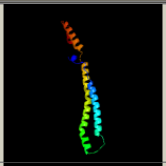
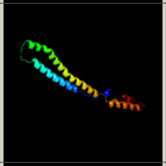
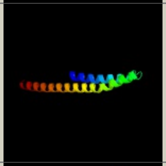
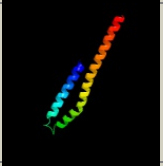
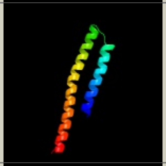
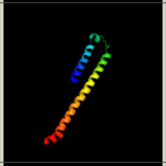
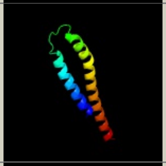
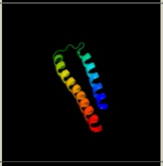
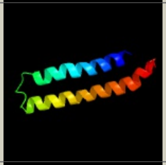
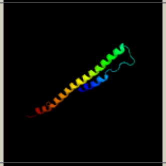
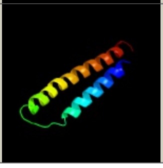
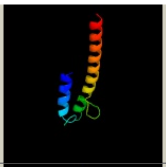
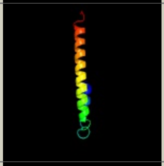
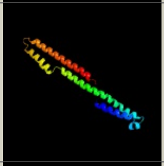
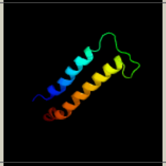
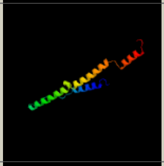
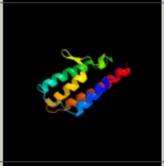
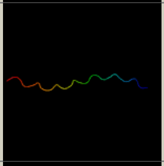
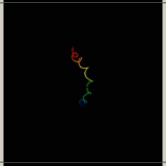
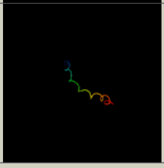
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3864_(-)_4340448_4341656
Date	Sat Aug 10 22:05:04 BST 2019
Unique Job ID	f8c4a8ce1bda4d92

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2g38B_	Alignment		96.7	7	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**ppe family protein; **PDBTitle:** a pe/ppe protein complex from mycobacterium tuberculosis
2	d2g38b1	Alignment		96.7	7	**Fold:**Ferritin-like **Superfamily:**PE/PPE dimer-like **Family:**PPE
3	c3zbhC_	Alignment		96.2	19	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**esxa; **PDBTitle:** geobacillus thermodenitrificans esxa crystal form i
4	c3gvmA_	Alignment		96.1	12	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein sag1039; **PDBTitle:** structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
5	c4iogD_	Alignment		96.1	12	**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
6	c4lwsA_	Alignment		95.8	6	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** esxa : esxb (semet) hetero-dimer from thermomonospora curvata
7	c2vs0B_	Alignment		95.8	20	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**virulence factor esxa; **PDBTitle:** structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
8	c4lwsB_	Alignment		95.0	16	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** esxa : esxb (semet) hetero-dimer from thermomonospora curvata
9	d1wa8b1	Alignment		94.5	14	**Fold:**Ferritin-like **Superfamily:**EsxAB dimer-like **Family:**ESAT-6 like
10	c4wj2A_	Alignment		94.2	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**antigen mtb48; **PDBTitle:** mycobacterial protein
11	d1wa8a1	Alignment		93.3	17	**Fold:**Ferritin-like **Superfamily:**EsxAB dimer-like **Family:**ESAT-6 like

12	c4i0xJ_	Alignment		92.5	17	**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
13	c4i0xA_	Alignment		89.9	17	**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
14	c5xfsB_	Alignment		88.8	12	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**ppe family protein ppe15; **PDBTitle:** crystal structure of pe8-ppe15 in complex with espg5 from m.2 tuberculosis
15	c2kg7B_	Alignment		87.8	5	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**esat-6-like protein esxh; **PDBTitle:** structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
16	c4xy3A_	Alignment		72.6	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**esx-1 secretion-associated protein espb; **PDBTitle:** structure of esx-1 secreted protein espb
17	c2kvpA_	Alignment		50.8	9	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**talin-1; **PDBTitle:** nmr structure of the talin vbs3 domain, 1815-1973
18	c2cuoA_	Alignment		48.9	50	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**collagen model peptide (pro-pro-gly)9; **PDBTitle:** collagen model peptide (pro-pro-gly)9
19	c2cuoE_	Alignment		48.9	50	**PDB header:**structural protein **Chain:** E: **PDB Molecule:**collagen model peptide (pro-pro-gly)9; **PDBTitle:** collagen model peptide (pro-pro-gly)9
20	c2cuoB_	Alignment		48.9	50	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**collagen model peptide (pro-pro-gly)9; **PDBTitle:** collagen model peptide (pro-pro-gly)9
21	c2cuoD_	Alignment	not modelled	48.9	50	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**collagen model peptide (pro-pro-gly)9; **PDBTitle:** collagen model peptide (pro-pro-gly)9
22	d1qkra_	Alignment	not modelled	48.8	12	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
23	c2cuoF_	Alignment	not modelled	47.7	48	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**collagen model peptide (pro-pro-gly)9; **PDBTitle:** collagen model peptide (pro-pro-gly)9
24	c2cuoC_	Alignment	not modelled	47.7	48	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**collagen model peptide (pro-pro-gly)9; **PDBTitle:** collagen model peptide (pro-pro-gly)9
25	c3ah9A_	Alignment	not modelled	41.4	50	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)9 at 1.1 a resolution
26	c3ah9F_	Alignment	not modelled	39.7	50	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)9 at 1.1 a resolution
27	c3ah9B_	Alignment	not modelled	37.0	48	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)9 at 1.1 a resolution
28	c3ah9E_	Alignment	not modelled	37.0	48	**PDB header:**structural protein **Chain:** E: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)9 at 1.1 a resolution
29	c3ah9C_	Alignment	not modelled	37.0	48	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**collagen-like peptide;

						PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
30	c3ah9D_	Alignment	not modelled	28.6	50	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)9 at 1.1 a resolution
31	c2vqkA_	Alignment	not modelled	25.2	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**uncharacterized protein cgl0972; **PDBTitle:** crystal structure of porb from corynebacterium glutamicum (2 crystal form iv)
32	c2vqlD_	Alignment	not modelled	24.1	21	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**uncharacterized protein cgl0972; **PDBTitle:** crystal structure of porb from corynebacterium glutamicum (2 crystal form iii)
33	c6b87C_	Alignment	not modelled	23.3	5	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**tmhc2_e; **PDBTitle:** crystal structure of transmembrane protein tmhc2_e
34	c2ic6B_	Alignment	not modelled	21.8	32	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**nucleocapsid protein; **PDBTitle:** the coiled-coil domain (residues 1-75) structure of the sin nombre2 virus nucleocapsid protein
35	c4anjA_	Alignment	not modelled	20.9	11	**PDB header:**motor protein/metal-bindng protein **Chain:** A: **PDB Molecule:**unconventional myosin-vi, green fluorescent protein; **PDBTitle:** myosin vi (mdinsert2-gfp fusion) pre-powerstroke state (mg.adp.alf4)
36	c3iykA_	Alignment	not modelled	18.5	32	**PDB header:**virus **Chain:** A: **PDB Molecule:**vp5; **PDBTitle:** bluetongue virus structure reveals a sialic acid binding domain,2 amphipathic helices and a central coiled coil in the outer capsid3 proteins
37	c4rvqA_	Alignment	not modelled	18.1	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**pre-mrna splicing helicase-like protein; **PDBTitle:** pwi-like domain of chaetomium thermophilum brr2
38	c4ng2E_	Alignment	not modelled	18.1	27	**PDB header:**transcription regulator **Chain:** E: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of lasr lbd-qsla complex from pseudomonas aeruginosa
39	d1ov9a_	Alignment	not modelled	17.9	33	**Fold:**H-NS histone-like proteins **Superfamily:**H-NS histone-like proteins **Family:**H-NS histone-like proteins
40	c2e4gB_	Alignment	not modelled	17.8	10	**PDB header:**biosynthetic protein, flavoprotein **Chain:** B: **PDB Molecule:**tryptophan halogenase; **PDBTitle:** rebh with bound l-trp
41	c5zt3A_	Alignment	not modelled	17.1	36	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**wa352; **PDBTitle:** crystal structure of wa352 from oryza sativa
42	c2mc7A_	Alignment	not modelled	16.3	22	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**regulatory peptide; **PDBTitle:** structure of salmonella mgtr
43	c3a0mF_	Alignment	not modelled	16.2	43	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**collagen-like peptide; **PDBTitle:** structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
44	c6j7bB_	Alignment	not modelled	15.9	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**small vasohibin-binding protein; **PDBTitle:** crystal structure of vash1-svbp in complex with epoy
45	d1ji5a_	Alignment	not modelled	15.3	13	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
46	c2d3fD_	Alignment	not modelled	14.9	48	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**collagen model peptides (pro-pro-gly)4-pro-hyp- **PDBTitle:** crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
47	c2d3fE_	Alignment	not modelled	14.9	48	**PDB header:**structural protein **Chain:** E: **PDB Molecule:**collagen model peptides (pro-pro-gly)4-pro-hyp- **PDBTitle:** crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
48	c2d3fF_	Alignment	not modelled	14.9	48	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**collagen model peptides (pro-pro-gly)4-pro-hyp- **PDBTitle:** crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
49	c1x1kD_	Alignment	not modelled	14.9	48	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**host-guest peptide (pro-pro-gly)4-(pro-allohyp- **PDBTitle:** host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
50	c1x1kA_	Alignment	not modelled	14.9	48	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**host-guest peptide (pro-pro-gly)4-(pro-allohyp- **PDBTitle:** host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
51	c1x1kC_	Alignment	not modelled	14.9	48	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**host-guest peptide (pro-pro-gly)4-(pro-allohyp- **PDBTitle:** host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
52	c1x1kB_	Alignment	not modelled	14.9	48	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**host-guest peptide (pro-pro-gly)4-(pro-allohyp- **PDBTitle:** host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
53	c6msrA_	Alignment	not modelled	14.6	18	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**pro-2.5; **PDBTitle:** crystal structure of pro-2.5

54	d1a9xa1	Alignment	not modelled	14.1	15	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
55	d1tqza1	Alignment	not modelled	14.1	35	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Necap1 N-terminal domain-like
56	c3ggzC_	Alignment	not modelled	13.8	11	**PDB header:**protein transport, endocytosis **Chain:** C: **PDB Molecule:**increased sodium tolerance protein 1; **PDBTitle:** crystal structure of s.cerevisiae ist1 n-terminal domain in complex2 with did2 mim motif
57	c3ddlB_	Alignment	not modelled	13.7	16	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**xanthorhodopsin; **PDBTitle:** crystallographic structure of xanthorhodopsin, a light-driven ion pump2 with dual chromophore
58	c3p42D_	Alignment	not modelled	13.4	14	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**predicted protein; **PDBTitle:** structure of gfcc (ymcb), protein encoded by the e. coli group 42 capsule operon
59	c6j9hA_	Alignment	not modelled	12.6	25	**PDB header:**peptide binding protein/hydrolase **Chain:** A: **PDB Molecule:**small vasohibin-binding protein; **PDBTitle:** crystal structure of svbp-vash1 complex
60	c5x70D_	Alignment	not modelled	12.6	24	**PDB header:**transferase/rna **Chain:** D: **PDB Molecule:**mrna capping enzyme p5; **PDBTitle:** crystal structure of rice dwarf virus p5 in complex with a ssrna2 oligomer
61	c6j4uB_	Alignment	not modelled	12.2	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**small vasohibin-binding protein; **PDBTitle:** structural basis of tubulin detyrosination by vasohibins-svbp enzyme2 complex and functional implications
62	c2k48A_	Alignment	not modelled	12.2	19	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**nucleoprotein; **PDBTitle:** nmr structure of the n-terminal coiled coil domain of the2 andes hantavirus nucleocapsid protein
63	c6cv0C_	Alignment	not modelled	12.1	12	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**spike glycoprotein; **PDBTitle:** cryo-electron microscopy structure of infectious bronchitis2 coronavirus spike protein
64	c3j38T_	Alignment	not modelled	11.6	21	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**40s ribosomal protein s19a; **PDBTitle:** structure of the d. melanogaster 40s ribosomal proteins
65	c6j4pB_	Alignment	not modelled	11.4	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**small vasohibin-binding protein; **PDBTitle:** structural basis of tubulin detyrosination by vasohibins-svbp enzyme2 complex and functional implications
66	c1x1kF_	Alignment	not modelled	10.9	50	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**host-guest peptide (pro-pro-gly)4-(pro-allohyp- **PDBTitle:** host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
67	c6j4sB_	Alignment	not modelled	10.8	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**small vasohibin-binding protein; **PDBTitle:** structural basis of tubulin detyrosination by vasohibins-svbp enzyme2 complex and functional implications
68	d1m98a1	Alignment	not modelled	10.8	19	**Fold:**Orange carotenoid protein, N-terminal domain **Superfamily:**Orange carotenoid protein, N-terminal domain **Family:**Orange carotenoid protein, N-terminal domain
69	c2dbfA_	Alignment	not modelled	10.5	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**nuclear factor nf-kappa-b p105 subunit; **PDBTitle:** solution structure of the death domain in human nuclear2 factor nf-kappa-b p105 subunit
70	c6j4vB_	Alignment	not modelled	10.3	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**small vasohibin-binding protein; **PDBTitle:** structural basis of tubulin detyrosination by vasohibins-svbp enzyme2 complex and functional implications
71	c6j8nA_	Alignment	not modelled	10.3	21	**PDB header:**peptide binding protein/hydrolase **Chain:** A: **PDB Molecule:**small vasohibin-binding protein; **PDBTitle:** crystal structure of svbp-vash1 complex, mutation c169a of vash1
72	c6j8nC_	Alignment	not modelled	10.3	21	**PDB header:**peptide binding protein/hydrolase **Chain:** C: **PDB Molecule:**small vasohibin-binding protein; **PDBTitle:** crystal structure of svbp-vash1 complex, mutation c169a of vash1
73	c3wt9A_	Alignment	not modelled	10.2	8	**PDB header:**proton transport **Chain:** A: **PDB Molecule:**rhodopsin i; **PDBTitle:** crystal structure of the cell-free synthesized membrane protein,2 acetabularia rhodopsin i, at 1.48 angstrom
74	c2i9nA_	Alignment	not modelled	10.1	46	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**mhb4a peptide; **PDBTitle:** design of bivalent miniprotein consisting of two2 independent elements, a b-hairpin peptide and a-helix3 peptide, tethered by four glycines
75	c3iq1A_	Alignment	not modelled	10.0	16	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**dps family protein; **PDBTitle:** crystal structure of dps protein from vibrio cholerae o1, a member of2 a broad superfamily of ferritin-like diiron-carboxylate proteins
76	c3frrA_	Alignment	not modelled	9.7	4	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**uncharacterized protein kiaa0174; **PDBTitle:** structure of human ist1(ntd) - (residues 1-189)(p21)
77	c6j9hC_	Alignment	not modelled	9.6	22	**PDB header:**peptide binding protein/hydrolase **Chain:** C: **PDB Molecule:**small vasohibin-binding protein; **PDBTitle:** crystal structure of svbp-vash1 complex
78	c1ciiA_	Alignment	not modelled	9.5	11	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia

79	c5jxlA_	Alignment	not modelled	9.4	25	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**flagellar hook protein flge; **PDBTitle:** cryo-em structure of the flagellar hook of campylobacter jejuni
80	c3admC_	Alignment	not modelled	9.2	44	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
81	c2d3fA_	Alignment	not modelled	9.2	46	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**collagen model peptides (pro-pro-gly)4-pro-hyp- **PDBTitle:** crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
82	c2d3fC_	Alignment	not modelled	9.2	46	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**collagen model peptides (pro-pro-gly)4-pro-hyp- **PDBTitle:** crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
83	c2d3fB_	Alignment	not modelled	9.2	46	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**collagen model peptides (pro-pro-gly)4-pro-hyp- **PDBTitle:** crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
84	c1x1kE_	Alignment	not modelled	9.2	46	**PDB header:**structural protein **Chain:** E: **PDB Molecule:**host-guest peptide (pro-pro-gly)4-(pro-allohyp- **PDBTitle:** host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
85	c6ocgB_	Alignment	not modelled	8.8	22	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**small vasohibin-binding protein; **PDBTitle:** crystal structure of vash1-svbp complex bound with epoy
86	c4ednL_	Alignment	not modelled	8.7	46	**PDB header:**signaling protein/cell adhesion **Chain:** L: **PDB Molecule:**paxillin; **PDBTitle:** crystal structure of beta-parvin ch2 domain in complex with paxillin2 ld1 motif
87	c3vf0A_	Alignment	not modelled	8.6	10	**PDB header:**cell adhesion/protein binding **Chain:** A: **PDB Molecule:**vinculin; **PDBTitle:** raver1 in complex with metavinculin l954 deletion mutant
88	c6ochD_	Alignment	not modelled	8.5	22	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** D: **PDB Molecule:**small vasohibin-binding protein; **PDBTitle:** crystal structure of vash1-svbp complex bound with parthenolide
89	c2l7nA_	Alignment	not modelled	8.5	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**talin-1; **PDBTitle:** nmr structure of the b domain of talin
90	c4ednQ_	Alignment	not modelled	8.4	46	**PDB header:**signaling protein/cell adhesion **Chain:** Q: **PDB Molecule:**paxillin; **PDBTitle:** crystal structure of beta-parvin ch2 domain in complex with paxillin2 ld1 motif
91	c2vzdD_	Alignment	not modelled	8.4	46	**PDB header:**cell adhesion **Chain:** D: **PDB Molecule:**paxillin; **PDBTitle:** crystal structure of the c-terminal calponin homology2 domain of alpha parvin in complex with paxillin ld1 motif
92	c6gbrA_	Alignment	not modelled	8.2	19	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**polymerase cofactor vp35; **PDBTitle:** crystal structure of the oligomerization domain of vp35 from reston2 virus, mercury derivative
93	c1m98A_	Alignment	not modelled	8.0	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**orange carotenoid protein; **PDBTitle:** crystal structure of orange carotenoid protein
94	c3admE_	Alignment	not modelled	7.9	44	**PDB header:**structural protein **Chain:** E: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
95	c3admF_	Alignment	not modelled	7.9	44	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
96	c3admB_	Alignment	not modelled	7.9	44	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
97	c3admA_	Alignment	not modelled	7.9	44	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
98	c4hyjB_	Alignment	not modelled	7.9	12	**PDB header:**proton transport **Chain:** B: **PDB Molecule:**rhodopsin; **PDBTitle:** crystal structure of exiguobacterium sibiricum rhodopsin
99	c3wvbA_	Alignment	not modelled	7.7	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**upf0254 protein mj1251; **PDBTitle:** hcgf from methanocaldococcus jannaschii