

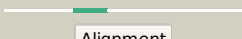

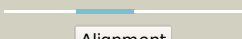
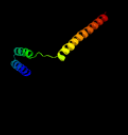





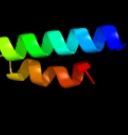












# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2236c_cobD_2508442_2509383
Date	Mon Aug 5 13:25:37 BST 2019
Unique Job ID	d9e8abcca759d4c7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5h93C_</a>	 Alignment		77.7	43	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> geobacter metallireducens smug1; <b>PDBTitle:</b> crystal structure of geobacter metallireducens smug1
2	<a href="#">c6iiuA_</a>	 Alignment		43.1	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> soluble cytochrome b562,thromboxane a2 receptor,rubredoxin, <b>PDBTitle:</b> crystal structure of the human thromboxane a2 receptor bound to2 ramatroban
3	<a href="#">c4l6rA_</a>	 Alignment		32.2	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> soluble cytochrome b562 and glucagon receptor chimera; <b>PDBTitle:</b> structure of the class b human glucagon g protein coupled receptor
4	<a href="#">d256ba_</a>	 Alignment		28.5	19	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Cytochromes <b>Family:</b> Cytochrome b562
5	<a href="#">c4er9A_</a>	 Alignment		28.1	19	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> soluble cytochrome b562; <b>PDBTitle:</b> crystal structure of cytochrome b562 from salmonella enterica subsp.2 enterica serovar typhimurium str. 14028s
6	<a href="#">c6g7oA_</a>	 Alignment		23.9	19	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> alkaline ceramidase 3,soluble cytochrome b562; <b>PDBTitle:</b> crystal structure of human alkaline ceramidase 3 (acer3) at 2.72 angstrom resolution
7	<a href="#">d1sxc1</a>	 Alignment		12.7	16	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> DNA polymerase III clamp loader subunits, C-terminal domain
8	<a href="#">d1sr2a_</a>	 Alignment		12.6	12	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Histidine-containing phosphotransfer domain, HPT domain <b>Family:</b> Sensor-like histidine kinase YojN, C-terminal domain
9	<a href="#">c3nrtC_</a>	 Alignment		12.2	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> putative ryanodine receptor; <b>PDBTitle:</b> the crystal structure of putative ryanodine receptor from bacteroides2 thetaiotaomicron vpi-5482
10	<a href="#">d1iqpa1</a>	 Alignment		10.4	18	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> DNA polymerase III clamp loader subunits, C-terminal domain
11	<a href="#">c3u8pB_</a>	 Alignment		8.6	19	<b>PDB header:</b> fluorescent protein, electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome b562 integral fusion with enhanced green <b>PDBTitle:</b> cytochrome b562 integral fusion with egfp

12	<a href="#">c4etvA_</a>	Alignment		8.3	22	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> ryanodine receptor 2; <b>PDBTitle:</b> crystal structure of mouse ryanodine receptor 2 (2699-2904)
13	<a href="#">c1t6zB_</a>	Alignment		7.8	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> riboflavin kinase/fmn adenyllyltransferase; <b>PDBTitle:</b> crystal structure of riboflavin bound tm379
14	<a href="#">c3j3vN_</a>	Alignment		7.4	12	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 50s ribosomal protein l17; <b>PDBTitle:</b> atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
15	<a href="#">d1hw1a2</a>	Alignment		7.1	7	<b>Fold:</b> GntR ligand-binding domain-like <b>Superfamily:</b> GntR ligand-binding domain-like <b>Family:</b> GntR ligand-binding domain-like
16	<a href="#">c4g78A_</a>	Alignment		7.1	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine phosphotransfer protein; <b>PDBTitle:</b> subatomic resolution crystal structure of histidine-containing2 phosphotransfer protein mthpt2 from medicago truncatula
17	<a href="#">d1khda2</a>	Alignment		7.0	19	<b>Fold:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
18	<a href="#">c3op1A_</a>	Alignment		6.7	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> macrolide-efflux protein; <b>PDBTitle:</b> crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
19	<a href="#">c3ixzB_</a>	Alignment		6.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> potassium-transporting atpase subunit beta; <b>PDBTitle:</b> pig gastric h+/k+-atpase complexed with aluminium fluoride
20	<a href="#">d1wn0a1</a>	Alignment		6.5	15	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Histidine-containing phosphotransfer domain, HPT domain <b>Family:</b> Phosphorelay protein-like
21	<a href="#">c2mkbA_</a>	Alignment	not modelled	5.8	20	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protease ns2-3; <b>PDBTitle:</b> structure of ns2(113-137) gbvb protein
22	<a href="#">c3frrA_</a>	Alignment	not modelled	5.8	14	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein kiaa0174; <b>PDBTitle:</b> structure of human ist1(ntd) - (residues 1-189)(p21)
23	<a href="#">c3rqrA_</a>	Alignment	not modelled	5.7	14	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> ryanodine receptor 1; <b>PDBTitle:</b> crystal structure of the ryr domain of the rabbit ryanodine receptor
24	<a href="#">c4or2A_</a>	Alignment	not modelled	5.4	19	<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
25	<a href="#">d2peqa1</a>	Alignment	not modelled	5.3	17	<b>Fold:</b> RbcX-like <b>Superfamily:</b> RbcX-like <b>Family:</b> RbcX-like
26	<a href="#">d2py8a1</a>	Alignment	not modelled	5.2	17	<b>Fold:</b> RbcX-like <b>Superfamily:</b> RbcX-like <b>Family:</b> RbcX-like