

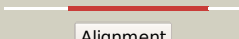

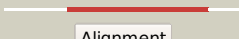



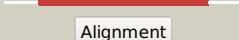



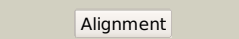

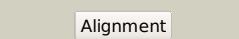

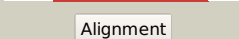






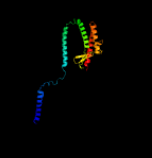

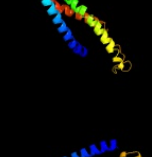
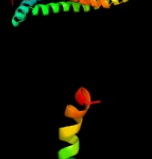

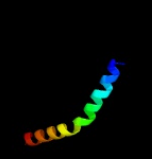

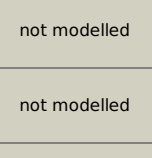


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3665c\_(dppB)\_4104709\_4105635  
 Date Fri Aug 9 18:20:35 BST 2019  
 Unique Job ID a748acc6d4b08ba0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4ymuC_</a>	 Alignment		99.9	13	<b>PDB header:</b> protein binding/transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> abc-type amino acid transport system, permease component; <b>PDBTitle:</b> crystal structure of an amino acid abc transporter complex with 2 arginines and atps
2	<a href="#">d3dhwa1</a>	 Alignment		99.9	17	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
3	<a href="#">c3d31D_</a>	 Alignment		99.9	14	<b>PDB header:</b> transport protein <b>Chain:</b> D; <b>PDB Molecule:</b> sulfate/molybdate abc transporter, permease protein; <b>PDBTitle:</b> modbc from methanosarcina acetivorans
4	<a href="#">d3d31c1</a>	 Alignment		99.9	14	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
5	<a href="#">d2onkc1</a>	 Alignment		99.9	17	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
6	<a href="#">c2onkC_</a>	 Alignment		99.9	17	<b>PDB header:</b> membrane protein <b>Chain:</b> C; <b>PDB Molecule:</b> molybdate/tungstate abc transporter, permease <b>PDBTitle:</b> abc transporter modbc in complex with its binding protein2 moda
7	<a href="#">c4tqvl_</a>	 Alignment		99.9	10	<b>PDB header:</b> transport protein <b>Chain:</b> I; <b>PDB Molecule:</b> algm1; <b>PDBTitle:</b> crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate
8	<a href="#">d2r6gf2</a>	 Alignment		99.8	12	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
9	<a href="#">c2r6qF_</a>	 Alignment		99.8	13	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> F; <b>PDB Molecule:</b> maltose transport system permease protein malF; <b>PDBTitle:</b> the crystal structure of the e. coli maltose transporter
10	<a href="#">c3fh6F_</a>	 Alignment		99.8	12	<b>PDB header:</b> transport protein <b>Chain:</b> F; <b>PDB Molecule:</b> maltose transport system permease protein malF; <b>PDBTitle:</b> crystal structure of the resting state maltose transporter from e.2 coli
11	<a href="#">c4tqvl_</a>	 Alignment		99.6	9	<b>PDB header:</b> transport protein <b>Chain:</b> J; <b>PDB Molecule:</b> algm2; <b>PDBTitle:</b> crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate

12	<a href="#">d2r6gg1</a>	Alignment		99.4	12	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
13	<a href="#">c5kbuA</a>	Alignment		90.9	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate receptor 2,voltage-dependent calcium channel <b>PDBTitle:</b> cryo-em structure of glua2-2xstz complex at 7.8 angstrom resolution
14	<a href="#">c5lj7B</a>	Alignment		39.9	14	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> structure of aggregatibacter actinomycetemcomitans macb bound to atp2 (p21)
15	<a href="#">c5xu1M</a>	Alignment		38.7	11	<b>PDB header:</b> transport protein <b>Chain:</b> M: <b>PDB Molecule:</b> abc transporter permeae; <b>PDBTitle:</b> structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
16	<a href="#">c5nikK</a>	Alignment		35.5	11	<b>PDB header:</b> transport protein <b>Chain:</b> K: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> structure of the macab-tolc abc-type tripartite multidrug efflux pump
17	<a href="#">c2nd4A</a>	Alignment		25.0	21	<b>PDB header:</b> hydrolase receptor <b>Chain:</b> A: <b>PDB Molecule:</b> amylase-binding protein abpa; <b>PDBTitle:</b> a distinct sortase srtb anchors and processes a streptococcal adhesin2 abpa with a novel structural property
18	<a href="#">c6r6bl</a>	Alignment		22.7	15	<b>PDB header:</b> protein transport <b>Chain:</b> I: <b>PDB Molecule:</b> surface presentation of antigens protein spaq; <b>PDBTitle:</b> structure of the core shigella flexneri type iii secretion system2 export gate complex sctrst (spa24/spa9/spa29).
19	<a href="#">c6f2dj</a>	Alignment		22.3	24	<b>PDB header:</b> protein transport <b>Chain:</b> J: <b>PDB Molecule:</b> flagellar biosynthetic protein fliq; <b>PDBTitle:</b> a flipqr complex forms the core of the salmonella type iii secretion2 system export apparatus.
20	<a href="#">c6f2dl</a>	Alignment		22.3	24	<b>PDB header:</b> protein transport <b>Chain:</b> I: <b>PDB Molecule:</b> flagellar biosynthetic protein fliq; <b>PDBTitle:</b> a flipqr complex forms the core of the salmonella type iii secretion2 system export apparatus.
21	<a href="#">c5x5yG</a>	Alignment	not modelled	16.3	17	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> a membrane protein complex
22	<a href="#">c1wz4A</a>	Alignment	not modelled	13.6	67	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> major surface antigen; <b>PDBTitle:</b> solution conformation of adr subtype hbv pre-s2 epitope
23	<a href="#">c4aezC</a>	Alignment	not modelled	13.3	12	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> mitotic spindle checkpoint component mad3; <b>PDBTitle:</b> crystal structure of mitotic checkpoint complex
24	<a href="#">c2cw1A</a>	Alignment	not modelled	11.5	26	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> sn4m; <b>PDBTitle:</b> solution structure of the de novo-designed lambda cro fold2 protein
25	<a href="#">c2hw2A</a>	Alignment	not modelled	11.5	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rifampin adp-ribosyl transferase; <b>PDBTitle:</b> crystal structure of rifampin adp-ribosyl transferase in complex with2 rifampin
26	<a href="#">c6mjpG</a>	Alignment	not modelled	9.4	16	<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="#">c4p16A</a>	Alignment	not modelled	9.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> orf1a; <b>PDBTitle:</b> crystal structure of the papain-like protease of middle-east2 respiratory syndrome coronavirus
28	<a href="#">c2jwaA</a>	Alignment	not modelled	9.1	30	<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
						<b>PDB header:</b> transferase

29	<a href="#">c2ks1A_</a>	Alignment	not modelled	9.1	30	<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 erbb2 receptors enabling kinase activation
30	<a href="#">c5ws4A_</a>	Alignment	not modelled	8.9	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> crystal structure of tripartite-type abc transporter macb from <i>2 acinetobacter baumannii</i>
31	<a href="#">c2yevC_</a>	Alignment	not modelled	8.5	30	<b>PDB header:</b> electron transport <b>Chain:</b> C: <b>PDB Molecule:</b> caa3-type cytochrome oxidase subunit iv; <b>PDBTitle:</b> structure of caa3-type cytochrome oxidase
32	<a href="#">d1n0ua5</a>	Alignment	not modelled	7.6	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V
33	<a href="#">d2d6fc1</a>	Alignment	not modelled	7.5	15	<b>Fold:</b> GatB/YqeY motif <b>Superfamily:</b> GatB/YqeY motif <b>Family:</b> GatB/GatE C-terminal domain-like
34	<a href="#">c5I75F_</a>	Alignment	not modelled	7.3	17	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> fig000988: predicted permease; <b>PDBTitle:</b> a protein structure
35	<a href="#">c5I75G_</a>	Alignment	not modelled	7.0	18	<b>PDB header:</b> transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> fig000906: predicted permease; <b>PDBTitle:</b> a protein structure
36	<a href="#">d1qy9a1</a>	Alignment	not modelled	6.8	10	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PhzC/PhzF-like
37	<a href="#">d1tdpa_</a>	Alignment	not modelled	6.7	19	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Bacteriocin immunity protein-like <b>Family:</b> Carnobacteriocin B2 immunity protein
38	<a href="#">c3ednB_</a>	Alignment	not modelled	6.7	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> phenazine biosynthesis protein, phzf family; <b>PDBTitle:</b> crystal structure of the bacillus anthracis phenazine2 biosynthesis protein, phzf family
39	<a href="#">c4yptA_</a>	Alignment	not modelled	6.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> replicase polyprotein 1ab; <b>PDBTitle:</b> x-ray structural of three tandemly linked domains of nsp3 from murine2 hepatitis virus at 2.60 angstroms resolution
40	<a href="#">c4ndiC_</a>	Alignment	not modelled	6.3	28	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> enh-c2b, computational designed homodimer; <b>PDBTitle:</b> computational design and experimental verification of a symmetric2 homodimer
41	<a href="#">c1g2hA_</a>	Alignment	not modelled	6.2	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein tyrr homolog; <b>PDBTitle:</b> solution structure of the dna-binding domain of the tyrr2 protein of haemophilus influenzae
42	<a href="#">d1g2ha_</a>	Alignment	not modelled	6.2	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
43	<a href="#">c2ka1A_</a>	Alignment	not modelled	6.1	32	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> bcl2/adenovirus e1b 19 kda protein-interacting <b>PDBTitle:</b> solution nmr structure of bnp3 transmembrane peptide dimer2 in detergent micelles
44	<a href="#">c2ka2B_</a>	Alignment	not modelled	6.1	32	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> bcl2/adenovirus e1b 19 kda protein-interacting <b>PDBTitle:</b> solution nmr structure of bnp3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
45	<a href="#">c2ka1B_</a>	Alignment	not modelled	6.1	32	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> bcl2/adenovirus e1b 19 kda protein-interacting <b>PDBTitle:</b> solution nmr structure of bnp3 transmembrane peptide dimer2 in detergent micelles
46	<a href="#">c2ka2A_</a>	Alignment	not modelled	6.1	32	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> bcl2/adenovirus e1b 19 kda protein-interacting <b>PDBTitle:</b> solution nmr structure of bnp3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
47	<a href="#">d1xuba1</a>	Alignment	not modelled	6.1	28	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PhzC/PhzF-like
48	<a href="#">d1u0ka1</a>	Alignment	not modelled	5.8	15	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PhzC/PhzF-like
49	<a href="#">c5lj3C_</a>	Alignment	not modelled	5.7	31	<b>PDB header:</b> splicing <b>Chain:</b> C: <b>PDB Molecule:</b> pre-mrna-splicing factor snu114; <b>PDBTitle:</b> structure of the core of the yeast spliceosome immediately after2 branching
50	<a href="#">d1ntca_</a>	Alignment	not modelled	5.7	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
51	<a href="#">c2m8gX_</a>	Alignment	not modelled	5.2	9	<b>PDB header:</b> transcription <b>Chain:</b> X: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> structure, function, and tethering of dna-binding domains in 542 transcriptional activators
52	<a href="#">c2b9sB_</a>	Alignment	not modelled	5.1	67	<b>PDB header:</b> isomerase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna topoisomerase i-like protein; <b>PDBTitle:</b> crystal structure of heterodimeric i. donovani topoisomerase i-2 vanadate-dna complex