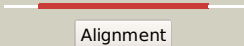
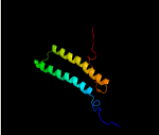
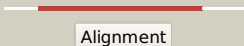

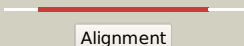







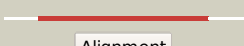
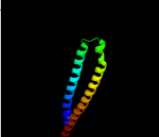



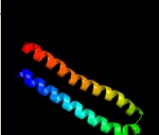
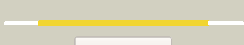
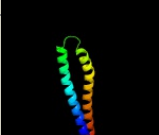


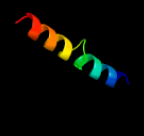

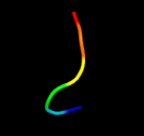
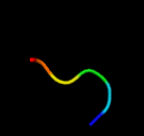
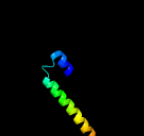



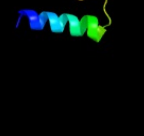


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3020c_(esxS)_3379046_3379339
Date	Thu Aug 8 16:20:19 BST 2019
Unique Job ID	96103b4a9f412afb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kg7A_			100.0	92	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein esxg (pe family protein); PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
2	c3h6pB_			100.0	100	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: esat-6 like protein esxs; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
3	c2kg7B_			95.7	18	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
4	d1wa8a1			95.3	30	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
5	d1wa8b1			95.3	16	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
6	c3zbhC_			93.9	20	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
7	c4lwsA_			93.1	21	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
8	c3gvmA_			90.3	17	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
9	c4lwsB_			88.2	17	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
10	c2vs0B_			74.2	14	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
11	c4iogD_			66.9	19	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

12	c2v0xB_	Alignment		11.2	52	PDB header: cell cycle Chain: B; PDB Molecule: lamina-associated polypeptide 2 isoforms alpha/zeta; PDBTitle: the dimerization domain of lap2alpha
13	c2q6mA_	Alignment		9.3	30	PDB header: toxin Chain: A; PDB Molecule: cholix toxin; PDBTitle: catalytic fragment of cholix toxin from vibrio cholerae in complex2 with the pj34 inhibitor
14	c1xrxD_	Alignment		7.9	83	PDB header: replication inhibitor Chain: D; PDB Molecule: seqa protein; PDBTitle: crystal structure of a dna-binding protein
15	d1xrx1	Alignment		7.9	83	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: SeqA N-terminal domain-like
16	c3u0cA_	Alignment		6.8	18	PDB header: cell invasion Chain: A; PDB Molecule: invasin ipab; PDBTitle: crystal structure of n-terminal region of type iii secretion first2 translocator ipab (residues 74-224)
17	d1hbna1	Alignment		6.7	44	Fold: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Superfamily: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Family: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
18	c5v6hC_	Alignment		6.1	42	PDB header: protein binding Chain: C; PDB Molecule: pdz domain-containing protein gipc2; PDBTitle: crystal structure of myosin vi in complex with gh2 domain of gipc2
19	d1e6va1	Alignment		5.7	38	Fold: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Superfamily: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Family: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
20	c4e1rA_	Alignment		5.4	30	PDB header: dna binding protein Chain: A; PDB Molecule: protein lsr2; PDBTitle: crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 31 2 1 space group
21	c4e1pA_	Alignment	not modelled	5.4	30	PDB header: dna binding protein Chain: A; PDB Molecule: protein lsr2; PDBTitle: crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 1 21 1 space group
22	c1wd6B_	Alignment	not modelled	5.1	39	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: protein ydhr; PDBTitle: crystal structure of jw1657 from escherichia coli