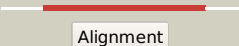



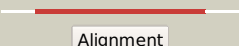





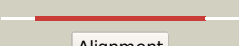




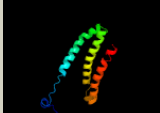

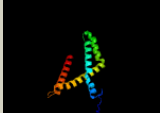








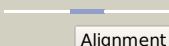
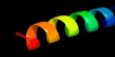
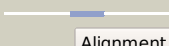

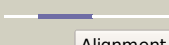
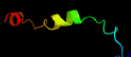
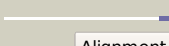



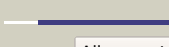



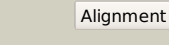

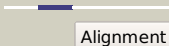
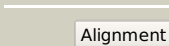
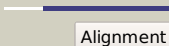
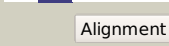



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3317_(sdhD)_3704608_3705042
Date	Thu Aug 8 16:20:52 BST 2019
Unique Job ID	b1ca53d2b1fb93e6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1nekd_</a>	 Alignment		99.9	20	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Fumarate reductase respiratory complex transmembrane subunits <b>Family:</b> Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
2	<a href="#">d2bs2c1</a>	 Alignment		99.8	23	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Fumarate reductase respiratory complex transmembrane subunits <b>Family:</b> Fumarate reductase respiratory complex cytochrome b subunit, FrdC
3	<a href="#">c5xmjG_</a>	 Alignment		99.6	25	<b>PDB header:</b> electron transport <b>Chain:</b> G: <b>PDB Molecule:</b> fumarate reductase respiratory complex; <b>PDBTitle:</b> crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
4	<a href="#">d1nekc_</a>	 Alignment		99.4	16	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Fumarate reductase respiratory complex transmembrane subunits <b>Family:</b> Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
5	<a href="#">c1yq3C_</a>	 Alignment		99.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> succinate dehydrogenase cytochrome b, large subunit; <b>PDBTitle:</b> avian respiratory complex ii with oxaloacetate and ubiquinone
6	<a href="#">c3vr6G_</a>	 Alignment		99.0	15	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> G: <b>PDB Molecule:</b> cytochrome b-large subunit; <b>PDBTitle:</b> mitochondrial rholoquinol-fumarate reductase from the parasitic2 nematode ascaris suum with the specific inhibitor flutolanil and3 substrate fumarate
7	<a href="#">c1zp0D_</a>	 Alignment		98.3	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> small cytochrome binding protein; <b>PDBTitle:</b> crystal structure of mitochondrial respiratory complex ii2 bound with 3-nitropropionate and 2-thenoyltrifluoroacetone
8	<a href="#">c3vr8H_</a>	 Alignment		98.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> succinate dehydrogenase [ubiquinone] cytochrome b small <b>PDBTitle:</b> mitochondrial rholoquinol-fumarate reductase from the parasitic2 nematode ascaris suum
9	<a href="#">d1kf6c_</a>	 Alignment		96.5	18	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Fumarate reductase respiratory complex transmembrane subunits <b>Family:</b> Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
10	<a href="#">d1kf6d_</a>	 Alignment		95.9	16	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Fumarate reductase respiratory complex transmembrane subunits <b>Family:</b> Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
11	<a href="#">c6hrbD_</a>	 Alignment		27.5	42	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> potassium-transporting atpase kdpf subunit; <b>PDBTitle:</b> cryo-em structure of the kdpfabc complex in an e2 inward-facing state2 (state 2)

12	<a href="#">c5mrwD_</a>	 Alignment		27.5	42	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> potassium-transporting atpase kdpf subunit; <b>PDBTitle:</b> structure of the kdpfabc complex
13	<a href="#">c6hraD_</a>	 Alignment		27.5	42	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> potassium-transporting atpase kdpf subunit; <b>PDBTitle:</b> cryo-em structure of the kdpfabc complex in an e1 outward-facing state2 (state 1)
14	<a href="#">c5mrwL_</a>	 Alignment		27.5	42	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> potassium-transporting atpase kdpf subunit; <b>PDBTitle:</b> structure of the kdpfabc complex
15	<a href="#">c5mrwH_</a>	 Alignment		27.5	42	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> potassium-transporting atpase kdpf subunit; <b>PDBTitle:</b> structure of the kdpfabc complex
16	<a href="#">c3izbE_</a>	 Alignment		14.2	31	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> 40s ribosomal protein rps2 (s5p); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
17	<a href="#">c5vkvA_</a>	 Alignment		13.4	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c-type biogenesis protein ccda; <b>PDBTitle:</b> solution nmr structure of the membrane electron transporter ccda
18	<a href="#">c5o0tA_</a>	 Alignment		9.3	22	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative ferric reductase; <b>PDBTitle:</b> crystal structure of trans-membrane domain of cylindrospermum stagnale2 nadph-oxidase 5 (nox5)
19	<a href="#">c6btmC_</a>	 Alignment		7.4	12	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> alternative complex iii subunit c; <b>PDBTitle:</b> structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
20	<a href="#">c2zxeG_</a>	 Alignment		7.0	9	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> phospholemman-like protein; <b>PDBTitle:</b> crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
21	<a href="#">c2jo1A_</a>	 Alignment	not modelled	6.9	14	<b>PDB header:</b> hydrolase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> phospholemman; <b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
22	<a href="#">c2ezdA_</a>	 Alignment	not modelled	6.1	31	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> high mobility group protein hmg-i/hmg-y; <b>PDBTitle:</b> solution structure of a complex of the second dna binding2 domain of human hmg-i(y) bound to dna dodecamer containing3 the prdii site of the interferon-beta promoter, nmr,4 minimized average structure
23	<a href="#">c2ezeA_</a>	 Alignment	not modelled	5.6	31	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> high mobility group protein hmg-i/hmg-y; <b>PDBTitle:</b> solution structure of a complex of the second dna binding2 domain of human hmg-i(y) bound to dna dodecamer containing3 the prdii site of the interferon-beta promoter, nmr, 354 structures
24	<a href="#">c2mkvA_</a>	 Alignment	not modelled	5.4	5	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/potassium-transporting atpase subunit gamma; <b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd2b in micelles
25	<a href="#">c5ir6B_</a>	 Alignment	not modelled	5.2	11	<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
26	<a href="#">c6hwhR_</a>	 Alignment	not modelled	5.2	17	<b>PDB header:</b> electron transport <b>Chain:</b> R: <b>PDB Molecule:</b> msmeg_4693; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
27	<a href="#">c2jp3A_</a>	 Alignment	not modelled	5.1	9	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fxyd domain-containing ion transport regulator 4;

		<b>PDBTitle:</b> solution structure of the human fxyd4 (chif) protein in sds2 micelles	
28 <a href="#">c6f0kC_</a>	Alignment not modelled	5.0	9 <b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> polysulphide reductase nrfd; <b>PDBTitle:</b> alternative complex iii