
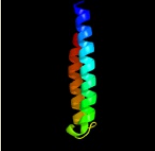

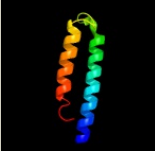

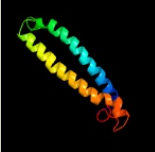

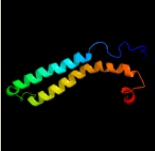

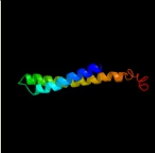

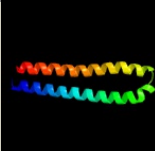



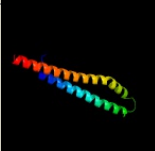
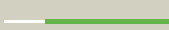
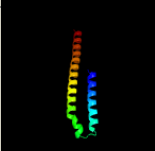
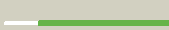
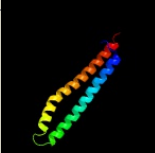

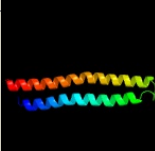
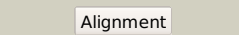
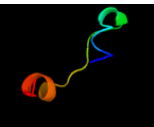
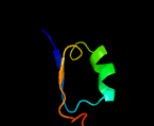




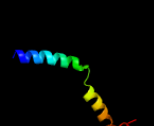






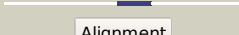

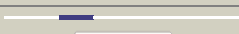

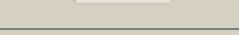
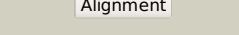
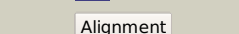


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1037c_(esxl)_1160548_1160832
 Date Wed Jul 31 22:05:11 BST 2019
 Unique Job ID 7f07c11aba1b3e12

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4gzaA_	 Alignment		100.0	88	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	86	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		95.9	21	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
4	c2kg7B_	 Alignment		95.3	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		83.5	14	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
6	c4lwsB_	 Alignment		63.6	18	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
7	c3zbhC_	 Alignment		63.2	18	PDB header: unknown function Chain: C; PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
8	c3gvmA_	 Alignment		60.4	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
9	c4lwsA_	 Alignment		57.2	13	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
10	c2vs0B_	 Alignment		55.3	10	PDB header: cell invasion Chain: B; PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
11	c4iogD_	 Alignment		17.1	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

12	c3nza1	 Alignment		15.8	33	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
13	c4rc1B	 Alignment		10.2	41	PDB header: unknown function Chain: B; PDB Molecule: upf0264 protein mj1099; PDBTitle: structure of the methanofuran/methanopterin biosynthetic enzyme mj10992 from methanocaldococcus jannaschii with prpp
14	d2diia1	 Alignment		9.1	42	Fold: BSD domain-like Superfamily: BSD domain-like Family: BSD domain
15	d2evra1	 Alignment		8.8	35	Fold: SH3-like barrel Superfamily: Prokaryotic SH3-related domain Family: Spr N-terminal domain-like
16	d2bsqe1	 Alignment		8.5	20	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like
17	d1njha	 Alignment		8.5	50	Fold: Hypothetical protein YojF Superfamily: Hypothetical protein YojF Family: Hypothetical protein YojF
18	c2diiA	 Alignment		8.5	42	PDB header: transcription Chain: A; PDB Molecule: tfiih basal transcription factor complex p62 PDBTitle: solution structure of the bsd domain of human tfiih basal2 transcription factor complex p62 subunit
19	c5oqj1	 Alignment		8.0	36	PDB header: transcription Chain: 1; PDB Molecule: rna polymerase ii transcription factor b subunit 1; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
20	c4rs7R	 Alignment		7.3	60	PDB header: dna binding protein Chain: R; PDB Molecule: parb-c; PDBTitle: structure of pnob8 parb-c
21	c5oqm1	 Alignment	not modelled	6.5	36	PDB header: transcription Chain: 1; PDB Molecule: general transcription and dna repair factor iih subunit PDBTitle: structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
22	c2ds2A	 Alignment	not modelled	6.3	83	PDB header: plant protein Chain: A; PDB Molecule: sweet protein mabinlin-2 chain a; PDBTitle: crystal structure of mabinlin ii
23	c2ds2C	 Alignment	not modelled	6.1	83	PDB header: plant protein Chain: C; PDB Molecule: sweet protein mabinlin-2 chain a; PDBTitle: crystal structure of mabinlin ii
24	c3bc1F	 Alignment	not modelled	5.9	53	PDB header: signaling protein/transport protein Chain: F; PDB Molecule: synaptotagmin-like protein 2; PDBTitle: crystal structure of the complex rab27a-slp2a
25	c2dtuA	 Alignment	not modelled	5.9	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
26	c3zh6B	 Alignment	not modelled	5.6	60	PDB header: cell adhesion Chain: B; PDB Molecule: protein e; PDBTitle: the structure of haemophilus influenzae se_met form of protein e
27	c6gym1	 Alignment	not modelled	5.4	36	PDB header: transcription Chain: 1; PDB Molecule: general transcription and dna repair factor iih subunit PDBTitle: structure of a yeast closed complex with distorted dna (ccdist)
28	c6hqaJ	 Alignment	not modelled	5.3	45	PDB header: transcription Chain: J; PDB Molecule: tfiid subunit (48 kda); PDBTitle: molecular structure of promoter-bound yeast tfiid