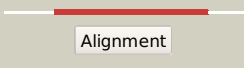
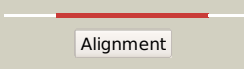
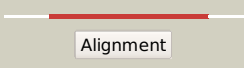
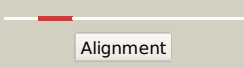
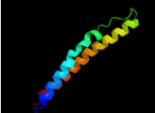
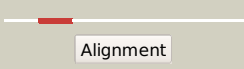
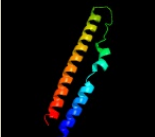
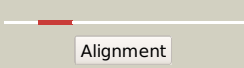
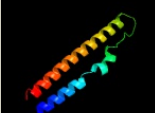
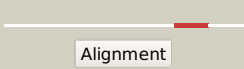

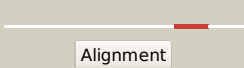

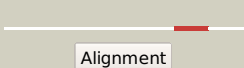

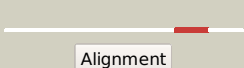

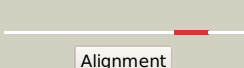






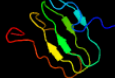


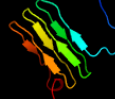


# Phyre2

Email	mdejesus@rockefeller.edu
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Date	Fri Jul 26 01:50:13 BST 2019
Unique Job ID	0bd498cb083e4215

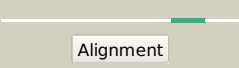
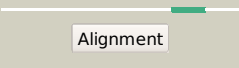
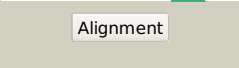
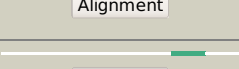
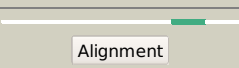
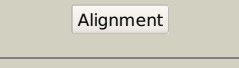

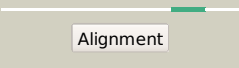
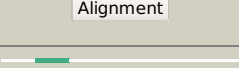
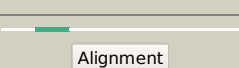
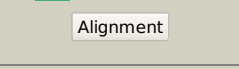
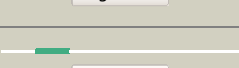
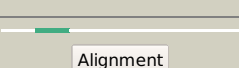
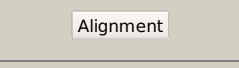
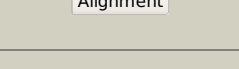
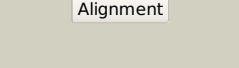
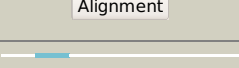
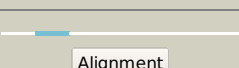
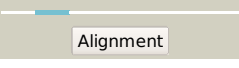

Detailed template information

#	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	26	<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	28	<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	44	<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	32	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PE
6	<a href="#">c2g38A_</a>	 Alignment		99.9	32	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> pe family protein; <b>PDBTitle:</b> a pe/ppe protein complex from mycobacterium tuberculosis
7	<a href="#">c3bogB_</a>	 Alignment		97.7	37	<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
8	<a href="#">c3bogA_</a>	 Alignment		97.7	37	<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
9	<a href="#">c2pneA_</a>	 Alignment		97.7	36	<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
10	<a href="#">c3boiB_</a>	 Alignment		97.6	36	<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
11	<a href="#">c3boiA_</a>	 Alignment		97.6	36	<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

12	<a href="#">c5ctiC_</a>	Alignment		96.1	36	<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)
13	<a href="#">c1nayC_</a>	Alignment		96.0	27	<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
14	<a href="#">c5ctdB_</a>	Alignment		96.0	35	<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
15	<a href="#">c5ctdA_</a>	Alignment		96.0	33	<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
16	<a href="#">c1k7qA_</a>	Alignment		95.4	21	<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
17	<a href="#">c2ml3A_</a>	Alignment		94.1	21	<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
18	<a href="#">c3gvmA_</a>	Alignment		93.5	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
19	<a href="#">c4iogD_</a>	Alignment		93.4	14	<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
20	<a href="#">d1k7ia1</a>	Alignment		93.2	23	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
21	<a href="#">d1kapp1</a>	Alignment	not modelled	92.3	23	<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="#">c1jiwP_</a>	Alignment	not modelled	92.3	24	<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
23	<a href="#">c2ml2A_</a>	Alignment	not modelled	92.2	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 alge6r2 subunit from the azotobacter vinelandii2 mannuronan c5-epimerase
24	<a href="#">c1satA_</a>	Alignment	not modelled	91.4	24	<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
25	<a href="#">c2zj6A_</a>	Alignment	not modelled	91.0	23	<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
26	<a href="#">c1om8A_</a>	Alignment	not modelled	91.0	24	<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
27	<a href="#">c2agmA_</a>	Alignment	not modelled	90.4	18	<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
28	<a href="#">d1wa8a1</a>	Alignment	not modelled	90.1	12	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like

29	<a href="#">c2vs0B</a>	Alignment	not modelled	89.5	12	<b>PDB header:</b> cell invasion <b>Chain:</b> B: <b>PDB Molecule:</b> virulence factor esxa; <b>PDBTitle:</b> structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
30	<a href="#">c3zbc</a>	Alignment	not modelled	85.3	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
31	<a href="#">c2klwA</a>	Alignment	not modelled	83.7	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
32	<a href="#">c3fkeB</a>	Alignment	not modelled	83.7	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> polymerase cofactor vp35; <b>PDBTitle:</b> structure of the ebola vp35 interferon inhibitory domain
33	<a href="#">c2cuoC</a>	Alignment	not modelled	82.5	41	<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
34	<a href="#">c2cuoF</a>	Alignment	not modelled	82.5	41	<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
35	<a href="#">c5cxlA</a>	Alignment	not modelled	81.7	23	<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
36	<a href="#">c2qubG</a>	Alignment	not modelled	80.0	15	<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
37	<a href="#">c3p4gD</a>	Alignment	not modelled	79.9	17	<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
38	<a href="#">c2cuoD</a>	Alignment	not modelled	75.5	38	<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
39	<a href="#">c2cuoE</a>	Alignment	not modelled	75.5	38	<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
40	<a href="#">c2cuoA</a>	Alignment	not modelled	75.5	38	<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
41	<a href="#">c2cuoB</a>	Alignment	not modelled	75.5	38	<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
42	<a href="#">c1k6fC</a>	Alignment	not modelled	75.0	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
43	<a href="#">c1k6fD</a>	Alignment	not modelled	75.0	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
44	<a href="#">c1k6fE</a>	Alignment	not modelled	75.0	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
45	<a href="#">c1k6fF</a>	Alignment	not modelled	75.0	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
46	<a href="#">c1k6fA</a>	Alignment	not modelled	75.0	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
47	<a href="#">c1k6fB</a>	Alignment	not modelled	75.0	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
48	<a href="#">d1g9ka1</a>	Alignment	not modelled	74.8	19	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
49	<a href="#">c3ah9A</a>	Alignment	not modelled	74.6	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)9 at 1.1 a resolution
50	<a href="#">c3ah9F</a>	Alignment	not modelled	74.4	36	<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
51	<a href="#">c3a0mF</a>	Alignment	not modelled	74.4	36	<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
52	<a href="#">c3ah9C</a>	Alignment	not modelled	74.0	40	<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
53	<a href="#">c3ah9B</a>	Alignment	not modelled	74.0	40	<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
54	<a href="#">c3ah9E</a>	Alignment	not modelled	74.0	40	<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
55	<a href="#">c4lwsA</a>	Alignment	not modelled	70.9	18	<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

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56	<a href="#">c3ah9D_</a>	Alignment	not modelled	70.7	38	<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
57	<a href="#">c2kg7B_</a>	Alignment	not modelled	70.6	16	<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
58	<a href="#">c4gh9A_</a>	Alignment	not modelled	70.2	27	<b>PDB header:</b> viral protein,rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> polymerase cofactor vp35; <b>PDBTitle:</b> crystal structure of marburg virus vp35 rna binding domain
59	<a href="#">c3v4cB_</a>	Alignment	not modelled	67.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aldehyde dehydrogenase (nadp+); <b>PDBTitle:</b> crystal structure of a semialdehyde dehydrogenase from sinorhizobium2 melliloti 1021
60	<a href="#">c3ks8D_</a>	Alignment	not modelled	63.6	24	<b>PDB header:</b> viral protein/rna <b>Chain:</b> D: <b>PDB Molecule:</b> polymerase cofactor vp35; <b>PDBTitle:</b> crystal structure of reston ebolavirus vp35 rna binding domain in2 complex with 18bp dsrna
61	<a href="#">c6hxoH_</a>	Alignment	not modelled	60.2	9	<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)
62	<a href="#">c6dkuA_</a>	Alignment	not modelled	59.5	25	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> vp35; <b>PDBTitle:</b> crystal structure of myotis vp35 mutant of interferon inhibitory2 domain
63	<a href="#">c3lr6A_</a>	Alignment	not modelled	58.1	16	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> major ampullate spidroin 1; <b>PDBTitle:</b> self-assembly of spider silk proteins is controlled by a ph-sensitive2 relay
64	<a href="#">d1sata1</a>	Alignment	not modelled	57.7	18	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
65	<a href="#">c4wj2A_</a>	Alignment	not modelled	57.4	16	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> antigen mtb48; <b>PDBTitle:</b> mycobacterial protein
66	<a href="#">c4f9iA_</a>	Alignment	not modelled	57.2	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> proline dehydrogenase/delta-1-pyrroline-5-carboxylate <b>PDBTitle:</b> crystal structure of proline utilization a (puta) from geobacter2 sulfurreducens pca
67	<a href="#">c3i0uA_</a>	Alignment	not modelled	55.6	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphothreonine lyase ospf; <b>PDBTitle:</b> structure of the type iii effector/phosphothreonine lyase ospf from2 shigella flexneri
68	<a href="#">c3w5mA_</a>	Alignment	not modelled	53.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative rhamnosidase; <b>PDBTitle:</b> crystal structure of streptomyces avermitilis alpha-l-rhamnosidase
69	<a href="#">c2z8nB_</a>	Alignment	not modelled	53.0	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 27.5 kda virulence protein; <b>PDBTitle:</b> structural basis for the catalytic mechanism of phosphothreonine lyase
70	<a href="#">c4idmA_</a>	Alignment	not modelled	52.3	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> delta-1-pyrroline-5-carboxylate dehydrogenase; <b>PDBTitle:</b> crystal structure of the delta-pyrroline-5-carboxylate dehydrogenase2 from mycobacterium tuberculosis
71	<a href="#">c3abnA_</a>	Alignment	not modelled	51.1	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
72	<a href="#">c4f7gB_</a>	Alignment	not modelled	50.8	17	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> stalin-1; <b>PDBTitle:</b> crystal structure of talin autoinhibition complex
73	<a href="#">c3ed6B_</a>	Alignment	not modelled	50.4	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> betaine aldehyde dehydrogenase; <b>PDBTitle:</b> 1.7 angstrom resolution crystal structure of betaine aldehyde2 dehydrogenase (betb) from staphylococcus aureus
74	<a href="#">c5kf6B_</a>	Alignment	not modelled	49.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein puta; <b>PDBTitle:</b> structure of proline utilization a from sinorhizobium melliloti2 complexed with l-tetrahydrofuroic acid and nad+ in space group p21
75	<a href="#">c4rglA_</a>	Alignment	not modelled	48.7	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> filamentation induced by camp protein fic; <b>PDBTitle:</b> crystal structure of a fic family protein (dde_2494) from2 desulfovibrio desulfuricans g20 at 2.70 a resolution
76	<a href="#">c1x1kB_</a>	Alignment	not modelled	48.3	42	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-pro-gly)4 <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2-pro-gly)4
77	<a href="#">c2d3fD_</a>	Alignment	not modelled	48.3	42	<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
78	<a href="#">c2d3fF_</a>	Alignment	not modelled	48.3	42	<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
79	<a href="#">c2d3fE_</a>	Alignment	not modelled	48.3	42	<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

80	<a href="#">c1x1kD</a>	 Alignment	not modelled	48.3	42	<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
81	<a href="#">c1x1kA</a>	 Alignment	not modelled	48.3	42	<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
82	<a href="#">c1x1kC</a>	 Alignment	not modelled	48.3	42	<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
83	<a href="#">d1wa8b1</a>	 Alignment	not modelled	48.0	13	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
84	<a href="#">c3a0mC</a>	 Alignment	not modelled	46.9	40	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
85	<a href="#">c3admC</a>	 Alignment	not modelled	45.4	38	<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)4-hyp-ser-gly-(pro-pro-gly)4
86	<a href="#">c3h6pB</a>	 Alignment	not modelled	43.6	35	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> esat-6 like protein esxs; <b>PDBTitle:</b> crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
87	<a href="#">c3admB</a>	 Alignment	not modelled	43.5	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
88	<a href="#">c3admA</a>	 Alignment	not modelled	43.5	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
89	<a href="#">c3admF</a>	 Alignment	not modelled	43.5	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
90	<a href="#">c3admE</a>	 Alignment	not modelled	43.5	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
91	<a href="#">c2vsgB</a>	 Alignment	not modelled	43.4	3	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> variant surface glycoprotein iltat 1.24; <b>PDBTitle:</b> a structural motif in the variant surface glycoproteins of trypanosoma2 brucei
92	<a href="#">c1vsgB</a>	 Alignment	not modelled	42.4	15	<b>PDB header:</b> glycoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> variant surface glycoprotein mitat 1.2; <b>PDBTitle:</b> 2.9 angstroms resolution structure of the n-terminal domain of a2 variant surface glycoprotein from trypanosoma brucei
93	<a href="#">c5x5fC</a>	 Alignment	not modelled	40.7	18	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> s protein; <b>PDBTitle:</b> prefusion structure of mers-cov spike glycoprotein, conformation 2
94	<a href="#">c2hm8A</a>	 Alignment	not modelled	40.6	19	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> pdcd4 c-terminal ma-3 domain; <b>PDBTitle:</b> solution structure of the c-terminal ma-3 domain of pdcd4
95	<a href="#">c4dngB</a>	 Alignment	not modelled	40.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized aldehyde dehydrogenase aldy; <b>PDBTitle:</b> crystal structure of putative aldehyde dehydrogenase from bacillus2 subtilis subsp. subtilis str. 168
96	<a href="#">c2iosA</a>	 Alignment	not modelled	40.4	19	<b>PDB header:</b> antitumor protein <b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death 4, pdcd4; <b>PDBTitle:</b> crystal structure of the c-terminal ma3 domain of pdcd42 (mouse); form 3
97	<a href="#">d2cj4a1</a>	 Alignment	not modelled	39.8	17	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Plant invertase/pectin methylesterase inhibitor <b>Family:</b> Plant invertase/pectin methylesterase inhibitor
98	<a href="#">c3jywF</a>	 Alignment	not modelled	39.0	32	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> 60s ribosomal protein l7(a); <b>PDBTitle:</b> structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
99	<a href="#">c1yiqA</a>	 Alignment	not modelled	38.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> quinohemoprotein alcohol dehydrogenase; <b>PDBTitle:</b> molecular cloning and structural analysis of2 quinohemoprotein alcohol dehydrogenase adhiig from3 pseudomonas putida hk5. comparison to the other4 quinohemoprotein alcohol dehydrogenase adhiib found in the5 same microorganism.
100	<a href="#">c2kbbA</a>	Alignment	not modelled	37.6	14	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> taln-1; <b>PDBTitle:</b> nmr structure of the talin rod domain, 1655-1822
101	<a href="#">c5jggB</a>	Alignment	not modelled	36.4	19	<b>PDB header:</b> oxygen binding/transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> beta chain; <b>PDBTitle:</b> x-ray sequence and high resolution crystal structure of persian2 sturgeon methemoglobin
102	<a href="#">c3ptwA</a>	Alignment	not modelled	36.1	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyl coa-acyl carrier protein transacylase; <b>PDBTitle:</b> crystal structure of malonyl coa-acyl carrier protein transacylase2 from clostridium perfringens atcc 13124
103	<a href="#">c4lwsB</a>	Alignment	not modelled	36.0	11	<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

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104	<a href="#">c3a19D_</a>	Alignment	not modelled	35.7	36	<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
105	<a href="#">d1pa2a_</a>	Alignment	not modelled	34.5	19	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> CCP-like
106	<a href="#">d1v59a3</a>	Alignment	not modelled	34.3	13	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
107	<a href="#">c5ujuA_</a>	Alignment	not modelled	34.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of nad-dependent aldehyde dehydrogenase from2 burkholderia multivorans
108	<a href="#">c3wa8B_</a>	Alignment	not modelled	33.8	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> crispr-associated protein, cse2 family; <b>PDBTitle:</b> crystal structure of m. ruber casb
109	<a href="#">c3cazA_</a>	Alignment	not modelled	33.3	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> bar protein; <b>PDBTitle:</b> crystal structure of a bar protein from galdieria sulphuraria
110	<a href="#">c3oniA_</a>	Alignment	not modelled	33.3	9	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> t-snare vti1; <b>PDBTitle:</b> crystal structure of yeast vti1p_habc domain
111	<a href="#">c2kvpA_</a>	Alignment	not modelled	32.5	20	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> talin-1; <b>PDBTitle:</b> nmr structure of the talin vbs3 domain, 1815-1973
112	<a href="#">d1ojta3</a>	Alignment	not modelled	32.3	6	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
113	<a href="#">d1gwua_</a>	Alignment	not modelled	32.2	22	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> CCP-like
114	<a href="#">c2kztB_</a>	Alignment	not modelled	31.9	19	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> programmed cell death protein 4; <b>PDBTitle:</b> structure of the tandem ma-3 region of pdcd4
115	<a href="#">c2d3hD_</a>	Alignment	not modelled	31.8	38	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-hyp-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4
116	<a href="#">c3a08D_</a>	Alignment	not modelled	31.8	38	<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, monoclinic, twinned crystal
117	<a href="#">c3a19F_</a>	Alignment	not modelled	31.8	38	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
118	<a href="#">c4c3sA_</a>	Alignment	not modelled	31.3	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde dehydrogenase; <b>PDBTitle:</b> structure of a propionaldehyde dehydrogenase from the clostridium2 phytofermentans fucose utilisation bacterial microcompartment
119	<a href="#">c3a0mB_</a>	Alignment	not modelled	30.8	38	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
120	<a href="#">c4dllB_</a>	Alignment	not modelled	30.5	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-hydroxy-3-oxopropionate reductase; <b>PDBTitle:</b> crystal structure of a 2-hydroxy-3-oxopropionate reductase from2 polaromonas sp. js666