


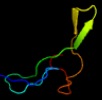
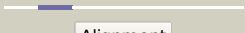

















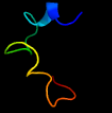
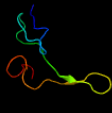

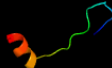
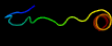






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0610c_(-)_704755_705912
Date	Fri Jul 26 01:50:17 BST 2019
Unique Job ID	1811181430128922

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6d0tA_	 Alignment		25.8	100	PDB header: de novo protein Chain: A: PDB Molecule: bb1; PDBTitle: de novo design of a fluorescence-activating beta barrel - bb1
2	c2e76D_	 Alignment		18.3	30	PDB header: photosynthesis Chain: D: PDB Molecule: cytochrome b6-f complex iron-sulfur subunit; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
3	d1ysrA1	 Alignment		18.2	25	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
4	c1iqpF_	 Alignment		17.3	30	PDB header: replication Chain: F: PDB Molecule: rfdc; PDBTitle: crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
5	c5muul_	 Alignment		16.8	67	PDB header: virus Chain: I: PDB Molecule: major outer capsid protein; PDBTitle: dsrna bacteriophage phi6 nucleocapsid
6	d1e5qa2	 Alignment		15.8	26	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Homoserine dehydrogenase-like
7	c2jrtA_	 Alignment		14.8	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr solution structure of the protein coded by gene2 rhos4_12090 of rhodobacter sphaeroides. northeast3 structural genomics target rhr5
8	d2oa4a1	 Alignment		14.6	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: SPO1678-like
9	c4lqdH_	 Alignment		12.7	44	PDB header: signaling protein Chain: H: PDB Molecule: ras association domain family member 5, rassf5; PDBTitle: structural basis for autoactivation of human mst2 kinase and its2 regulation by rassf5
10	c2p5dA_	 Alignment		12.1	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0310 protein mjec136; PDBTitle: crystal structure of mjec136 from methanocaldococcus2 jannaschii dsm 2661
11	d1jsxA_	 Alignment		12.1	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glucose-inhibited division protein B (GidB)

12	d2hd9a1	Alignment		12.1	22	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
13	d2e74d1	Alignment		10.6	30	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
14	c2ymyB_	Alignment		10.0	50	PDB header: apoptosis Chain: B; PDB Molecule: ras association domain-containing protein 5; PDBTitle: structure of the murine nore1-sarah domain
15	c5cwsF_	Alignment		9.7	35	PDB header: protein transport Chain: F; PDB Molecule: nucleoporin nic96; PDBTitle: crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
16	c5cwsL_	Alignment		9.7	35	PDB header: protein transport Chain: L; PDB Molecule: nucleoporin nic96; PDBTitle: crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
17	c2v3cC_	Alignment		9.5	25	PDB header: signaling protein Chain: C; PDB Molecule: signal recognition 54 kda protein; PDBTitle: crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
18	d1vh1b_	Alignment		8.8	50	Fold: Ferredoxin-like Superfamily: Viral DNA-binding domain Family: Viral DNA-binding domain
19	c5fnoB_	Alignment		8.6	30	PDB header: oxidoreductase Chain: B; PDB Molecule: manganese lipoxigenase; PDBTitle: manganese lipoxigenase
20	c2px0D_	Alignment		8.5	26	PDB header: biosynthetic protein Chain: D; PDB Molecule: flagellar biosynthesis protein flhf; PDBTitle: crystal structure of flhf complexed with gmpnp/mg(2+)
21	d1iqa2	Alignment	not modelled	8.2	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
22	d1txka2	Alignment	not modelled	8.0	36	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: MdoG-like
23	c2la3A_	Alignment	not modelled	8.0	23	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: the nmr structure of the protein np_344798.1 reveals a cca-adding2 enzyme head domain
24	d3dhpa1	Alignment	not modelled	7.8	31	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
25	d1hx0a1	Alignment	not modelled	7.6	38	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
26	d1g94a1	Alignment	not modelled	7.4	38	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
27	c1sr9A_	Alignment	not modelled	7.2	28	PDB header: transferase Chain: A; PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of leua from mycobacterium tuberculosis
28	d1b3ta_	Alignment	not modelled	7.1	50	Fold: Ferredoxin-like Superfamily: Viral DNA-binding domain Family: Viral DNA-binding domain
						PDB header: dna binding protein/protein binding Chain: B; PDB Molecule: anti-sigma-k factor rska;

29	c3vdoB_	Alignment	not modelled	7.0	33	PDBTitle: structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rskA from mycobacterium3 tuberculosis
30	c1txkA_	Alignment	not modelled	7.0	36	PDB header: biosynthetic protein Chain: A: PDB Molecule: glucans biosynthesis protein g; PDBTitle: crystal structure of escherichia coli oppg
31	c3vuoa_	Alignment	not modelled	6.9	64	PDB header: toxin Chain: A: PDB Molecule: ntnha; PDBTitle: crystal structure of nontoxic nonhemagglutinin subcomponent (ntnha)2 from clostridium botulinum serotype d strain 4947
32	c2ovcA_	Alignment	not modelled	6.9	40	PDB header: transport protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily kqt member 4; PDBTitle: crystal structure of a coiled-coil tetramerization domain from kv7.42 channels
33	c2rn5B_	Alignment	not modelled	6.5	57	PDB header: hormone Chain: B: PDB Molecule: insulin; PDBTitle: humal insulin mutant b31lys-b32arg
34	c4qccA_	Alignment	not modelled	6.2	21	PDB header: structural protein, lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase, peptidyl- PDBTitle: structure of a cube-shaped, highly porous protein cage designed by2 fusing symmetric oligomeric domains
35	d1kzyc2	Alignment	not modelled	6.2	36	Fold: BRCT domain Superfamily: BRCT domain Family: 53BP1
36	d1jaea1	Alignment	not modelled	6.1	54	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
37	c3vcmP_	Alignment	not modelled	6.0	44	PDB header: hydrolase Chain: P: PDB Molecule: prorenin; PDBTitle: crystal structure of human prorenin
38	c1hisB_	Alignment	not modelled	5.9	78	PDB header: hormone Chain: B: PDB Molecule: insulin; PDBTitle: structure and dynamics of des-pentapeptide-insulin in2 solution: the molten-globule hypothesis.
39	c5wuqD_	Alignment	not modelled	5.9	14	PDB header: metal binding protein Chain: D: PDB Molecule: anti-sigma-w factor rsiw; PDBTitle: crystal structure of sigw in complex with its anti-sigma rsiw, a zinc2 binding form
40	c4aupA_	Alignment	not modelled	5.8	44	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase a2 group xiii; PDBTitle: tuber borchii phospholipase a2
41	c5wknD_	Alignment	not modelled	5.6	86	PDB header: viral protein Chain: D: PDB Molecule: phosphoprotein; PDBTitle: crystal structure of the parainfluenza virus 5 nucleoprotein-2 phosphoprotein complex
42	c4lqdF_	Alignment	not modelled	5.3	44	PDB header: signaling protein Chain: F: PDB Molecule: ras association domain family member 5, rassf5; PDBTitle: structural basis for autoactivation of human mst2 kinase and its2 regulation by rassf5
43	c2j289_	Alignment	not modelled	5.3	25	PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
44	c5vbaA_	Alignment	not modelled	5.3	26	PDB header: chaperone, hydrolase Chain: A: PDB Molecule: lysozyme, esx-1 secretion-associated protein espg1 chimera; PDBTitle: structure of espg1 chaperone from the type vii (esx-1) secretion2 system determined with the assistance of n-terminal t4 lysozyme3 fusion
45	c5y88S_	Alignment	not modelled	5.2	83	PDB header: splicing Chain: S: PDB Molecule: pre-mrna-processing factor 17; PDBTitle: cryo-em structure of the intron-lariat spliceosome ready for2 disassembly from s.cerevisiae at 3.5 angstrom
46	c1z65A_	Alignment	not modelled	5.1	71	PDB header: unknown function Chain: A: PDB Molecule: prion-like protein doppel; PDBTitle: mouse doppel 1-30 peptide