







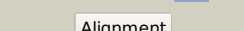

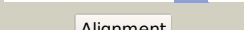
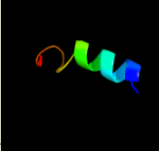
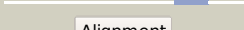
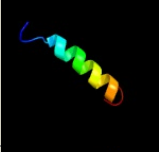


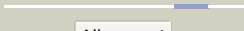
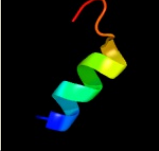

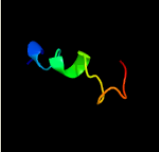
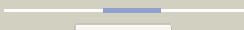
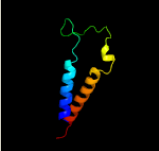
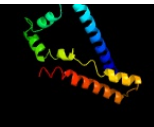





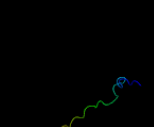




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3005c_(-)_3363703_3364542
Date	Thu Aug 8 16:20:17 BST 2019
Unique Job ID	e7a01146d476c4bd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2bs2c1	 Alignment		55.0	13	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Fumarate reductase respiratory complex cytochrome b subunit, FrdC
2	c5gjqZ_	 Alignment		47.9	16	PDB header: hydrolase Chain: Z: PDB Molecule: 26s proteasome non-atpase regulatory subunit 2; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
3	c6hwhB_	 Alignment		34.4	15	PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
4	c5khrA_	 Alignment		34.3	33	PDB header: cell cycle Chain: A: PDB Molecule: anaphase-promoting complex subunit 1; PDBTitle: model of human anaphase-promoting complex/cyclosome complex (apc152 deletion mutant) in complex with the e2 ube2c/ubch10 poised for3 ubiquitin ligation to substrate (apc/c-cdc20-substrate-ube2c)
5	c5a31A_	 Alignment		28.3	37	PDB header: cell cycle Chain: A: PDB Molecule: anaphase-promoting complex subunit 1; PDBTitle: structure of the human apc-cdh1-hsl1-ubch10 complex.
6	c4ui9A_	 Alignment		27.5	37	PDB header: cell cycle Chain: A: PDB Molecule: anaphase-promoting complex subunit 1; PDBTitle: atomic structure of the human anaphase-promoting complex
7	c2lzsE_	 Alignment		26.7	21	PDB header: protein transport Chain: E: PDB Molecule: sec-independent protein translocase protein tata; PDBTitle: tata oligomer
8	c5xj6A_	 Alignment		26.4	19	PDB header: transferase Chain: A: PDB Molecule: glycerol-3-phosphate acyltransferase; PDBTitle: crystal structure of pscy (ygih), an integral membrane glycerol 3-2 phosphate acyltransferase - the glycerol 3-phosphate form
9	c2mi2A_	 Alignment		25.0	29	PDB header: transport protein Chain: A: PDB Molecule: sec-independent protein translocase protein tatb; PDBTitle: solution structure of the e. coli tatb protein in dpc micelles
10	c5khuA_	 Alignment		24.7	37	PDB header: cell cycle Chain: A: PDB Molecule: anaphase-promoting complex subunit 1; PDBTitle: model of human anaphase-promoting complex/cyclosome (apc15 deletion2 mutant), in complex with the mitotic checkpoint complex (apc/c-cdc20-3 mcc) based on cryo em data at 4.8 angstrom resolution
11	c5awwG_	 Alignment		23.1	19	PDB header: protein transport/immune system Chain: G: PDB Molecule: putative preprotein translocase, secg subunit; PDBTitle: precise resting state of thermus thermophilus secyeg

12	c3vrBG_	Alignment		21.2	18	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: G: PDB Molecule: cytochrome b-large subunit; PDBTitle: mitochondrial rhoquinol-fumarate reductase from the parasitic2 nematode ascaris suum with the specific inhibitor flutolanil and3 substrate fumarate
13	c5l9uA_	Alignment		20.9	35	PDB header: signaling protein Chain: A: PDB Molecule: anaphase-promoting complex subunit 1; PDBTitle: model of human anaphase-promoting complex/cyclosome (apc/c-cdh1) with2 a cross linked ubiquitin variant-substrate-ube2c (ubch10) complex3 representing key features of multiubiquitination
14	c4ezdB_	Alignment		20.2	20	PDB header: transport protein Chain: B: PDB Molecule: urea transporter 1; PDBTitle: crystal structure of the ut-b urea transporter from bos taurus bound2 to selenourea
15	c6iu3A_	Alignment		19.7	16	PDB header: metal transport Chain: A: PDB Molecule: vit1; PDBTitle: crystal structure of iron transporter vit1 with zinc ions
16	c5xmjG_	Alignment		19.2	13	PDB header: electron transport Chain: G: PDB Molecule: fumarate reductase respiratory complex; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
17	c2lcnA_	Alignment		19.1	31	PDB header: membrane protein Chain: A: PDB Molecule: walp19-p10 peptide; PDBTitle: 1h and 15n assignments of walp19-p10 peptide in sds micelles
18	d1jvra_	Alignment		15.3	21	Fold: Retroviral matrix proteins Superfamily: Retroviral matrix proteins Family: HTLV-II matrix protein
19	c2lcoA_	Alignment		14.7	31	PDB header: membrane protein Chain: A: PDB Molecule: walp19-p8 peptide; PDBTitle: 1h and 15n assignments of walp19-p8 peptide in sds micelles
20	c2l16A_	Alignment		12.7	17	PDB header: protein transport Chain: A: PDB Molecule: sec-independent protein translocase protein tatad; PDBTitle: solution structure of bacillus subtilis tatad protein in dpc micelles
21	c2k9yB_	Alignment	not modelled	12.3	29	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
22	c2k9yA_	Alignment	not modelled	11.5	29	PDB header: transferase Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
23	c3k3gA_	Alignment	not modelled	11.2	24	PDB header: transport protein Chain: A: PDB Molecule: urea transporter; PDBTitle: crystal structure of the urea transporter from desulfovibrio vulgaris2 bound to 1,3-dimethylurea
24	c5sxpF_	Alignment	not modelled	7.7	47	PDB header: signaling protein/ligase Chain: F: PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: structural basis for the interaction between itch prr and beta-pix
25	c6ffvA_	Alignment	not modelled	7.3	11	PDB header: transport protein Chain: A: PDB Molecule: btum; PDBTitle: the crystal structure of btum cobalamin transporter
26	c5l6nI_	Alignment	not modelled	7.2	27	PDB header: hydrolase Chain: I: PDB Molecule: thrombin inhibitor madanin 1; PDBTitle: disulfated madanin-thrombin complex
27	c5ldwc_	Alignment	not modelled	6.9	11	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 3, PDBTitle: structure of mammalian respiratory complex i, class1
28	c5lc5c_	Alignment	not modelled	6.9	11	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 3, PDBTitle: structure of mammalian respiratory complex i, class2
29	c2miiA_	Alignment	not modelled	6.9	12	PDB header: protein binding Chain: A: PDB Molecule: penicillin-binding protein activator lpob; PDBTitle: nmr structure of e. coli lpob

30	d3boea1	Alignment	not modelled	6.9	33	Fold: CdCA1 repeat-like Superfamily: CdCA1 repeat-like Family: CdCA1 repeat-like
31	d1xm5a_	Alignment	not modelled	6.3	36	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Predicted metal-dependent hydrolase
32	c3rkoK_	Alignment	not modelled	6.2	23	PDB header: oxidoreductase Chain: K: PDB Molecule: nadh-quinone oxidoreductase subunit k; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
33	c5sxpG_	Alignment	not modelled	6.2	44	PDB header: signaling protein/ligase Chain: G: PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: structural basis for the interaction between itch prr and beta-pix
34	c2cpbA_	Alignment	not modelled	6.0	11	PDB header: viral protein Chain: A: PDB Molecule: m13 major coat protein; PDBTitle: solution nmr structures of the major coat protein of2 filamentous bacteriophage m13 solubilized in3 dodecylphosphocholine micelles, 25 lowest energy structures
35	c3ipkA_	Alignment	not modelled	5.8	7	PDB header: cell adhesion Chain: A: PDB Molecule: agi/ii; PDBTitle: crystal structure of a3vp1 of agi/ii of streptococcus mutans
36	c1xaxA_	Alignment	not modelled	5.8	36	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0054 protein hi0004; PDBTitle: nmr structure of hi0004, a putative essential gene product2 from haemophilus influenzae
37	c4heaK_	Alignment	not modelled	5.5	18	PDB header: oxidoreductase Chain: K: PDB Molecule: nadh-quinone oxidoreductase subunit 11; PDBTitle: crystal structure of the entire respiratory complex i from thermus2 thermophilus
38	c5azcA_	Alignment	not modelled	5.4	16	PDB header: transferase Chain: A: PDB Molecule: prolipoprotein diacylglycerol transferase; PDBTitle: crystal structure of escherichia coli lgt in complex with2 phosphatidylglycerol
39	c4gvsA_	Alignment	not modelled	5.4	22	PDB header: hydrolase Chain: A: PDB Molecule: methenyltetrahydromethanopterin cyclohydrolase; PDBTitle: x-ray structure of the archaeoglobus fulgidus methenyl-2 tetrahydromethanopterin cyclohydrolase in complex with n5-formyl-3 tetrahydromethanopterin
40	c4cdiC_	Alignment	not modelled	5.3	23	PDB header: membrane protein Chain: C: PDB Molecule: predicted protein; PDBTitle: crystal structure of acrb-acrz complex
41	c4cz8A_	Alignment	not modelled	5.3	6	PDB header: membrane protein Chain: A: PDB Molecule: na+/h+ antiporter, putative; PDBTitle: structure of the sodium proton antiporter panhap from2 pyrococcus abyssii at ph 8.
42	c5z62N_	Alignment	not modelled	5.3	29	PDB header: electron transport Chain: N: PDB Molecule: cytochrome c oxidase subunit ndufa4; PDBTitle: structure of human cytochrome c oxidase
43	c6cfwl_	Alignment	not modelled	5.1	27	PDB header: membrane protein Chain: I: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase