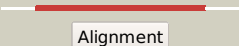



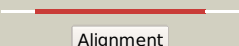




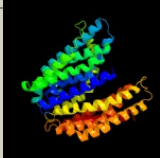
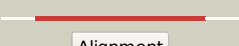
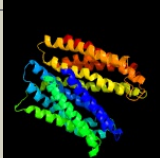









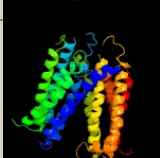






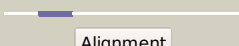

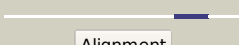
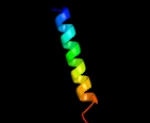
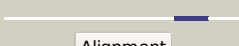
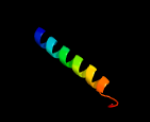
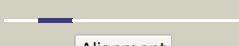
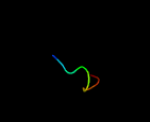

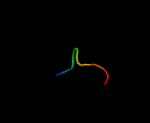

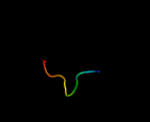

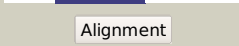

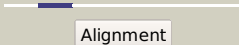

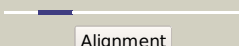
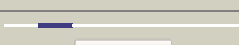



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3630_(-)_4069354_4070649
Date	Fri Aug 9 18:20:31 BST 2019
Unique Job ID	6291fc92afbdbc7a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6cc4A_	 Alignment		100.0	11	PDB header: transport protein Chain: A: PDB Molecule: soluble cytochrome b562, lipid ii flippase murj chimera; PDBTitle: structure of murj from escherichia coli
2	c5y50A_	 Alignment		100.0	10	PDB header: membrane protein Chain: A: PDB Molecule: protein detoxification 14; PDBTitle: crystal structure of eukaryotic mate transporter atdtx14
3	c5xjjA_	 Alignment		100.0	9	PDB header: transport protein Chain: A: PDB Molecule: multi drug efflux transporter; PDBTitle: crystal structure of a mate family protein
4	c6idrA_	 Alignment		100.0	11	PDB header: transport protein Chain: A: PDB Molecule: mate family efflux transporter; PDBTitle: crystal structure of vibrio cholerae mate transporter vcmn in the bent2 form
5	c5t77A_	 Alignment		100.0	10	PDB header: transport protein Chain: A: PDB Molecule: putative lipid ii flippase murj; PDBTitle: crystal structure of the mop flippase murj
6	c6fv6A_	 Alignment		100.0	8	PDB header: membrane protein Chain: A: PDB Molecule: aq128; PDBTitle: monomer structure of the mate family multidrug resistance transporter2 aq_128 from aquifex aeolicus in the outward-facing state
7	c4lz9A_	 Alignment		100.0	8	PDB header: transport protein Chain: A: PDB Molecule: bh2163 protein; PDBTitle: structure of mate multidrug transporter dinf-bh in complex with r6g
8	c4z3pA_	 Alignment		100.0	10	PDB header: transport protein Chain: A: PDB Molecule: putative drug/sodium antiporter; PDBTitle: mate transporter clbm in complex with rb+
9	c3vvpA_	 Alignment		100.0	14	PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of mate in complex with br-nrf
10	c3mkuB_	 Alignment		99.9	11	PDB header: transport protein Chain: B: PDB Molecule: multi antimicrobial extrusion protein (na+)/drug PDBTitle: structure of a cation-bound multidrug and toxin compound extrusion2 (mate) transporter
11	c3mkuA_	 Alignment		99.9	12	PDB header: transport protein Chain: A: PDB Molecule: multi antimicrobial extrusion protein (na+)/drug PDBTitle: structure of a cation-bound multidrug and toxin compound extrusion2 (mate) transporter

12	c4hunA_	 Alignment		99.4	11	PDB header: transport protein Chain: A: PDB Molecule: multidrug efflux protein; PDBTitle: mate transporter norm-ng in complex with r6g and monobody
13	c4n7wA_	 Alignment		86.5	12	PDB header: transport protein Chain: A: PDB Molecule: transporter, sodium/bile acid symporter family; PDBTitle: crystal structure of the sodium bile acid symporter from yersinia2 frederiksenii
14	c6n3qA_	 Alignment		11.7	11	PDB header: transport protein Chain: A: PDB Molecule: protein transport protein sec61; PDBTitle: cryo-em structure of the yeast sec complex
15	c2luvA_	 Alignment		10.0	18	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-x; PDBTitle: structure and binding interface of the cytosolic tails of axb22 integrin
16	c2momB_	 Alignment		8.6	12	PDB header: membrane protein Chain: B: PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles
17	c2momC_	 Alignment		8.6	12	PDB header: membrane protein Chain: C: PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles
18	c5lo2A_	 Alignment		8.0	45	PDB header: structural protein Chain: A: PDB Molecule: ppatyr; PDBTitle: engineering protein stability with atomic precision in a monomeric2 miniprotein
19	c5lo4A_	 Alignment		8.0	45	PDB header: structural protein Chain: A: PDB Molecule: ppa-ch3; PDBTitle: engineering protein stability with atomic precision in a monomeric2 miniprotein
20	c5lo3A_	 Alignment		8.0	45	PDB header: structural protein Chain: A: PDB Molecule: ppaome; PDBTitle: engineering protein stability with atomic precision in a monomeric2 miniprotein
21	d3ehbb2	 Alignment	not modelled	7.0	10	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
22	c4iu8A_	 Alignment	not modelled	6.7	8	PDB header: transport protein Chain: A: PDB Molecule: nitrite extrusion protein 2; PDBTitle: crystal structure of a membrane transporter (selenomethionine2 derivative)
23	d3dtub2	 Alignment	not modelled	6.6	13	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
24	c3h1cL_	 Alignment	not modelled	6.6	20	PDB header: transferase Chain: L: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnpase)2 core bound to rnase e and tungstate
25	c3h1cE_	 Alignment	not modelled	6.6	20	PDB header: transferase Chain: E: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnpase)2 core bound to rnase e and tungstate
26	c3h1cY_	 Alignment	not modelled	6.6	20	PDB header: transferase Chain: Y: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnpase)2 core bound to rnase e and tungstate
27	c3h1cS_	 Alignment	not modelled	6.6	20	PDB header: transferase Chain: S: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnpase)2 core bound to rnase e and tungstate
28	c3h1cH_	 Alignment	not modelled	6.6	20	PDB header: transferase Chain: H: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnpase)2 core bound to rnase e and tungstate

29	c3h1cP_	Alignment	not modelled	6.6	20	PDB header: transferase Chain: P: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnpase)2 core bound to rnase e and tungstate
30	c3h1cJ_	Alignment	not modelled	6.6	20	PDB header: transferase Chain: J: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnpase)2 core bound to rnase e and tungstate
31	c3h1cW_	Alignment	not modelled	6.6	20	PDB header: transferase Chain: W: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnpase)2 core bound to rnase e and tungstate
32	c3gmeD_	Alignment	not modelled	6.6	20	PDB header: transferase / protein binding Chain: D: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase in complex2 with rnase e and manganese
33	c3h1cN_	Alignment	not modelled	6.6	20	PDB header: transferase Chain: N: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnpase)2 core bound to rnase e and tungstate
34	c3h1cF_	Alignment	not modelled	6.6	20	PDB header: transferase Chain: F: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnpase)2 core bound to rnase e and tungstate
35	c3h1cU_	Alignment	not modelled	6.6	20	PDB header: transferase Chain: U: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnpase)2 core bound to rnase e and tungstate
36	c3gcmF_	Alignment	not modelled	6.6	20	PDB header: transferase / protein binding Chain: F: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of e. coli polynucleotide phosphorylase2 bound to rna and rnase e
37	c3h1cD_	Alignment	not modelled	6.6	20	PDB header: transferase Chain: D: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnpase)2 core bound to rnase e and tungstate
38	c3gcmD_	Alignment	not modelled	6.6	20	PDB header: transferase / protein binding Chain: D: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of e. coli polynucleotide phosphorylase2 bound to rna and rnase e
39	c2zqpY_	Alignment	not modelled	6.5	13	PDB header: protein transport Chain: Y: PDB Molecule: preprotein translocase secy subunit; PDBTitle: crystal structure of secye translocon from thermus2 thermophilus
40	c3gcmE_	Alignment	not modelled	6.4	18	PDB header: transferase / protein binding Chain: E: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of e. coli polynucleotide phosphorylase2 bound to rna and rnase e
41	c3wdoA_	Alignment	not modelled	6.3	12	PDB header: transport protein Chain: A: PDB Molecule: mfs transporter; PDBTitle: structure of e. coli yajr transporter
42	c3j01A_	Alignment	not modelled	6.3	15	PDB header: ribosome/ribosomal protein Chain: A: PDB Molecule: preprotein translocase secy subunit; PDBTitle: structure of the ribosome-secye complex in the membrane environment
43	c4e6nC_	Alignment	not modelled	6.0	36	PDB header: protein binding Chain: C: PDB Molecule: metallophosphoesterase; PDBTitle: crystal structure of bacterial pnpk-c/hen1-n heterodimer
44	d1pw4a_	Alignment	not modelled	5.8	10	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: Glycerol-3-phosphate transporter
45	c3ty8A_	Alignment	not modelled	5.8	36	PDB header: transferase Chain: A: PDB Molecule: polynucleotide 2',3'-cyclic phosphate phosphodiesterase / PDBTitle: crystal structure of c. thermocellum pnpk ligase domain apo form
46	c4dblB_	Alignment	not modelled	5.8	12	PDB header: transport protein Chain: B: PDB Molecule: vitamin b12 import system permease protein btuc; PDBTitle: crystal structure of e159q mutant of btucdf
47	c2bf9A_	Alignment	not modelled	5.5	33	PDB header: hormone Chain: A: PDB Molecule: pancreatic hormone; PDBTitle: anisotropic refinement of avian (turkey) pancreatic polypeptide at 0.2 99 angstroms resolution.
48	c4c9qB_	Alignment	not modelled	5.5	12	PDB header: transport protein Chain: B: PDB Molecule: adp, atp carrier protein 3; PDBTitle: structure of yeast mitochondrial adp/atp carrier isoform 32 inhibited by carboxyatractyloside (p21 crystal form)
49	c1g2cN_	Alignment	not modelled	5.5	30	PDB header: viral protein Chain: N: PDB Molecule: fusion protein (f); PDBTitle: human respiratory syncytial virus fusion protein core
50	c1tz5A_	Alignment	not modelled	5.4	27	PDB header: hormone/growth factor Chain: A: PDB Molecule: chimera of pancreatic hormone and neuropeptide y; PDBTitle: [pnpy19-23]-hpp bound to dpc micelles
51	c4xruE_	Alignment	not modelled	5.1	7	PDB header: protein binding Chain: E: PDB Molecule: rnl; PDBTitle: structure of pnpk1/rnl/hen1 complex
52	c5z62M_	Alignment	not modelled	5.1	17	PDB header: electron transport Chain: M: PDB Molecule: cytochrome c oxidase subunit 8a, mitochondrial; PDBTitle: structure of human cytochrome c oxidase
53	c3v5uA_	Alignment	not modelled	5.0	9	PDB header: metal transport Chain: A: PDB Molecule: uncharacterized membrane protein mj0091; PDBTitle: structure of sodium/calcium exchanger from methanocaldococcus2 jannaschii dsm 2661
54	c2jwaA_	Alignment	not modelled	5.0	21	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2;

