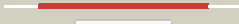
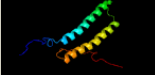

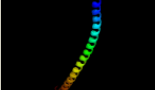
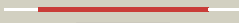
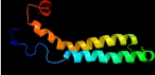







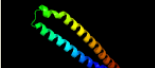

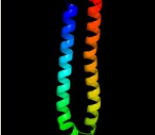




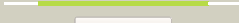

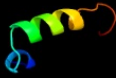






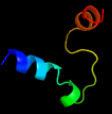
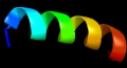


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0287_(esxG)_351525_351818
Date	Tue Jul 23 14:50:35 BST 2019
Unique Job ID	6318e440e8d82b4b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kg7A_	 Alignment		100.0	100	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_	 Alignment		100.0	91	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_	 Alignment		95.0	19	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	d1wa8b1	 Alignment		94.7	17	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
5	d1wa8a1	 Alignment		94.3	31	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
6	c3zbcC_	 Alignment		92.5	21	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
7	c4lwsA_	 Alignment		92.1	24	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
8	c4lwsB_	 Alignment		89.1	17	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
9	c3gvmA_	 Alignment		89.0	18	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
10	c2vs0B_	 Alignment		73.0	15	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
11	c4iogD_	 Alignment		65.6	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

12	d2i9fa1	Alignment		13.0	38	Fold: Nucleocapsid protein dimerization domain Superfamily: Nucleocapsid protein dimerization domain Family: Arterivirus nucleocapsid protein
13	c3u0cA_	Alignment		12.5	20	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)
14	c2i9fB_	Alignment		12.2	38	PDB header: viral protein Chain: B: PDB Molecule: nucleocapsid; PDBTitle: structure of the equine arterivirus nucleocapsid protein
15	c5j9iH_	Alignment		11.2	29	PDB header: antitoxin Chain: H: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 antitoxin c-terminal domain
16	d1e6va1	Alignment		11.1	41	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
17	c3bd1B_	Alignment		10.6	37	PDB header: transcription Chain: B: PDB Molecule: cro protein; PDBTitle: structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
18	d1x57a1	Alignment		10.0	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
19	d1hbna1	Alignment		9.6	41	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	c2ri1A_	Alignment		9.4	28	PDB header: oxidoreductase Chain: A: PDB Molecule: antibiotic biosynthesis monooxygenase; PDBTitle: crystal structure of a putative monooxygenase (yp_001095275.1) from2 shewanella loihica pv-4 at 1.26 a resolution
21	d2ppxa1	Alignment	not modelled	9.0	29	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
22	c2ppxA_	Alignment	not modelled	9.0	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1735; PDBTitle: crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
23	d1xbwa_	Alignment	not modelled	8.6	45	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
24	c2osza_	Alignment	not modelled	8.4	20	PDB header: structural protein Chain: A: PDB Molecule: nucleoporin p58/p45; PDBTitle: structure of nup58/45 suggests flexible nuclear pore diameter by2 intermolecular sliding
25	c2jv1A_	Alignment	not modelled	8.3	19	PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
26	c5v6hC_	Alignment	not modelled	7.7	42	PDB header: protein binding Chain: C: PDB Molecule: pdz domain-containing protein gjpc2; PDBTitle: crystal structure of myosin vi in complex with gh2 domain of gjpc2
27	c1wd6B_	Alignment	not modelled	7.5	39	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein ydhr; PDBTitle: crystal structure of jw1657 from escherichia coli
28	c5d4zF_	Alignment	not modelled	7.4	24	PDB header: dna binding protein Chain: F: PDB Molecule: repressor; PDBTitle: crystal structure of repressor from salmonella-temperate phage
						PDB header: protein transport

29	c4xy3A_	Alignment	not modelled	7.3	15	Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
30	c4ghjA_	Alignment	not modelled	7.2	43	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: 1.75 angstrom crystal structure of transcriptional regulator ftom2 vibrio vulnificus.
31	c4ybaA_	Alignment	not modelled	7.1	24	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein c; PDBTitle: the structure of the c.kpn2i controller protein
32	d1xrx1	Alignment	not modelled	7.0	67	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: SeqA N-terminal domain-like
33	c1xrxD_	Alignment	not modelled	7.0	67	PDB header: replication inhibitor Chain: D: PDB Molecule: seqa protein; PDBTitle: crystal structure of a dna-binding protein
34	c6csuA_	Alignment	not modelled	6.9	75	PDB header: cell cycle Chain: A: PDB Molecule: centrosomal protein of 63 kda; PDBTitle: the structure of the cep63-cep152 heterotetrameric complex
35	c3fmyA_	Alignment	not modelled	6.8	14	PDB header: dna binding protein Chain: A: PDB Molecule: hth-type transcriptional regulator mqsa PDBTitle: structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
36	d1sq8a_	Alignment	not modelled	6.5	33	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
37	c4pu4C_	Alignment	not modelled	6.2	25	PDB header: toxin/antitoxin/dna Chain: C: PDB Molecule: toxin-antitoxin system antidote transcriptional repressor PDBTitle: shewanella oneidensis mr-1 toxin antitoxin system hipa, hipb and its2 operator dna complex (space group p21)
38	c5jaaB_	Alignment	not modelled	6.0	29	PDB header: toxin Chain: B: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higba2 toxin-antitoxin complex
39	c5bu3A_	Alignment	not modelled	5.7	35	PDB header: lyase Chain: A: PDB Molecule: pyri4; PDBTitle: crystal structure of diels-alderase pyri4 in complex with its product
40	c2eouA_	Alignment	not modelled	5.6	75	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 473; PDBTitle: solution structure of the c2h2 type zinc finger (region 370-2 400) of human zinc finger protein 473
41	c2ebyA_	Alignment	not modelled	5.4	10	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
42	c5n1qD_	Alignment	not modelled	5.3	44	PDB header: transferase Chain: D: PDB Molecule: methyl-coenzyme m reductase iii from methanothermococcus PDBTitle: methyl-coenzyme m reductase iii from methanothermococcus2 thermolithotrophicus at 1.9 a resolution
43	c4e1pA_	Alignment	not modelled	5.3	20	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
44	c4e1rA_	Alignment	not modelled	5.3	20	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
45	c5z1yA_	Alignment	not modelled	5.2	83	PDB header: antibiotic Chain: A: PDB Molecule: mbjamp1 peptide; PDBTitle: mbjamp1 structure