


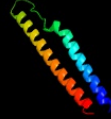

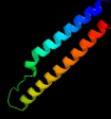
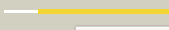

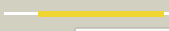
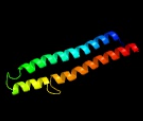

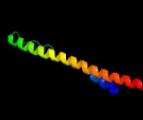





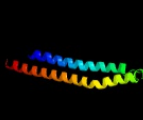



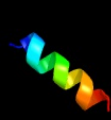


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1088_(PE9)_1214518_1214952
Date	Wed Jul 31 22:05:16 BST 2019
Unique Job ID	5eacfc8443444a31

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsA_	 Alignment		100.0	42	PDB header: protein transport Chain: A; PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	d2g38a1	 Alignment		100.0	30	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
3	c2g38A_	 Alignment		100.0	30	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
4	c3gvmA_	 Alignment		79.6	13	PDB header: viral protein Chain: A; PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
5	c4iogD_	 Alignment		75.4	13	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
6	c4wj2A_	 Alignment		67.9	9	PDB header: unknown function Chain: A; PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
7	c2vs0B_	 Alignment		66.5	7	PDB header: cell invasion Chain: B; PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
8	d1wa8a1	 Alignment		63.1	11	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
9	c3zbhC_	 Alignment		47.1	15	PDB header: unknown function Chain: C; PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	c2y0mB_	 Alignment		32.3	41	PDB header: transcription Chain: B; PDB Molecule: male-specific lethal 1 homolog; PDBTitle: crystal structure of the complex between dosage2 compensation factors msl1 and mof
11	d1lghb_	 Alignment		26.3	20	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits

12	c3lphD_	Alignment		21.5	27	PDB header: viral protein Chain: D: PDB Molecule: protein rev; PDBTitle: crystal structure of the hiv-1 rev dimer
13	d1bg1a1	Alignment		19.4	47	Fold: STAT-like Superfamily: STAT Family: STAT
14	c1wrgA_	Alignment		16.9	14	PDB header: membrane protein Chain: A: PDB Molecule: light-harvesting protein b-880, beta chain; PDBTitle: light-harvesting complex 1 beta subunit from wild-type2 rhodospirillum rubrum
15	c4lwsA_	Alignment		16.6	17	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
16	c1g70B_	Alignment		14.7	64	PDB header: viral protein/rna Chain: B: PDB Molecule: rsg-1.2 peptide; PDBTitle: complex of hiv-1 rre-iiib rna with rsg-1.2 peptide
17	c4lwsB_	Alignment		14.1	11	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
18	c2x7IP_	Alignment		13.9	29	PDB header: immune system Chain: P: PDB Molecule: protein rev; PDBTitle: implications of the hiv-1 rev dimer structure at 3.2a resolution for2 multimeric binding to the rev response element
19	c3oniA_	Alignment		13.6	13	PDB header: protein transport Chain: A: PDB Molecule: t-snare vti1; PDBTitle: crystal structure of yeast vti1p_habc domain
20	d1bf5a1	Alignment		12.2	47	Fold: STAT-like Superfamily: STAT Family: STAT
21	c3zs9C_	Alignment	not modelled	11.1	50	PDB header: hydrolase/transport protein Chain: C: PDB Molecule: golgi to er traffic protein 2; PDBTitle: s. cerevisiae get3-adp-alf4- complex with a cytosolic get2 fragment
22	c6et5u_	Alignment	not modelled	11.1	21	PDB header: photosynthesis Chain: U: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
23	c4rg1A_	Alignment	not modelled	10.7	18	PDB header: dna binding protein Chain: A: PDB Molecule: filamentation induced by camp protein fic; PDBTitle: crystal structure of a fic family protein (dde_2494) from2 desulfovibrio desulfuricans g20 at 2.70 a resolution
24	c4qlbG_	Alignment	not modelled	9.2	13	PDB header: transferase Chain: G: PDB Molecule: protein gyg-1, isoform b; PDBTitle: structural basis for the recruitment of glycogen synthase by2 glycogenin
25	c3sjdE_	Alignment	not modelled	9.0	50	PDB header: hydrolase/transport protein Chain: E: PDB Molecule: golgi to er traffic protein 2; PDBTitle: crystal structure of s. cerevisiae get3 with bound adp-mg2+ in complex2 with get2 cytosolic domain
26	c3sjdD_	Alignment	not modelled	9.0	50	PDB header: hydrolase/transport protein Chain: D: PDB Molecule: golgi to er traffic protein 2; PDBTitle: crystal structure of s. cerevisiae get3 with bound adp-mg2+ in complex2 with get2 cytosolic domain
27	d1f0la3	Alignment	not modelled	8.8	35	Fold: Toxins' membrane translocation domains Superfamily: Diphtheria toxin, middle domain Family: Diphtheria toxin, middle domain
28	c5y88S_	Alignment	not modelled	8.3	54	PDB header: splicing Chain: S: PDB Molecule: pre-mrna-processing factor 17; PDBTitle: cryo-em structure of the intron-lariat spliceosome ready for2 disassembly from s.cerevisiae at 3.5 angstrom PDB header: immune system/viral protein

29	c4jo8B_	Alignment	not modelled	8.3	50	Chain: B; PDB Molecule: killer cell lectin-like receptor 8; PDBTitle: crystal structure of the activating ly49h receptor in complex with2 m157 (g1f strain)
30	c2w0cR_	Alignment	not modelled	7.5	17	PDB header: virus Chain: R; PDB Molecule: protein p3; PDBTitle: x-ray structure of the entire lipid-containing bacteriophage pm2
31	d2ga1a1	Alignment	not modelled	7.5	45	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Alr1493-like
32	c4hg6A_	Alignment	not modelled	7.0	27	PDB header: transferase Chain: A; PDB Molecule: cellulose synthase subunit a; PDBTitle: structure of a cellulose synthase - cellulose translocation2 intermediate
33	c3ukzC_	Alignment	not modelled	6.7	63	PDB header: protein transport/protein binding Chain: C; PDB Molecule: nuclear cap-binding protein subunit 1; PDBTitle: mouse importin alpha: mouse cbp80 cnl5 complex
34	c3ul0C_	Alignment	not modelled	6.6	63	PDB header: protein transport/protein binding Chain: C; PDB Molecule: nuclear cap-binding protein subunit 1; PDBTitle: mouse importin alpha: mouse cbp80y8d cnl5 complex
35	c1qfqB_	Alignment	not modelled	6.2	30	PDB header: transcription/rna Chain: B; PDB Molecule: 36-mer n-terminal peptide of the n protein; PDBTitle: bacteriophage lambda n-protein-nutboxb-rna complex
36	c5firH_	Alignment	not modelled	6.1	44	PDB header: hydrolase Chain: H; PDB Molecule: paxt-1; PDBTitle: crystal structure of c. elegans xrn2 in complex with the2 xrn2-binding domain of paxt-1
37	c4qlbH_	Alignment	not modelled	6.0	20	PDB header: transferase Chain: H; PDB Molecule: protein gyy-1, isoform b; PDBTitle: structural basis for the recruitment of glycogen synthase by2 glycogenin
38	c2m1aA_	Alignment	not modelled	5.8	67	PDB header: viral protein Chain: A; PDB Molecule: hiv-1 rev arginine-rich motif (arm); PDBTitle: hiv-1 rev arm peptide (residues t34-r50)
39	c3zmnA_	Alignment	not modelled	5.7	78	PDB header: viral protein Chain: A; PDB Molecule: vp17; PDBTitle: vp17, a capsid protein of bacteriophage p23-77
40	c1etfB_	Alignment	not modelled	5.5	67	PDB header: viral protein/rna Chain: B; PDB Molecule: rev peptide; PDBTitle: rev response element (rre) rna complexed with rev peptide,2 nmr, minimized average structure
41	c1etgB_	Alignment	not modelled	5.5	67	PDB header: viral protein/rna Chain: B; PDB Molecule: rev peptide; PDBTitle: rev response element (rre) rna complexed with rev peptide,2 nmr, 19 structures
42	c2gqcA_	Alignment	not modelled	5.3	56	PDB header: hydrolase Chain: A; PDB Molecule: rhomboid intramembrane protease; PDBTitle: solution structure of the n-terminal domain of rhomboid intramembrane2 protease from p. aeruginosa
43	c2npiC_	Alignment	not modelled	5.2	33	PDB header: transcription Chain: C; PDB Molecule: protein pcf11; PDBTitle: clp1-atp-pcf11 complex