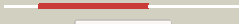
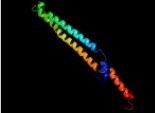


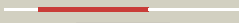
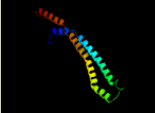

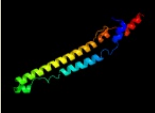

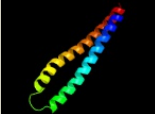

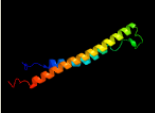

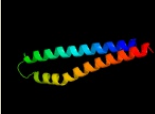

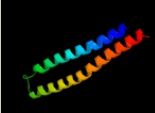

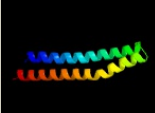

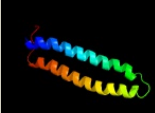

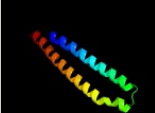


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3426\_(PPE58)\_3843216\_3843914  
 Date Fri Aug 9 18:20:09 BST 2019  
 Unique Job ID 9aecad02c6dfd850

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xfsB_</a>	 Alignment		100.0	33	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> ppe family protein ppe15; <b>PDBTitle:</b> crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	<a href="#">c2g38B_</a>	 Alignment		100.0	34	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ppe family protein; <b>PDBTitle:</b> a pe/ppe protein complex from mycobacterium tuberculosis
3	<a href="#">d2g38b1</a>	 Alignment		100.0	34	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PPE
4	<a href="#">c4xy3A_</a>	 Alignment		100.0	7	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> esx-1 secretion-associated protein espb; <b>PDBTitle:</b> structure of esx-1 secreted protein espb
5	<a href="#">c2vs0B_</a>	 Alignment		98.0	18	<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
6	<a href="#">c4wj2A_</a>	 Alignment		98.0	18	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> antigen mtb48; <b>PDBTitle:</b> mycobacterial protein
7	<a href="#">c3gvmA_</a>	 Alignment		97.8	14	<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
8	<a href="#">c4iogD_</a>	 Alignment		97.8	9	<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
9	<a href="#">c3zbhC_</a>	 Alignment		97.8	15	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> esxa; <b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i
10	<a href="#">d1wa8a1</a>	 Alignment		97.2	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
11	<a href="#">c4lwsA_</a>	 Alignment		96.6	19	<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

12	<a href="#">c4lwsB_</a>	Alignment		96.2	10	<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
13	<a href="#">d1wa8b1</a>	Alignment		96.1	19	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
14	<a href="#">c4i0xA_</a>	Alignment		95.8	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> esat-6-like protein mab_3112; <b>PDBTitle:</b> crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
15	<a href="#">c2kg7B_</a>	Alignment		92.5	10	<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
16	<a href="#">c4i0xJ_</a>	Alignment		69.5	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> J; <b>PDB Molecule:</b> esat-6-like protein mab_3113; <b>PDBTitle:</b> crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
17	<a href="#">c3ogiD_</a>	Alignment		30.3	62	<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)
18	<a href="#">c1bkvA_</a>	Alignment		20.7	13	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
19	<a href="#">c1bkvB_</a>	Alignment		19.6	13	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
20	<a href="#">c1bkvC_</a>	Alignment		19.6	13	<b>PDB header:</b> structural protein <b>Chain:</b> C; <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
21	<a href="#">c2lcrA_</a>	Alignment	not modelled	18.3	42	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> activin receptor-like kinase 1; <b>PDBTitle:</b> nmr structure of alk1 extracellular domain
22	<a href="#">c3urkA_</a>	Alignment	not modelled	13.9	67	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; <b>PDBTitle:</b> isph in complex with propynyl diphosphate (1061)
23	<a href="#">c3ke8A_</a>	Alignment	not modelled	13.9	67	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; <b>PDBTitle:</b> crystal structure of isph:hmbpp-complex
24	<a href="#">c3dnfB_</a>	Alignment	not modelled	13.2	56	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; <b>PDBTitle:</b> structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
25	<a href="#">c5sybB_</a>	Alignment	not modelled	12.6	27	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> phd finger-like domain-containing protein 5a; <b>PDBTitle:</b> crystal structure of human phf5a
26	<a href="#">c4n7bA_</a>	Alignment	not modelled	12.6	56	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> lytb; <b>PDBTitle:</b> structure of the e-1-hydroxy-2-methyl-but-2-enyl-4-diphosphate2 reductase from plasmodium falciparum
27	<a href="#">d1uura2</a>	Alignment	not modelled	12.5	22	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> p53-like transcription factors <b>Family:</b> STAT DNA-binding domain <b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> collagen alpha-2(i) chain,collagen alpha-

28	<a href="#">c5ctdB_</a>	Alignment	not modelled	11.3	43	Z(ix) chain; <b>PDBTitle:</b> crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen
29	<a href="#">d1o9ga_</a>	Alignment	not modelled	10.7	29	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> rRNA methyltransferase AviRa
30	<a href="#">c5ctdA_</a>	Alignment	not modelled	10.6	38	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen alpha-1(i) chain,collagen alpha-1(ix) chain; <b>PDBTitle:</b> crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen
31	<a href="#">c3dmwA_</a>	Alignment	not modelled	9.4	45	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen alpha-1(iii) chain; <b>PDBTitle:</b> crystal structure of human type iii collagen g982-g10232 containing c-terminal cystine knot
32	<a href="#">c3dmwB_</a>	Alignment	not modelled	9.2	45	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen alpha-1(iii) chain; <b>PDBTitle:</b> crystal structure of human type iii collagen g982-g10232 containing c-terminal cystine knot
33	<a href="#">c1xu2R_</a>	Alignment	not modelled	9.2	75	<b>PDB header:</b> cytokine, hormone/growth factor receptor <b>Chain:</b> R: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 17; <b>PDBTitle:</b> the crystal structure of april bound to bcma
34	<a href="#">d1xu2r_</a>	Alignment	not modelled	9.2	75	<b>Fold:</b> TNF receptor-like <b>Superfamily:</b> TNF receptor-like <b>Family:</b> BAFF receptor-like
35	<a href="#">c3dmwC_</a>	Alignment	not modelled	9.1	45	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen alpha-1(iii) chain; <b>PDBTitle:</b> crystal structure of human type iii collagen g982-g10232 containing c-terminal cystine knot
36	<a href="#">c2kkrA_</a>	Alignment	not modelled	8.9	56	<b>PDB header:</b> transcription, protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ataxin-7; <b>PDBTitle:</b> solution structure of sca7 zinc finger domain from human ataxin-7 protein
37	<a href="#">c2mviA_</a>	Alignment	not modelled	8.8	60	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriocin plantarican asm1; <b>PDBTitle:</b> structure of the s-glycosylated bacteriocin asm1
38	<a href="#">c4gyxC_</a>	Alignment	not modelled	8.4	27	<b>PDB header:</b> structural protein, blood clotting <b>Chain:</b> C: <b>PDB Molecule:</b> type iii collagen fragment in a host peptide stabilized by <b>PDBTitle:</b> the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
39	<a href="#">c1vytF_</a>	Alignment	not modelled	8.3	50	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> voltage-dependent l-type calcium channel <b>PDBTitle:</b> beta3 subunit complexed with aid
40	<a href="#">c2mtyA_</a>	Alignment	not modelled	8.3	27	<b>PDB header:</b> peptide binding <b>Chain:</b> A: <b>PDB Molecule:</b> starp antigen; <b>PDBTitle:</b> 3d structure determination of starp peptides implicated in p.2 falciparum invasion of hepatic cells
41	<a href="#">c2mz0A_</a>	Alignment	not modelled	8.2	78	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> defensin-like protein 32; <b>PDBTitle:</b> solution nmr structure of pdf12.1 from arabidopsis thaliana
42	<a href="#">c4gyxB_</a>	Alignment	not modelled	8.0	27	<b>PDB header:</b> structural protein, blood clotting <b>Chain:</b> B: <b>PDB Molecule:</b> type iii collagen fragment in a host peptide stabilized by <b>PDBTitle:</b> the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
43	<a href="#">c4gyxA_</a>	Alignment	not modelled	8.0	27	<b>PDB header:</b> structural protein, blood clotting <b>Chain:</b> A: <b>PDB Molecule:</b> type iii collagen fragment in a host peptide stabilized by <b>PDBTitle:</b> the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
44	<a href="#">c6g3bA_</a>	Alignment	not modelled	7.8	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> type ii site-specific deoxyribonuclease; <b>PDBTitle:</b> avaii restriction endonuclease in complex with an rna/dna hybrid
45	<a href="#">d1omba_</a>	Alignment	not modelled	7.6	47	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> omega toxin-like <b>Family:</b> Spider toxins
46	<a href="#">d1jixa_</a>	Alignment	not modelled	7.4	67	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> beta-Glycosyltransferase (DNA-modifying)
47	<a href="#">c4dmtB_</a>	Alignment	not modelled	7.4	23	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen iii derived peptide; <b>PDBTitle:</b> crystal structure of a vwf binding collagen iii derived triple helical2 peptide
48	<a href="#">c4dmtC_</a>	Alignment	not modelled	7.4	23	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen iii derived peptide; <b>PDBTitle:</b> crystal structure of a vwf binding collagen iii derived triple helical2 peptide
49	<a href="#">c4dmtA_</a>	Alignment	not modelled	7.4	23	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen iii derived peptide; <b>PDBTitle:</b> crystal structure of a vwf binding collagen iii derived triple helical2 peptide
50	<a href="#">c2y5tG_</a>	Alignment	not modelled	7.1	33	<b>PDB header:</b> immune system <b>Chain:</b> G: <b>PDB Molecule:</b> c1; <b>PDBTitle:</b> crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide
51	<a href="#">c2iu1A_</a>	Alignment	not modelled	6.8	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5; <b>PDBTitle:</b> crystal structure of eif5 c-terminal domain
52	<a href="#">c2y5tE_</a>	Alignment	not modelled	6.8	33	<b>PDB header:</b> immune system <b>Chain:</b> E: <b>PDB Molecule:</b> c1; <b>PDBTitle:</b> crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide

53	<a href="#">c2lyyB_</a>	Alignment	not modelled	6.7	32	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr structure of the protein nb7890a from shewanella sp
54	<a href="#">c2f6aJ_</a>	Alignment	not modelled	6.5	86	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> J: <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
55	<a href="#">c1qloA_</a>	Alignment	not modelled	6.5	42	<b>PDB header:</b> membrane proteins <b>Chain:</b> A: <b>PDB Molecule:</b> herpes simplex virus protein icp47; <b>PDBTitle:</b> structure of the active domain of the herpes simplex virus2 protein icp47 in water/sodium dodecyl sulfate solution3 determined by nuclear magnetic resonance spectroscopy
56	<a href="#">c2f6aG_</a>	Alignment	not modelled	6.5	86	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> G: <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
57	<a href="#">c2f6aE_</a>	Alignment	not modelled	6.5	86	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
58	<a href="#">c2f6aH_</a>	Alignment	not modelled	6.5	86	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> H: <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
59	<a href="#">c2f6aI_</a>	Alignment	not modelled	6.5	86	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> I: <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
60	<a href="#">c2f6aF_</a>	Alignment	not modelled	6.5	86	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
61	<a href="#">c2kn1A_</a>	Alignment	not modelled	6.4	75	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 17; <b>PDBTitle:</b> solution nmr structure of bcma
62	<a href="#">c6dzsD_</a>	Alignment	not modelled	6.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> mycobacterial homoserine dehydrogenase thra in complex with nadp
63	<a href="#">d1un8a4</a>	Alignment	not modelled	6.2	50	<b>Fold:</b> DAK1/DegV-like <b>Superfamily:</b> DAK1/DegV-like <b>Family:</b> DAK1
64	<a href="#">d1a0aa_</a>	Alignment	not modelled	6.1	16	<b>Fold:</b> HLH-like <b>Superfamily:</b> HLH, helix-loop-helix DNA-binding domain <b>Family:</b> HLH, helix-loop-helix DNA-binding domain
65	<a href="#">d1agga_</a>	Alignment	not modelled	6.1	47	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> omega toxin-like <b>Family:</b> Spider toxins
66	<a href="#">c5uc0B_</a>	Alignment	not modelled	6.1	60	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein cog5400; <b>PDBTitle:</b> crystal structure of beta-barrel-like, uncharacterized protein of2 cog5400 from brucella abortus
67	<a href="#">c2kg7A_</a>	Alignment	not modelled	5.9	29	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein esxg (pe family protein); <b>PDBTitle:</b> structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
68	<a href="#">c2wuhD_</a>	Alignment	not modelled	5.8	33	<b>PDB header:</b> receptor/peptide <b>Chain:</b> D: <b>PDB Molecule:</b> collagen peptide; <b>PDBTitle:</b> crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
69	<a href="#">c2y5tF_</a>	Alignment	not modelled	5.7	33	<b>PDB header:</b> immune system <b>Chain:</b> F: <b>PDB Molecule:</b> c1; <b>PDBTitle:</b> crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide
70	<a href="#">c2fulE_</a>	Alignment	not modelled	5.6	28	<b>PDB header:</b> translation <b>Chain:</b> E: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5; <b>PDBTitle:</b> crystal structure of the c-terminal domain of s. cerevisiae eif5
71	<a href="#">c4deyB_</a>	Alignment	not modelled	5.6	22	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> voltage-dependent l-type calcium channel subunit alpha-1c; <b>PDBTitle:</b> crystal structure of the voltage dependent calcium channel beta-22 subunit in complex with the cav1.2 i-ii linker.
72	<a href="#">d1iyxa1</a>	Alignment	not modelled	5.5	29	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> Enolase
73	<a href="#">c2wuhB_</a>	Alignment	not modelled	5.5	33	<b>PDB header:</b> receptor/peptide <b>Chain:</b> B: <b>PDB Molecule:</b> collagen peptide; <b>PDBTitle:</b> crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
74	<a href="#">c2wuhC_</a>	Alignment	not modelled	5.5	33	<b>PDB header:</b> receptor/peptide <b>Chain:</b> C: <b>PDB Molecule:</b> collagen peptide; <b>PDBTitle:</b> crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
75	<a href="#">d2c4fl3</a>	Alignment	not modelled	5.4	78	<b>Fold:</b> GLA-domain <b>Superfamily:</b> GLA-domain <b>Family:</b> GLA-domain
76	<a href="#">c2fwtA_</a>	Alignment	not modelled	5.3	38	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> dhc, diheme cytochrome c; <b>PDBTitle:</b> crystal structure of dhc purified from rhodobacter2 sphaeroides
77	<a href="#">c2k0aA_</a>	Alignment	not modelled	5.3	27	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna-splicing factor rds3; <b>PDBTitle:</b> 1h, 15n and 13c chemical shift assignments for rds3 protein
78	<a href="#">c4auoE_</a>	Alignment	not modelled	5.2	33	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> E: <b>PDB Molecule:</b> triple-helical collagen peptide; <b>PDBTitle:</b> crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide

79	<a href="#">c4auoH_</a>	Alignment	not modelled	5.2	33	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> H: <b>PDB Molecule:</b> triple-helical collagen peptide; <b>PDBTitle:</b> crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide
80	<a href="#">c3u99A_</a>	Alignment	not modelled	5.2	38	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> diheme cytochrome c; <b>PDBTitle:</b> the experimental x-ray structure of the new diheme cytochrome type c2 from shewanella baltica os155 sb-dhc
81	<a href="#">c6iczX_</a>	Alignment	not modelled	5.1	29	<b>PDB header:</b> splicing <b>Chain:</b> X: <b>PDB Molecule:</b> prkr-interacting protein 1; <b>PDBTitle:</b> cryo-em structure of a human post-catalytic spliceosome (p complex) at 2.3 angstrom
82	<a href="#">c6a0aA_</a>	Alignment	not modelled	5.1	25	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen type iii peptide; <b>PDBTitle:</b> structure of a triple-helix region of human collagen type iii
83	<a href="#">c2drxB_</a>	Alignment	not modelled	5.0	33	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen like peptide; <b>PDBTitle:</b> structure analysis of (pog)4-(log)2-(pog)4
84	<a href="#">c3ct4B_</a>	Alignment	not modelled	5.0	60	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pts-dependent dihydroxyacetone kinase, dihydroxyacetone- <b>PDBTitle:</b> structure of dha-kinase subunit dhak from l. lactis
85	<a href="#">c2drxA_</a>	Alignment	not modelled	5.0	33	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen like peptide; <b>PDBTitle:</b> structure analysis of (pog)4-(log)2-(pog)4