Phyre2

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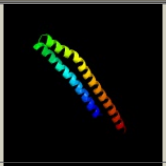
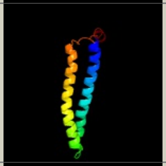
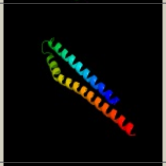
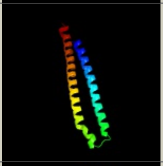
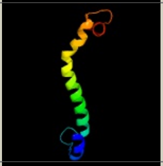
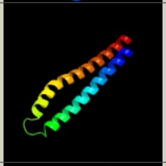
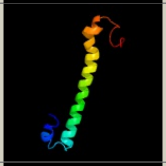
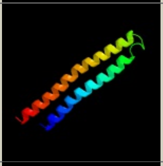
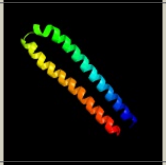
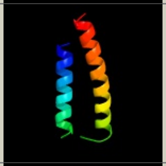
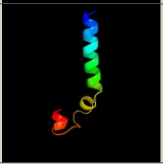
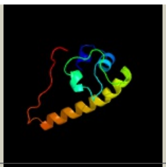
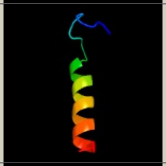
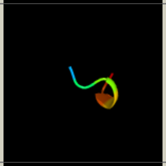
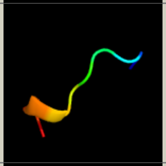
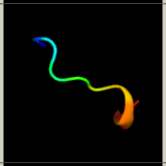
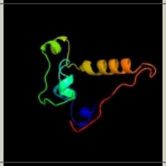
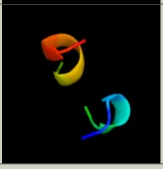
Description	RVBD0965c_(-)_1076782_1077201
Date	Wed Jul 31 22:05:03 BST 2019
Unique Job ID	a57be8882f7607b9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3zbhC_	Alignment		96.2	15	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**esxa; **PDBTitle:** geobacillus thermodenitrificans esxa crystal form i
2	d1wa8a1	Alignment		95.8	18	**Fold:**Ferritin-like **Superfamily:**EsxAB dimer-like **Family:**ESAT-6 like
3	c3gvmA_	Alignment		95.5	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
4	c4lwsA_	Alignment		95.3	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** esxa : esxb (semet) hetero-dimer from thermomonospora curvata
5	c2kg7B_	Alignment		88.9	11	**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
6	c2vs0B_	Alignment		87.9	10	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**virulence factor esxa; **PDBTitle:** structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	d1wa8b1	Alignment		86.4	18	**Fold:**Ferritin-like **Superfamily:**EsxAB dimer-like **Family:**ESAT-6 like
8	c4iogD_	Alignment		80.1	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
9	c4lwsB_	Alignment		63.1	18	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** esxa : esxb (semet) hetero-dimer from thermomonospora curvata
10	c4i0xJ_	Alignment		42.1	18	**PDB header:**structural genomics, unknown function **Chain:** J: **PDB Molecule:**esat-6-like protein mab_3113; **PDBTitle:** crystal structure of the mycobacterum abscessus esxef (mab_3112-2 mab_3113) complex
11	d2fefa1	Alignment		13.5	30	**Fold:**Bromodomain-like **Superfamily:**PA2201 N-terminal domain-like **Family:**PA2201 N-terminal domain-like

12	c4xwhA_	Alignment		11.4	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylglucosaminidase; **PDBTitle:** crystal structure of the human n-acetyl-alpha-glucosaminidase
13	c2p7vA_	Alignment		11.3	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulator of sigma d; **PDBTitle:** crystal structure of the escherichia coli regulator of sigma 70, rsd,2 in complex with sigma 70 domain 4
14	c6iczX_	Alignment		8.8	35	**PDB header:**splicing **Chain:** X: **PDB Molecule:**prkr-interacting protein 1; **PDBTitle:** cryo-em structure of a human post-catalytic spliceosome (p complex) at2 3.0 angstrom
15	c5vkoB_	Alignment		8.8	86	**PDB header:**transcription **Chain:** B: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb1; **PDBTitle:** spt6 tsh2-rpb1 1468-1500 pt1471, ps1493
16	d1v8da_	Alignment		7.8	60	**Fold:**TTHA0583/YokD-like **Superfamily:**TTHA0583/YokD-like **Family:**Hypothetical protein TT1679
17	c1v8dC_	Alignment		7.6	60	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein (tt1679); **PDBTitle:** crystal structure of the conserved hypothetical protein2 tt1679 from thermus thermophilus
18	c2vcbA_	Alignment		6.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylglucosaminidase; **PDBTitle:** family 89 glycoside hydrolase from clostridium perfringens2 in complex with pugnac
19	c3fajA_	Alignment		6.6	54	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structure of the structural protein p131 of the archaeal virus2 acidianus two-tailed virus (atv)
20	d1v7ra_	Alignment		6.2	62	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
21	d1v97a6	Alignment	not modelled	6.0	20	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
22	c4ln0C_	Alignment	not modelled	5.8	33	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcription cofactor vestigial-like protein 4; **PDBTitle:** crystal structure of the vgll4-tead4 complex
23	c3eyxB_	Alignment	not modelled	5.7	6	**PDB header:**lyase **Chain:** B: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** crystal structure of carbonic anhydrase nce103 from2 saccharomyces cerevisiae
24	d1au7a2	Alignment	not modelled	5.2	28	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**POU-specific domain