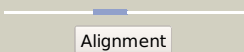

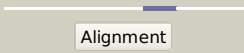



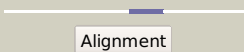
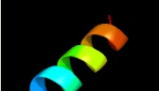
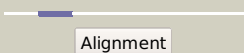
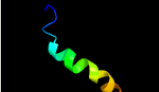
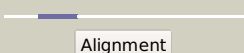


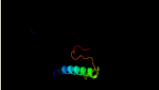
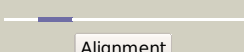
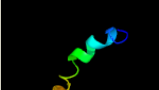
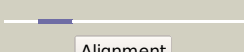

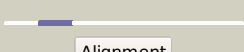
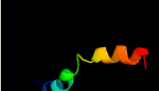




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2180c (-)_2442335_2443222
Date	Mon Aug 5 13:25:30 BST 2019
Unique Job ID	57b3a5d822df9d1b

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2cnyB_	 Alignment		21.3	60	PDB header: fibril protein Chain: B: PDB Molecule: putative outer membrane protein; PDBTitle: salmonella enterica safA pilin in complex with a 19-residue2 safA nte peptide (i15a mutant)
2	c2dw3A_	 Alignment		17.0	33	PDB header: photosynthesis Chain: A: PDB Molecule: intrinsic membrane protein pufx; PDBTitle: solution structure of the rhodobacter sphaeroides pufx2 membrane protein
3	d2axtk1	 Alignment		15.3	45	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein K, PsbK Family: PsbK-like
4	c4y3uB_	 Alignment		14.7	29	PDB header: membrane protein Chain: B: PDB Molecule: cardiac phospholamban; PDBTitle: the structure of phospholamban bound to the calcium pump serca1a
5	c3jcku_	 Alignment		14.5	31	PDB header: membrane protein Chain: K: PDB Molecule: photosystem ii reaction center protein k; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
6	c5jngA_	 Alignment		13.5	10	PDB header: transferase/antibiotic Chain: A: PDB Molecule: phospho-n-acetylmuramoyl-pentapeptide-transferase; PDBTitle: mray tunicamycin complex
7	c4j72A_	 Alignment		13.3	11	PDB header: transferase Chain: A: PDB Molecule: phospho-n-acetylmuramoyl-pentapeptide-transferase; PDBTitle: crystal structure of polyprenyl-phosphate n-acetyl hexosamine 1-2 phosphate transferase
8	c3a0bK_	 Alignment		11.6	23	PDB header: electron transport Chain: K: PDB Molecule: photosystem ii reaction center protein k; PDBTitle: crystal structure of br-substituted photosystem ii complex
9	c3a0hK_	 Alignment		11.6	23	PDB header: electron transport Chain: K: PDB Molecule: photosystem ii reaction center protein k; PDBTitle: crystal structure of i-substituted photosystem ii complex
10	c3a0bk_	 Alignment		11.6	23	PDB header: electron transport Chain: K: PDB Molecule: photosystem ii reaction center protein k; PDBTitle: crystal structure of br-substituted photosystem ii complex
11	c1zllE_	 Alignment		11.0	29	PDB header: membrane protein/signaling protein Chain: E: PDB Molecule: cardiac phospholamban; PDBTitle: nmr structure of unphosphorylated human phospholamban2 pentamer

12	c1d8wa_	Alignment		10.5	19	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: L-rhamnose isomerase
13	c4kv3A_	Alignment		10.2	38	PDB header: protein transport Chain: A: PDB Molecule: chimera fusion protein of esx-1 secretion system protein PDBTitle: ubiquitin-like domain of the mycobacterium tuberculosis type vii2 secretion system protein eccd1 as maltose-binding protein fusion
14	c2bzwB_	Alignment		9.3	39	PDB header: transcription Chain: B: PDB Molecule: bcl2-antagonist of cell death; PDBTitle: the crystal structure of bcl-xl in complex with full-length bad
15	c3a0hj_	Alignment		9.2	27	PDB header: electron transport Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: crystal structure of i-substituted photosystem ii complex
16	d2axtj1	Alignment		9.2	27	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein J, Psbj Family: Psbj-like
17	c2ziiA_	Alignment		9.1	31	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 74; PDBTitle: crystal structure of yeast vps74-n-term truncation variant
18	c6k1hF_	Alignment		8.5	30	PDB header: protein transport Chain: F: PDB Molecule: pts system mannose-specific eiid component; PDBTitle: structure of membrane protein
19	c2zihC_	Alignment		8.5	31	PDB header: protein transport Chain: C: PDB Molecule: vacuolar protein sorting-associated protein 74; PDBTitle: crystal structure of yeast vps74
20	c3rqrA_	Alignment		8.5	15	PDB header: metal transport Chain: A: PDB Molecule: ryanodine receptor 1; PDBTitle: crystal structure of the ryr domain of the rabbit ryanodine receptor
21	c3a0hk_	Alignment	not modelled	8.3	45	PDB header: electron transport Chain: K: PDB Molecule: photosystem ii reaction center protein k; PDBTitle: crystal structure of i-substituted photosystem ii complex
22	d2q07a2	Alignment	not modelled	7.8	22	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: AF0587 domain-like
23	d1g7oa1	Alignment	not modelled	7.8	14	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
24	c1vd9A_	Alignment	not modelled	7.2	50	PDB header: transcription Chain: A: PDB Molecule: fibroin-modulator-binding-protein-1; PDBTitle: solution structure of fmbp-1 tandem repeat 3
25	d1b93a_	Alignment	not modelled	6.0	19	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA
26	c2jlnA_	Alignment	not modelled	6.0	17	PDB header: membrane protein Chain: A: PDB Molecule: mhp1; PDBTitle: structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
27	c2qn5B_	Alignment	not modelled	5.9	44	PDB header: hydrolase inhibitor/hydrolase Chain: B: PDB Molecule: bowman-birk type bran trypsin inhibitor; PDBTitle: crystal structure and functional study of the bowman-birk2 inhibitor from rice bran in complex with bovine trypsin
28	c2lw6A_	Alignment	not modelled	5.8	40	PDB header: apoptosis Chain: A: PDB Molecule: avrpiz-t protein; PDBTitle: solution structure of an avirulence protein avrpiz-t from pathogen2 magnaportheorzyae
						Fold: Dodecin subunit-like

29	d2cc6a1	Alignment	not modelled	5.8	50	Superfamily: Dodecin-like Family: Dodecin-like
30	c3gioA	Alignment	not modelled	5.7	50	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the tnf-alpha inducing protein (tip2 alpha) from helicobacter pylori
31	d1m9sa2	Alignment	not modelled	5.5	26	Fold: SH3-like barrel Superfamily: Prokaryotic SH3-related domain Family: GW domain
32	c1tx6j	Alignment	not modelled	5.5	33	PDB header: hydrolase/protein binding Chain: J: PDB Molecule: bowman-birk type trypsin inhibitor; PDBTitle: trypsin:bbi complex
33	c4pkcC	Alignment	not modelled	5.3	67	PDB header: lyase Chain: C: PDB Molecule: tutf; PDBTitle: benzylsuccinate alpha-gamma complex
34	d1iq3a	Alignment	not modelled	5.2	30	Fold: EF Hand-like Superfamily: EF-hand Family: Eps15 homology domain (EH domain)
35	c4pkfC	Alignment	not modelled	5.2	67	PDB header: lyase Chain: C: PDB Molecule: tutf; PDBTitle: benzylsuccinate synthase alpha-beta-gamma complex