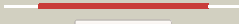


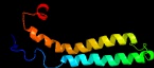
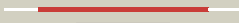




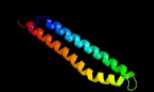

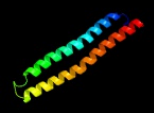

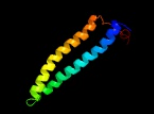











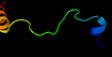


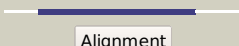



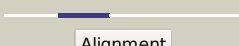

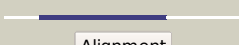


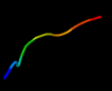




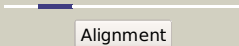
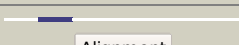




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3890c_(esxC)_4373904_4374191
 Date Sat Aug 10 22:05:07 BST 2019
 Unique Job ID 25947df0e6e54f20

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1wa8b1	 Alignment		98.7	14	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
2	c2kg7B_	 Alignment		97.4	25	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein esxh; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
3	c3gvmA_	 Alignment		97.3	16	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
4	c4lwsB_	 Alignment		96.8	19	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
5	c2vs0B_	 Alignment		94.7	13	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
6	c4iogD_	 Alignment		94.5	20	PDB header: unknown function Chain: D: PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
7	d1wa8a1	 Alignment		94.3	11	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
8	c3zbhC_	 Alignment		94.1	14	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
9	c4lwsA_	 Alignment		90.9	12	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
10	c5xugB_	 Alignment		34.8	26	PDB header: hydrolase Chain: B: PDB Molecule: endo-1,4-beta-mannanase; PDBTitle: complex structure(rmman134a-m5).
11	c5jtsA_	 Alignment		32.2	28	PDB header: hydrolase Chain: A: PDB Molecule: beta-1,4-mannanase; PDBTitle: structure of a beta-1,4-mannanase, ssg134.

12	d1gxma_	 Alignment		9.6	13	Fold: alpha/alpha toroid Superfamily: Family 10 polysaccharide lyase Family: Family 10 polysaccharide lyase
13	c5zjih_	 Alignment		8.9	33	PDB header: membrane protein Chain: H: PDB Molecule: photosystem i reaction center subunit vi, chloroplastic; PDBTitle: structure of photosystem i supercomplex with light-harvesting2 complexes i and ii
14	c3c4nB_	 Alignment		7.4	30	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein dr_0571; PDBTitle: crystal structure of dr_0571 protein from deinococcus radiodurans in2 complex with adp. northeast structural genomics consortium target3 drr125
15	c3q4hB_	 Alignment		7.3	25	PDB header: metal transport Chain: B: PDB Molecule: low molecular weight protein antigen 7; PDBTitle: crystal structure of the mycobacterium smegmatis esx9 complex2 (msmeg_0620-msmeg_0621)
16	c4awaA_	 Alignment		7.2	36	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: legumain; PDBTitle: crystal structure of active legumain in complex with yvad-cmk2 at ph 5.0
17	d1lp1a_	 Alignment		7.1	19	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
18	c3lraA_	 Alignment		7.1	25	PDB header: membrane protein Chain: A: PDB Molecule: disks large homolog 1, maguk p55 subfamily member 7, PDBTitle: structural basis for assembling a human tripartite complex dlg1-mpp7-2 mals3
19	c4f6oA_	 Alignment		6.3	50	PDB header: hydrolase Chain: A: PDB Molecule: metacaspase-1; PDBTitle: crystal structure of the yeast metacaspase yca1
20	c5h0iB_	 Alignment		6.1	36	PDB header: hydrolase Chain: B: PDB Molecule: asparaginyl endopeptidase; PDBTitle: name to be released when published
21	c6k4vA_	 Alignment	not modelled	6.1	60	PDB header: antibiotic Chain: A: PDB Molecule: smart chimeric peptide g6; PDBTitle: the solution structure of the smart chimeric peptide g6
22	c5zbiB_	 Alignment	not modelled	5.6	27	PDB header: plant protein Chain: B: PDB Molecule: peptide asparaginyl ligase; PDBTitle: crystal structure of asparaginyl endopeptidases from viola canadensis
23	c1ambA_	 Alignment	not modelled	5.6	86	PDB header: proteinase inhibitor(trypsin) Chain: A: PDB Molecule: amyloid beta-peptide; PDBTitle: solution structure of residues 1-28 of the amyloid beta-2 peptide
24	c1am1A_	 Alignment	not modelled	5.4	70	PDB header: serine protease inhibitor Chain: A: PDB Molecule: amyloid a4; PDBTitle: the alzheimer's disease amyloid a4 peptide (residues 1-40)
25	d1ledla_	 Alignment	not modelled	5.4	29	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
26	c4fquB_	 Alignment	not modelled	5.1	36	PDB header: hydrolase Chain: B: PDB Molecule: legumain; PDBTitle: crystal structure of prolegumain