



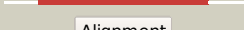

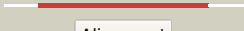




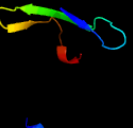



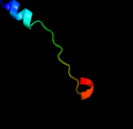
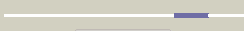




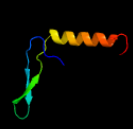

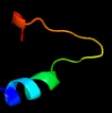
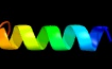

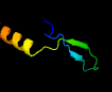
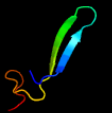

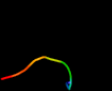
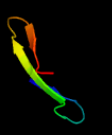


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3889c_(-)_4372978_4373808
Date	Sat Aug 10 22:05:07 BST 2019
Unique Job ID	a181f909f5ff29a8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4kxrC_	 Alignment		100.0	23	PDB header: protein transport Chain: C: PDB Molecule: espg5; PDBTitle: structure of the mycobacterium tuberculosis type vii secretion system2 chaperone espg5 in complex with pe25-ppe41 dimer
2	c4l4wB_	 Alignment		100.0	25	PDB header: protein transport Chain: B: PDB Molecule: espg3; PDBTitle: structure of espg3 chaperone from the type vii (esx-3) secretion2 system
3	c5vbaA_	 Alignment		100.0	27	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
4	c4w4iA_	 Alignment		100.0	23	PDB header: protein transport Chain: A: PDB Molecule: esx-3 secretion-associated protein espg3; PDBTitle: crystal structure of espg3 from the esx-3 type vii secretion system of2 m. tuberculosis
5	c4rcIB_	 Alignment		100.0	26	PDB header: chaperone Chain: B: PDB Molecule: espg3; PDBTitle: structure of espg3 chaperone from the type vii (esx-3) secretion2 system, space group p43212
6	c4rdkB_	 Alignment		24.3	19	PDB header: viral protein Chain: B: PDB Molecule: capsid; PDBTitle: crystal structure of norovirus boxer p domain in complex with lewis b2 tetrasaccharide
7	d1hynp_	 Alignment		14.1	19	Fold: Phoshotransferase/anion transport protein Superfamily: Phoshotransferase/anion transport protein Family: Anion transport protein, cytoplasmic domain
8	c1hynQ_	 Alignment		12.8	19	PDB header: membrane protein Chain: Q: PDB Molecule: band 3 anion transport protein; PDBTitle: crystal structure of the cytoplasmic domain of human erythrocyte band-2 3 protein
9	d1rk8C_	 Alignment		11.5	55	Fold: WW domain-like Superfamily: Pym (Within the bgcn gene intron protein, WIBG), N-terminal domain Family: Pym (Within the bgcn gene intron protein, WIBG), N-terminal domain
10	c1rk8C_	 Alignment		11.5	55	PDB header: translation Chain: C: PDB Molecule: within the bgcn gene intron protein; PDBTitle: structure of the cytosolic protein pym bound to the mago-2 y14 core of the exon junction complex
11	c4qyID_	 Alignment		9.7	19	PDB header: oxidoreductase Chain: D: PDB Molecule: aldehyde dehydrogenase; PDBTitle: structure of phenylacetaldehyde dehydrogenase from pseudomonas putida2 s12

12	c5iuuA_	Alignment		9.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase family protein; PDBTitle: crystal structure of indole-3-acetaldehyde dehydrogenase in apo form
13	d1mgta1	Alignment		7.2	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
14	c3zdlB_	Alignment		7.2	24	PDB header: cell adhesion Chain: B: PDB Molecule: amyloid beta a4 precursor protein-binding family b member PDBTitle: vinculin head (1-258) in complex with a riam fragment
15	d1g26a_	Alignment		6.7	63	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Granulin repeat Family: Granulin repeat
16	c3ed6B_	Alignment		6.3	23	PDB header: oxidoreductase Chain: B: PDB Molecule: betaine aldehyde dehydrogenase; PDBTitle: 1.7 angstrom resolution crystal structure of betaine aldehyde2 dehydrogenase (betb) from staphylococcus aureus
17	c1fwxB_	Alignment		6.2	6	PDB header: oxidoreductase Chain: B: PDB Molecule: nitrous oxide reductase; PDBTitle: crystal structure of nitrous oxide reductase from p. denitrificans
18	d1mo6a2	Alignment		6.2	43	Fold: Anti-LPS factor/recA domain Superfamily: RecA protein, C-terminal domain Family: RecA protein, C-terminal domain
19	d1u94a2	Alignment		6.0	86	Fold: Anti-LPS factor/recA domain Superfamily: RecA protein, C-terminal domain Family: RecA protein, C-terminal domain
20	c2zl5A_	Alignment		5.8	23	PDB header: viral protein Chain: A: PDB Molecule: 58 kd capsid protein; PDBTitle: atomic resolution structural characterization of2 recognition of histo-blood group antigen by norwalk virus
21	c5zcrB_	Alignment	not modelled	5.7	18	PDB header: hydrolase Chain: B: PDB Molecule: maltoooligosyl trehalose synthase; PDBTitle: dsm5389 glycosyltrehalose synthase
22	d1xp8a2	Alignment	not modelled	5.7	71	Fold: Anti-LPS factor/recA domain Superfamily: RecA protein, C-terminal domain Family: RecA protein, C-terminal domain
23	d1ubea2	Alignment	not modelled	5.4	43	Fold: Anti-LPS factor/recA domain Superfamily: RecA protein, C-terminal domain Family: RecA protein, C-terminal domain
24	d1kdga2	Alignment	not modelled	5.4	19	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: GMC oxidoreductases
25	c5fgoA_	Alignment	not modelled	5.4	9	PDB header: dna binding protein Chain: A: PDB Molecule: cg1507-pb, isoform b; PDBTitle: crystal structure of d. melanogaster pur-alpha repeat iii.
26	c3b4wA_	Alignment	not modelled	5.3	10	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of mycobacterium tuberculosis aldehyde dehydrogenase2 complexed with nad+
27	c3u5gK_	Alignment	not modelled	5.1	17	PDB header: ribosome Chain: K: PDB Molecule: 40s ribosomal protein s10-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome b