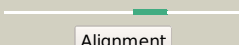
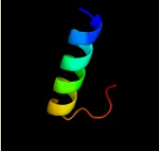
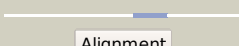

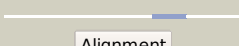

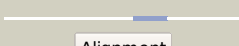


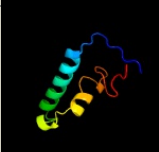



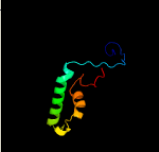










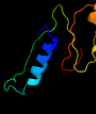








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0964c_(-)_1076200_1076682
Date	Wed Jul 31 22:05:02 BST 2019
Unique Job ID	bda083b278860d4a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3solA_	 Alignment		42.3	41	PDB header: protein transport Chain: A: PDB Molecule: type ii secretion pathway related protein; PDBTitle: crystal structure of the type 2 secretion system pilotin gsp5
2	c3utkA_	 Alignment		26.7	41	PDB header: protein transport Chain: A: PDB Molecule: lipoprotein outs; PDBTitle: structure of the pilotin of the type ii secretion system
3	d1nera_	 Alignment		22.9	50	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
4	c4a56A_	 Alignment		21.1	23	PDB header: protein transport Chain: A: PDB Molecule: pullulanase secretion protein pul5; PDBTitle: crystal structure of the type 2 secretion system pilotin2 from klebsiella oxytoca
5	c5hxpA_	 Alignment		16.0	15	PDB header: transferase Chain: A: PDB Molecule: (2z,6z)-farnesyl diphosphate synthase, chloroplastic; PDBTitle: crystal structure of z,z-farnesyl diphosphate synthase (d71m, e75a and2 h103y mutants) complexed with ipp
6	d1uxya2	 Alignment		13.5	20	Fold: Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain Superfamily: Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain Family: Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
7	c6jcnB_	 Alignment		13.0	16	PDB header: transferase Chain: B: PDB Molecule: dehydrodolichyl diphosphate synthase complex subunit nus1; PDBTitle: yeast dehydrodolichyl diphosphate synthase complex subunit nus1
8	c2knpA_	 Alignment		10.6	55	PDB header: unknown function Chain: A: PDB Molecule: mcocc-1; PDBTitle: isolation and characterization of peptides from momordica2 cochinchinensis seeds.
9	c3nvnA_	 Alignment		10.5	26	PDB header: viral protein/signaling protein Chain: A: PDB Molecule: evm139; PDBTitle: molecular mechanism of guidance cue recognition
10	c1plpA_	 Alignment		10.5	47	PDB header: membrane protein Chain: A: PDB Molecule: phospholamban; PDBTitle: solution structure of the cytoplasmic domain of2 phospholamban
11	d2bmta_	 Alignment		8.5	71	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins

12	c4xa1A_	Alignment		8.4	41	PDB header: viral protein Chain: A: PDB Molecule: tegument protein vp22; PDBTitle: crystal structure of the conserved core domain of vp22 from hsv-1
13	c2m0dA_	Alignment		7.4	57	PDB header: transcription Chain: A: PDB Molecule: zinc finger and btb domain-containing protein 17; PDBTitle: solution structure of miz-1 zinc finger 5
14	d2c8ma1	Alignment		7.3	13	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: LpIA-like
15	d1hska2	Alignment		7.2	13	Fold: Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain Superfamily: Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain Family: Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
16	c3vh5D_	Alignment		6.9	62	PDB header: dna binding protein Chain: D: PDB Molecule: cenp-x; PDBTitle: crystal structure of the chicken cenp-t histone fold/cenp-w/cenp-2 s/cenp-x heterotetrameric complex, crystal form i
17	c5hc7A_	Alignment		6.3	32	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: prenyltransferase for protein; PDBTitle: crystal structure of lavenderyl diphosphate synthase from lavandula x2 intermedia in complex with s-thiolisopentenyl diphosphate
18	c5z1vA_	Alignment		6.1	67	PDB header: antibiotic Chain: A: PDB Molecule: mbjamp1 peptide; PDBTitle: mbjamp1 structure
19	c4v1av_	Alignment		5.9	56	PDB header: ribosome Chain: V: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
20	c4pytA_	Alignment		5.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvylglucosamine reductase; PDBTitle: crystal structure of a murB family ep-udp-n-acetylglucosamine2 reductase
21	c3s0xB_	Alignment	not modelled	5.4	36	PDB header: hydrolase Chain: B: PDB Molecule: peptidase a24b, flak domain protein; PDBTitle: the crystal structure of gxgd membrane protease flak
22	c4vj0C_	Alignment	not modelled	5.2	67	PDB header: transcription Chain: C: PDB Molecule: doublesex- and mab-3-related transcription factor 1; PDBTitle: crystal structure of the dm domain of human dmrt1 bound to 25mer2 target dna
23	d1deca_	Alignment	not modelled	5.1	67	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Leech antihemostatic proteins Family: Hirudin-like
24	c1decA_	Alignment	not modelled	5.1	67	PDB header: blood coagulation Chain: A: PDB Molecule: decorsin; PDBTitle: structure of the rgd protein decorsin: conserved motif and distinct2 function in leech proteins that affect blood clotting