




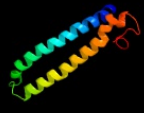




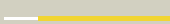
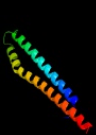





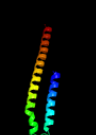
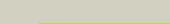



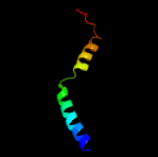
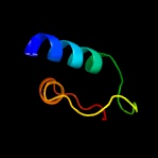
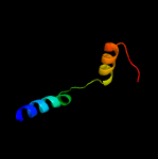
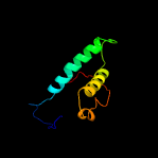


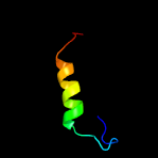

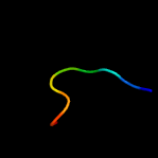


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1793_(esxN)_2030701_2030985
 Date Fri Aug 2 13:30:40 BST 2019
 Unique Job ID 909eb0c0194c3c77

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4gzaA_	 Alignment		100.0	97	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: esat-6-like protein 6; PDBTitle: crystal structure of the mycobacterium tuberculosis h37rv esxp2 (rv2346c-rv2347c) complex in space group c2221
2	c3ogiC_	 Alignment		100.0	95	PDB header: structural genomics, unknown function Chain: C; PDB Molecule: putative esat-6-like protein 6; PDBTitle: crystal structure of the mycobacterium tuberculosis h37rv esxp2 complex (rv2346c-rv2347c)
3	d1wa8b1	 Alignment		96.4	20	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
4	c2kg7B_	 Alignment		96.2	18	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
5	d1wa8a1	 Alignment		86.5	12	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
6	c3gvmA_	 Alignment		77.2	11	PDB header: viral protein Chain: A; PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
7	c3zbhC_	 Alignment		77.0	17	PDB header: unknown function Chain: C; PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
8	c4lwsB_	 Alignment		71.8	18	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
9	c4lwsA_	 Alignment		68.3	12	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
10	c2vs0B_	 Alignment		67.7	12	PDB header: cell invasion Chain: B; PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
11	c4iogD_	 Alignment		27.8	11	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	d2bsqe1	Alignment		22.6	22	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like
13	d1zuna1	Alignment		15.7	31	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
14	c2h1oH_	Alignment		13.8	24	PDB header: gene regulation/dna complex Chain: H: PDB Molecule: trafficking protein a; PDBTitle: structure of fitab bound to ir36 dna fragment
15	c4p63A_	Alignment		10.2	22	PDB header: transferase Chain: A: PDB Molecule: probable deoxyhypusine synthase; PDBTitle: crystal structure of deoxyhypusine synthase from pyrococcus horikoshii
16	c4dwnB_	Alignment		10.1	32	PDB header: apoptosis Chain: B: PDB Molecule: bcl10-interacting card protein; PDBTitle: crystal structure of human bincard card
17	c2xuvB_	Alignment		9.5	100	PDB header: unknown function Chain: B: PDB Molecule: hdeb; PDBTitle: the structure of hdeb
18	d1q8ia2	Alignment		9.0	30	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I
19	c2dtuA_	Alignment		8.9	30	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase; PDBTitle: crystal structure of the beta hairpin loop deletion variant of rb692 gp43 in complex with dna containing an abasic site analog
20	c1nwaA_	Alignment		8.9	67	PDB header: oxidoreductase Chain: A: PDB Molecule: peptide methionine sulfoxide reductase msra; PDBTitle: structure of mycobacterium tuberculosis methionine2 sulfoxide reductase a in complex with protein-bound3 methionine
21	d1nwaa_	Alignment	not modelled	8.9	67	Fold: Ferredoxin-like Superfamily: Peptide methionine sulfoxide reductase Family: Peptide methionine sulfoxide reductase
22	c4d8mA_	Alignment	not modelled	8.4	18	PDB header: lipid binding protein Chain: A: PDB Molecule: pesticidal crystal protein cry5ba; PDBTitle: crystal structure of bacillus thuringiensis cry5b nematocidal toxin
23	c3bqhA_	Alignment	not modelled	8.3	67	PDB header: oxidoreductase Chain: A: PDB Molecule: peptide methionine sulfoxide reductase msra/msrb; PDBTitle: structure of the central domain (msra) of neisseria meningitidis pilb2 (oxidized form)
24	c2ds2A_	Alignment	not modelled	8.2	83	PDB header: plant protein Chain: A: PDB Molecule: sweet protein mabinlin-2 chain a; PDBTitle: crystal structure of mabinlin ii
25	d1ih7a2	Alignment	not modelled	8.1	30	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I
26	c4xvvB_	Alignment	not modelled	8.0	80	PDB header: chaperone Chain: B: PDB Molecule: acid stress chaperone hdeb; PDBTitle: crystal structure of an acid stress chaperone hdeb (kpn_03484) from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578 at 1.70 a3 resolution
27	c2ds2C_	Alignment	not modelled	7.9	83	PDB header: plant protein Chain: C: PDB Molecule: sweet protein mabinlin-2 chain a; PDBTitle: crystal structure of mabinlin ii
28	d1njha_	Alignment	not modelled	7.8	50	Fold: Hypothetical protein YojF Superfamily: Hypothetical protein YojF Family: Hypothetical protein YojF

29	d2fyuk1	Alignment	not modelled	7.7	23	Fold: Single transmembrane helix Superfamily: Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
30	c4rs7R	Alignment	not modelled	7.5	60	PDB header: dna binding protein Chain: R: PDB Molecule: parb-c; PDBTitle: structure of pnob8 parb-c
31	c3nzlA	Alignment	not modelled	7.1	27	PDB header: transcription Chain: A: PDB Molecule: dna-binding protein satb1; PDBTitle: crystal structure of the n-terminal domain of dna-binding protein2 satb1 from homo sapiens, northeast structural genomics consortium3 target hr4435b
32	c4hetA	Alignment	not modelled	6.9	32	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical glycoside hydrolase; PDBTitle: crystal structure of a putative glycoside hydrolase (bt3745) from2 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution
33	d1mq0a	Alignment	not modelled	6.9	31	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
34	c2j89A	Alignment	not modelled	5.8	56	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine sulfoxide reductase a; PDBTitle: functional and structural aspects of poplar cytosolic and2 plastidial type a methionine sulfoxide reductases
35	c1dlcA	Alignment	not modelled	5.8	41	PDB header: toxin Chain: A: PDB Molecule: delta-endotoxin cryiiia; PDBTitle: crystal structure of insecticidal delta-endotoxin from2 bacillus thuringiensis at 2.5 angstroms resolution
36	c1w99A	Alignment	not modelled	5.6	32	PDB header: toxin Chain: A: PDB Molecule: pesticidal crystal protein cry4ba; PDBTitle: mosquito-larvicidal toxin cry4ba from bacillus thuringiensis ssp.2 israelensis
37	c5fa9B	Alignment	not modelled	5.5	67	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase msra; PDBTitle: bifunctional methionine sulfoxide reductase ab (msrab) from treponema2 denticola
38	c3pilA	Alignment	not modelled	5.5	67	PDB header: oxidoreductase Chain: A: PDB Molecule: peptide methionine sulfoxide reductase; PDBTitle: crystal structure of mxr1 from saccharomyces cerevisiae in reduced2 form
39	c4itqA	Alignment	not modelled	5.5	33	PDB header: gene regulation, structural protein/dna Chain: A: PDB Molecule: putative uncharacterized protein sco1480; PDBTitle: crystal structure of hypothetical protein sco1480 bound to dna
40	d2fr5a1	Alignment	not modelled	5.2	25	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
41	c3eb7B	Alignment	not modelled	5.2	45	PDB header: toxin Chain: B: PDB Molecule: insecticidal delta-endotoxin cry8ea1; PDBTitle: crystal structure of insecticidal delta-endotoxin cry8ea1 from2 bacillus thuringiensis at 2.2 angstroms resolution