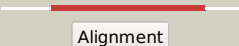


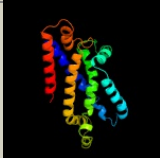
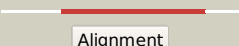





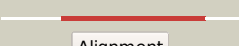
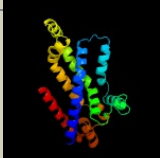



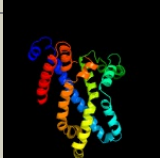

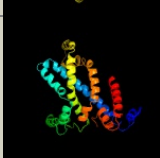



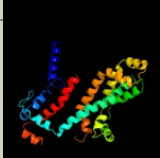

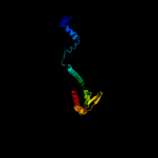

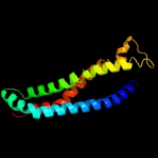

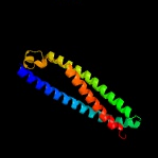

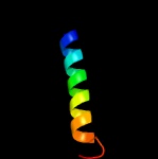
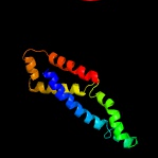


# Phyre2


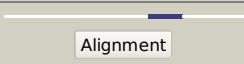
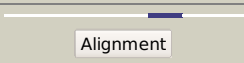
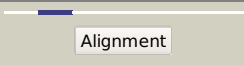
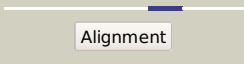
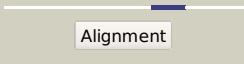
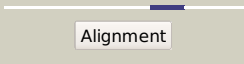
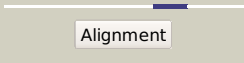
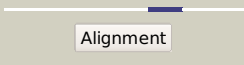
Email	mdejesus@rockefeller.edu
Description	RVBD1283c_oppB_1436146_1437123
Date	Wed Jul 31 22:05:37 BST 2019
Unique Job ID	fc4e564503ad43bc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4ymuC_</a>	 Alignment		99.9	14	<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 with2 arginines and atps
2	<a href="#">d3dhwa1</a>	 Alignment		99.9	21	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
3	<a href="#">c3d31D_</a>	 Alignment		99.8	13	<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		99.8	13	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
5	<a href="#">c2onkC_</a>	 Alignment		99.8	9	<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
6	<a href="#">d2onkc1</a>	 Alignment		99.8	9	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
7	<a href="#">c4tqvI_</a>	 Alignment		99.8	14	<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		99.6	15	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
9	<a href="#">c2r6gF_</a>	 Alignment		99.5	12	<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		99.5	13	<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="#">c4tqvI_</a>	 Alignment		99.2	17	<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		99.0	15	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
13	<a href="#">c5kbuA</a>	Alignment		94.3	16	<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="#">c2nd4A</a>	Alignment		59.8	43	<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
15	<a href="#">c5xu1M</a>	Alignment		45.1	14	<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		32.4	16	<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="#">c5lj7B</a>	Alignment		31.6	16	<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)
18	<a href="#">c1wz4A</a>	Alignment		22.6	78	<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
19	<a href="#">c2yevC</a>	Alignment		19.6	33	<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
20	<a href="#">c5l75F</a>	Alignment		16.9	20	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> fig000988: predicted permease; <b>PDBTitle:</b> a protein structure
21	<a href="#">c2m8gX</a>	Alignment	not modelled	14.8	26	<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
22	<a href="#">d1g2ha</a>	Alignment	not modelled	14.8	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
23	<a href="#">c1g2hA</a>	Alignment	not modelled	14.8	19	<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
24	<a href="#">c2ka2B</a>	Alignment	not modelled	13.8	12	<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
25	<a href="#">c2ka1A</a>	Alignment	not modelled	13.8	12	<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
26	<a href="#">c2ka1B</a>	Alignment	not modelled	13.8	12	<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
27	<a href="#">c2ka2A</a>	Alignment	not modelled	13.8	12	<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
28	<a href="#">c6f2dL</a>	Alignment	not modelled	12.9	18	<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.
29	<a href="#">c6f2dJ</a>	Alignment	not modelled	12.9	18	<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.
30	<a href="#">c6r6bL</a>	Alignment	not modelled	12.5	18	<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).
31	<a href="#">c5x3tA</a>	Alignment	not modelled	12.2	23	<b>PDB header:</b> antitoxin/toxin <b>Chain:</b> A: <b>PDB Molecule:</b> antitoxin vapp26; <b>PDBTitle:</b> vappc from mycobacterium tuberculosis
32	<a href="#">c4g1uB</a>	Alignment	not modelled	12.0	18	<b>PDB header:</b> transport protein/hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hemin transport system permease protein hmuu; <b>PDBTitle:</b> x-ray structure of the bacterial heme transporter hmuuv from yersinia2 pestis
33	<a href="#">d1umqA</a>	Alignment	not modelled	11.9	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
34	<a href="#">c1umqA</a>	Alignment	not modelled	11.9	19	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> photosynthetic apparatus regulatory protein; <b>PDBTitle:</b> solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
35	<a href="#">c2j5dA</a>	Alignment	not modelled	10.3	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> bcl2/adenovirus e1b 19 kda protein-interacting protein 3; <b>PDBTitle:</b> nmr structure of bnip3 transmembrane domain in lipid bicelles
36	<a href="#">d2auwa1</a>	Alignment	not modelled	9.4	29	<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
37	<a href="#">d1ntca</a>	Alignment	not modelled	9.3	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
38	<a href="#">c5b57B</a>	Alignment	not modelled	8.6	15	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> putative hemin abc transport system, membrane protein; <b>PDBTitle:</b> inward-facing conformation of abc heme importer bhuuv from2 burkholderia cenocepacia
39	<a href="#">c2b9sB</a>	Alignment	not modelled	8.1	36	<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
40	<a href="#">d1a9xa1</a>	Alignment	not modelled	7.8	16	<b>Fold:</b> Carbamoyl phosphate synthetase, large subunit connection domain <b>Superfamily:</b> Carbamoyl phosphate synthetase, large subunit connection domain <b>Family:</b> Carbamoyl phosphate synthetase, large subunit connection domain
41	<a href="#">c4I5eA</a>	Alignment	not modelled	7.7	9	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of a. aeolicus ntrc1 dna binding domain
42	<a href="#">c1y66D</a>	Alignment	not modelled	7.4	21	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> engrailed homeodomain; <b>PDBTitle:</b> dioxane contributes to the altered conformation and2 oligomerization state of a designed engrailed homeodomain3 variant
43	<a href="#">c5ws4A</a>	Alignment	not modelled	6.6	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 from2 acinetobacter baumannii
44	<a href="#">c1ciiA</a>	Alignment	not modelled	6.4	20	<b>PDB header:</b> transmembrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> colicin ia; <b>PDBTitle:</b> colicin ia
45	<a href="#">c2nq2A</a>	Alignment	not modelled	6.3	11	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical abc transporter permease protein <b>PDBTitle:</b> an inward-facing conformation of a putative metal-chelate2 type abc transporter.
46	<a href="#">d1etob</a>	Alignment	not modelled	6.2	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
47	<a href="#">d1zq1c1</a>	Alignment	not modelled	6.2	23	<b>Fold:</b> GatB/YqeY motif <b>Superfamily:</b> GatB/YqeY motif <b>Family:</b> GatB/GatE C-terminal domain-like
48	<a href="#">c6ac5A</a>	Alignment	not modelled	6.1	24	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> receptor-interacting serine/threonine-protein kinase 1; <b>PDBTitle:</b> crystal structure of ripk1 death domain glcnacylated by epec effector2 nleb
49	<a href="#">d1fipa</a>	Alignment	not modelled	6.1	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
50	<a href="#">c4ndIC</a>	Alignment	not modelled	6.0	18	<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

51	<a href="#">c5m7nA_</a>	 Alignment	not modelled	5.8	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen assimilation regulatory protein; <b>PDBTitle:</b> crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystaldirect automated mounting and cryo-cooling3 technology
52	<a href="#">c2cw1A_</a>	 Alignment	not modelled	5.8	30	<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
53	<a href="#">d3orca_</a>	 Alignment	not modelled	5.5	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
54	<a href="#">c5l75G_</a>	 Alignment	not modelled	5.4	11	<b>PDB header:</b> transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> fig000906: predicted permease; <b>PDBTitle:</b> a protein structure
55	<a href="#">c3td7A_</a>	 Alignment	not modelled	5.4	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fad-linked sulfhydryl oxidase r596; <b>PDBTitle:</b> crysal structure of the mimivirus sulfhydryl oxidase r596
56	<a href="#">c2d7dB_</a>	 Alignment	not modelled	5.3	19	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> 40-mer from uvrabc system protein b; <b>PDBTitle:</b> structural insights into the cryptic dna dependent atp-ase2 activity of uvrbc
57	<a href="#">d1gt1a_</a>	 Alignment	not modelled	5.2	18	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Retinol binding protein-like
58	<a href="#">c2knaA_</a>	 Alignment	not modelled	5.1	11	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> baculoviral iap repeat-containing protein 4; <b>PDBTitle:</b> solution structure of uba domain of xiap
59	<a href="#">c3oq9C_</a>	 Alignment	not modelled	5.1	13	<b>PDB header:</b> apoptosis <b>Chain:</b> C: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> structure of the fas/fadd death domain assembly