



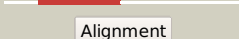
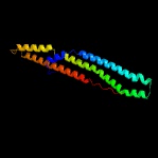
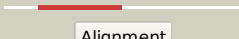
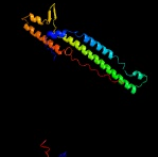
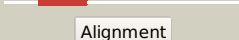
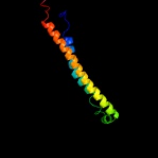
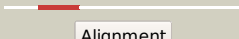
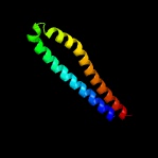
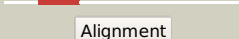

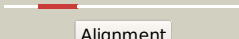
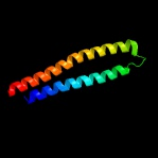


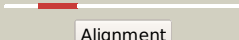


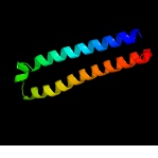
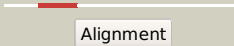

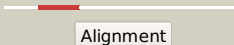

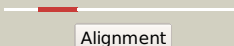
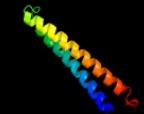
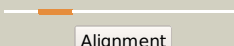
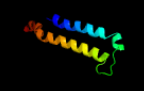
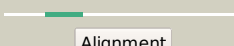

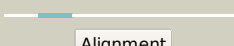

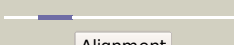
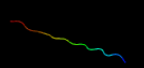




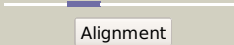
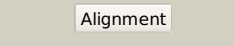
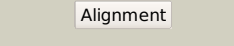
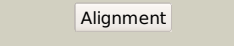
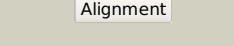
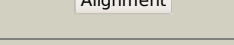

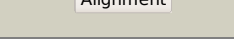


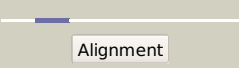
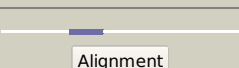
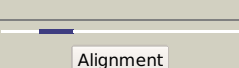
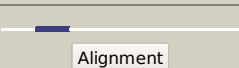
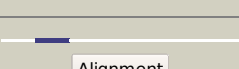
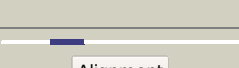
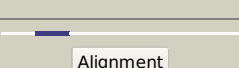
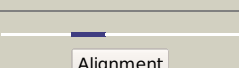
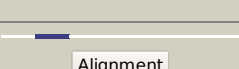
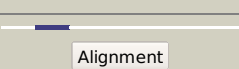
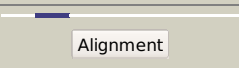
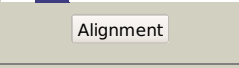
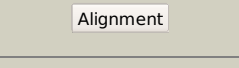
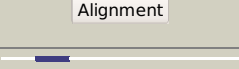
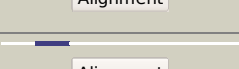
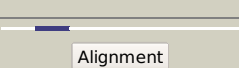
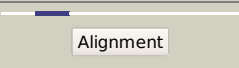
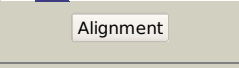
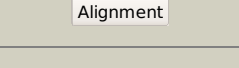
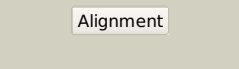
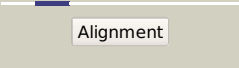
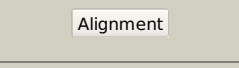
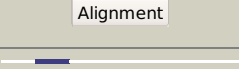
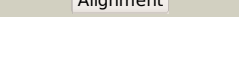

Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3021c_(PPE47)_3379386_3380693
 Date Thu Aug 8 16:20:19 BST 2019
 Unique Job ID 122b4f0c37628f2f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	39	PDB header: protein transport Chain: B: PDB Molecule: ppe family protein ppe15; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	c2g38B_	 Alignment		100.0	29	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
3	d2g38b1	 Alignment		100.0	29	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
4	c4xy3A_	 Alignment		100.0	21	PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
5	c4wj2A_	 Alignment		97.9	21	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.6	11	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c3gvmA_	 Alignment		97.4	16	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
8	c4iogD_	 Alignment		97.4	14	PDB header: unknown function Chain: D: PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
9	c3zbhC_	 Alignment		97.1	16	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		96.2	13	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsB_	 Alignment		93.6	16	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	d1wa8b1	 Alignment		92.7	14	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
13	c4lwsA	 Alignment		92.0	10	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
14	c4i0xA	 Alignment		90.3	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein mab_3112; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
15	c2kg7B	 Alignment		84.5	17	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein eshx; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
16	d1ui5a2	 Alignment		40.6	20	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
17	c4i0xJ	 Alignment		39.2	16	PDB header: structural genomics, unknown function Chain: J: PDB Molecule: esat-6-like protein mab_3113; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
18	c1bkvA	 Alignment		19.5	50	PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen
19	c1bkvC	 Alignment		18.5	50	PDB header: structural protein Chain: C: PDB Molecule: t3-785; PDBTitle: collagen
20	c1bkvB	 Alignment		18.5	50	PDB header: structural protein Chain: B: PDB Molecule: t3-785; PDBTitle: collagen
21	d1zeeal	 Alignment	not modelled	18.5	54	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Indoleamine 2,3-dioxygenase-like
22	d1dlpa1	 Alignment	not modelled	17.1	18	Fold: beta-Prism II Superfamily: alpha-D-mannose-specific plant lectins Family: alpha-D-mannose-specific plant lectins
23	c5i85B	 Alignment	not modelled	16.2	36	PDB header: signaling protein Chain: B: PDB Molecule: nuclear fragile x mental retardation-interacting protein 1; PDBTitle: solution structure of the complex between human znhit3 and nufip12 proteins
24	c4xb6D	 Alignment	not modelled	14.4	33	PDB header: transferase Chain: D: PDB Molecule: alpha-d-ribose 1-methylphosphonate 5-phosphate c-p lyase; PDBTitle: structure of the e. coli c-p lyase core complex
25	c3sjrB	 Alignment	not modelled	12.2	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved unknwn function protein cv_1783 from2 chromobacterium violaceum atcc 12472
26	c6aokA	 Alignment	not modelled	11.8	25	PDB header: hydrolase Chain: A: PDB Molecule: ceg4; PDBTitle: crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
27	d1vlfn1	 Alignment	not modelled	10.8	100	Fold: Prealbumin-like Superfamily: Cna protein B-type domain Family: Cna protein B-type domain
28	c6cglA	 Alignment	not modelled	10.8	38	PDB header: hydrolase Chain: A: PDB Molecule: effector protein lem4 (lpg1101); PDBTitle: structure of the had domain of effector protein lem4 (lpg1101) from2 legionella pneumophila

29	c4gyxC	 Alignment	not modelled	10.4	45	PDB header: structural protein, blood clotting Chain: C: PDB Molecule: type iii collagen fragment in a host peptide stabilized by PDBTitle: the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
30	c2nviA	 Alignment	not modelled	10.0	40	PDB header: hydrolase Chain: A: PDB Molecule: 25mer peptide from vacuolar atp synthase subunit PDBTitle: nmr structures of transmembrane segment from subunit a from2 the yeast proton v-atpase
31	c1vytF	 Alignment	not modelled	9.9	50	PDB header: transport protein Chain: F: PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
32	c4gyxA	 Alignment	not modelled	9.8	45	PDB header: structural protein, blood clotting Chain: A: PDB Molecule: type iii collagen fragment in a host peptide stabilized by PDBTitle: the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
33	c4gyxB	 Alignment	not modelled	9.8	45	PDB header: structural protein, blood clotting Chain: B: PDB Molecule: type iii collagen fragment in a host peptide stabilized by PDBTitle: the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
34	c2ahmG	 Alignment	not modelled	9.3	24	PDB header: viral protein, replication Chain: G: PDB Molecule: replicase polyprotein 1ab, heavy chain; PDBTitle: crystal structure of sars-cov super complex of non-structural2 proteins: the hexadecamer
35	c2y5tG	 Alignment	not modelled	9.0	83	PDB header: immune system Chain: G: PDB Molecule: c1; PDBTitle: crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide
36	c1bzgA	 Alignment	not modelled	9.0	14	PDB header: hormone Chain: A: PDB Molecule: parathyroid hormone-related protein; PDBTitle: the solution structure of human parathyroid hormone-related2 protein (1-34) in near-physiological solution, nmr, 303 structures
37	c2y5tE	 Alignment	not modelled	8.4	83	PDB header: immune system Chain: E: PDB Molecule: c1; PDBTitle: crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide
38	c2y5tF	 Alignment	not modelled	7.6	83	PDB header: immune system Chain: F: PDB Molecule: c1; PDBTitle: crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide
39	c2iu1A	 Alignment	not modelled	7.5	28	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
40	c2f6aJ	 Alignment	not modelled	7.4	71	PDB header: cell adhesion/structural protein Chain: J: PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure
41	c2lkqA	 Alignment	not modelled	7.3	44	PDB header: immune system Chain: A: PDB Molecule: immunoglobulin lambda-like polypeptide 1; PDBTitle: nmr structure of the lambda 5 22-45 peptide
42	c2wuhD	 Alignment	not modelled	7.1	83	PDB header: receptor/peptide Chain: D: PDB Molecule: collagen peptide; PDBTitle: crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
43	c6a0aA	 Alignment	not modelled	7.1	63	PDB header: structural protein Chain: A: PDB Molecule: collagen type iii peptide; PDBTitle: structure of a triple-helix region of human collagen type iii
44	c2f6aF	 Alignment	not modelled	7.1	71	PDB header: cell adhesion/structural protein Chain: F: PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure
45	c2f6aE	 Alignment	not modelled	7.1	71	PDB header: cell adhesion/structural protein Chain: E: PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure
46	c2f6aI	 Alignment	not modelled	7.1	71	PDB header: cell adhesion/structural protein Chain: I: PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure
47	c2f6aG	 Alignment	not modelled	7.1	71	PDB header: cell adhesion/structural protein Chain: G: PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure
48	c2f6aH	 Alignment	not modelled	7.1	71	PDB header: cell adhesion/structural protein Chain: H: PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure
49	c5hl8B	 Alignment	not modelled	7.0	30	PDB header: protein transport Chain: B: PDB Molecule: type ii secretion system protein I; PDBTitle: 1.93 angstrom resolution crystal structure of a pullulanase-specific2 type ii secretion system integral cytoplasmic membrane protein gspi3 (c-terminal fragment; residues 309-397) from klebsiella pneumoniae4 subsp. pneumoniae ntuH-k2044
50	c5uc0B	 Alignment	not modelled	6.9	100	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein cog5400; PDBTitle: crystal structure of beta-barrel-like, uncharacterized protein of2 cog5400 from brucella abortus
51	c2fulE	 Alignment	not modelled	6.9	28	PDB header: translation Chain: E: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of the c-terminal domain of s. cerevisiae eif5
52	c5vmoB	 Alignment	not modelled	6.9	50	PDB header: viral protein/apoptosis Chain: B: PDB Molecule: bcl-2 interacting mediator of cell death; PDBTitle: crystal structure of grouper iridovirus giv66: bim complex
53	c2wuhC	 Alignment	not modelled	6.8	83	PDB header: receptor/peptide Chain: C: PDB Molecule: collagen peptide; PDBTitle: crystal structure of the ddr2 discoidin domain bound to a2

						triple-helical collagen peptide
54	c2wuhB_	Alignment	not modelled	6.8	83	PDB header: receptor/peptide Chain: B: PDB Molecule: collagen peptide; PDBTitle: crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
55	c1vytE_	Alignment	not modelled	6.7	50	PDB header: transport protein Chain: E: PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
56	c2kg7A_	Alignment	not modelled	6.6	47	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein esxg (pe family protein); PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
57	c6a0cB_	Alignment	not modelled	6.6	63	PDB header: structural protein Chain: B: PDB Molecule: collagen type iii peptide; PDBTitle: structure of a triple-helix region of human collagen type iii
58	c2iunD_	Alignment	not modelled	6.6	50	PDB header: viral protein Chain: D: PDB Molecule: avian adenovirus celo long fibre; PDBTitle: structure of the c-terminal head domain of the avian adenovirus celo2 long fibre (p21 crystal form)
59	c3ub0D_	Alignment	not modelled	6.6	20	PDB header: replication Chain: D: PDB Molecule: non-structural protein 6, nsp6,; PDBTitle: crystal structure of the nonstructural protein 7 and 8 complex of f2 feline coronavirus
60	c6nbiP_	Alignment	not modelled	6.4	60	PDB header: signaling protein Chain: P: PDB Molecule: long-acting parathyroid hormone analog; PDBTitle: cryo-em structure of parathyroid hormone receptor type 1 in complex2 with a long-acting parathyroid hormone analog and g protein
61	c5dn4A_	Alignment	not modelled	6.4	43	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan hydrolase flgj; PDBTitle: structure of the glycoside hydrolase domain from salmonella2 typhimurium flgj
62	c3h6pB_	Alignment	not modelled	6.4	47	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: esat-6 like protein esxs; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
63	c1t0jC_	Alignment	not modelled	6.4	43	PDB header: signaling protein Chain: C: PDB Molecule: voltage-dependent l-type calcium channel alpha-1c subunit; PDBTitle: crystal structure of a complex between voltage-gated calcium channel2 beta2a subunit and a peptide of the alpha1c subunit
64	c2drxB_	Alignment	not modelled	6.3	83	PDB header: structural protein Chain: B: PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-(log)2-(pog)4
65	c4dexB_	Alignment	not modelled	6.3	38	PDB header: transport protein Chain: B: PDB Molecule: voltage-dependent n-type calcium channel subunit alpha-1b; PDBTitle: crystal structure of the voltage dependent calcium channel beta-22 subunit in complex with the cav2.2 i-ii linker.
66	c2drxA_	Alignment	not modelled	6.2	83	PDB header: structural protein Chain: A: PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-(log)2-(pog)4
67	d1fcda3	Alignment	not modelled	6.2	23	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
68	c6a0aB_	Alignment	not modelled	6.1	83	PDB header: structural protein Chain: B: PDB Molecule: collagen type iii peptide; PDBTitle: structure of a triple-helix region of human collagen type iii
69	c6a0aC_	Alignment	not modelled	6.1	83	PDB header: structural protein Chain: C: PDB Molecule: collagen type iii peptide; PDBTitle: structure of a triple-helix region of human collagen type iii
70	c2drxC_	Alignment	not modelled	6.0	83	PDB header: structural protein Chain: C: PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-(log)2-(pog)4
71	c2drtB_	Alignment	not modelled	5.9	83	PDB header: structural protein Chain: B: PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-log-(pog)5
72	c2drtA_	Alignment	not modelled	5.9	83	PDB header: structural protein Chain: A: PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-log-(pog)5
73	c6fxoA_	Alignment	not modelled	5.9	67	PDB header: hydrolase Chain: A: PDB Molecule: bifunctional autolysin; PDBTitle: crystal structure of major bifunctional autolysin
74	c1qsuC_	Alignment	not modelled	5.9	83	PDB header: structural protein Chain: C: PDB Molecule: protein ((pro-hyp-gly)4- glu-lys-gly(pro-hyp-gly)5); PDBTitle: crystal structure of the triple-helical collagen-like peptide, (pro-2 hyp-gly)4-glu-lys-gly(pro-hyp-gly)5
75	c2drtC_	Alignment	not modelled	5.8	83	PDB header: structural protein Chain: C: PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-log-(pog)5
76	c3ponB_	Alignment	not modelled	5.8	55	PDB header: unknown function Chain: B: PDB Molecule: mb1 collagen-like peptide; PDBTitle: crystal structure of mbl collagen-like peptide
77	c3ponA_	Alignment	not modelled	5.8	55	PDB header: unknown function Chain: A: PDB Molecule: mb1 collagen-like peptide; PDBTitle: crystal structure of mbl collagen-like peptide
78	c3pobB_	Alignment	not modelled	5.8	55	PDB header: hydrolase Chain: B: PDB Molecule: mb1 collagen-like peptide; PDBTitle: crystal structure of masp-1 cub2 domain in complex with

						the collagen-2 like domain of mbl
79	c3pobC_	Alignment	not modelled	5.8	55	PDB header: hydrolase Chain: C: PDB Molecule: mbl collagen-like peptide; PDBTitle: crystal structure of masp-1 cub2 domain in complex with the collagen-2 like domain of mbl
80	c3pobD_	Alignment	not modelled	5.8	55	PDB header: hydrolase Chain: D: PDB Molecule: mbl collagen-like peptide; PDBTitle: crystal structure of masp-1 cub2 domain in complex with the collagen-2 like domain of mbl
81	c1cagA_	Alignment	not modelled	5.8	83	PDB header: collagen Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution
82	c1cagC_	Alignment	not modelled	5.8	83	PDB header: collagen Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution
83	c6a0cA_	Alignment	not modelled	5.7	83	PDB header: structural protein Chain: A: PDB Molecule: collagen type iii peptide; PDBTitle: structure of a triple-helix region of human collagen type iii
84	c6a0cC_	Alignment	not modelled	5.7	83	PDB header: structural protein Chain: C: PDB Molecule: collagen type iii peptide; PDBTitle: structure of a triple-helix region of human collagen type iii
85	c3zfsA_	Alignment	not modelled	5.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: f420-reducing hydrogenase, subunit alpha; PDBTitle: cryo-em structure of the f420-reducing nife-hydrogenase from a2 methanogenic archaeon with bound substrate
86	c1qsuB_	Alignment	not modelled	5.6	83	PDB header: structural protein Chain: B: PDB Molecule: protein ((pro-hyp-gly)4- glu-lys-gly((pro-hyp-gly)5); PDBTitle: crystal structure of the triple-helical collagen-like peptide, (pro-2 hyp-gly)4-glu-lys-gly((pro-hyp-gly)5
87	c1qsuA_	Alignment	not modelled	5.6	83	PDB header: structural protein Chain: A: PDB Molecule: protein ((pro-hyp-gly)4- glu-lys-gly((pro-hyp-gly)5); PDBTitle: crystal structure of the triple-helical collagen-like peptide, (pro-2 hyp-gly)4-glu-lys-gly((pro-hyp-gly)5
88	c4f3fC_	Alignment	not modelled	5.5	47	PDB header: immune system Chain: C: PDB Molecule: mesothelin; PDBTitle: crystal structure of msln7-64 morab-009 fab complex
89	c1cagB_	Alignment	not modelled	5.5	83	PDB header: collagen Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution
90	c1cgdC_	Alignment	not modelled	5.5	83	PDB header: collagen Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: hydration structure of a collagen peptide
91	c1cgdB_	Alignment	not modelled	5.5	83	PDB header: collagen Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: hydration structure of a collagen peptide
92	c1cgdA_	Alignment	not modelled	5.5	83	PDB header: collagen Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: hydration structure of a collagen peptide
93	c6hg7B_	Alignment	not modelled	5.5	83	PDB header: structural protein Chain: B: PDB Molecule: collagen alpha-1(ii) chain; PDBTitle: crystal structure of a collagen ii fragment containing the binding2 site of pedf and comp, (pog)4-lkg hrg ftg lqq-pog(4)
94	c6hg7A_	Alignment	not modelled	5.5	83	PDB header: structural protein Chain: A: PDB Molecule: collagen alpha-1(ii) chain; PDBTitle: crystal structure of a collagen ii fragment containing the binding2 site of pedf and comp, (pog)4-lkg hrg ftg lqq-pog(4)
95	c6hg7C_	Alignment	not modelled	5.5	83	PDB header: structural protein Chain: C: PDB Molecule: collagen alpha-1(ii) chain; PDBTitle: crystal structure of a collagen ii fragment containing the binding2 site of pedf and comp, (pog)4-lkg hrg ftg lqq-pog(4)
96	c2zycA_	Alignment	not modelled	5.4	60	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan hydrolase flgj; PDBTitle: crystal structure of peptidoglycan hydrolase from2 sphingomonas sp. a1
97	c2qnuB_	Alignment	not modelled	5.4	29	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein pa0076; PDBTitle: crystal structure of pa0076 from pseudomonas aeruginosa pao12 at 2.05 a resolution
98	c2jtwA_	Alignment	not modelled	5.3	50	PDB header: membrane protein Chain: A: PDB Molecule: transmembrane helix 7 of yeast vatpase; PDBTitle: solution structure of tm7 bound to dpc micelles
99	c2wseE_	Alignment	not modelled	5.3	43	PDB header: photosynthesis Chain: E: PDB Molecule: photosystem i reaction center subunit iv a, chloroplastic; PDBTitle: improved model of plant photosystem i