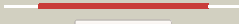


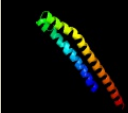
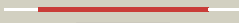



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3440c_(-)_3859845_3860156
Date	Fri Aug 9 18:20:11 BST 2019
Unique Job ID	872ac183d79c6ad6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gvmA_	 Alignment		96.3	15	PDB header: viral protein Chain: A; PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
2	c3zbc_	 Alignment		96.1	14	PDB header: unknown function Chain: C; PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
3	d1wa8a1	 Alignment		96.1	18	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
4	c2vs0B_	 Alignment		95.0	12	PDB header: cell invasion Chain: B; PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
5	c4lwsA_	 Alignment		92.9	14	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
6	c2kg7B_	 Alignment		87.1	14	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
7	d1wa8b1	 Alignment		82.6	12	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
8	c4iogD_	 Alignment		82.6	14	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
9	c4i0xA_	 Alignment		65.5	22	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
10	c4lwsB_	 Alignment		43.2	15	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
11	c5ezaE_	 Alignment		33.7	38	PDB header: de novo protein Chain: E; PDB Molecule: cc-hept-c-h-i; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i18c-i22h

12	c5ezaF_	Alignment		33.7	38	PDB header: de novo protein Chain: F: PDB Molecule: cc-hept-c-h-i; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i18c-l22h
13	c5ezaD_	Alignment		33.7	38	PDB header: de novo protein Chain: D: PDB Molecule: cc-hept-c-h-i; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i18c-l22h
14	c5ezaC_	Alignment		33.7	38	PDB header: de novo protein Chain: C: PDB Molecule: cc-hept-c-h-i; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i18c-l22h
15	c5ezaB_	Alignment		33.7	38	PDB header: de novo protein Chain: B: PDB Molecule: cc-hept-c-h-i; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i18c-l22h
16	c5ezaG_	Alignment		33.7	38	PDB header: de novo protein Chain: G: PDB Molecule: cc-hept-c-h-i; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i18c-l22h
17	c5ezaA_	Alignment		33.7	38	PDB header: de novo protein Chain: A: PDB Molecule: cc-hept-c-h-i; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i18c-l22h
18	c5ez9A_	Alignment		29.6	38	PDB header: de novo protein Chain: A: PDB Molecule: cc-hept-l22h; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i-h-i
19	c5ez9C_	Alignment		29.6	38	PDB header: de novo protein Chain: C: PDB Molecule: cc-hept-l22h; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i-h-i
20	c5ez9G_	Alignment		29.6	38	PDB header: de novo protein Chain: G: PDB Molecule: cc-hept-l22h; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i-h-i
21	c5ez9D_	Alignment	not modelled	29.6	38	PDB header: de novo protein Chain: D: PDB Molecule: cc-hept-l22h; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i-h-i
22	c5ez9E_	Alignment	not modelled	29.6	38	PDB header: de novo protein Chain: E: PDB Molecule: cc-hept-l22h; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i-h-i
23	c5ez9B_	Alignment	not modelled	29.4	38	PDB header: de novo protein Chain: B: PDB Molecule: cc-hept-l22h; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i-h-i
24	c5ez9F_	Alignment	not modelled	29.4	38	PDB header: de novo protein Chain: F: PDB Molecule: cc-hept-l22h; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i-h-i
25	d2g38b1	Alignment	not modelled	28.3	18	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
26	c2g38B_	Alignment	not modelled	28.3	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
27	c3p9a_	Alignment	not modelled	23.9	25	PDB header: dna binding protein Chain: I: PDB Molecule: dna-packaging protein gp3; PDBTitle: an atomic view of the nonameric small terminase subunit of 2 bacteriophage p22
28	c5xfsb_	Alignment	not modelled	22.2	20	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
29	c5hb3A_	Alignment	not modelled	13.1	11	PDB header: transport protein Chain: A: PDB Molecule: nucleoporin nic96;

29	c1nb3A	Alignment	not modelled	13.1	11	PDBTitle: crystal structure of chaetomium thermophilum nic96 sol-nup53 complex
30	c6qfmB	Alignment	not modelled	12.7	40	PDB header: apoptosis Chain: B; PDB Molecule: bcl-2-binding component 3; PDBTitle: structure of human mcl-1 in complex with puma bh3 peptide
31	c6qg8B	Alignment	not modelled	12.0	40	PDB header: apoptosis Chain: B; PDB Molecule: bcl-2-binding component 3; PDBTitle: structure of human bcl-2 in complex with puma bh3 peptide
32	c2ltuA	Alignment	not modelled	11.0	23	PDB header: transferase Chain: A; PDB Molecule: 5'-amp-activated protein kinase catalytic subunit alpha-2; PDBTitle: solution structure of autoinhibitory domain of human amp-activated2 protein kinase catalytic subunit
33	c4hnjC	Alignment	not modelled	10.7	40	PDB header: apoptosis/protein binding Chain: C; PDB Molecule: bcl-2-binding component 3; PDBTitle: crystallographic structure of bcl-xl domain-swapped dimer in complex2 with puma bh3 peptide at 2.9a resolution
34	c2m04B	Alignment	not modelled	9.4	40	PDB header: apoptosis/protein binding Chain: B; PDB Molecule: bcl-2-binding component 3; PDBTitle: solution structure of bcl-xl in complex with puma bh3 peptide
35	c5jnbG	Alignment	not modelled	8.5	55	PDB header: transferase Chain: G; PDB Molecule: rnp (rrm rna binding domain) containing; PDBTitle: structure of gld-2/rnp-8 complex
36	c2kngA	Alignment	not modelled	8.4	28	PDB header: dna binding protein Chain: A; PDB Molecule: protein lsr2; PDBTitle: solution structure of c-domain of lsr2
37	c1sy9B	Alignment	not modelled	7.5	46	PDB header: calcium-binding protein Chain: B; PDB Molecule: cyclic-nucleotide-gated olfactory channel; PDBTitle: structure of calmodulin complexed with a fragment of the2 olfactory cng channel
38	c6eikE	Alignment	not modelled	7.3	38	PDB header: de novo protein Chain: E; PDB Molecule: cc-hept-i24e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i24e
39	c2vofB	Alignment	not modelled	6.9	40	PDB header: apoptosis Chain: B; PDB Molecule: bcl-2-binding component 3; PDBTitle: structure of mouse a1 bound to the puma bh3-domain
40	c6eikG	Alignment	not modelled	6.5	38	PDB header: de novo protein Chain: G; PDB Molecule: cc-hept-i24e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i24e
41	c6eikA	Alignment	not modelled	6.5	38	PDB header: de novo protein Chain: A; PDB Molecule: cc-hept-i24e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i24e
42	c6eikB	Alignment	not modelled	6.5	38	PDB header: de novo protein Chain: B; PDB Molecule: cc-hept-i24e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i24e
43	c6eikF	Alignment	not modelled	6.5	38	PDB header: de novo protein Chain: F; PDB Molecule: cc-hept-i24e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i24e
44	c6eikC	Alignment	not modelled	6.5	38	PDB header: de novo protein Chain: C; PDB Molecule: cc-hept-i24e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i24e
45	c6eikD	Alignment	not modelled	6.5	38	PDB header: de novo protein Chain: D; PDB Molecule: cc-hept-i24e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i24e
46	c5jnbE	Alignment	not modelled	6.0	55	PDB header: transferase Chain: E; PDB Molecule: rnp (rrm rna binding domain) containing; PDBTitle: structure of gld-2/rnp-8 complex
47	c2rocB	Alignment	not modelled	5.8	40	PDB header: apoptosis Chain: B; PDB Molecule: bcl-2-binding component 3; PDBTitle: solution structure of mcl-1 complexed with puma
48	c5ijoI	Alignment	not modelled	5.5	15	PDB header: transport protein Chain: I; PDB Molecule: nuclear pore complex protein nup93; PDBTitle: alternative composite structure of the inner ring of the human nuclear2 pore complex (16 copies of nup188, 16 copies of nup205)
49	d3c7ba1	Alignment	not modelled	5.4	23	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
50	c2qx5B	Alignment	not modelled	5.3	14	PDB header: transport protein Chain: B; PDB Molecule: nucleoporin nic96; PDBTitle: structure of nucleoporin nic96
51	c1pyvA	Alignment	not modelled	5.3	45	PDB header: hydrolase Chain: A; PDB Molecule: atp synthase beta chain, mitochondrial precursor; PDBTitle: nmr solution structure of the mitochondrial f1b presequence2 peptide from nicotiana plumbaginifolia