






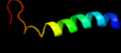



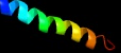







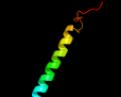


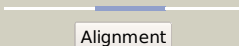
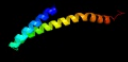




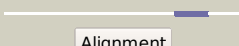

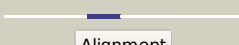

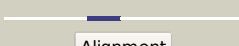


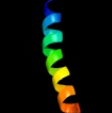

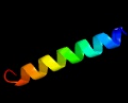

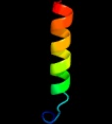
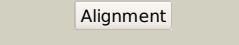
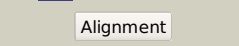

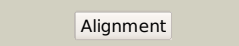
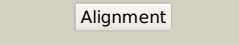

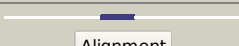



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1164_(narI)_1293411_1294151
 Date Wed Jul 31 22:05:25 BST 2019
 Unique Job ID 2879f536305408ef

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1y5ic1	 Alignment		100.0	29	Fold: Heme-binding four-helical bundle Superfamily: Respiratory nitrate reductase 1 gamma chain Family: Respiratory nitrate reductase 1 gamma chain
2	c5oc0A	 Alignment		77.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome b561; PDBTitle: structure of e. coli superoxide oxidase
3	c2kncA	 Alignment		70.8	17	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
4	c2kluA	 Alignment		65.2	23	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
5	d1kqfc	 Alignment		57.6	10	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Formate dehydrogenase N, cytochrome (gamma) subunit
6	c3kdpH	 Alignment		49.9	22	PDB header: hydrolase Chain: H: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
7	c3kdpG	 Alignment		49.9	22	PDB header: hydrolase Chain: G: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
8	c2k1aA	 Alignment		46.2	17	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: bicelle-embedded integrin alpha(iiB) transmembrane segment
9	c5ir6B	 Alignment		45.0	11	PDB header: oxidoreductase Chain: B: PDB Molecule: bd-type quinol oxidase subunit ii; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
10	c2mkvA	 Alignment		32.8	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
11	c2l8sA	 Alignment		27.0	23	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-1; PDBTitle: solution nmr structure of transmembrane and cytosolic regions of2 integrin alpha1 in detergent micelles

12	c2uuiA_	 Alignment		22.7	16	PDB header: lyase Chain: A: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
13	c2jo1A_	 Alignment		12.6	29	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
14	c2jp3A_	 Alignment		12.5	18	PDB header: transcription Chain: A: PDB Molecule: fxyd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles
15	c2ww9B_	 Alignment		12.1	28	PDB header: ribosome Chain: B: PDB Molecule: protein transport protein sss1; PDBTitle: cryo-em structure of the active yeast ssh1 complex bound to the yeast2 80s ribosome
16	c2k1kA_	 Alignment		9.4	38	PDB header: signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
17	c2k11B_	 Alignment		9.4	38	PDB header: signaling protein Chain: B: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
18	c2k11A_	 Alignment		9.4	38	PDB header: signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
19	c2k1kB_	 Alignment		9.4	38	PDB header: signaling protein Chain: B: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
20	c4hqjG_	 Alignment		8.8	21	PDB header: hydrolase/transport protein Chain: G: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of na+,k+-atpase in the na+-bound state
21	c4hqjE_	 Alignment	not modelled	8.4	21	PDB header: hydrolase/transport protein Chain: E: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of na+,k+-atpase in the na+-bound state
22	c6g72A_	 Alignment	not modelled	8.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: na-d-ubiquinone oxidoreductase chain 3; PDBTitle: mouse mitochondrial complex i in the deactive state
23	c4p6vB_	 Alignment	not modelled	8.1	15	PDB header: oxidoreductase Chain: B: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit b; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
24	c2kncB_	 Alignment	not modelled	7.6	22	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
25	c2zxeG_	 Alignment	not modelled	6.9	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
26	c2dymB_	 Alignment	not modelled	6.7	25	PDB header: protein turnover/protein turnover Chain: B: PDB Molecule: autophagy protein 16; PDBTitle: the crystal structure of saccharomyces cerevisiae atg5-2 atg16(1-46) complex
27	c2dymH_	 Alignment	not modelled	6.7	25	PDB header: protein turnover/protein turnover Chain: H: PDB Molecule: autophagy protein 16; PDBTitle: the crystal structure of saccharomyces cerevisiae atg5-2 atg16(1-46) complex
28	c2dymF_	 Alignment	not modelled	6.7	25	PDB header: protein turnover/protein turnover Chain: F: PDB Molecule: autophagy protein 16; PDBTitle: the crystal structure of saccharomyces cerevisiae atg5-2 atg16(1-46) complex

29	c2dymD_	Alignment	not modelled	6.7	25	PDB header: protein turnover/protein turnover Chain: D: PDB Molecule: autophagy protein 16; PDBTitle: the crystal structure of saccharomyces cerevisiae atg5-2 atg16(1-46) complex
30	c3w1sB_	Alignment	not modelled	6.6	25	PDB header: ligase Chain: B: PDB Molecule: autophagy protein 16; PDBTitle: crystal structure of saccharomyces cerevisiae atg12-atg5 conjugate2 bound to the n-terminal domain of atg16
31	c6n52B_	Alignment	not modelled	5.9	11	PDB header: membrane protein Chain: B: PDB Molecule: metabotropic glutamate receptor 5; PDBTitle: metabotropic glutamate receptor 5 apo form
32	c3wmmP_	Alignment	not modelled	5.6	23	PDB header: photosynthesis Chain: P: PDB Molecule: lh1 beta polypeptide; PDBTitle: crystal structure of the lh1-rc complex from thermochromatium tepidum2 in c2 form
33	d1ar1a_	Alignment	not modelled	5.6	15	Fold: Cytochrome c oxidase subunit I-like Superfamily: Cytochrome c oxidase subunit I-like Family: Cytochrome c oxidase subunit I-like
34	c2dyoB_	Alignment	not modelled	5.4	25	PDB header: protein turnover/protein turnover Chain: B: PDB Molecule: autophagy protein 16; PDBTitle: the crystal structure of saccharomyces cerevisiae atg5-2 atg16(1-57) complex
35	c3b8eH_	Alignment	not modelled	5.3	24	PDB header: hydrolase/transport protein Chain: H: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
36	c3n23E_	Alignment	not modelled	5.2	17	PDB header: hydrolase Chain: E: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the high affinity complex between ouabain and the2 e2p form of the sodium-potassium pump