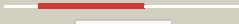
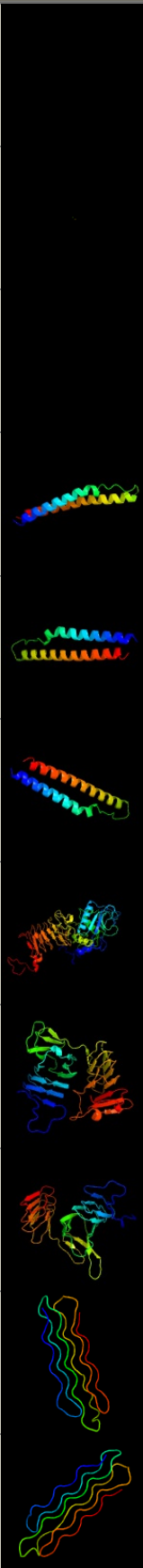

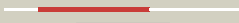








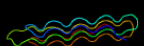
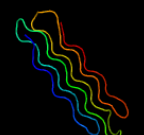


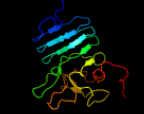


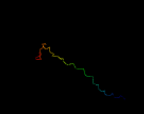



# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD3508\_(PE\_PGR554)\_3931184\_3936889  
 Date Fri Aug 9 18:20:18 BST 2019  
 Unique Job ID f91f8a94f14afc97

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1ygvA_</a>	 Alignment		100.0	28	<b>PDB header:</b> structural protein/contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen i alpha 1; <b>PDBTitle:</b> the structure of collagen type i. single type i collagen2 molecule: rigid refinement
2	<a href="#">c1y0fB_</a>	 Alignment		100.0	28	<b>PDB header:</b> structural protein/contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen i alpha 2; <b>PDBTitle:</b> the structure of collagen type i. single type i collagen2 molecule
3	<a href="#">c3hqvB_</a>	 Alignment		100.0	31	<b>PDB header:</b> structural protein, contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen alpha-2(i) chain; <b>PDBTitle:</b> low resolution, molecular envelope structure of type i2 collagen in situ determined by fiber diffraction. single3 type i collagen molecule, rigid body refinement
4	<a href="#">c5xfA_</a>	 Alignment		99.9	47	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> pe family protein pe8; <b>PDBTitle:</b> crystal structure of pe8-ppe15 in complex with espg5 from m.2 tuberculosis
5	<a href="#">d2g38a1</a>	 Alignment		99.9	31	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PE
6	<a href="#">c2g38A_</a>	 Alignment		99.9	31	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> pe family protein; <b>PDBTitle:</b> a pe/pep protein complex from mycobacterium tuberculosis
7	<a href="#">c1k7qA_</a>	 Alignment		98.6	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> secreted protease c; <b>PDBTitle:</b> prtC from erwinia chrysanthemi: e189a mutant
8	<a href="#">c2zj6A_</a>	 Alignment		97.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> crystal structure of d337a mutant of pseudomonas sp. mis38 lipase
9	<a href="#">c2qubG_</a>	 Alignment		97.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> extracellular lipase; <b>PDBTitle:</b> crystal structure of extracellular lipase lipa from serratia2 marcescens
10	<a href="#">c3bogB_</a>	 Alignment		97.4	41	<b>PDB header:</b> antifreeze protein <b>Chain:</b> B: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein; <b>PDBTitle:</b> snow flea antifreeze protein quasi-racemate
11	<a href="#">c3bogA_</a>	 Alignment		97.4	41	<b>PDB header:</b> antifreeze protein <b>Chain:</b> A: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein; <b>PDBTitle:</b> snow flea antifreeze protein quasi-racemate

12	<a href="#">c2pneA</a>	Alignment		97.2	42	<b>PDB header:</b> antifreeze protein <b>Chain:</b> A: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein; <b>PDBTitle:</b> crystal structure of the snow flea antifreeze protein
13	<a href="#">c3boiB</a>	Alignment		97.2	42	<b>PDB header:</b> antifreeze protein <b>Chain:</b> B: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein; <b>PDBTitle:</b> snow flea antifreeze protein racemate
14	<a href="#">c3boiA</a>	Alignment		97.2	42	<b>PDB header:</b> antifreeze protein <b>Chain:</b> A: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein; <b>PDBTitle:</b> snow flea antifreeze protein racemate
15	<a href="#">d1kapp1</a>	Alignment		96.8	16	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
16	<a href="#">c2ml3A</a>	Alignment		96.7	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(beta-d-mannuronate) c5 epimerase 6; <b>PDBTitle:</b> solution structure of alge6r3 subunit from the azotobacter vinelandii2 mannuronan c5-epimerase
17	<a href="#">d1sata1</a>	Alignment		96.4	15	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
18	<a href="#">c1satA</a>	Alignment		96.3	16	<b>PDB header:</b> hydrolase (serine protease) <b>Chain:</b> A: <b>PDB Molecule:</b> serratia protease; <b>PDBTitle:</b> crystal structure of the 50 kda metallo protease from s.2 marcescens
19	<a href="#">c1nayC</a>	Alignment		95.9	25	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> gpp-foldon:x-ray structure
20	<a href="#">c2ml2A</a>	Alignment		95.4	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(beta-d-mannuronate) c5 epimerase 6; <b>PDBTitle:</b> solution structure of alge6r2 subunit from the azotobacter vinelandii2 mannuronan c5-epimerase
21	<a href="#">d1k7ia1</a>	Alignment	not modelled	95.2	14	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
22	<a href="#">d1g9ka1</a>	Alignment	not modelled	94.8	18	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
23	<a href="#">c2agmA</a>	Alignment	not modelled	94.3	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(beta-d-mannuronate) c5 epimerase 4; <b>PDBTitle:</b> solution structure of the r-module from alge4
24	<a href="#">c5ctdB</a>	Alignment	not modelled	94.1	33	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen alpha-2(i) chain,collagen alpha-2(ix) chain; <b>PDBTitle:</b> crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen
25	<a href="#">c5ctiC</a>	Alignment	not modelled	93.8	33	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen alpha-1(i) chain,collagen alpha-3(ix) chain; <b>PDBTitle:</b> crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen (native form)
26	<a href="#">c1jiwP</a>	Alignment	not modelled	93.7	22	<b>PDB header:</b> hydrolase/hyrolase inhibitor <b>Chain:</b> P: <b>PDB Molecule:</b> alkaline metalloproteinase; <b>PDBTitle:</b> crystal structure of the apr-aprin complex
27	<a href="#">c5ctdA</a>	Alignment	not modelled	93.7	31	<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
28	<a href="#">c1om8A_</a>	Alignment	not modelled	93.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serralysin; <b>PDBTitle:</b> crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallized with 10 mm edta
29	<a href="#">c5cxIA_</a>	Alignment	not modelled	87.4	26	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional hemolysin/adenylate cyclase; <b>PDBTitle:</b> crystal structure of rtx domain block v of adenylate cyclase toxin2 from bordetella pertussis
30	<a href="#">c2klwA_</a>	Alignment	not modelled	80.4	33	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> (pkg)10; <b>PDBTitle:</b> solution structure of an abc collagen heterotrimer reveals a2 single-register helix stabilized by electrostatic3 interactions
31	<a href="#">c2cuoF_</a>	Alignment	not modelled	73.5	37	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
32	<a href="#">c2cuoC_</a>	Alignment	not modelled	73.5	37	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
33	<a href="#">c1k6fF_</a>	Alignment	not modelled	69.3	38	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen triple helix; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
34	<a href="#">c1k6fB_</a>	Alignment	not modelled	69.3	38	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen triple helix; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
35	<a href="#">c1k6fD_</a>	Alignment	not modelled	69.3	38	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen triple helix; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
36	<a href="#">c1k6fA_</a>	Alignment	not modelled	69.3	38	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen triple helix; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
37	<a href="#">c1k6fC_</a>	Alignment	not modelled	69.3	38	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen triple helix; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
38	<a href="#">c1k6fE_</a>	Alignment	not modelled	69.3	38	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen triple helix; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
39	<a href="#">c3p4gD_</a>	Alignment	not modelled	67.5	14	<b>PDB header:</b> antifreeze protein <b>Chain:</b> D: <b>PDB Molecule:</b> antifreeze protein; <b>PDBTitle:</b> x-ray crystal structure of a hyperactive, ca2+-dependent, beta-helical2 antifreeze protein from an antarctic bacterium
40	<a href="#">c3ah9F_</a>	Alignment	not modelled	66.9	35	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
41	<a href="#">c3ah9E_</a>	Alignment	not modelled	65.9	35	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
42	<a href="#">c3ah9B_</a>	Alignment	not modelled	65.9	35	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
43	<a href="#">c3ah9C_</a>	Alignment	not modelled	65.9	35	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
44	<a href="#">c3a0mF_</a>	Alignment	not modelled	61.5	35	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
45	<a href="#">c2cuoA_</a>	Alignment	not modelled	59.9	35	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
46	<a href="#">c2cuoE_</a>	Alignment	not modelled	59.9	35	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
47	<a href="#">c2cuoB_</a>	Alignment	not modelled	59.9	35	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
48	<a href="#">c2cuoD_</a>	Alignment	not modelled	59.9	35	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
49	<a href="#">c3ah9D_</a>	Alignment	not modelled	58.0	33	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
50	<a href="#">c3ah9A_</a>	Alignment	not modelled	51.8	32	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
51	<a href="#">c3gvmA_</a>	Alignment	not modelled	46.2	19	<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
52	<a href="#">d1n7ka_</a>	Alignment	not modelled	45.5	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
53	<a href="#">c4iogD_</a>	Alignment	not modelled	39.5	15	<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 <b>PDB header:</b> unknown function

54	<a href="#">c2mgxA_</a>	Alignment	not modelled	37.4	27	<b>Chain:</b> A: <b>PDB Molecule:</b> steroid receptor rna activator 1; <b>PDBTitle:</b> nmr structure of sra1p c-terminal domain
55	<a href="#">c2vs0B_</a>	Alignment	not modelled	35.3	17	<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
56	<a href="#">c3ngiC_</a>	Alignment	not modelled	31.6	25	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> deoxyribose-phosphate aldolase; <b>PDBTitle:</b> crystal structure of a putative deoxyribose-phosphate aldolase from2 entamoeba histolytica
57	<a href="#">c6cfzj_</a>	Alignment	not modelled	31.5	28	<b>PDB header:</b> nuclear protein <b>Chain:</b> J: <b>PDB Molecule:</b> spc34; <b>PDBTitle:</b> structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
58	<a href="#">c2gp4A_</a>	Alignment	not modelled	30.7	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydratase; <b>PDBTitle:</b> structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
59	<a href="#">d1wa8a1</a>	Alignment	not modelled	30.1	8	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
60	<a href="#">d1p1xa_</a>	Alignment	not modelled	27.2	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
61	<a href="#">c3abnA_</a>	Alignment	not modelled	25.7	42	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-asp-gly-(pro-pro-gly)4 at 1.022 a
62	<a href="#">c3admB_</a>	Alignment	not modelled	24.9	42	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
63	<a href="#">c3admE_</a>	Alignment	not modelled	24.9	42	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
64	<a href="#">c3admF_</a>	Alignment	not modelled	24.9	42	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
65	<a href="#">c3admA_</a>	Alignment	not modelled	24.9	42	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
66	<a href="#">c4xbsA_</a>	Alignment	not modelled	23.2	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> deoxyribose-phosphate aldolase; <b>PDBTitle:</b> 2-deoxyribose-5-phosphate aldolase mutant - e78k
67	<a href="#">c6bjcP_</a>	Alignment	not modelled	22.8	36	<b>PDB header:</b> cell cycle <b>Chain:</b> P: <b>PDB Molecule:</b> targeting protein for xklp2; <b>PDBTitle:</b> tpx2_mini decorated gmpcpp-microtubule
68	<a href="#">c6bjcT_</a>	Alignment	not modelled	22.8	36	<b>PDB header:</b> cell cycle <b>Chain:</b> T: <b>PDB Molecule:</b> targeting protein for xklp2; <b>PDBTitle:</b> tpx2_mini decorated gmpcpp-microtubule
69	<a href="#">d1ub3a_</a>	Alignment	not modelled	22.8	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
70	<a href="#">c5f5ul_</a>	Alignment	not modelled	22.0	53	<b>PDB header:</b> splicing <b>Chain:</b> I: <b>PDB Molecule:</b> zinc finger domain-containing protein; <b>PDBTitle:</b> crystal structure of the snu23-prp38-mfap1(217-258) complex of2 chaetomium thermophilum
71	<a href="#">d1o0ya_</a>	Alignment	not modelled	21.3	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
72	<a href="#">c5f5uF_</a>	Alignment	not modelled	20.6	53	<b>PDB header:</b> splicing <b>Chain:</b> F: <b>PDB Molecule:</b> zinc finger domain-containing protein; <b>PDBTitle:</b> crystal structure of the snu23-prp38-mfap1(217-258) complex of2 chaetomium thermophilum
73	<a href="#">c3zbhC_</a>	Alignment	not modelled	20.5	16	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> esxa; <b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i
74	<a href="#">c6hxoH_</a>	Alignment	not modelled	20.4	13	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> atp-citrate lyase alpha-subunit; <b>PDBTitle:</b> structure of the citryl-coa lyase core module of chlorobium limicola2 atp citrate lyase (space group p21)
75	<a href="#">c2kg7B_</a>	Alignment	not modelled	20.2	13	<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
76	<a href="#">c3l6dB_</a>	Alignment	not modelled	20.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
77	<a href="#">c1x1kD_</a>	Alignment	not modelled	19.9	38	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp- <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
78	<a href="#">c1x1kA_</a>	Alignment	not modelled	19.9	38	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp- <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
79	<a href="#">c2d3fD_</a>	Alignment	not modelled	19.9	38	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4

80	<a href="#">c1x1kB</a>	Alignment	not modelled	19.9	38	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp- <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
81	<a href="#">c2d3fE</a>	Alignment	not modelled	19.9	38	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
82	<a href="#">c2d3ff</a>	Alignment	not modelled	19.9	38	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
83	<a href="#">c1x1kC</a>	Alignment	not modelled	19.9	38	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp- <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
84	<a href="#">c3qyqC</a>	Alignment	not modelled	19.3	21	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> deoxyribose-phosphate aldolase, putative; <b>PDBTitle:</b> 1.8 angstrom resolution crystal structure of a putative deoxyribose-2 phosphate aldolase from toxoplasma gondii me49
85	<a href="#">c5f5uC</a>	Alignment	not modelled	19.2	53	<b>PDB header:</b> splicing <b>Chain:</b> C: <b>PDB Molecule:</b> zinc finger domain-containing protein; <b>PDBTitle:</b> crystal structure of the snu23-prp38-mfap1(217-258) complex of2 chaetomium thermophilum
86	<a href="#">c2a4aB</a>	Alignment	not modelled	18.9	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> deoxyribose-phosphate aldolase; <b>PDBTitle:</b> deoxyribose-phosphate aldolase from p. yoelii
87	<a href="#">d1liab</a>	Alignment	not modelled	18.7	21	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
88	<a href="#">c2yruA</a>	Alignment	not modelled	18.4	24	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> steroid receptor rna activator 1; <b>PDBTitle:</b> solution structure of mouse steroid receptor rna activator2 1 (sra1) protein
89	<a href="#">d1lt7a</a>	Alignment	not modelled	18.3	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Homocysteine S-methyltransferase <b>Family:</b> Homocysteine S-methyltransferase
90	<a href="#">d2odfa1</a>	Alignment	not modelled	17.1	15	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> FGase-like
91	<a href="#">c5odoA</a>	Alignment	not modelled	16.6	44	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> isomerase; <b>PDBTitle:</b> crystal structure of the oleate hydratase of rhodococcus erythropolis
92	<a href="#">c3h6pB</a>	Alignment	not modelled	16.5	63	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> esat-6 like protein exs; <b>PDBTitle:</b> crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
93	<a href="#">c3ng3A</a>	Alignment	not modelled	15.7	29	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> deoxyribose-phosphate aldolase; <b>PDBTitle:</b> crystal structure of deoxyribose phosphate aldolase from mycobacterium2 avium 104 in a schiff base with an unknown aldehyde
94	<a href="#">c3a19D</a>	Alignment	not modelled	15.7	54	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
95	<a href="#">c4an5F</a>	Alignment	not modelled	15.4	34	<b>PDB header:</b> virus <b>Chain:</b> F: <b>PDB Molecule:</b> coat protein; <b>PDBTitle:</b> capsid structure and its stability at the late stages of bacteriophage2 spp1 assembly
96	<a href="#">c2o01H</a>	Alignment	not modelled	15.1	24	<b>PDB header:</b> photosynthesis <b>Chain:</b> H: <b>PDB Molecule:</b> photosystem i reaction center subunit vi, chloroplast; <b>PDBTitle:</b> the structure of a plant photosystem i supercomplex at 3.4 angstrom2 resolution
97	<a href="#">c2kg7A</a>	Alignment	not modelled	14.2	44	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein exsg (pe family protein); <b>PDBTitle:</b> structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
98	<a href="#">d1h72c2</a>	Alignment	not modelled	14.2	2	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> Homoserine kinase
99	<a href="#">c5dbul</a>	Alignment	not modelled	13.5	33	<b>PDB header:</b> lyase <b>Chain:</b> I: <b>PDB Molecule:</b> deoxyribose-phosphate aldolase; <b>PDBTitle:</b> crystal structure of 2-deoxyribose-5-phosphate aldolase (1-220) from2 streptococcus suis