PDBTitle:</b> structure of trpv1 in complex with capsazepine, determined in lipid2 nanodisc
22	<a href="#">c6dvyC_</a>	Alignment	not modelled	19.7	15	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily v <b>PDBTitle:</b> cryo-em structure of mouse trpv3 in complex with 2-aminoethoxydiphenyl2 borate (2-apb)
23	<a href="#">c4xtrG_</a>	Alignment	not modelled	17.9	60	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> pep12p; <b>PDBTitle:</b> structure of get3 bound to the transmembrane domain of pep12
24	<a href="#">c5o9zE_</a>	Alignment	not modelled	17.7	20	<b>PDB header:</b> splicing <b>Chain:</b> E: <b>PDB Molecule:</b> u4/u6 small nuclear ribonucleoprotein prp3; <b>PDBTitle:</b> cryo-em structure of a pre-catalytic human spliceosome primed for2 activation (b complex)
25	<a href="#">c5lq3F_</a>	Alignment	not modelled	17.4	6	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> cmeb; <b>PDBTitle:</b> structures and transport dynamics of the campylobacter jejuni2 multidrug efflux pump cmeb
26	<a href="#">c6mhvD_</a>	Alignment	not modelled	16.9	17	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily v <b>PDBTitle:</b> structure of human trpv3 in the presence of 2-apb in c4 symmetry
27	<a href="#">c1ql6B_</a>	Alignment	not modelled	16.1	6	<b>PDB header:</b> oxidoreductase/immune system <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide ii; <b>PDBTitle:</b> cryo-structure of the paracoccus denitrificans four-subunit cytochrome2 c oxidase in the completely oxidized state

						complexed with an antibody3 fv fragment
28	<a href="#">c6iedA</a>	Alignment	not modelled	15.2	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> heme a synthase; <b>PDBTitle:</b> crystal structure of heme a synthase from bacillus subtilis
29	<a href="#">c5wdaL</a>	Alignment	not modelled	14.1	21	<b>PDB header:</b> protein transport <b>Chain:</b> L: <b>PDB Molecule:</b> general secretion pathway protein g; <b>PDBTitle:</b> structure of the pulg pseudopilus
30	<a href="#">c6humB</a>	Alignment	not modelled	13.8	14	<b>PDB header:</b> proton transport <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p)h-quinone oxidoreductase subunit 2; <b>PDBTitle:</b> structure of the photosynthetic complex i from thermosynechococcus2 elongatus
31	<a href="#">c2qtsA</a>	Alignment	not modelled	13.3	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> acid-sensing ion channel; <b>PDBTitle:</b> structure of an acid-sensing ion channel 1 at 1.9 a resolution and low2 ph
32	<a href="#">c6bo5D</a>	Alignment	not modelled	13.2	14	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily v <b>PDBTitle:</b> trpv2 ion channel in partially closed state
33	<a href="#">c6basA</a>	Alignment	not modelled	12.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan glycosyltransferase roda; <b>PDBTitle:</b> crystal structure of thermus thermophilus rod shape determining2 protein roda d255a mutant (q5six3_thet8)
34	<a href="#">c1ar1B</a>	Alignment	not modelled	12.2	6	<b>PDB header:</b> complex (oxidoreductase/antibody) <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase; <b>PDBTitle:</b> structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment
35	<a href="#">c4he8L</a>	Alignment	not modelled	11.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit 14; <b>PDBTitle:</b> crystal structure of the membrane domain of respiratory complex i from2 thermus thermophilus
36	<a href="#">c5vkqC</a>	Alignment	not modelled	11.3	13	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> no mechanoreceptor potential c isoform I; <b>PDBTitle:</b> structure of a mechanotransduction ion channel drosophila nompc in2 nanodisc
37	<a href="#">c3j5pB</a>	Alignment	not modelled	11.2	14	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily v <b>PDBTitle:</b> structure of trpv1 ion channel determined by single particle electron2 cryo-microscopy
38	<a href="#">c6humE</a>	Alignment	not modelled	10.9	16	<b>PDB header:</b> proton transport <b>Chain:</b> E: <b>PDB Molecule:</b> nad(p)h-quinone oxidoreductase subunit 4l; <b>PDBTitle:</b> structure of the photosynthetic complex i from thermosynechococcus2 elongatus
39	<a href="#">d2j8c1</a>	Alignment	not modelled	10.8	13	<b>Fold:</b> Bacterial photosystem II reaction centre, L and M subunits <b>Superfamily:</b> Bacterial photosystem II reaction centre, L and M subunits <b>Family:</b> Bacterial photosystem II reaction centre, L and M subunits
40	<a href="#">c3jcmK</a>	Alignment	not modelled	10.6	27	<b>PDB header:</b> transcription <b>Chain:</b> K: <b>PDB Molecule:</b> u4/u6 small nuclear ribonucleoprotein prp3; <b>PDBTitle:</b> cryo-em structure of the spliceosomal u4/u6.u5 tri-snrnp
41	<a href="#">c5ldwM</a>	Alignment	not modelled	10.4	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> M: <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 4; <b>PDBTitle:</b> structure of mammalian respiratory complex i, class1
42	<a href="#">d2nn6i2</a>	Alignment	not modelled	10.0	41	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Ribosomal L27 protein-like <b>Family:</b> ECR1 N-terminal domain-like
43	<a href="#">c5kdaA</a>	Alignment	not modelled	9.8	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aromatic prenyltransferase; <b>PDBTitle:</b> crystal structure of the aromatic prenyltransferase aptp from2 aspergillus terreus a8-4 in complex with dimethylallyl s-3 thiolodiphosphate and genistein
44	<a href="#">c5ogeE</a>	Alignment	not modelled	9.8	12	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> gdp-mannose transporter 1; <b>PDBTitle:</b> crystal structure of a nucleotide sugar transporter
45	<a href="#">c6epcN</a>	Alignment	not modelled	9.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> N: <b>PDB Molecule:</b> 26s proteasome non-atpase regulatory subunit 1; <b>PDBTitle:</b> ground state 26s proteasome (gs2)
46	<a href="#">c4heaK</a>	Alignment	not modelled	8.3	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> K: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit 11; <b>PDBTitle:</b> crystal structure of the entire respiratory complex i from thermus2 thermophilus
47	<a href="#">d2dsya1</a>	Alignment	not modelled	7.7	20	<b>Fold:</b> TTHA1013/TTHA0281-like <b>Superfamily:</b> TTHA1013/TTHA0281-like <b>Family:</b> TTHA0281-like
48	<a href="#">c4ld7N</a>	Alignment	not modelled	7.5	23	<b>PDB header:</b> transferase <b>Chain:</b> N: <b>PDB Molecule:</b> dimethylallyl tryptophan synthase; <b>PDBTitle:</b> crystal structure of anapt from neosartorya fischeri
49	<a href="#">c3ih1A</a>	Alignment	not modelled	7.0	24	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> methylisocitrate lyase; <b>PDBTitle:</b> crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
50	<a href="#">c4b1yM</a>	Alignment	not modelled	7.0	31	<b>PDB header:</b> structural protein <b>Chain:</b> M: <b>PDB Molecule:</b> phosphatase and actin regulator 1; <b>PDBTitle:</b> structure of the phactr1 rpel-3 bound to g-actin
51	<a href="#">c3j9pD</a>	Alignment	not modelled	5.9	7	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> maltose-binding periplasmic protein, transient receptor <b>PDBTitle:</b> structure of the trpa1 ion channel determined by electron cryo-2 microscopy
52	<a href="#">c5xeaB</a>	Alignment	not modelled	5.6	42	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> envelope glycoprotein; <b>PDBTitle:</b> structure of thogoto virus envelope glycoprotein

53	<a href="#">c5do7B_</a>	Alignment	not modelled	5.6	7	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> atp-binding cassette sub-family g member 8; <b>PDBTitle:</b> crystal structure of the human sterol transporter abcg5/abcg8
54	<a href="#">c4ifdl_</a>	Alignment	not modelled	5.5	43	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> I: <b>PDB Molecule:</b> exosome complex component csl4; <b>PDBTitle:</b> crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
55	<a href="#">c6hwhX_</a>	Alignment	not modelled	5.4	25	<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 from2 mycobacterium smegmatis
56	<a href="#">c5wtiZ_</a>	Alignment	not modelled	5.4	23	<b>PDB header:</b> hydrolase/dna/rna <b>Chain:</b> Z: <b>PDB Molecule:</b> crispr-associated protein; <b>PDBTitle:</b> crystal structure of the crispr-associated protein in complex with2 crrna and dna
57	<a href="#">c6eznC_</a>	Alignment	not modelled	5.2	20	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> dolichyl-diphosphooligosaccharide--protein <b>PDBTitle:</b> cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
58	<a href="#">c2k27A_</a>	Alignment	not modelled	5.2	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> paired box protein pax-8; <b>PDBTitle:</b> solution structure of human pax8 paired box domain
59	<a href="#">d1q90n_</a>	Alignment	not modelled	5.1	36	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> PetN subunit of the cytochrome b6f complex <b>Family:</b> PetN subunit of the cytochrome b6f complex
60	<a href="#">c1h2sB_</a>	Alignment	not modelled	5.0	42	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> sensory rhodopsin ii transducer; <b>PDBTitle:</b> molecular basis of transmenbrane signalling by sensory rhodopsin ii-2 transducer complex
61	<a href="#">d1h2sb_</a>	Alignment	not modelled	5.0	42	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Htr2 transmembrane domain-like <b>Family:</b> Htr2 transmembrane domain-like