




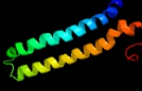



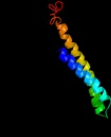


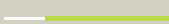
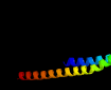

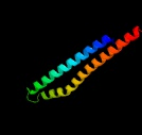

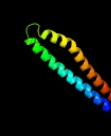

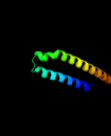




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2346c_(esxO)_2625898_2626182
Date	Mon Aug 5 13:25:50 BST 2019
Unique Job ID	61c5264433dcb9d0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4gzaA_</a>	 Alignment		100.0	100	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> esat-6-like protein 6; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis h37rv esxp2 (rv2346c-rv2347c) complex in space group c2221
2	<a href="#">c3ogiC_</a>	 Alignment		100.0	98	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C; <b>PDB Molecule:</b> putative esat-6-like protein 6; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis h37rv esxp2 complex (rv2346c-rv2347c)
3	<a href="#">d1wa8b1</a>	 Alignment		96.2	18	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
4	<a href="#">c2kg7B_</a>	 Alignment		95.8	20	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> esat-6-like protein eshx; <b>PDBTitle:</b> structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
5	<a href="#">d1wa8a1</a>	 Alignment		82.6	13	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
6	<a href="#">c4lwsB_</a>	 Alignment		67.3	18	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> esxa : esxb (semet) hetero-dimer from thermomonospora curvata
7	<a href="#">c3zbhC_</a>	 Alignment		66.9	17	<b>PDB header:</b> unknown function <b>Chain:</b> C; <b>PDB Molecule:</b> esxa; <b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i
8	<a href="#">c3gvmA_</a>	 Alignment		64.0	11	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein sag1039; <b>PDBTitle:</b> structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
9	<a href="#">c2vs0B_</a>	 Alignment		62.2	12	<b>PDB header:</b> cell invasion <b>Chain:</b> B; <b>PDB Molecule:</b> virulence factor esxa; <b>PDBTitle:</b> structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
10	<a href="#">c4lwsA_</a>	 Alignment		60.5	12	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> esxa : esxb (semet) hetero-dimer from thermomonospora curvata
11	<a href="#">c2mijA_</a>	 Alignment		20.0	34	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> spbc2 prophage-derived bacteriocin sublancin-168; <b>PDBTitle:</b> nmr structure of the s-linked glycopeptide sublancin 168

12	<a href="#">c4iogD_</a>	Alignment		18.8	12	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> secreted protein esxb; <b>PDBTitle:</b> the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. sterne
13	<a href="#">c4p63A_</a>	Alignment		17.6	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable deoxyhypusine synthase; <b>PDBTitle:</b> crystal structure of deoxyhypusine synthase from pyrococcus horikoshii
14	<a href="#">d1zua1</a>	Alignment		16.3	31	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PAPS reductase-like
15	<a href="#">d2fyuk1</a>	Alignment		13.2	22	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) <b>Family:</b> Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
16	<a href="#">d1b4ua_</a>	Alignment		12.7	31	<b>Fold:</b> LigA subunit of an aromatic-ring-opening dioxygenase LigAB <b>Superfamily:</b> LigA subunit of an aromatic-ring-opening dioxygenase LigAB <b>Family:</b> LigA subunit of an aromatic-ring-opening dioxygenase LigAB
17	<a href="#">c5m1mA_</a>	Alignment		11.4	38	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> matrix protein 1; <b>PDBTitle:</b> crystal structure of matrix protein 1 from influenza c virus (strain2 c/ann arbor/1/1950)
18	<a href="#">c4dwnB_</a>	Alignment		10.5	32	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bc110-interacting card protein; <b>PDBTitle:</b> crystal structure of human bincard card
19	<a href="#">c2xuvB_</a>	Alignment		10.1	100	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hdeb; <b>PDBTitle:</b> the structure of hdeb
20	<a href="#">d1q8ia2</a>	Alignment		9.4	30	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> DNA polymerase I
21	<a href="#">c2dtuA_</a>	Alignment	not modelled	9.4	30	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase; <b>PDBTitle:</b> crystal structure of the beta hairpin loop deletion variant of rb692 gp43 in complex with dna containing an abasic site analog
22	<a href="#">c1nwaA_</a>	Alignment	not modelled	9.0	67	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> peptide methionine sulfoxide reductase msra; <b>PDBTitle:</b> structure of mycobacterium tuberculosis methionine2 sulfoxide reductase a in complex with protein-bound3 methionine
23	<a href="#">d1nwa_</a>	Alignment	not modelled	9.0	67	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Peptide methionine sulfoxide reductase <b>Family:</b> Peptide methionine sulfoxide reductase
24	<a href="#">c2goyC_</a>	Alignment	not modelled	8.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosine phosphosulfate reductase; <b>PDBTitle:</b> crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps
25	<a href="#">c2ds2A_</a>	Alignment	not modelled	8.8	83	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> sweet protein mabinlin-2 chain a; <b>PDBTitle:</b> crystal structure of mabinlin ii
26	<a href="#">c2ds2C_</a>	Alignment	not modelled	8.5	83	<b>PDB header:</b> plant protein <b>Chain:</b> C: <b>PDB Molecule:</b> sweet protein mabinlin-2 chain a; <b>PDBTitle:</b> crystal structure of mabinlin ii
27	<a href="#">c4xvvB_</a>	Alignment	not modelled	8.5	80	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> acid stress chaperone hdeb; <b>PDBTitle:</b> crystal structure of an acid stress chaperone hdeb (kpn_03484) from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578 at 1.70 a3 resolution
28	<a href="#">c3bqhA_</a>	Alignment	not modelled	8.4	67	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> peptide methionine sulfoxide reductase msra/msrb;

						<b>PDBTitle:</b> structure of the central domain (msra) of neisseria meningitidis pilb2 (oxidized form)
29	<a href="#">d1ih7a2</a>	Alignment	not modelled	8.4	30	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> DNA polymerase I
30	<a href="#">d1njha</a>	Alignment	not modelled	8.4	50	<b>Fold:</b> Hypothetical protein YojF <b>Superfamily:</b> Hypothetical protein YojF <b>Family:</b> Hypothetical protein YojF
31	<a href="#">c4rs7R</a>	Alignment	not modelled	7.8	60	<b>PDB header:</b> dna binding protein <b>Chain:</b> R: <b>PDB Molecule:</b> parb-c; <b>PDBTitle:</b> structure of pnob8 parb-c
32	<a href="#">c2kwaA</a>	Alignment	not modelled	7.6	24	<b>PDB header:</b> transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> kinase a inhibitor; <b>PDBTitle:</b> 1h, 13c and 15n backbone and side chain resonance assignments of the2 n-terminal domain of the histidine kinase inhibitor kipi from3 bacillus subtilis
33	<a href="#">c3nzaA</a>	Alignment	not modelled	7.5	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein satb1; <b>PDBTitle:</b> crystal structure of the n-terminal domain of dna-binding protein2 satb1 from homo sapiens, northeast structural genomics consortium3 target hr4435b
34	<a href="#">d1mq0a</a>	Alignment	not modelled	7.3	31	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
35	<a href="#">c4hetA</a>	Alignment	not modelled	6.9	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical glycoside hydrolase; <b>PDBTitle:</b> crystal structure of a putative glycoside hydrolase (bt3745) from2 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution
36	<a href="#">c2j89A</a>	Alignment	not modelled	6.0	56	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine sulfoxide reductase a; <b>PDBTitle:</b> functional and structural aspects of poplar cytosolic and2 plastidial type a methionine sulfoxide reductases
37	<a href="#">c4itqA</a>	Alignment	not modelled	5.8	33	<b>PDB header:</b> gene regulation, structural protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein sco1480; <b>PDBTitle:</b> crystal structure of hypothetical protein sco1480 bound to dna
38	<a href="#">c5fa9B</a>	Alignment	not modelled	5.7	67	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peptide methionine sulfoxide reductase msra; <b>PDBTitle:</b> bifunctional methionine sulfoxide reductase ab (msrab) from treponema2 denticola
39	<a href="#">c3pila</a>	Alignment	not modelled	5.7	67	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> peptide methionine sulfoxide reductase; <b>PDBTitle:</b> crystal structure of mxr1 from saccharomyces cerevisiae in reduced2 form
40	<a href="#">d2fr5a1</a>	Alignment	not modelled	5.6	25	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
41	<a href="#">c4uz0B</a>	Alignment	not modelled	5.5	56	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> nucleolar protein 3; <b>PDBTitle:</b> crystal structure of apoptosis repressor with card (arc)
42	<a href="#">c6qfbB</a>	Alignment	not modelled	5.4	35	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> atp-citrate synthase; <b>PDBTitle:</b> structure of the human atp citrate lyase holoenzyme in complex with2 citrate, coenzyme a and mg.adp
43	<a href="#">d1l0nk</a>	Alignment	not modelled	5.2	22	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) <b>Family:</b> Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)