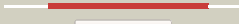
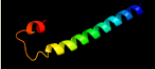
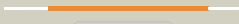

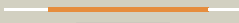
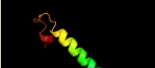



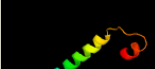

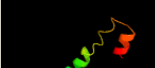
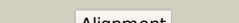
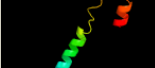
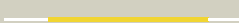


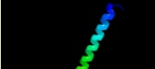

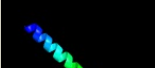


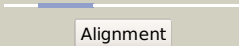
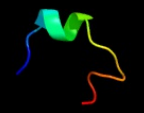
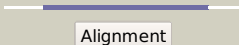
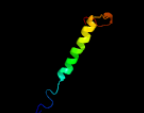

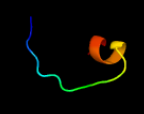
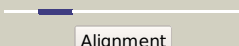

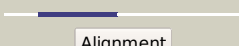
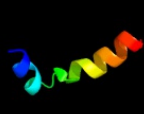
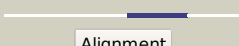
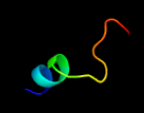
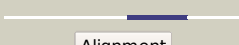


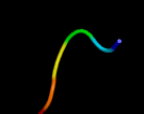



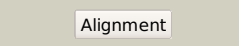

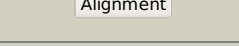
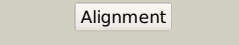
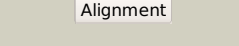





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1950c (-) _2200005_2200196
Date	Mon Aug 5 13:25:04 BST 2019
Unique Job ID	a8f96f51b78f0b91

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vs0B_	 Alignment		91.2	15	PDB header: cell invasion Chain: B; PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
2	c4iogD_	 Alignment		89.7	17	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
3	c3gvmA_	 Alignment		89.5	22	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	c3zbhC_	 Alignment		83.7	20	PDB header: unknown function Chain: C; PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
5	d1wa8a1	 Alignment		81.2	16	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
6	c2g38B_	 Alignment		80.6	21	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
7	d2g38b1	 Alignment		80.6	21	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
8	c4lwsA_	 Alignment		73.0	15	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
9	c4lwsB_	 Alignment		71.9	17	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
10	c5xfsB_	 Alignment		66.6	12	PDB header: protein transport Chain: B; PDB Molecule: ppe family protein ppe15; PDBTitle: crystal structure of pe8-ppe15 in complex with espg5 from m.2 tuberculosis
11	d1wa8b1	 Alignment		36.9	22	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like

12	c2eapA	 Alignment		20.4	29	PDB header: signaling protein Chain: A: PDB Molecule: lymphocyte cytosolic protein 2; PDBTitle: solution structure of the n-terminal sam-domain of human2 lymphocyte cytosolic protein 2
13	c2kg7B	 Alignment		18.8	15	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein eshx; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
14	c3adyA	 Alignment		11.4	11	PDB header: proton transport Chain: A: PDB Molecule: dotd; PDBTitle: crystal structure of dotd from legionella
15	c2kfvA	 Alignment		8.7	50	PDB header: isomerase Chain: A: PDB Molecule: fk506-binding protein 3; PDBTitle: structure of the amino-terminal domain of human fk506-2 binding protein 3 / northeast structural genomics3 consortium target ht99a
16	c2jq3A	 Alignment		8.5	26	PDB header: lipid binding protein Chain: A: PDB Molecule: apolipoprotein c-iii; PDBTitle: structure and dynamics of human apolipoprotein c-iii
17	d2axth1	 Alignment		7.0	24	Fold: Single transmembrane helix Superfamily: Photosystem II 10 kDa phosphoprotein PsbH Family: PsbH-like
18	c2axtH	 Alignment		7.0	24	PDB header: electron transport Chain: H: PDB Molecule: photosystem ii reaction center h protein; PDBTitle: crystal structure of photosystem ii from thermosynechococcus elongatus
19	c2rf9C	 Alignment		6.6	50	PDB header: transferase Chain: C: PDB Molecule: erbb receptor feedback inhibitor 1; PDBTitle: crystal structure of the complex between the egfr kinase domain and a2 mig6 peptide
20	c2pheC	 Alignment		6.6	25	PDB header: transcription Chain: C: PDB Molecule: alpha trans-inducing protein; PDBTitle: model for vp16 binding to pc4
21	c4gegF	 Alignment	not modelled	6.6	44	PDB header: cell cycle Chain: F: PDB Molecule: kinetochore-associated protein cnn1; PDBTitle: crystal structure of the spc24-spc25/cnn1 binding interface
22	c5zt3A	 Alignment	not modelled	6.5	20	PDB header: plant protein Chain: A: PDB Molecule: wa352; PDBTitle: crystal structure of wa352 from oryza sativa
23	c2rfeF	 Alignment	not modelled	6.4	50	PDB header: transferase Chain: F: PDB Molecule: erbb receptor feedback inhibitor 1; PDBTitle: crystal structure of the complex between the egfr kinase domain and a2 mig6 peptide
24	c4i21D	 Alignment	not modelled	6.4	50	PDB header: transferase/transferase inhibitor Chain: D: PDB Molecule: erbb receptor feedback inhibitor 1; PDBTitle: crystal structure of l858r + t790m egfr kinase domain in complex with2 mig6 peptide
25	c2rfeE	 Alignment	not modelled	6.4	50	PDB header: transferase Chain: E: PDB Molecule: erbb receptor feedback inhibitor 1; PDBTitle: crystal structure of the complex between the egfr kinase domain and a2 mig6 peptide
26	c2rf9D	 Alignment	not modelled	6.4	50	PDB header: transferase Chain: D: PDB Molecule: erbb receptor feedback inhibitor 1; PDBTitle: crystal structure of the complex between the egfr kinase domain and a2 mig6 peptide
27	c3a56B	 Alignment	not modelled	6.4	23	PDB header: hydrolase Chain: B: PDB Molecule: protein-glutaminase; PDBTitle: crystal structure of pro- protein-glutaminase
28	c4i0xA	 Alignment	not modelled	6.0	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein mab_3112; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
		 Alignment				PDB header: transferase/transferase inhibitor

29	c4i21C_	Alignment	not modelled	5.7	50	Chain: C: PDB Molecule: erbb receptor feedback inhibitor 1; PDBTitle: crystal structure of l858r + t790m egfr kinase domain in complex with2 mig6 peptide
30	c2lpuA_	Alignment	not modelled	5.7	10	PDB header: protein transport Chain: A: PDB Molecule: kmatg10; PDBTitle: solution structures of kmatg10
31	d1byra_	Alignment	not modelled	5.6	17	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Nuclease
32	c5tpvB_	Alignment	not modelled	5.5	40	PDB header: isomerase Chain: B: PDB Molecule: wlara, tdp-fucose-3,4-ketoisomerase; PDBTitle: x-ray structure of wlara (tdp-fucose-3,4-ketoisomerase) from2 campylobacter jejuni