Phyre2

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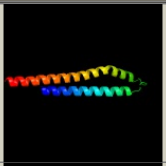
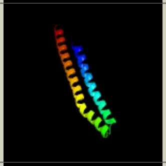
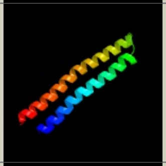
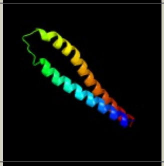
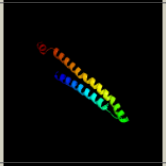
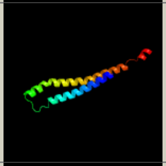
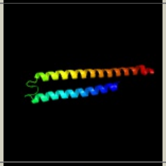
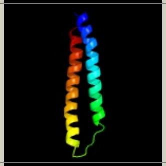
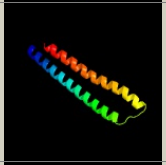
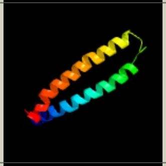
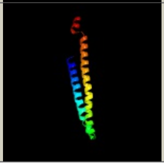
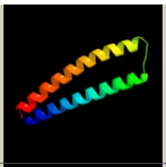
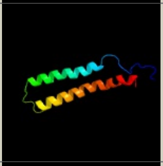
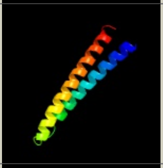
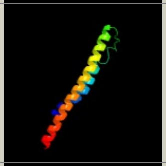
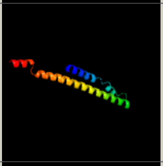
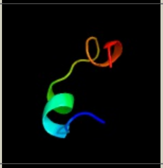
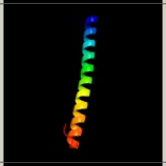
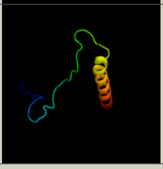
Description	RVBD2077c_(-)_2333331_2334302
Date	Mon Aug 5 13:25:19 BST 2019
Unique Job ID	9a2cf034d76ee35d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gvmA_	Alignment		98.2	15	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein sag1039; **PDBTitle:** structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
2	c3zbhC_	Alignment		98.1	14	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**esxa; **PDBTitle:** geobacillus thermodenitrificans esxa crystal form i
3	c4iogD_	Alignment		98.1	16	**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
4	c2vs0B_	Alignment		98.1	13	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**virulence factor esxa; **PDBTitle:** structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
5	c2g38B_	Alignment		97.8	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**ppe family protein; **PDBTitle:** a pe/ppe protein complex from mycobacterium tuberculosis
6	d2g38b1	Alignment		97.8	12	**Fold:**Ferritin-like **Superfamily:**PE/PPE dimer-like **Family:**PPE
7	c4lwsA_	Alignment		97.8	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** esxa : esxb (semet) hetero-dimer from thermomonospora curvata
8	d1wa8a1	Alignment		97.6	17	**Fold:**Ferritin-like **Superfamily:**EsxAB dimer-like **Family:**ESAT-6 like
9	c4lwsB_	Alignment		97.5	11	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** esxa : esxb (semet) hetero-dimer from thermomonospora curvata
10	d1wa8b1	Alignment		97.5	16	**Fold:**Ferritin-like **Superfamily:**EsxAB dimer-like **Family:**ESAT-6 like
11	c5xfsB_	Alignment		97.2	13	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**ppe family protein ppe15; **PDBTitle:** crystal structure of pe8-ppe15 in complex with espg5 from m.2 tuberculosis

12	c4i0xJ_	Alignment		96.4	14	**PDB header:**structural genomics, unknown function **Chain:** J: **PDB Molecule:**esat-6-like protein mab_3113; **PDBTitle:** crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
13	c2kg7B_	Alignment		95.7	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
14	c4i0xA_	Alignment		94.9	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**esat-6-like protein mab_3112; **PDBTitle:** crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
15	c4wj2A_	Alignment		93.9	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**antigen mtb48; **PDBTitle:** mycobacterial protein
16	c4xy3A_	Alignment		89.5	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**esx-1 secretion-associated protein espb; **PDBTitle:** structure of esx-1 secreted protein espb
17	c2eapA_	Alignment		56.1	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**lymphocyte cytosolic protein 2; **PDBTitle:** solution structure of the n-terminal sam-domain of human2 lymphocyte cytosolic protein 2
18	c5j1hB_	Alignment		19.7	19	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**plectin,plectin; **PDBTitle:** structure of the spectrin repeats 5 and 6 of the plakin domain of2 plectin
19	c6cg8A_	Alignment		15.8	17	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**upf0335 protein b7z12_12435; **PDBTitle:** structure of c. crescentus gapr-dna
20	c2mwqA_	Alignment		13.7	24	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**oxygen-evolving enhancer protein 3, chloroplastic; **PDBTitle:** solution structure of psbq from spinacia oleracea
21	c4wxmD_	Alignment	not modelled	12.8	37	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator fleq; **PDBTitle:** fleq rec domain from pseudomonas aeruginosa pao1
22	c4gwpB_	Alignment	not modelled	11.1	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**mediator of rna polymerase ii transcription subunit 17; **PDBTitle:** structure of the mediator head module from s. cerevisiae
23	c6cfxD_	Alignment	not modelled	10.5	15	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**upf0335 protein ase63_04290; **PDBTitle:** bosea sp gapr solved in the presence of dna
24	d1q08a_	Alignment	not modelled	10.2	11	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
25	c2phcB_	Alignment	not modelled	9.5	38	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein ph0987; **PDBTitle:** crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
26	d1dfma_	Alignment	not modelled	9.3	9	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease BglII
27	c5dudB_	Alignment	not modelled	8.1	38	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**ybgj; **PDBTitle:** crystal structure of e. coli ybgjk
28	c1mi1A_	Alignment	not modelled	7.9	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**neurobeachin; **PDBTitle:** crystal structure of the ph-beach domain of human2 neurobeachin
						PDB header:transferase inhibitor

29	c2zp2B_	Alignment	not modelled	7.7	50	**Chain:** B: **PDB Molecule:**kinase a inhibitor; **PDBTitle:** c-terminal domain of kipi from bacillus subtilis
30	c4nncA_	Alignment	not modelled	7.5	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**obca, oxalate biosynthetic component a; **PDBTitle:** ternary complex of obca with c4-coa adduct and oxalate
31	d2phcb1	Alignment	not modelled	7.4	38	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**PH0987 C-terminal domain-like
32	c5yrzC_	Alignment	not modelled	7.1	6	**PDB header:**antitoxin/hydrolase **Chain:** C: **PDB Molecule:**hicb; **PDBTitle:** toxin-antitoxin complex from streptococcus pneumoniae
33	c3mmlD_	Alignment	not modelled	7.0	25	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**allophanate hydrolase subunit 1; **PDBTitle:** allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
34	c3cjxE_	Alignment	not modelled	6.7	11	**PDB header:**unknown function **Chain:** E: **PDB Molecule:**protein of unknown function with a cupin-like fold; **PDBTitle:** crystal structure of a protein of unknown function with a cupin-like2 fold (reut_b4571) from ralstonia eutropha jmp134 at 2.60 a resolution
35	c5aeoA_	Alignment	not modelled	6.5	26	**PDB header:**immune system **Chain:** A: **PDB Molecule:**r. equi vapg protein; **PDBTitle:** virulence-associated protein vapg from the intracellular2 pathogen rhodococcus equi
36	c3pm7A_	Alignment	not modelled	6.4	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of ef_3132 protein from enterococcus faecalis at the2 resolution 2a, northeast structural genomics consortium target efr184
37	c3obhA_	Alignment	not modelled	6.1	75	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** x-ray crystal structure of protein sp_0782 (7-79) from streptococcus2 pneumoniae. northeast structural genomics consortium target spr104
38	c4csbA_	Alignment	not modelled	5.8	30	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**virulence associated protein vapd; **PDBTitle:** structure of the virulence-associated protein vapd from the2 intracellular pathogen rhodococcus equi.
39	c3r84O_	Alignment	not modelled	5.7	23	**PDB header:**transcription **Chain:** O: **PDB Molecule:**mediator of rna polymerase ii transcription subunit 11; **PDBTitle:** structure of the mediator head subcomplex med11/22
40	c2ltdA_	Alignment	not modelled	5.6	63	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ydbc; **PDBTitle:** solution nmr structure of apo ydbc from lactococcus lactis, northeast2 structural genomics consortium (nesg) target kr150
41	c5nf2A_	Alignment	not modelled	5.6	23	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**minor fimbrium subunit mfa1; **PDBTitle:** the fimbrial shaft protein mfa1 from porphyromonas gingivalis
42	c1ygyA_	Alignment	not modelled	5.3	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
43	c2l3aA_	Alignment	not modelled	5.3	75	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of homodimer protein sp_0782 (7-79) from2 streptococcus pneumoniae northeast structural genomics consortium3 target spr104 .
44	c4cv7A_	Alignment	not modelled	5.1	22	**PDB header:**toxin **Chain:** A: **PDB Molecule:**virulence associated protein vapb; **PDBTitle:** crystal structure of rhodococcus equi vapb
45	d1mi1a1	Alignment	not modelled	5.1	22	**Fold:**BEACH domain **Superfamily:**BEACH domain **Family:**BEACH domain