
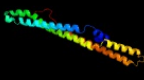

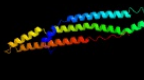

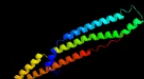



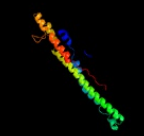





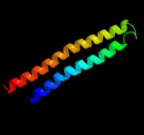



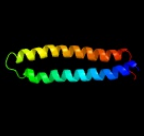

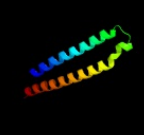


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2108_(PPE36)_2367719_2368450
Date	Mon Aug 5 13:25:22 BST 2019
Unique Job ID	c64a468eafe6288b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xfsB_</a>	 Alignment		100.0	43	<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	16	<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="#">c4wj2A_</a>	 Alignment		98.5	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> antigen mtb48; <b>PDBTitle:</b> mycobacterial protein
6	<a href="#">c2vs0B_</a>	 Alignment		97.9	16	<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
7	<a href="#">c3gvmA_</a>	 Alignment		97.8	18	<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		97.7	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
9	<a href="#">c3zbhC_</a>	 Alignment		97.6	23	<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		96.9	12	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
11	<a href="#">c4lwsA_</a>	 Alignment		96.5	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	13	<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		96.0	17	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
14	<a href="#">c4i0xA_</a>	Alignment		95.4	16	<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		91.4	13	<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		75.3	19	<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="#">c3txaA_</a>	Alignment		44.7	57	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> cell wall surface anchor family protein; <b>PDBTitle:</b> structural analysis of adhesive tip pilin, gbs104 from group b2 streptococcus agalactiae
18	<a href="#">d1zyea1</a>	Alignment		20.5	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
19	<a href="#">d2f8aa1</a>	Alignment		19.8	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
20	<a href="#">d1gp1a_</a>	Alignment		17.1	17	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
21	<a href="#">c3drnB_</a>	Alignment	not modelled	16.9	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> peroxiredoxin, bacterioferritin comigratory protein <b>PDBTitle:</b> the crystal structure of bcp1 from sulfobolus sulfataricus
22	<a href="#">d1st9a_</a>	Alignment	not modelled	16.8	31	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
23	<a href="#">d1jfma_</a>	Alignment	not modelled	16.6	14	<b>Fold:</b> MHC antigen-recognition domain <b>Superfamily:</b> MHC antigen-recognition domain <b>Family:</b> MHC antigen-recognition domain
24	<a href="#">c1bkvA_</a>	Alignment	not modelled	16.4	50	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
25	<a href="#">c1bkvC_</a>	Alignment	not modelled	15.4	50	<b>PDB header:</b> structural protein <b>Chain:</b> C; <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
26	<a href="#">c1bkvB_</a>	Alignment	not modelled	15.4	50	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
27	<a href="#">c2p5qA_</a>	Alignment	not modelled	15.2	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> glutathione peroxidase 5; <b>PDBTitle:</b> crystal structure of the poplar glutathione peroxidase 5 in the2 reduced form
28	<a href="#">c3tw0D_</a>	Alignment	not modelled	14.8	33	<b>PDB header:</b> cell adhesion <b>Chain:</b> D; <b>PDB Molecule:</b> cell wall surface anchor family protein; <b>PDBTitle:</b> structural analysis of adhesive tip pilin, gbs104 from group b2 streptococcus agalactiae
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> alkyl hydroperoxide reductase/ thiol

29	<a href="#">c5enuB</a>	Alignment	not modelled	13.8	25	specific antioxidant/ <b>PDBTitle:</b> crystal structure of an alkyl hydroperoxide reductase from burkholderia2 ambifaria
30	<a href="#">c2n5uA</a>	Alignment	not modelled	13.4	21	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> tsr0524 protein; <b>PDBTitle:</b> solution structure of the cyanobacterial cytochrome b6f complex2 subunit petp
31	<a href="#">c3lorB</a>	Alignment	not modelled	13.3	38	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> thiol-disulfide isomerase and thioredoxins; <b>PDBTitle:</b> the crystal structure of a thiol-disulfide isomerase from2 corynebacterium glutamicum to 2.2a
32	<a href="#">c2hyxA</a>	Alignment	not modelled	12.1	33	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein dipz; <b>PDBTitle:</b> structure of the c-terminal domain of dipz from mycobacterium2 tuberculosis
33	<a href="#">c2v1mA</a>	Alignment	not modelled	11.9	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione peroxidase; <b>PDBTitle:</b> crystal structure of schistosoma mansoni glutathione peroxidase
34	<a href="#">c4ka0C</a>	Alignment	not modelled	11.5	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative thiol-disulfide oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative thiol-disulfide oxidoreductase from2 bacteroides vulgatus (target nysgrc-011676), space group p21221
35	<a href="#">c2wpyA</a>	Alignment	not modelled	11.4	50	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4 leucine zipper mutant with one vxxnxxx motif2 coordinating chloride
36	<a href="#">d1qxha</a>	Alignment	not modelled	10.9	9	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
37	<a href="#">c3pmdA</a>	Alignment	not modelled	10.8	29	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> conserved domain protein; <b>PDBTitle:</b> crystal structure of the sporulation inhibitor pxo1-118 from bacillus2 anthracis
38	<a href="#">c2yp6A</a>	Alignment	not modelled	10.7	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin family protein; <b>PDBTitle:</b> crystal structure of the pneumococcal exposed lipoprotein2 thioredoxin sp_1000 (etrx2) from streptococcus pneumoniae3 strain tigr4 in complex with cyclofos 3 tm
39	<a href="#">c3eytA</a>	Alignment	not modelled	10.4	31	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein spoa0173; <b>PDBTitle:</b> crystal structure of thioredoxin-like superfamily protein spoa0173
40	<a href="#">c2h66G</a>	Alignment	not modelled	10.4	12	<b>PDB header:</b> structural genomics/oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> pv-pf14_0368; <b>PDBTitle:</b> the crystal structure of plasmodium vivax 2-cys2 peroxiredoxin
41	<a href="#">c3mp6A</a>	Alignment	not modelled	10.3	53	<b>PDB header:</b> histone binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,linker,saga-associated <b>PDBTitle:</b> complex structure of sgf29 and dimethylated h3k4
42	<a href="#">c4g7xB</a>	Alignment	not modelled	10.2	17	<b>PDB header:</b> protein binding/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> tola protein; <b>PDBTitle:</b> crystal structure of a complex between the ctxphi piiii n-terminal2 domain and the vibrio cholerae tola c-terminal domain
43	<a href="#">c2iu1A</a>	Alignment	not modelled	10.2	14	<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
44	<a href="#">c3ixrA</a>	Alignment	not modelled	10.1	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bacterioferritin comigratory protein; <b>PDBTitle:</b> crystal structure of xylella fastidiosa prqx c47s mutant
45	<a href="#">c4je1A</a>	Alignment	not modelled	9.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable thiol peroxidase; <b>PDBTitle:</b> crystal structure of thiol peroxidase from burkholderia cenocepacia2 j2315
46	<a href="#">d3e9va1</a>	Alignment	not modelled	9.6	27	<b>Fold:</b> BTG domain-like <b>Superfamily:</b> BTG domain-like <b>Family:</b> BTG domain-like
47	<a href="#">c4yk3B</a>	Alignment	not modelled	9.4	20	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> bepe protein; <b>PDBTitle:</b> crystal structure of the bid domain of bepe from bartonella henselae
48	<a href="#">c4yk2B</a>	Alignment	not modelled	9.1	14	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> bartonella effector protein (bep) substrate of virb t4ss; <b>PDBTitle:</b> crystal structure of the bid domain of bep9 from bartonella2 clarridgeiae
49	<a href="#">c2eqmA</a>	Alignment	not modelled	9.1	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> phd finger protein 20-like 1; <b>PDBTitle:</b> solution structure of the tudor domain of phd finger2 protein 20-like 1 [homo sapiens]
50	<a href="#">c2l5oA</a>	Alignment	not modelled	8.9	47	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioredoxin; <b>PDBTitle:</b> solution structure of a putative thioredoxin from neisseria2 meningitidis
51	<a href="#">d1knga</a>	Alignment	not modelled	8.7	44	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
52	<a href="#">d1e6yb1</a>	Alignment	not modelled	8.6	26	<b>Fold:</b> Methyl-coenzyme M reductase alpha and beta chain C-terminal domain <b>Superfamily:</b> Methyl-coenzyme M reductase alpha and beta chain C-terminal domain <b>Family:</b> Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
53	<a href="#">d1rqba1</a>	Alignment	not modelled	8.6	48	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> post-HMGL domain-like <b>Family:</b> Conserved carboxylase domain

54	<a href="#">d2bzba1</a>	Alignment	not modelled	8.6	35	<b>Fold:</b> ROP-like <b>Superfamily:</b> BAS1536-like <b>Family:</b> BAS1536-like
55	<a href="#">c3rmrA</a>	Alignment	not modelled	8.4	32	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> avirulence protein; <b>PDBTitle:</b> crystal structure of hyaloperonospora arabidopsidis atr1 effector2 domain
56	<a href="#">c2r37A</a>	Alignment	not modelled	8.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> glutathione peroxidase 3; <b>PDBTitle:</b> crystal structure of human glutathione peroxidase 3 (selenocysteine to2 glycine mutant)
57	<a href="#">c2x5rA</a>	Alignment	not modelled	8.3	37	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein orf126; <b>PDBTitle:</b> crystal structure of the hypothetical protein orf126 from pyrobaculum2 spherical virus
58	<a href="#">c3gknA</a>	Alignment	not modelled	8.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> bacterioferritin comigratory protein; <b>PDBTitle:</b> insights into the alkyl peroxide reduction activity of xanthomonas2 campestris bacterioferritin comigratory protein from the trapped3 intermediate/ligand complex structures
59	<a href="#">d1hbnb1</a>	Alignment	not modelled	8.3	38	<b>Fold:</b> Methyl-coenzyme M reductase alpha and beta chain C-terminal domain <b>Superfamily:</b> Methyl-coenzyme M reductase alpha and beta chain C-terminal domain <b>Family:</b> Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
60	<a href="#">c3cmiA</a>	Alignment	not modelled	8.2	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> peroxiredoxin hyr1; <b>PDBTitle:</b> crystal structure of glutathione-dependent phospholipid peroxidase2 hyr1 from the yeast saccharomyces cerevisiae
61	<a href="#">c4luqD</a>	Alignment	not modelled	8.1	100	<b>PDB header:</b> protein binding/toxin inhibitor <b>Chain:</b> D; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of virulence effector tse3 in complex with2 neutralizer tsi3
62	<a href="#">c4mm1E</a>	Alignment	not modelled	8.1	24	<b>PDB header:</b> transferase <b>Chain:</b> E; <b>PDB Molecule:</b> geranylgeranylglyceryl phosphate synthase; <b>PDBTitle:</b> gggps from methanothermobacter thermautotrophicus
63	<a href="#">c6mn5A</a>	Alignment	not modelled	8.1	25	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A; <b>PDB Molecule:</b> aminoglycoside n(3)-acetyltransferase, aac(3)-iva; <b>PDBTitle:</b> crystal structure of aminoglycoside acetyltransferase aac(3)-iva,2 h154a mutant, in complex with gentamicin c1a
64	<a href="#">c2fulE</a>	Alignment	not modelled	8.0	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
65	<a href="#">d1zupa1</a>	Alignment	not modelled	7.8	33	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> TM1739-like
66	<a href="#">c4gyxC</a>	Alignment	not modelled	7.8	45	<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
67	<a href="#">c6a97A</a>	Alignment	not modelled	7.8	19	<b>PDB header:</b> immune system <b>Chain:</b> A; <b>PDB Molecule:</b> mhc i-like leukocyte 2 long form; <b>PDBTitle:</b> crystal structure of mhc-like mill2
68	<a href="#">c2lndA</a>	Alignment	not modelled	7.8	44	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> de novo designed protein, pfk fold; <b>PDBTitle:</b> solution nmr structure of de novo designed protein, pfk fold,2 northeast structural genomics consortium target or134
69	<a href="#">c3hfxA</a>	Alignment	not modelled	7.8	23	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> l-carnitine/gamma-butyrobetaine antiporter; <b>PDBTitle:</b> crystal structure of carnitine transporter
70	<a href="#">c2b1kA</a>	Alignment	not modelled	7.8	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbe; <b>PDBTitle:</b> crystal structure of e. coli ccmg protein
71	<a href="#">c5frgA</a>	Alignment	not modelled	7.8	63	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> formin-binding protein 1-like; <b>PDBTitle:</b> the nmr structure of the cdc42-interacting region of toca1
72	<a href="#">c3hm6X</a>	Alignment	not modelled	7.7	17	<b>PDB header:</b> signaling protein <b>Chain:</b> X; <b>PDB Molecule:</b> plexin-b1; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of human plexin b1
73	<a href="#">d2b0ja2</a>	Alignment	not modelled	7.7	70	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
74	<a href="#">c2wpzA</a>	Alignment	not modelled	7.7	50	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4 leucine zipper mutant with two vxxnxxx motifs2 coordinating chloride
75	<a href="#">c5j4fB</a>	Alignment	not modelled	7.6	22	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the n-terminally his6-tagged hp0902, an2 uncharacterized protein from helicobacter pylori 26695
76	<a href="#">c2y5tG</a>	Alignment	not modelled	7.5	83	<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
77	<a href="#">c6qm7V</a>	Alignment	not modelled	7.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> V; <b>PDB Molecule:</b> proteasome beta1 chain; <b>PDBTitle:</b> leishmania tarentolae proteasome 20s subunit complexed with gsk3494245
78	<a href="#">c4gyxB</a>	Alignment	not modelled	7.5	45	<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
79	<a href="#">c4gyxA</a>	Alignment	not modelled	7.5	45	<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
80	<a href="#">c5e6pA</a>	Alignment	not modelled	7.4	24	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> plexin-b2; <b>PDBTitle:</b> plexinb2 cytoplasmic region/pdz-rhogef pdz domain complex
81	<a href="#">c3dvvB</a>	Alignment	not modelled	7.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione peroxidase-like protein; <b>PDBTitle:</b> glutathione peroxidase-type tryparedoxin peroxidase, oxidized form
82	<a href="#">d2b5xa1</a>	Alignment	not modelled	7.3	31	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
83	<a href="#">d1ui5a2</a>	Alignment	not modelled	7.2	17	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
84	<a href="#">c5v6rB</a>	Alignment	not modelled	7.2	17	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> plexin-d1; <b>PDBTitle:</b> structure of plexin d1 intracellular domain
85	<a href="#">c2y5tE</a>	Alignment	not modelled	7.2	83	<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
86	<a href="#">c3lwaA</a>	Alignment	not modelled	7.2	31	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> secreted thiol-disulfide isomerase; <b>PDBTitle:</b> the crystal structure of a secreted thiol-disulfide isomerase from2 corynebacterium glutamicum to 1.75a
87	<a href="#">c2wpzB</a>	Alignment	not modelled	7.2	50	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4 leucine zipper mutant with two vxxnxxx motifs2 coordinating chloride
88	<a href="#">c3ig3A</a>	Alignment	not modelled	7.1	24	<b>PDB header:</b> signaling protein, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> plxn3 protein; <b>PDBTitle:</b> crystal structure of mouse plexin a3 intracellular domain
89	<a href="#">c2c0dA</a>	Alignment	not modelled	7.1	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin peroxidase 2; <b>PDBTitle:</b> structure of the mitochondrial 2-cys peroxidoredoxin from2 plasmodium falciparum
90	<a href="#">c4h5bB</a>	Alignment	not modelled	7.1	34	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> dr_1245 protein; <b>PDBTitle:</b> crystal structure of dr_1245 from deinococcus radiodurans
91	<a href="#">c1de4A</a>	Alignment	not modelled	7.1	16	<b>PDB header:</b> metal transport inhibitor/receptor <b>Chain:</b> A: <b>PDB Molecule:</b> hemochromatosis protein; <b>PDBTitle:</b> hemochromatosis protein hfe complexed with transferrin receptor
92	<a href="#">c3ia1A</a>	Alignment	not modelled	7.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thio-disulfide isomerase/thioredoxin; <b>PDBTitle:</b> crystal structure of thio-disulfide isomerase from thermus2 thermophilus
93	<a href="#">c2wpzC</a>	Alignment	not modelled	7.0	50	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4 leucine zipper mutant with two vxxnxxx motifs2 coordinating chloride
94	<a href="#">d1jfua</a>	Alignment	not modelled	7.0	22	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
95	<a href="#">c3su8X</a>	Alignment	not modelled	6.9	17	<b>PDB header:</b> apoptosis/signaling protein <b>Chain:</b> X: <b>PDB Molecule:</b> plexin-b1; <b>PDBTitle:</b> crystal structure of a truncated intracellular domain of plexin-b1 in2 complex with rac1
96	<a href="#">c4dmtC</a>	Alignment	not modelled	6.9	38	<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
97	<a href="#">c4dmtB</a>	Alignment	not modelled	6.9	38	<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
98	<a href="#">c4dmtA</a>	Alignment	not modelled	6.9	38	<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
99	<a href="#">d1we0a1</a>	Alignment	not modelled	6.7	17	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like