











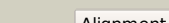
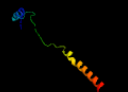

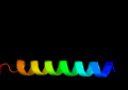



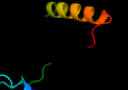

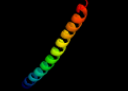

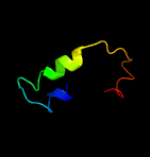

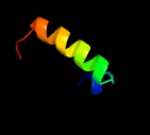


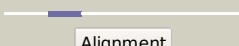

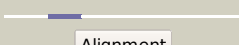
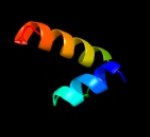
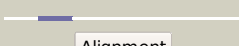

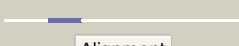
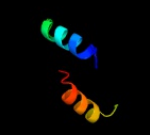

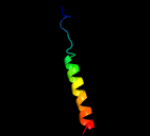

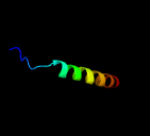
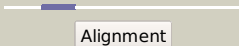


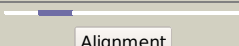
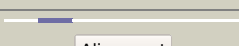
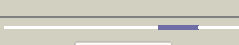
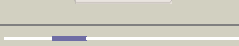
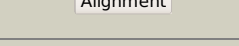
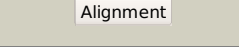


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3921c_(-)_4409146_4410246
Date	Sat Aug 10 22:05:11 BST 2019
Unique Job ID	0e879177a625abef

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3wvfA_	 Alignment		100.0	30	PDB header: chaperone Chain: A: PDB Molecule: membrane protein insertase yidc; PDBTitle: crystal structure of yidc from escherichia coli
2	c3wo6A_	 Alignment		100.0	31	PDB header: membrane protein Chain: A: PDB Molecule: membrane protein insertase yidc 2; PDBTitle: crystal structure of yidc from bacillus halodurans (form i)
3	c5y83A_	 Alignment		100.0	28	PDB header: transport protein Chain: A: PDB Molecule: membrane protein insertase yidc; PDBTitle: crystal structure of yidc from thermotoga maritima
4	c4utqA_	 Alignment		100.0	31	PDB header: protein transport Chain: A: PDB Molecule: membrane protein insertase yidc; PDBTitle: a structural model of the active ribosome-bound membrane protein2 insertase yidc
5	c6n3qD_	 Alignment		45.2	21	PDB header: transport protein Chain: D: PDB Molecule: protein translocation protein sec63; PDBTitle: cryo-em structure of the yeast sec complex
6	d1v54d_	 Alignment		43.5	17	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit IV Family: Mitochondrial cytochrome c oxidase subunit IV
7	c2y69Q_	 Alignment		42.8	17	PDB header: electron transport Chain: Q: PDB Molecule: cytochrome c oxidase subunit 4 isoform 1; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular oxygen
8	c3r45C_	 Alignment		36.7	28	PDB header: nuclear protein Chain: C: PDB Molecule: holliday junction recognition protein; PDBTitle: structure of a cenp-a-histone h4 heterodimer in complex with chaperone2 hjurp
9	c2avuF_	 Alignment		26.2	26	PDB header: transcription activator Chain: F: PDB Molecule: flagellar transcriptional activator flhC; PDBTitle: structure of the escherichia coli flhdc complex, a2 prokaryotic heteromeric regulator of transcription
10	d2avue1	 Alignment		24.3	25	Fold: FlhC-like Superfamily: FlhC-like Family: FlhC-like
11	c5dayA_	 Alignment		22.2	9	PDB header: chaperone Chain: A: PDB Molecule: nap1-related protein 1; PDBTitle: the structure of nap1-related protein(nrp1) in arabidopsis

12	c6k1hF_			21.9	8	PDB header: protein transport Chain: F: PDB Molecule: pts system mannose-specific eiid component; PDBTitle: structure of membrane protein
13	d1ryka_			21.5	15	Fold: SAM domain-like Superfamily: Hypothetical protein Yjbj Family: Hypothetical protein Yjbj
14	c6iu8C_			19.3	19	PDB header: metal transport Chain: C: PDB Molecule: vit1; PDBTitle: crystal structure of cytoplasmic metal binding domain with cobalt ions
15	c2hyxA_			18.9	14	PDB header: unknown function Chain: A: PDB Molecule: protein dipz; PDBTitle: structure of the c-terminal domain of dipz from mycobacterium2 tuberculosis
16	c2do5A_			18.7	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: splicing factor 3b subunit 2; PDBTitle: solution structure of the sap domain of human splicing2 factor 3b subunit 2
17	c1p58C_			16.9	15	PDB header: virus Chain: C: PDB Molecule: major envelope protein e; PDBTitle: complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
18	c6gc1A_			16.7	14	PDB header: unknown function Chain: A: PDB Molecule: nhl repeat-containing protein 2; PDBTitle: crystal structure of trx-like and nhl repeat containing domains of2 human nhlrc2
19	c4l0nG_			14.4	27	PDB header: transferase Chain: G: PDB Molecule: serine/threonine-protein kinase 3; PDBTitle: crystal structure of stk3 (mst2) sarah domain
20	c2jo8B_			14.1	24	PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase 4; PDBTitle: solution structure of c-terminal domain of human mammalian2 sterile 20-like kinase 1 (mst1)
21	d2e50a1		not modelled	12.1	18	Fold: NAP-like Superfamily: NAP-like Family: NAP-like
22	d2ea9a1		not modelled	11.8	30	Fold: Profilin-like Superfamily: YeeU-like Family: YagB/YeeU/YfjZ-like
23	c2ymyB_		not modelled	11.5	41	PDB header: apoptosis Chain: B: PDB Molecule: ras association domain-containing protein 5; PDBTitle: structure of the murine nore1-sarah domain
24	d2h28a1		not modelled	11.4	20	Fold: Profilin-like Superfamily: YeeU-like Family: YagB/YeeU/YfjZ-like
25	d2inwa1		not modelled	10.5	20	Fold: Profilin-like Superfamily: YeeU-like Family: YagB/YeeU/YfjZ-like
26	c6a70B_		not modelled	10.5	14	PDB header: membrane protein Chain: B: PDB Molecule: polycystin-1; PDBTitle: structure of the human pkd1/pkd2 complex
27	c6onpA_		not modelled	10.1	7	PDB header: unknown function Chain: A: PDB Molecule: periplasmic binding protein xoxj; PDBTitle: crystal structure of periplasmic binding protein xoxj from2 methylobacterium extorquens am1
28	d1lvaa3		not modelled	9.9	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal fragment of elongation factor SelB
29	c2ncaA		not modelled	9.9	18	PDB header: chaperone Chain: A: PDB Molecule: hsp90 co-chaperone cdc37;

29	c2itcA_	Alignment	not modelled	9.5	10	PDBTitle: structural model for the n-terminal domain of human cdc37
30	c6iu3A_	Alignment	not modelled	9.6	14	PDB header: metal transport Chain: A; PDB Molecule: vit1; PDBTitle: crystal structure of iron transporter vit1 with zinc ions
31	d1ojra_	Alignment	not modelled	9.4	25	Fold: AraD/HMP-PK domain-like Superfamily: AraD/HMP-PK domain-like Family: AraD-like aldolase/epimerase
32	c5z10C_	Alignment	not modelled	9.2	10	PDB header: membrane protein Chain: C; PDB Molecule: piezo-type mechanosensitive ion channel component 1; PDBTitle: structure of the mechanosensitive piezo1 channel
33	c5sv6A_	Alignment	not modelled	9.1	14	PDB header: unknown function Chain: A; PDB Molecule: extracellular solute-binding protein, family 3; PDBTitle: crystal structure of mxaj from methlophaga aminisulfidivorans mpt
34	c2ayuA_	Alignment	not modelled	8.1	7	PDB header: chaperone Chain: A; PDB Molecule: nucleosome assembly protein; PDBTitle: the structure of nucleosome assembly protein suggests a mechanism for2 histone binding and shuttling
35	d2ayu1	Alignment	not modelled	8.1	7	Fold: NAP-like Superfamily: NAP-like Family: NAP-like
36	d2cp8a1	Alignment	not modelled	8.0	28	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
37	c2mbyA_	Alignment	not modelled	7.5	28	PDB header: rna binding protein Chain: A; PDB Molecule: ribosomal rna-processing protein 7; PDBTitle: nmr structure of rrp7 c-terminal domain
38	c6n2gC_	Alignment	not modelled	7.4	10	PDB header: chaperone Chain: C; PDB Molecule: nucleosome assembly protein; PDBTitle: crystal structure of caenorhabditis elegans nap1
39	c1ywwA_	Alignment	not modelled	7.3	26	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein pa4738; PDBTitle: nmr structure of p. aeruginosa protein pa4738: northeast2 structural genomics consortium target pap2
40	c4a1qB_	Alignment	not modelled	7.1	38	PDB header: viral protein Chain: B; PDB Molecule: orf e73; PDBTitle: solution structure of e73 protein from sulfolobus spindle-2 shaped virus ragged hills, a hyperthermophilic3 crenarchaeal virus from yellowstone national park
41	c4aaiB_	Alignment	not modelled	7.1	38	PDB header: viral protein Chain: B; PDB Molecule: orf e73; PDBTitle: thermostable protein from hyperthermophilic virus ssv-rh
42	c3emxB_	Alignment	not modelled	7.1	14	PDB header: oxidoreductase Chain: B; PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from aeropyrum pernix
43	c3fs3A_	Alignment	not modelled	6.9	12	PDB header: chaperone Chain: A; PDB Molecule: nucleosome assembly protein 1, putative; PDBTitle: crystal structure of malaria parasite nucleosome assembly protein2 (nap)
44	c2kuaA_	Alignment	not modelled	6.8	23	PDB header: apoptosis Chain: A; PDB Molecule: bcl-2-like protein 10; PDBTitle: solution structure of a divergent bcl-2 protein
45	c3hfdA_	Alignment	not modelled	6.5	12	PDB header: chaperone, protein transport Chain: A; PDB Molecule: nucleosome assembly protein 1; PDBTitle: nucleosome assembly protein 1 from plasmodium knowlesi
46	c6hl2C_	Alignment	not modelled	6.4	25	PDB header: electron transport Chain: C; PDB Molecule: nadh-quinone oxidoreductase subunit e; PDBTitle: wild-type nuoef from aquifex aeolicus - oxidized form
47	c2kmuA_	Alignment	not modelled	6.3	16	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent dna helicase q4; PDBTitle: recq14 amino-terminal domain
48	c2k1aA_	Alignment	not modelled	6.3	12	PDB header: cell adhesion Chain: A; PDB Molecule: integrin alpha-iiB; PDBTitle: bicelle-embedded integrin alpha(iiB) transmembrane segment
49	c6nd1A_	Alignment	not modelled	6.1	23	PDB header: protein transport Chain: A; PDB Molecule: protein translocation protein sec63; PDBTitle: cryoem structure of the sec complex from yeast
50	c2kncA_	Alignment	not modelled	6.0	11	PDB header: cell adhesion Chain: A; PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alfaIiB-beta3 transmembrane-cytoplasmic2 heterocomplex
51	c3gyvA_	Alignment	not modelled	6.0	12	PDB header: chaperone Chain: A; PDB Molecule: nucleosome assembly protein 1, putative; PDBTitle: crystal structure of nucleosome assembly protein from plasmodium2 falciparum
52	c2qf9B_	Alignment	not modelled	5.8	3	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: putative secreted protein; PDBTitle: crystal structure of putative secreted protein duf305 from2 streptomyces coelicolor
53	c2rmrA_	Alignment	not modelled	5.8	12	PDB header: transcription Chain: A; PDB Molecule: paired amphipathic helix protein sin3a; PDBTitle: solution structure of msin3a pah1 domain
54	c3tijA_	Alignment	not modelled	5.7	17	PDB header: membrane protein Chain: A; PDB Molecule: nupc family protein; PDBTitle: crystal structure of a concentrative nucleoside transporter from2 vibrio cholerae
55	c5ireA_	Alignment	not modelled	5.6	16	PDB header: virus Chain: A; PDB Molecule: e protein; PDBTitle: the cryo-em structure of zika virus

56	d2axtk1	Alignment	not modelled	5.6	18	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein K, PsbK Family: PsbK-like
57	c5hvdA	Alignment	not modelled	5.6	10	PDB header: transport protein Chain: A: PDB Molecule: ion transport protein; PDBTitle: full length open-form sodium channel navms i218c
58	c5b16C	Alignment	not modelled	5.6	33	PDB header: hydrolase Chain: C: PDB Molecule: microprocessor complex subunit dgcr8; PDBTitle: x-ray structure of drosha in complex with the c-terminal tail of2 dgcr8.
59	c1vw4a	Alignment	not modelled	5.5	20	PDB header: ribosome Chain: A: PDB Molecule: PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
60	c3bt5A	Alignment	not modelled	5.4	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein duf305; PDBTitle: crystal structure of duf305 fragment from deinococcus radiodurans
61	c4b4sA	Alignment	not modelled	5.4	22	PDB header: apoptosis Chain: A: PDB Molecule: bcl-2-like protein 10; PDBTitle: crystal structure of a pro-survival bcl-2:bim bh3 complex
62	c2okqB	Alignment	not modelled	5.4	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein ybaa; PDBTitle: crystal structure of unknown conserved ybaa protein from shigella2 flexneri
63	c1z65A	Alignment	not modelled	5.4	7	PDB header: unknown function Chain: A: PDB Molecule: prion-like protein doppel; PDBTitle: mouse doppel 1-30 peptide
64	c5b16B	Alignment	not modelled	5.3	33	PDB header: hydrolase Chain: B: PDB Molecule: microprocessor complex subunit dgcr8; PDBTitle: x-ray structure of drosha in complex with the c-terminal tail of2 dgcr8.
65	c4pvzC	Alignment	not modelled	5.3	13	PDB header: protein binding Chain: C: PDB Molecule: inner nuclear membrane protein heh2; PDBTitle: structure of yeast importin a bound to the membrane protein nuclear2 localization signal sequence of inm protein heh2
66	c2lckA	Alignment	not modelled	5.2	14	PDB header: transport protein Chain: A: PDB Molecule: mitochondrial uncoupling protein 2; PDBTitle: structure of the mitochondrial uncoupling protein 2 determined by nmr2 molecular fragment replacement
67	c2jv5A	Alignment	not modelled	5.2	21	PDB header: protein binding Chain: A: PDB Molecule: reticulon-4; PDBTitle: nogo54