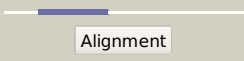
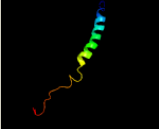
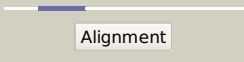
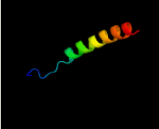
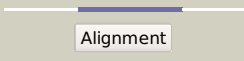

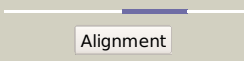
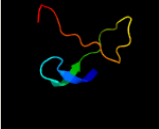
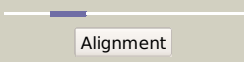
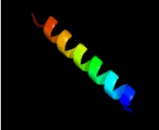
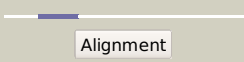
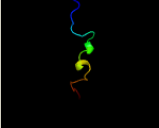
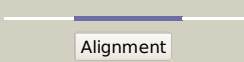

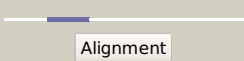

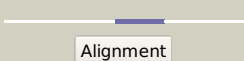
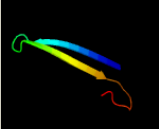
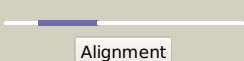
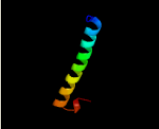
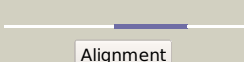
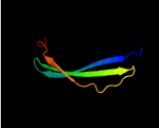
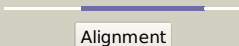

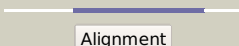


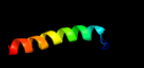
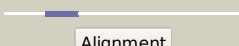
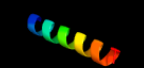
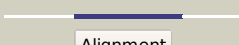

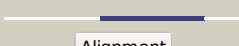

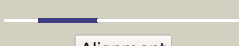

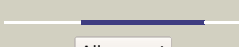


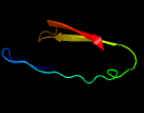
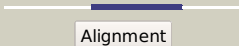
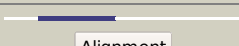

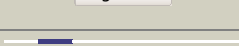
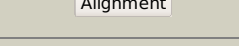
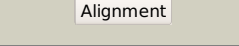

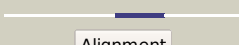



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1081c_(-)_1205989_1206423
Date	Wed Jul 31 22:05:15 BST 2019
Unique Job ID	194d4a50124e8133

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6f0kA_	 Alignment		19.8	20	PDB header: membrane protein Chain: A; PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii
2	c2kncA_	 Alignment		19.0	3	PDB header: cell adhesion Chain: A; PDB Molecule: integrin alpha-iib; PDBTitle: platelet integrin alfaIib-beta3 transmembrane-cytoplasmic2 heterocomplex
3	d3cnva1	 Alignment		15.4	15	Fold: Chorismate lyase-like Superfamily: Chorismate lyase-like Family: UTRA domain
4	d2g5da1	 Alignment		13.9	8	Fold: Double psi beta-barrel Superfamily: Barwin-like endoglucanases Family: MLTA-like
5	c6btmA_	 Alignment		13.6	13	PDB header: membrane protein Chain: A; PDB Molecule: alternative complex iii subunit a; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
6	d2aqaal	 Alignment		13.0	26	Fold: Rubredoxin-like Superfamily: Nop10-like SnoRNP Family: Nucleolar RNA-binding protein Nop10-like
7	c3f8lC_	 Alignment		12.8	22	PDB header: transcription Chain: C; PDB Molecule: hth-type transcriptional repressor phnf; PDBTitle: crystal structure of the effector domain of phnf from mycobacterium2 smegmatis
8	c2lx0A_	 Alignment		12.5	4	PDB header: membrane protein Chain: A; PDB Molecule: membrane fusion protein p14; PDBTitle: arced helix (arch) nmr structure of the reovirus p14 fusion-associated2 small transmembrane (fast) protein transmembrane domain (tmd) in3 dodecyl phosphocholine (dpc) micelles
9	d1ekra_	 Alignment		12.2	13	Fold: Ferredoxin-like Superfamily: Molybdenum cofactor biosynthesis protein C, MoaC Family: Molybdenum cofactor biosynthesis protein C, MoaC
10	c6f0kC_	 Alignment		12.1	19	PDB header: membrane protein Chain: C; PDB Molecule: polysulphide reductase nrfd; PDBTitle: alternative complex iii
11	c3ir3B_	 Alignment		11.6	11	PDB header: lyase Chain: B; PDB Molecule: 3-hydroxyacyl-thioester dehydratase 2; PDBTitle: crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2)

12	d1xo8a_	 Alignment		10.8	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: LEA14-like Family: LEA14-like
13	c1yycA_	 Alignment		10.7	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative late embryogenesis abundant protein; PDBTitle: solution structure of a putative late embryogenesis2 abundant (lea) protein at2g46140.1
14	c2l8sA_	 Alignment		10.6	10	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-1; PDBTitle: solution nmr structure of transmembrane and cytosolic regions of f2 integrin alpha1 in detergent micelles
15	c2k1aA_	 Alignment		10.3	0	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiib; PDBTitle: bicelle-embedded integrin alpha(iiib) transmembrane segment
16	c4zsiA_	 Alignment		9.9	16	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional repressor dasr; PDBTitle: crystal structure of the effector-binding domain of dasr (dasr-ebd) in2 complex with glucosamine-6-phosphate
17	c3cmgA_	 Alignment		9.8	16	PDB header: hydrolase Chain: A: PDB Molecule: putative beta-galactosidase; PDBTitle: crystal structure of putative beta-galactosidase from bacteroides2 fragilis
18	c6btmC_	 Alignment		9.3	16	PDB header: membrane protein Chain: C: PDB Molecule: alternative complex iii subunit c; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
19	c4zo9B_	 Alignment		9.2	14	PDB header: hydrolase Chain: B: PDB Molecule: lin1840 protein; PDBTitle: crystal structure of mutant (d270a) beta-glucosidase from listeria2 innocua in complex with laminaribiose
20	c5ow3C_	 Alignment		8.7	13	PDB header: membrane protein Chain: C: PDB Molecule: protein hapless 2; PDBTitle: crystal structure of a c-terminally truncated trimeric ectodomain of2 the arabidopsis thaliana gamete fusion protein hap2
21	d3bwga2	 Alignment	not modelled	8.5	19	Fold: Chorismate lyase-like Superfamily: Chorismate lyase-like Family: UTRA domain
22	c6mitC_	 Alignment	not modelled	8.2	20	PDB header: lipid transport Chain: C: PDB Molecule: lipopolysaccharide export system protein lptc; PDBTitle: lptbfgc from enterobacter cloacae
23	c5yotB_	 Alignment	not modelled	8.1	19	PDB header: hydrolase Chain: B: PDB Molecule: isoprimeverose-producing enzyme; PDBTitle: isoprimeverose-producing enzyme from aspergillus oryzae in complex2 with isoprimeverose
24	d2apob1	 Alignment	not modelled	8.1	22	Fold: Rubredoxin-like Superfamily: Nop10-like SnoRNP Family: Nucleolar RNA-binding protein Nop10-like
25	c5z62N_	 Alignment	not modelled	8.1	6	PDB header: electron transport Chain: N: PDB Molecule: cytochrome c oxidase subunit ndufa4; PDBTitle: structure of human cytochrome c oxidase
26	c4i3gB_	 Alignment	not modelled	7.7	22	PDB header: hydrolase Chain: B: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure of desr, a beta-glucosidase from streptomyces2 venezuelae in complex with d-glucose.
27	c2ideE_	 Alignment	not modelled	7.6	16	PDB header: biosynthetic protein Chain: E: PDB Molecule: molybdenum cofactor biosynthesis protein c; PDBTitle: crystal structure of the molybdenum cofactor biosynthesis protein c2 (ttha1789) from thermus thermophilus hb8
28	d2gkea2	 Alignment	not modelled	7.4	11	Fold: Diaminopimelate epimerase-like Superfamily: Diaminopimelate epimerase-like Family: Diaminopimelate epimerase

29	c6hu9e_	 Alignment	not modelled	7.4	7	PDB header: oxidoreductase/electron transport Chain: E: PDB Molecule: cytochrome b-c1 complex subunit rieske, mitochondrial; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
30	c3butA_	 Alignment	not modelled	7.1	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein af_0446; PDBTitle: crystal structure of protein af_0446 from archaeoglobus fulgidus
31	c4d0jD_	 Alignment	not modelled	7.0	15	PDB header: hydrolase Chain: D: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure of glycoside hydrolase family 3 beta-2 glucosidase cel3a from the moderately thermophilic fungus3 rasamsonia emersonii
32	c2ohdB_	 Alignment	not modelled	7.0	24	PDB header: biosynthetic protein Chain: B: PDB Molecule: probable molybdenum cofactor biosynthesis protein c; PDBTitle: crystal structure of hypothetical molybdenum cofactor biosynthesis2 protein c from sulfolobus tokodaii
33	d2e74g1	 Alignment	not modelled	6.8	20	Fold: Single transmembrane helix Superfamily: PetG subunit of the cytochrome b6f complex Family: PetG subunit of the cytochrome b6f complex
34	c2eknC_	 Alignment	not modelled	6.7	24	PDB header: biosynthetic protein Chain: C: PDB Molecule: probable molybdenum cofactor biosynthesis protein c; PDBTitle: structure of ph1811 protein from pyrococcus horikoshii
35	c3g3oA_	 Alignment	not modelled	6.3	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: vacuolar transporter chaperone 2; PDBTitle: crystal structure of the cytoplasmic tunnel domain in yeast2 vtc2p
36	d3ddva1	 Alignment	not modelled	6.3	13	Fold: Chorismate lyase-like Superfamily: Chorismate lyase-like Family: UTRA domain
37	d1gr0a1	 Alignment	not modelled	6.1	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
38	c5cpgA_	 Alignment	not modelled	5.9	18	PDB header: lyase Chain: A: PDB Molecule: (r)-specific enoyl-coa hydratase; PDBTitle: r-hydratase phaj1 from pseudomonas aeruginosa in the unliganded form
39	c3lheA_	 Alignment	not modelled	5.8	22	PDB header: transcription regulator Chain: A: PDB Molecule: gntr family transcriptional regulator; PDBTitle: the crystal structure of the c-terminal domain of a gntr2 family transcriptional regulator from bacillus anthracis3 str. sterne
40	d2oeza1	 Alignment	not modelled	5.7	25	Fold: YacF-like Superfamily: YacF-like Family: YacF-like
41	d2ey4e1	 Alignment	not modelled	5.6	35	Fold: Rubredoxin-like Superfamily: Nop10-like SnoRNP Family: Nucleolar RNA-binding protein Nop10-like
42	c4bq3A_	 Alignment	not modelled	5.5	15	PDB header: hydrolase Chain: A: PDB Molecule: b-agarase; PDBTitle: structural analysis of an exo-beta-agarase
43	c5tf0B_	 Alignment	not modelled	5.5	16	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase family 3 n-terminal domain protein; PDBTitle: crystal structure of glycosyl hydrolase family 3 n-terminal domain2 protein from bacteroides intestinalis
44	c6cfwG_	 Alignment	not modelled	5.5	36	PDB header: membrane protein Chain: G: PDB Molecule: monovalent cation/h+ antiporter subunit c; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
45	c1zzaA_	 Alignment	not modelled	5.4	32	PDB header: membrane protein Chain: A: PDB Molecule: stannin; PDBTitle: solution nmr structure of the membrane protein stannin
46	c2m6oA_	 Alignment	not modelled	5.3	19	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the actinobacterial transcription factor rbpA binds to the principal2 sigma subunit of rna polymerase
47	c5jp0A_	 Alignment	not modelled	5.3	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase bogh3b; PDBTitle: bacteroides ovatus xyloglucan pul gh3b with bound glucose
48	c6elhA_	 Alignment	not modelled	5.2	11	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric-oxide reductase; PDBTitle: low resolution structure of neisseria meningitidis qnor
49	c5dkoA_	 Alignment	not modelled	5.2	25	PDB header: replication Chain: A: PDB Molecule: cell division protein zapd; PDBTitle: the structure of escherichia coli zapd
50	c2r39A_	 Alignment	not modelled	5.2	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: fixg-related protein; PDBTitle: crystal structure of fixg-related protein from vibrio parahaemolyticus