


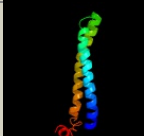

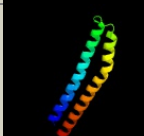

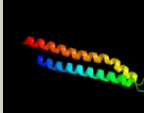

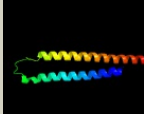



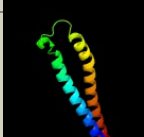

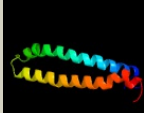





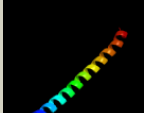


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2347c_(esxP)_2626233_2626529
Date	Mon Aug 5 13:25:50 BST 2019
Unique Job ID	ffc1df4961c84032

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3ogiD_</a>	 Alignment		100.0	92	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> putative esat-6-like protein 7; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis h37rv esxop2 complex (rv2346c-rv2347c)
2	<a href="#">d1wa8a1</a>	 Alignment		98.6	21	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
3	<a href="#">c3zbhC_</a>	 Alignment		97.9	20	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> esxa; <b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i
4	<a href="#">c3gvmA_</a>	 Alignment		97.6	15	<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
5	<a href="#">c4lwsA_</a>	 Alignment		97.6	22	<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
6	<a href="#">c4iogD_</a>	 Alignment		97.5	24	<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
7	<a href="#">c2vs0B_</a>	 Alignment		97.5	14	<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
8	<a href="#">d1wa8b1</a>	 Alignment		96.6	10	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
9	<a href="#">c4lwsB_</a>	 Alignment		95.9	14	<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
10	<a href="#">c2kg7B_</a>	 Alignment		94.9	21	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> esat-6-like protein esxh; <b>PDBTitle:</b> structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
11	<a href="#">c3m0dC_</a>	 Alignment		76.8	19	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> tnf receptor-associated factor 1; <b>PDBTitle:</b> crystal structure of the traf1:traf2:ciap2 complex

12	<a href="#">c3m06F_</a>	Alignment		67.3	19	<b>PDB header:</b> protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> tnf receptor-associated factor 2; <b>PDBTitle:</b> crystal structure of traf2
13	<a href="#">c2dw3A_</a>	Alignment		52.4	38	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> intrinsic membrane protein pufx; <b>PDBTitle:</b> solution structure of the rhodobacter sphaeroides pufx2 membrane protein
14	<a href="#">c3ag7A_</a>	Alignment		29.4	16	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein f9e10.5; <b>PDBTitle:</b> an auxilin-like j-domain containing protein, jac1 j-domain
15	<a href="#">d1pqua2</a>	Alignment		28.3	54	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
16	<a href="#">d1wtea_</a>	Alignment		26.0	42	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Restriction endonuclease EcoO109IR
17	<a href="#">d1mb4a2</a>	Alignment		20.8	54	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
18	<a href="#">d1t4ba2</a>	Alignment		20.7	46	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
19	<a href="#">d2gz1a2</a>	Alignment		20.5	46	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
20	<a href="#">c2la2A_</a>	Alignment		20.1	27	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> cecropin; <b>PDBTitle:</b> solution structure of papillocin isolated from the swallowtail2 butterfly, papilio xuthus
21	<a href="#">c5a3kA_</a>	Alignment	not modelled	17.1	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative pteridine-dependent dioxygenase; <b>PDBTitle:</b> chorismatase mechanisms reveal fundamentally different types of2 reaction in a single conserved protein fold
22	<a href="#">c3gtzA_</a>	Alignment	not modelled	17.1	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative translation initiation inhibitor; <b>PDBTitle:</b> crystal structure of a putative translation initiation inhibitor from2 salmonella typhimurium
23	<a href="#">c3h6pD_</a>	Alignment	not modelled	13.3	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> esat-6-like protein esxr; <b>PDBTitle:</b> crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
24	<a href="#">c1i8tB_</a>	Alignment	not modelled	11.2	40	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> strcuture of udp-galactopyranose mutase from e.coli
25	<a href="#">d1xbla_</a>	Alignment	not modelled	10.8	12	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Chaperone J-domain <b>Family:</b> Chaperone J-domain
26	<a href="#">c2dn9A_</a>	Alignment	not modelled	9.6	14	<b>PDB header:</b> apoptosis, chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> dnaj homolog subfamily a member 3; <b>PDBTitle:</b> solution structure of j-domain from the dnaj homolog, human2 tid1 protein
27	<a href="#">c3kjl_</a>	Alignment	not modelled	9.0	18	<b>PDB header:</b> unknown function <b>Chain:</b> L: <b>PDB Molecule:</b> nmb1025 protein; <b>PDBTitle:</b> crystal structure of nmb1025, a member of yjgf protein family, from2 neisseria meningitidis (hexagonal crystal form)
28	<a href="#">c3l32B_</a>	Alignment	not modelled	8.6	35	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoprotein; <b>PDBTitle:</b> structure of the dimerisation domain of the rabies virus2 phosphoprotein
						<b>Fold:</b> Ribosomal protein L6

29	<a href="#">d1vqpe1</a>	Alignment	not modelled	8.4	41	<b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
30	<a href="#">d2qamg1</a>	Alignment	not modelled	8.3	35	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
31	<a href="#">d2j01h1</a>	Alignment	not modelled	8.3	23	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
32	<a href="#">c2vq7B_</a>	Alignment	not modelled	8.1	53	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> flavin-containing monooxygenase; <b>PDBTitle:</b> bacterial flavin-containing monooxygenase in complex with2 nadp: native data
33	<a href="#">c4m70A_</a>	Alignment	not modelled	8.1	39	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> rx protein; <b>PDBTitle:</b> crystal structure of potato rx-cc domain in complex with rangap2-wpp2 domain
34	<a href="#">c2bi8A_</a>	Alignment	not modelled	7.9	47	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> udp-galactopyranose mutase from klebsiella pneumoniae with reduced fad
35	<a href="#">d1w4xa1</a>	Alignment	not modelled	7.9	40	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
36	<a href="#">d1jd1a_</a>	Alignment	not modelled	7.7	18	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> YjgF-like <b>Family:</b> YjgF/L-PSP
37	<a href="#">c3k0tA_</a>	Alignment	not modelled	7.6	14	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> endoribonuclease l-psp, putative; <b>PDBTitle:</b> crystal structure of pspto -psp protein in complex with d-beta-glucose2 from pseudomonas syringae pv. tomato str. dc3000
38	<a href="#">c5nmwA_</a>	Alignment	not modelled	7.6	47	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin-containing monooxygenase; <b>PDBTitle:</b> crystal structure of the pyrrolizidine alkaloid n-oxygenase from2 zonocerus variegatus in complex with fad
39	<a href="#">c5j7xA_</a>	Alignment	not modelled	7.5	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dimethylaniline monooxygenase, putative; <b>PDBTitle:</b> baeyer-villiger monooxygenase bvmoaf1838 from aspergillus flavus
40	<a href="#">d2hjsa2</a>	Alignment	not modelled	7.4	27	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
41	<a href="#">d2k49a2</a>	Alignment	not modelled	7.4	43	<b>Fold:</b> YegP-like <b>Superfamily:</b> YegP-like <b>Family:</b> YegP-like
42	<a href="#">c3we0A_</a>	Alignment	not modelled	7.3	47	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-amino acid oxidase/monooxygenase; <b>PDBTitle:</b> l-amino acid oxidase/monooxygenase from pseudomonas sp. aiu 813
43	<a href="#">d1nz6a_</a>	Alignment	not modelled	7.2	20	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Chaperone J-domain <b>Family:</b> Chaperone J-domain
44	<a href="#">d2k8ea1</a>	Alignment	not modelled	7.1	71	<b>Fold:</b> YegP-like <b>Superfamily:</b> YegP-like <b>Family:</b> YegP-like
45	<a href="#">c3bj4B_</a>	Alignment	not modelled	6.9	39	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily kqt <b>PDBTitle:</b> the kcnq1 (kv7.1) c-terminus, a multi-tiered scaffold for2 subunit assembly and protein interaction
46	<a href="#">d1j7ha_</a>	Alignment	not modelled	6.9	18	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> YjgF-like <b>Family:</b> YjgF/L-PSP
47	<a href="#">c1v0jB_</a>	Alignment	not modelled	6.9	27	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> udp-galactopyranose mutase from mycobacterium tuberculosis
48	<a href="#">c2ym9D_</a>	Alignment	not modelled	6.8	23	<b>PDB header:</b> cell invasion <b>Chain:</b> D: <b>PDB Molecule:</b> cell invasion protein sipd; <b>PDBTitle:</b> sipd from salmonella typhimurium
49	<a href="#">c4ap3A_</a>	Alignment	not modelled	6.6	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> steroid monooxygenase; <b>PDBTitle:</b> oxidized steroid monooxygenase bound to nadp
50	<a href="#">c3uoyB_</a>	Alignment	not modelled	6.5	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> otemo; <b>PDBTitle:</b> crystal structure of otemo complex with fad and nadp (form 1)
51	<a href="#">c5gsnD_</a>	Alignment	not modelled	6.4	40	<b>PDB header:</b> flavoprotein <b>Chain:</b> D: <b>PDB Molecule:</b> flavin-containing monooxygenase; <b>PDBTitle:</b> tmm in complex with methimazole
52	<a href="#">c3gwdA_</a>	Alignment	not modelled	6.4	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclohexanone monooxygenase; <b>PDBTitle:</b> closed crystal structure of cyclohexanone monooxygenase
53	<a href="#">c4tlxC_</a>	Alignment	not modelled	6.3	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> ktzi; <b>PDBTitle:</b> kutzneria sp. 744 ornithine n-hydroxylase, ktzi-fadred-nadp+-l-orn
54	<a href="#">d2bi7a1</a>	Alignment	not modelled	6.2	47	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> UDP-galactopyranose mutase, N-terminal domain
55	<a href="#">c3nj2B_</a>	Alignment	not modelled	6.2	18	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> duf269-containing protein; <b>PDBTitle:</b> crystal structure of cce_0566 from the cyanobacterium

						cyanothece2 51142, a protein associated with nitrogen fixation from the duf2693 family
56	<a href="#">d2ewca1</a>	Alignment	not modelled	6.2	23	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> YjgF-like <b>Family:</b> YjgF/L-PSP
57	<a href="#">c2jb1B_</a>	Alignment	not modelled	6.1	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-amino acid oxidase; <b>PDBTitle:</b> the l-amino acid oxidase from rhodococcus opacus in complex2 with l-alanine
58	<a href="#">c3lmeE_</a>	Alignment	not modelled	5.9	13	<b>PDB header:</b> translation <b>Chain:</b> E: <b>PDB Molecule:</b> possible translation initiation inhibitor; <b>PDBTitle:</b> structure of probable translation initiation inhibitor from (rpa2473)2 from rhodopseudomonas palustris
59	<a href="#">c1bq0A_</a>	Alignment	not modelled	5.9	12	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> dnaj; <b>PDBTitle:</b> j-domain (residues 1-77) of the escherichia coli n-terminal2 fragment (residues 1-104) of the molecular chaperone dnaj.3 nmr, 20 structures
60	<a href="#">c3r0pB_</a>	Alignment	not modelled	5.8	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> l-psp putative endoribonuclease; <b>PDBTitle:</b> crystal structure of l-psp putative endoribonuclease from uncultured2 organism
61	<a href="#">c2ip6A_</a>	Alignment	not modelled	5.7	29	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> papb; <b>PDBTitle:</b> crystal structure of pedb
62	<a href="#">c5jwcA_</a>	Alignment	not modelled	5.5	38	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> ndh dehydrogenase, putative; <b>PDBTitle:</b> structure of ndh2 from plasmodium falciparum in complex with ryl-552
63	<a href="#">c5o8rA_</a>	Alignment	not modelled	5.4	20	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-lysine 6-monooxygenase involved in desferrioxamine <b>PDBTitle:</b> the crystal structure of dfoa bound to fad and nadp; the2 desferrioxamine biosynthetic pathway cadaverine monooxygenase from3 the fire blight disease pathogen erwinia amylovora
64	<a href="#">c6fe8D_</a>	Alignment	not modelled	5.3	42	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> centromere dna-binding protein complex cbf3 subunit c; <b>PDBTitle:</b> cryo-em structure of the core centromere binding factor 3 complex
65	<a href="#">c3uteB_</a>	Alignment	not modelled	5.2	40	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> crystal structure of aspergillus fumigatus udp galactopyranose mutase2 sulfate complex
66	<a href="#">c2bbrA_</a>	Alignment	not modelled	5.2	44	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> viral casp8 and fadd-like apoptosis regulator; <b>PDBTitle:</b> crystal structure of mc159 reveals molecular mechanism of2 disc assembly and vflip inhibition
67	<a href="#">c6jdkA_</a>	Alignment	not modelled	5.1	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> baeyer-villiger monooxygenase; <b>PDBTitle:</b> crystal structure of baeyer-villiger monooxygenase from parvibaculum2 lavamentivorans
68	<a href="#">d2zjre2</a>	Alignment	not modelled	5.1	27	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
69	<a href="#">d2dw4a2</a>	Alignment	not modelled	5.1	53	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
70	<a href="#">c5m0zA_</a>	Alignment	not modelled	5.1	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclohexanone monooxygenase from thermocrispum municipale.; <b>PDBTitle:</b> cyclohexanone monooxygenase from t. municipale: reduced enzyme bound2 to nadp+