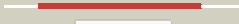

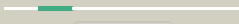






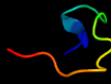

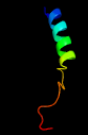







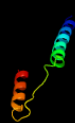

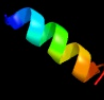


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD0156 (pntAb)\_184721\_185053  
 Date Tue Jul 23 14:50:20 BST 2019  
 Unique Job ID 0350ffe66826f531

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4o9pC_</a>	 Alignment		100.0	46	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> nad(p) transhydrogenase subunit alpha 2; <b>PDBTitle:</b> crystal structure of thermus thermophilis transhydrogeanse domain ii2 dimer semet derivative
2	<a href="#">c3arct_</a>	 Alignment		48.9	0	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
3	<a href="#">c3a0bT_</a>	 Alignment		44.8	0	<b>PDB header:</b> electron transport <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of br-substituted photosystem ii complex
4	<a href="#">c5sv9B_</a>	 Alignment		21.6	16	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> bor1p boron transporter; <b>PDBTitle:</b> structure of the slc4 transporter bor1p in an inward-facing2 conformation
5	<a href="#">d2auwa1</a>	 Alignment		18.2	11	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE0471 C-terminal domain-like
6	<a href="#">c2dw3A_</a>	 Alignment		16.8	47	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> intrinsic membrane protein pufx; <b>PDBTitle:</b> solution structure of the rhodobacter sphaeroides pufx2 membrane protein
7	<a href="#">c2hp0A_</a>	 Alignment		15.0	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ids-epimerase; <b>PDBTitle:</b> crystal structure of iminodisuccinate epimerase
8	<a href="#">d1qnta2</a>	 Alignment		12.8	38	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Methylated DNA-protein cysteine methyltransferase domain <b>Family:</b> Methylated DNA-protein cysteine methyltransferase domain
9	<a href="#">d1pbua_</a>	 Alignment		12.2	33	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> eEF1-gamma domain <b>Family:</b> eEF1-gamma domain
10	<a href="#">c6eznH_</a>	 Alignment		11.6	10	<b>PDB header:</b> membrane protein <b>Chain:</b> H: <b>PDB Molecule:</b> dolichyl-diphosphooligosaccharide--protein <b>PDBTitle:</b> cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
11	<a href="#">c2h3oA_</a>	 Alignment		11.2	31	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> structure of merf, a membrane protein with two trans-2 membrane helices

12	<a href="#">c6humQ_</a>	Alignment		10.8	29	<b>PDB header:</b> proton transport <b>Chain:</b> Q; <b>PDB Molecule:</b> proton-translocating nadh-quinone dehydrogenase subunit q <b>PDBTitle:</b> structure of the photosynthetic complex i from thermosynechococcus2 elongatus
13	<a href="#">c2g2oA_</a>	Alignment		10.5	33	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> malonyl coa-acyl carrier protein transacylase; <b>PDBTitle:</b> structure of e.coli fabd complexed with sulfate
14	<a href="#">c2kr6A_</a>	Alignment		9.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> presenilin-1; <b>PDBTitle:</b> solution structure of presenilin-1 ctf subunit
15	<a href="#">c5nvkF_</a>	Alignment		8.5	17	<b>PDB header:</b> translation <b>Chain:</b> F; <b>PDB Molecule:</b> grb10-interacting gyf protein 1; <b>PDBTitle:</b> crystal structure of the human 4ehp-gigyf1 complex
16	<a href="#">c5dz7A_</a>	Alignment		8.3	25	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> polyketide biosynthesis protein pkse; <b>PDBTitle:</b> structural basis of acyl transfer in a trans-at polyketide synthase
17	<a href="#">d1rh1a2</a>	Alignment		8.1	18	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Colicin <b>Family:</b> Colicin
18	<a href="#">c2auwB_</a>	Alignment		7.7	11	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> hypothetical protein ne0471; <b>PDBTitle:</b> crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
19	<a href="#">c5o5oD_</a>	Alignment		7.5	28	<b>PDB header:</b> chaperone <b>Chain:</b> D; <b>PDB Molecule:</b> rnase adapter protein rapz; <b>PDBTitle:</b> x-ray crystal structure of rapz from escherichia coli (p32 space2 group)
20	<a href="#">c5dz6A_</a>	Alignment		7.3	25	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> polyketide biosynthesis malonyl coa-acyl carrier protein <b>PDBTitle:</b> acyl transferase from bacillaene pks
21	<a href="#">c2c2nA_</a>	Alignment	not modelled	7.1	42	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> malonyl coa-acyl carrier protein transacylase; <b>PDBTitle:</b> structure of human mitochondrial malonyltransferase
22	<a href="#">c3vr6G_</a>	Alignment	not modelled	6.9	30	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> G; <b>PDB Molecule:</b> cytochrome b-large subunit; <b>PDBTitle:</b> mitochondrial rhoquoinol-fumarate reductase from the parasitic2 nematode ascaris suum with the specific inhibitor flutolanil and3 substrate fumarate
23	<a href="#">d2i53a2</a>	Alignment	not modelled	6.8	18	<b>Fold:</b> Cyclin-like <b>Superfamily:</b> Cyclin-like <b>Family:</b> Cyclin
24	<a href="#">c3ezoA_</a>	Alignment	not modelled	6.8	25	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> malonyl coa-acyl carrier protein transacylase; <b>PDBTitle:</b> crystal structure of acyl-carrier-protein s-malonyltransferase from2 burkholderia pseudomallei 1710b
25	<a href="#">c2cdh9_</a>	Alignment	not modelled	6.6	42	<b>PDB header:</b> transferase <b>Chain:</b> 9; <b>PDB Molecule:</b> acetyl transferase; <b>PDBTitle:</b> architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
26	<a href="#">c3rgiA_</a>	Alignment	not modelled	6.4	25	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> disd protein; <b>PDBTitle:</b> trans-acting transferase from disorazole synthase
27	<a href="#">c2jwaA_</a>	Alignment	not modelled	6.2	38	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbB-2; <b>PDBTitle:</b> erbB2 transmembrane segment dimer spatial structure
28	<a href="#">c2ks1A_</a>	Alignment	not modelled	6.2	38	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbB-2; <b>PDBTitle:</b> heterodimeric association of transmembrane domains of erbB1 and erbB22 receptors enabling kinase activation <b>PDB header:</b> transport protein

29	<a href="#">c1wazA_</a>	Alignment	not modelled	6.1	31	<b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> nmr structure determination of the bacterial mercury transporter;2 merf, in micelles
30	<a href="#">c2k1aA_</a>	Alignment	not modelled	6.1	50	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> bicelle-embedded integrin alpha(iiB) transmembrane segment
31	<a href="#">c5y79A_</a>	Alignment	not modelled	6.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative hexose phosphate translocator; <b>PDBTitle:</b> crystal structure of the triose-phosphate/phosphate translocator in2 complex with 3-phosphoglycerate
32	<a href="#">c5yq7C_</a>	Alignment	not modelled	5.9	17	<b>PDB header:</b> photosynthesis <b>Chain:</b> C: <b>PDB Molecule:</b> cytochrome subunit of photosynthetic reaction center; <b>PDBTitle:</b> cryo-em structure of the rc-lh core complex from roseiflexus2 castenholzii
33	<a href="#">c3im8A_</a>	Alignment	not modelled	5.8	42	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyl acyl carrier protein transacylase; <b>PDBTitle:</b> crystal structure of mcat from streptococcus pneumoniae
34	<a href="#">c4rl1A_</a>	Alignment	not modelled	5.8	45	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> type i polyketide synthase avcs 1; <b>PDBTitle:</b> structural and functional analysis of a loading acyltransferase from2 the avermectin modular polyketide synthase
35	<a href="#">c5ukvA_</a>	Alignment	not modelled	5.7	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-binding protein; <b>PDBTitle:</b> dhp domain of phor of m. tuberculosis - semet
36	<a href="#">c5m45I_</a>	Alignment	not modelled	5.6	25	<b>PDB header:</b> ligase <b>Chain:</b> I: <b>PDB Molecule:</b> acetone carboxylase gamma subunit; <b>PDBTitle:</b> structure of acetone carboxylase purified from xanthobacter2 autotrophicus
37	<a href="#">c3im9A_</a>	Alignment	not modelled	5.5	36	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyl coa-acyl carrier protein transacylase; <b>PDBTitle:</b> crystal structure of mcat from staphylococcus aureus
38	<a href="#">d1joya_</a>	Alignment	not modelled	5.3	25	<b>Fold:</b> ROP-like <b>Superfamily:</b> Homodimeric domain of signal transducing histidine kinase <b>Family:</b> Homodimeric domain of signal transducing histidine kinase
39	<a href="#">c2jxfA_</a>	Alignment	not modelled	5.2	50	<b>PDB header:</b> viral protein, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> the solution structure of hcv ns4b(40-69)
40	<a href="#">c5mx2T_</a>	Alignment	not modelled	5.2	0	<b>PDB header:</b> oxidoreductase <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> photosystem ii depleted of the mn4cao5 cluster at 2.55 a resolution