



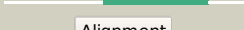


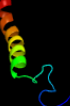








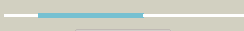


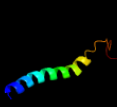




# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD2093c\_(tatC)\_2352111\_2353037  
 Date Mon Aug 5 13:25:21 BST 2019  
 Unique Job ID 9267a1eed26c9e9d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4b4aA_</a>	 Alignment		100.0	35	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> sec-independent protein translocase protein tatc; <b>PDBTitle:</b> structure of the tatc core of the twin arginine protein2 translocation system
2	<a href="#">d1v54I_</a>	 Alignment		41.9	22	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit VIIc (aka VIIla) <b>Family:</b> Mitochondrial cytochrome c oxidase subunit VIIc (aka VIIla)
3	<a href="#">c6c08C_</a>	 Alignment		41.4	11	<b>PDB header:</b> membrane protein <b>Chain:</b> C; <b>PDB Molecule:</b> sodium-coupled neutral amino acid transporter 9; <b>PDBTitle:</b> zebrafish slc38a9 with arginine bound in the cytosol open state
4	<a href="#">c2y69Y_</a>	 Alignment		39.2	22	<b>PDB header:</b> electron transport <b>Chain:</b> Y; <b>PDB Molecule:</b> cytochrome c oxidase subunit 7c; <b>PDBTitle:</b> bovine heart cytochrome c oxidase re-refined with molecular oxygen
5	<a href="#">c2mdfA_</a>	 Alignment		34.5	29	<b>PDB header:</b> proton transport <b>Chain:</b> A; <b>PDB Molecule:</b> sodium/hydrogen exchanger 1; <b>PDBTitle:</b> nmr structure of a two-transmembrane segment tm vi-vii of nhe1
6	<a href="#">c6ivuB_</a>	 Alignment		33.8	15	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> rna polymerase sigma factor sigi1; <b>PDBTitle:</b> solution structure of the sigma-anti-sigma factor complex rsgi1n-2 sigi1c from clostridium thermocellum
7	<a href="#">c2rddB_</a>	 Alignment		31.8	16	<b>PDB header:</b> membrane protein/transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> upf0092 membrane protein yajc; <b>PDBTitle:</b> x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
8	<a href="#">c3qodB_</a>	 Alignment		30.7	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> heterocyst differentiation protein; <b>PDBTitle:</b> crystal structure of heterocyst differentiation protein, hetr from2 fischerella mv11
9	<a href="#">c3rfuC_</a>	 Alignment		30.6	19	<b>PDB header:</b> hydrolase, membrane protein <b>Chain:</b> C; <b>PDB Molecule:</b> copper efflux atpase; <b>PDBTitle:</b> crystal structure of a copper-transporting pib-type atpase
10	<a href="#">c2kncA_</a>	 Alignment		29.9	18	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> platelet integrin alfaIIB-beta3 transmembrane-cytoplasmic2 heterocomplex
11	<a href="#">c2oaxC_</a>	 Alignment		29.7	16	<b>PDB header:</b> transcription <b>Chain:</b> C; <b>PDB Molecule:</b> mineralocorticoid receptor; <b>PDBTitle:</b> crystal structure of the s810I mutant mineralocorticoid2 receptor associated with sc9420

12	<a href="#">c5cwsF_</a>	Alignment		20.5	29	<b>PDB header:</b> protein transport <b>Chain:</b> F; <b>PDB Molecule:</b> nucleoporin nic96; <b>PDBTitle:</b> crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
13	<a href="#">c5cwsL_</a>	Alignment		17.6	29	<b>PDB header:</b> protein transport <b>Chain:</b> L; <b>PDB Molecule:</b> nucleoporin nic96; <b>PDBTitle:</b> crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
14	<a href="#">c3lk2B_</a>	Alignment		17.1	42	<b>PDB header:</b> protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> f-actin-capping protein subunit beta isoforms 1 and 2; <b>PDBTitle:</b> crystal structure of capz bound to the uncapping motif from carmil
15	<a href="#">c4akrB_</a>	Alignment		15.3	33	<b>PDB header:</b> actin-binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> f-actin-capping protein subunit beta; <b>PDBTitle:</b> crystal structure of the cytoplasmic actin capping protein2 cap32_34 from dictyostelium discoideum
16	<a href="#">c6roiA_</a>	Alignment		15.2	15	<b>PDB header:</b> lipid transport <b>Chain:</b> A; <b>PDB Molecule:</b> probable phospholipid-transporting atpase drs2; <b>PDBTitle:</b> cryo-em structure of the partially activated drs2p-cdc50p
17	<a href="#">c4ojkD_</a>	Alignment		14.6	47	<b>PDB header:</b> hydrolase/protein binding <b>Chain:</b> D; <b>PDB Molecule:</b> cgmp-dependent protein kinase 2; <b>PDBTitle:</b> structure of the cgmp dependent protein kinase ii and rab11b complex
18	<a href="#">d1iznb_</a>	Alignment		14.4	42	<b>Fold:</b> Subunits of heterodimeric actin filament capping protein Capz <b>Superfamily:</b> Subunits of heterodimeric actin filament capping protein Capz <b>Family:</b> Capz beta-1 subunit
19	<a href="#">c3ukxC_</a>	Alignment		14.4	29	<b>PDB header:</b> protein transport/inhibitor <b>Chain:</b> C; <b>PDB Molecule:</b> bimax2 peptide; <b>PDBTitle:</b> mouse importin alpha: bimax2 peptide complex
20	<a href="#">c3vw7A_</a>	Alignment		13.3	17	<b>PDB header:</b> signaling protein/antagonist <b>Chain:</b> A; <b>PDB Molecule:</b> proteinase-activated receptor 1, lysozyme; <b>PDBTitle:</b> crystal structure of human protease-activated receptor 1 (par1) bound2 with antagonist vorapaxar at 2.2 angstrom
21	<a href="#">c2ndjA_</a>	Alignment	not modelled	12.5	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> potassium voltage-gated channel subfamily e member 3; <b>PDBTitle:</b> structural basis for kcne3 and estrogen modulation of the kcnq12 channel
22	<a href="#">c4ojkC_</a>	Alignment	not modelled	12.1	47	<b>PDB header:</b> hydrolase/protein binding <b>Chain:</b> C; <b>PDB Molecule:</b> cgmp-dependent protein kinase 2; <b>PDBTitle:</b> structure of the cgmp dependent protein kinase ii and rab11b complex
23	<a href="#">c6c6IN_</a>	Alignment	not modelled	11.5	25	<b>PDB header:</b> membrane protein <b>Chain:</b> N; <b>PDB Molecule:</b> v0 assembly protein 1; <b>PDBTitle:</b> yeast vacuolar atpase vo in lipid nanodisc
24	<a href="#">c2k21A_</a>	Alignment	not modelled	10.8	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> potassium voltage-gated channel subfamily e <b>PDBTitle:</b> nmr structure of human kcne1 in Impg micelles at ph 6.0 and2 40 degree c
25	<a href="#">c5eulY_</a>	Alignment	not modelled	10.5	24	<b>PDB header:</b> protein transport <b>Chain:</b> Y; <b>PDB Molecule:</b> protein translocase subunit secy; <b>PDBTitle:</b> structure of the seca-secy complex with a translocating polypeptide2 substrate
26	<a href="#">c6mjpG_</a>	Alignment	not modelled	10.0	7	<b>PDB header:</b> lipid transport <b>Chain:</b> G; <b>PDB Molecule:</b> lps export abc transporter permease lptg; <b>PDBTitle:</b> lptb(e163q)fgc from vibrio cholerae
27	<a href="#">c4k1cA_</a>	Alignment	not modelled	8.9	14	<b>PDB header:</b> membrane protein/metal transport <b>Chain:</b> A; <b>PDB Molecule:</b> vacuolar calcium ion transporter; <b>PDBTitle:</b> vcx1 calcium/proton exchanger
28	<a href="#">c4k1cB_</a>	Alignment	not modelled	8.8	15	<b>PDB header:</b> membrane protein/metal transport <b>Chain:</b> B; <b>PDB Molecule:</b> vacuolar calcium ion transporter; <b>PDBTitle:</b> vcx1 calcium/proton exchanger
						<b>PDB header:</b> membrane protein

29	<a href="#">c6irtB_</a>	Alignment	not modelled	8.8	15	<b>Chain:</b> B: <b>PDB Molecule:</b> large neutral amino acids transporter small subunit 1; <b>PDBTitle:</b> human lat1-4f2hc complex bound with bch
30	<a href="#">c4r1iB_</a>	Alignment	not modelled	8.7	15	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> aminobenzoyl-glutamate transporter; <b>PDBTitle:</b> structure and function of neisseria gonorrhoeae mtrf illuminates a2 class of antimetabolite efflux pumps
31	<a href="#">c6m9tA_</a>	Alignment	not modelled	8.3	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> prostaglandin e2 receptor ep3 subtype, endolysin chimera; <b>PDBTitle:</b> crystal structure of ep3 receptor bound to misoprostol-fa
32	<a href="#">c3j01A_</a>	Alignment	not modelled	8.2	43	<b>PDB header:</b> ribosome/ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> preprotein translocase secy subunit; <b>PDBTitle:</b> structure of the ribosome-secy complex in the membrane environment
33	<a href="#">c2p14A_</a>	Alignment	not modelled	8.2	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> heterodimeric restriction endonuclease r.bspd6i small <b>PDBTitle:</b> crystal structure of small subunit (r.bspd6i2) of the heterodimeric2 restriction endonuclease r.bspd6i
34	<a href="#">c2kluA_</a>	Alignment	not modelled	8.1	23	<b>PDB header:</b> immune system, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> t-cell surface glycoprotein cd4; <b>PDBTitle:</b> nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
35	<a href="#">c5e5wB_</a>	Alignment	not modelled	6.8	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hemagglutinin-esterase; <b>PDBTitle:</b> hemagglutinin-esterase-fusion mutant structure of influenza d virus
36	<a href="#">c4xnwC_</a>	Alignment	not modelled	6.8	8	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> p2y purinoceptor 1,rubredoxin,p2y purinoceptor 1; <b>PDBTitle:</b> the human p2y1 receptor in complex with mrs2500
37	<a href="#">c4kppA_</a>	Alignment	not modelled	6.5	6	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of h+/ca2+ exchanger cax
38	<a href="#">c1gw4A_</a>	Alignment	not modelled	6.4	27	<b>PDB header:</b> high density lipoproteins <b>Chain:</b> A: <b>PDB Molecule:</b> apoa-i; <b>PDBTitle:</b> the helix-hinge-helix structural motif in human2 apolipoprotein a-i determined by nmr spectroscopy, 13 structure
39	<a href="#">c2ewfA_</a>	Alignment	not modelled	6.1	4	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nicking endonuclease n.bspd6i; <b>PDBTitle:</b> crystal structure of the site-specific dna nickase n.bspd6i
40	<a href="#">c4i0xl_</a>	Alignment	not modelled	5.9	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> J: <b>PDB Molecule:</b> esat-6-like protein mab_3113; <b>PDBTitle:</b> crystal structure of the mycobacterium abscessus esxf (mab_3112-2 mab_3113) complex
41	<a href="#">c3rkoK_</a>	Alignment	not modelled	5.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> K: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit k; <b>PDBTitle:</b> crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
42	<a href="#">c5x5yF_</a>	Alignment	not modelled	5.8	16	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> a membrane protein complex
43	<a href="#">c5jzfF_</a>	Alignment	not modelled	5.8	34	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> uncharacterized protein yhfg; <b>PDBTitle:</b> e. coli ecfict in complex with ecfica mutant e28g
44	<a href="#">c5jzfB_</a>	Alignment	not modelled	5.8	34	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein yhfg; <b>PDBTitle:</b> e. coli ecfict in complex with ecfica mutant e28g
45	<a href="#">c3aymB_</a>	Alignment	not modelled	5.7	8	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> rhodopsin; <b>PDBTitle:</b> crystal structure of the batho intermediate of squid rhodopsin
46	<a href="#">c4ib4A_</a>	Alignment	not modelled	5.6	10	<b>PDB header:</b> signaling protein, electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> chimera protein of human 5-hydroxytryptamine receptor 2b <b>PDBTitle:</b> crystal structure of the chimeric protein of 5-ht2b-bril in complex2 with ergotamine
47	<a href="#">c2e8pA_</a>	Alignment	not modelled	5.5	30	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> elf3 protein; <b>PDBTitle:</b> solution structure of the n-terminal sam-domain of e74-like2 factor 3
48	<a href="#">c6a94B_</a>	Alignment	not modelled	5.3	8	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> 5-hydroxytryptamine receptor 2a,soluble cytochrome b562; <b>PDBTitle:</b> crystal structure of 5-ht2ar in complex with zotepine
49	<a href="#">c5l75F_</a>	Alignment	not modelled	5.3	15	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> fig000988: predicted permease; <b>PDBTitle:</b> a protein structure
50	<a href="#">c3thgA_</a>	Alignment	not modelled	5.3	17	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ribulose bisphosphate carboxylase/oxygenase activase 1, <b>PDBTitle:</b> crystal structure of the creosote rubisco activase c-domain