














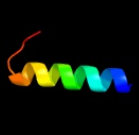

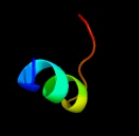






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2367c_(-)_2648374_2648922
Date	Mon Aug 5 13:25:52 BST 2019
Unique Job ID	e599b960295ce412

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1xm5a_</a>	 Alignment		100.0	32	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Predicted metal-dependent hydrolase
2	<a href="#">d1oz9a_</a>	 Alignment		100.0	34	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Predicted metal-dependent hydrolase
3	<a href="#">c1xaxA_</a>	 Alignment		100.0	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical upf0054 protein hi0004; <b>PDBTitle:</b> nmr structure of hi0004, a putative essential gene product2 from haemophilus influenzae
4	<a href="#">d1tvia_</a>	 Alignment		100.0	31	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Predicted metal-dependent hydrolase
5	<a href="#">c2xhqA_</a>	 Alignment		57.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> archaemetzincin; <b>PDBTitle:</b> crystal structure of archaemetzincin (amza) from archaeoglobus2 fulgidus at 1.45 a resolution
6	<a href="#">c1u9pA_</a>	 Alignment		57.7	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> parc; <b>PDBTitle:</b> permuted single-chain arc
7	<a href="#">d1lmla_</a>	 Alignment		57.5	17	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Leishmanolysin
8	<a href="#">c2x7mA_</a>	 Alignment		55.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> archaemetzincin; <b>PDBTitle:</b> crystal structure of archaemetzincin (amza) from methanopyrus2 kandleri at 1.5 a resolution
9	<a href="#">c3vtgA_</a>	 Alignment		51.6	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> high choriolytic enzyme 1; <b>PDBTitle:</b> high choriolytic enzyme 1 (hce-1), a hatching enzyme zinc-protease2 from oryzias latipes (medaka fish)
10	<a href="#">c5czwA_</a>	 Alignment		40.8	37	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> myroilysin; <b>PDBTitle:</b> crystal structure of myroilysin
11	<a href="#">c5th6D_</a>	 Alignment		38.8	26	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> matrix metalloproteinase-9,matrix metalloproteinase-9; <b>PDBTitle:</b> structure determination of a potent, selective antibody inhibitor of2 human mmp9 (apo mmp9)

12	<a href="#">d1hv5a_</a>	Alignment		38.1	30	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
13	<a href="#">c4q66j_</a>	Alignment		37.7	21	<b>PDB header:</b> protein transport <b>Chain:</b> J: <b>PDB Molecule:</b> chs5p; <b>PDBTitle:</b> structure of exomer bound to arf1.
14	<a href="#">d1asta_</a>	Alignment		37.4	36	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Astacin
15	<a href="#">c3edhA_</a>	Alignment		37.1	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bone morphogenetic protein 1; <b>PDBTitle:</b> crystal structure of bone morphogenetic protein 1 protease2 domain in complex with partially bound dmso
16	<a href="#">d2ovxa1</a>	Alignment		36.8	40	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
17	<a href="#">d1y93a1</a>	Alignment		36.8	35	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
18	<a href="#">c3lqbA_</a>	Alignment		35.3	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> loc792177 protein; <b>PDBTitle:</b> crystal structure of the hatching enzyme zhe1 from the zebrafish danio2 rerio
19	<a href="#">c4gwnA_</a>	Alignment		34.1	43	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> meprin a subunit beta; <b>PDBTitle:</b> crystal structure of human mature meprin beta
20	<a href="#">d1hova_</a>	Alignment		33.3	30	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
21	<a href="#">d1hfca_</a>	Alignment	not modelled	31.4	30	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
22	<a href="#">c4gwmA_</a>	Alignment	not modelled	31.4	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> meprin a subunit beta; <b>PDBTitle:</b> crystal structure of human promeprin beta
23	<a href="#">d1cglA_</a>	Alignment	not modelled	31.2	30	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
24	<a href="#">d1fbla2</a>	Alignment	not modelled	31.2	32	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
25	<a href="#">d1qiba_</a>	Alignment	not modelled	30.3	30	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
26	<a href="#">c2jsdA_</a>	Alignment	not modelled	29.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> matrix metalloproteinase-20; <b>PDBTitle:</b> solution structure of mmp20 complexed with nngH
27	<a href="#">d1i76a_</a>	Alignment	not modelled	28.8	35	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
28	<a href="#">d1xuca1</a>	Alignment	not modelled	28.3	42	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
29	<a href="#">c3lmcA_</a>	Alignment	not modelled	28.1	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidase, zinc-dependent; <b>PDBTitle:</b> crystal structure of zinc-dependent peptidase from

						methanocorpusculum2 labreanum (strain z), northeast structural genomics consortium target3 mur16
30	<a href="#">d1q3aa_</a>	Alignment	not modelled	27.5	37	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
31	<a href="#">c4yg8A_</a>	Alignment	not modelled	26.4	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> chitin biosynthesis protein chs5; <b>PDBTitle:</b> crystal structure of the chs5-chs6 exomer cargo adaptor complex
32	<a href="#">c4gnsA_</a>	Alignment	not modelled	26.4	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> chitin biosynthesis protein chs5; <b>PDBTitle:</b> crystal structure of the chs5-chs6 exomer cargo adaptor complex
33	<a href="#">d1rm8a_</a>	Alignment	not modelled	25.8	37	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
34	<a href="#">c5zwoO_</a>	Alignment	not modelled	25.6	16	<b>PDB header:</b> splicing <b>Chain:</b> O: <b>PDB Molecule:</b> 66 kda u4/u6.u5 small nuclear ribonucleoprotein component; <b>PDBTitle:</b> cryo-em structure of the yeast b complex at average resolution of 3.92 angstrom
35	<a href="#">c2xs4A_</a>	Alignment	not modelled	25.4	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> karilysin protease; <b>PDBTitle:</b> structure of karilysin catalytic mmp domain in complex with magnesium
36	<a href="#">c3lq0A_</a>	Alignment	not modelled	23.7	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> proastacin; <b>PDBTitle:</b> zymogen structure of crayfish astacin metallopeptidase
37	<a href="#">d1cxva_</a>	Alignment	not modelled	23.2	37	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
38	<a href="#">d1mmqa_</a>	Alignment	not modelled	22.9	25	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
39	<a href="#">d1hy7a_</a>	Alignment	not modelled	19.0	35	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
40	<a href="#">c1slmA_</a>	Alignment	not modelled	18.8	37	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> stromelysin-1; <b>PDBTitle:</b> crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
41	<a href="#">c5mslA_</a>	Alignment	not modelled	18.5	36	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> anti-sigma-f factor fin; <b>PDBTitle:</b> solution structure of the b. subtilis anti-sigma-f factor, fin
42	<a href="#">d1k7ia2</a>	Alignment	not modelled	13.3	19	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal) domain
43	<a href="#">c4g0dD_</a>	Alignment	not modelled	13.3	40	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> collagenase 3; <b>PDBTitle:</b> human collagenase 3 (mmp-13) full form with peptides from pro-domain
44	<a href="#">c1jmtB_</a>	Alignment	not modelled	13.1	38	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> splicing factor u2af 65 kda subunit; <b>PDBTitle:</b> x-ray structure of a core u2af65/u2af35 heterodimer
45	<a href="#">d1wgnA_</a>	Alignment	not modelled	12.8	19	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
46	<a href="#">d1eaka2</a>	Alignment	not modelled	12.5	32	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
47	<a href="#">d1qmya_</a>	Alignment	not modelled	11.5	44	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> FMDV leader protease
48	<a href="#">d1qola_</a>	Alignment	not modelled	11.4	44	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> FMDV leader protease
49	<a href="#">c2erpA_</a>	Alignment	not modelled	11.2	33	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> vascular apoptosis-inducing protein 1; <b>PDBTitle:</b> crystal structure of vascular apoptosis-inducing protein-1(inhibitor-2 bound form)
50	<a href="#">c2zw2B_</a>	Alignment	not modelled	11.0	18	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein sts178; <b>PDBTitle:</b> crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stspurs)
51	<a href="#">d1sata2</a>	Alignment	not modelled	10.6	15	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal) domain
52	<a href="#">c5fx8U_</a>	Alignment	not modelled	10.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> U: <b>PDB Molecule:</b> zonadhesin; <b>PDBTitle:</b> complete structure of manganese lipoxygenase of gaeumannomyces2 graminis and partial structure of zonadhesin of komagataella3 pastoris
53	<a href="#">c2cltB_</a>	Alignment	not modelled	10.4	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> interstitial collagenase; <b>PDBTitle:</b> crystal structure of the active form (full-length) of human2 fibroblast collagenase.
54	<a href="#">d2a6aa2</a>	Alignment	not modelled	10.2	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> YeaZ-like
55	<a href="#">d1atla_</a>	Alignment	not modelled	10.2	25	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like

56	<a href="#">c3wnnB_</a>	Alignment	not modelled	9.9	31	<b>PDB header:</b> metal binding protein/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> orff; <b>PDBTitle:</b> crystal structure of lysz from thermus thermophilus complex with lysw
57	<a href="#">c2dw1B_</a>	Alignment	not modelled	9.4	30	<b>PDB header:</b> apoptosis, toxin <b>Chain:</b> B: <b>PDB Molecule:</b> catrocollastatin; <b>PDBTitle:</b> crystal structure of vap2 from crotalus atrox venom (form 2-2 crystal)
58	<a href="#">c4cs7A_</a>	Alignment	not modelled	9.3	20	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> m2-1; <b>PDBTitle:</b> crystal structure of the asymmetric human metapneumovirus2 m2-1 tetramer, form 1
59	<a href="#">c1rm1C_</a>	Alignment	not modelled	9.2	23	<b>PDB header:</b> transcription/dna <b>Chain:</b> C: <b>PDB Molecule:</b> transcription initiation factor iia large chain; <b>PDBTitle:</b> structure of a yeast tfiia/tpb/tata-box dna complex
60	<a href="#">d1jyma_</a>	Alignment	not modelled	8.8	21	<b>Fold:</b> Peptide deformylase <b>Superfamily:</b> Peptide deformylase <b>Family:</b> Peptide deformylase
61	<a href="#">c2rjqA_</a>	Alignment	not modelled	8.8	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adamts-5; <b>PDBTitle:</b> crystal structure of adamts5 with inhibitor bound
62	<a href="#">c2mzeA_</a>	Alignment	not modelled	8.8	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> matrilysin; <b>PDBTitle:</b> nmr solution structure of the pro form of human matrilysin (prommp-7)
63	<a href="#">d1kufa_</a>	Alignment	not modelled	8.8	30	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like
64	<a href="#">c3bkdD_</a>	Alignment	not modelled	8.7	63	<b>PDB header:</b> viral protein, membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> transmembrane domain of matrix protein m2; <b>PDBTitle:</b> high resolution crystal structure of transmembrane domain of m22 protein
65	<a href="#">c3bkdB_</a>	Alignment	not modelled	8.7	63	<b>PDB header:</b> viral protein, membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> transmembrane domain of matrix protein m2; <b>PDBTitle:</b> high resolution crystal structure of transmembrane domain of m22 protein
66	<a href="#">c3bkdC_</a>	Alignment	not modelled	8.7	63	<b>PDB header:</b> viral protein, membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> transmembrane domain of matrix protein m2; <b>PDBTitle:</b> high resolution crystal structure of transmembrane domain of m22 protein
67	<a href="#">c3bkdA_</a>	Alignment	not modelled	8.7	63	<b>PDB header:</b> viral protein, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> transmembrane domain of matrix protein m2; <b>PDBTitle:</b> high resolution crystal structure of transmembrane domain of m22 protein
68	<a href="#">c3bkdE_</a>	Alignment	not modelled	8.7	63	<b>PDB header:</b> viral protein, membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> transmembrane domain of matrix protein m2; <b>PDBTitle:</b> high resolution crystal structure of transmembrane domain of m22 protein
69	<a href="#">c3bkdH_</a>	Alignment	not modelled	8.7	63	<b>PDB header:</b> viral protein, membrane protein <b>Chain:</b> H: <b>PDB Molecule:</b> transmembrane domain of matrix protein m2; <b>PDBTitle:</b> high resolution crystal structure of transmembrane domain of m22 protein
70	<a href="#">c3bkdG_</a>	Alignment	not modelled	8.7	63	<b>PDB header:</b> viral protein, membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> transmembrane domain of matrix protein m2; <b>PDBTitle:</b> high resolution crystal structure of transmembrane domain of m22 protein
71	<a href="#">c3bkdF_</a>	Alignment	not modelled	8.7	63	<b>PDB header:</b> viral protein, membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> transmembrane domain of matrix protein m2; <b>PDBTitle:</b> high resolution crystal structure of transmembrane domain of m22 protein
72	<a href="#">d1bqqm_</a>	Alignment	not modelled	8.3	32	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
73	<a href="#">c3ipfA_</a>	Alignment	not modelled	7.9	31	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the q251q8_deshy protein from desulfitobacterium2 hafniense. northeast structural genomics consortium target dhr8c.
74	<a href="#">d1r55a_</a>	Alignment	not modelled	7.9	29	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like
75	<a href="#">c2l0qA_</a>	Alignment	not modelled	7.7	55	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iota; <b>PDBTitle:</b> solution nmr structure of ubiquitin-binding motif (ubm2) of human2 polymerase iota
76	<a href="#">c2khuA_</a>	Alignment	not modelled	7.4	55	<b>PDB header:</b> transferase/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> immunoglobulin g-binding protein g, dna <b>PDBTitle:</b> solution structure of the ubiquitin-binding motif of human2 polymerase iota
77	<a href="#">c3e5aB_</a>	Alignment	not modelled	7.3	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> targeting protein for xklp2; <b>PDBTitle:</b> crystal structure of aurora a in complex with vx-680 and tpx2
78	<a href="#">c2oq2B_</a>	Alignment	not modelled	7.0	5	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoadenosine phosphosulfate reductase; <b>PDBTitle:</b> crystal structure of yeast paps reductase with pap, a product complex
						<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> C-terminal domain of alpha and beta subunits of F1

79	<a href="#">d1fx0b1</a>	Alignment	not modelled	7.0	16	ATP synthase <b>Family:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase
80	<a href="#">c3c0tB</a>	Alignment	not modelled	6.9	67	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> mediator of rna polymerase ii transcription <b>PDBTitle:</b> structure of the schizosaccharomyces pombe mediator2 subcomplex med8c/18
81	<a href="#">c3gr1A</a>	Alignment	not modelled	6.8	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein prgh; <b>PDBTitle:</b> periplasmic domain of the t3ss inner membrane protein prgh from <i>S.typhimurium</i> (fragment 170-392)
82	<a href="#">c5k2mF</a>	Alignment	not modelled	6.7	46	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> F: <b>PDB Molecule:</b> probable lysine biosynthesis protein; <b>PDBTitle:</b> bifunctional lysx/argx from thermococcus kodakarensis with lysw-gamma-2 aaa
83	<a href="#">d2i47a1</a>	Alignment	not modelled	6.6	33	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> TNF-alpha converting enzyme, TACE, catalytic domain
84	<a href="#">c3b8zB</a>	Alignment	not modelled	6.6	33	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein adamts-5; <b>PDBTitle:</b> high resolution crystal structure of the catalytic domain of adamts-52 (aggrecanase-2)
85	<a href="#">c2kwuA</a>	Alignment	not modelled	6.4	36	<b>PDB header:</b> protein binding/signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iota; <b>PDBTitle:</b> solution structure of ubm2 of murine polymerase iota in complex with 2 ubiquitin
86	<a href="#">c3ba0A</a>	Alignment	not modelled	6.3	36	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> macrophage metalloelastase; <b>PDBTitle:</b> crystal structure of full-length human mmp-12
87	<a href="#">d1t4aa</a>	Alignment	not modelled	6.0	25	<b>Fold:</b> PurS-like <b>Superfamily:</b> PurS-like <b>Family:</b> PurS subunit of FGAM synthetase
88	<a href="#">c3viqC</a>	Alignment	not modelled	5.7	27	<b>PDB header:</b> recombination activator <b>Chain:</b> C: <b>PDB Molecule:</b> swi5-dependent recombination dna repair protein 1; <b>PDBTitle:</b> crystal structure of swi5-sfr1 complex from fission yeast
89	<a href="#">c4in3C</a>	Alignment	not modelled	5.6	21	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> chitin biosynthesis protein chs5; <b>PDBTitle:</b> crystal structure of the chs5-bch1 exomer cargo adaptor complex
90	<a href="#">c4fipG</a>	Alignment	not modelled	5.6	47	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> saga-associated factor 11; <b>PDBTitle:</b> structure of the saga ubp8(s144n)/sgf11(1-72, delta-znf)/sus1/sgf732 dub module
91	<a href="#">c2v4bB</a>	Alignment	not modelled	5.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> adamts-1; <b>PDBTitle:</b> crystal structure of human adamts-1 catalytic domain and cysteine-2 rich domain (apo-form)
92	<a href="#">c1dowB</a>	Alignment	not modelled	5.5	24	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> beta-catenin; <b>PDBTitle:</b> crystal structure of a chimera of beta-catenin and alpha-2 catenin
93	<a href="#">c2dgbA</a>	Alignment	not modelled	5.5	42	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein purs; <b>PDBTitle:</b> structure of thermus thermophilus purs in the p21 form
94	<a href="#">c1l6jA</a>	Alignment	not modelled	5.3	39	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> matrix metalloproteinase-9; <b>PDBTitle:</b> crystal structure of human matrix metalloproteinase mmp92 (gelatinase b).
95	<a href="#">c3k7iA</a>	Alignment	not modelled	5.2	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atragin; <b>PDBTitle:</b> structures of two elapid snake venom metalloproteases with 2 distinct activities highlight the disulfide patterns in the 3 d domain of adamalysin family proteins
96	<a href="#">d3e11a1</a>	Alignment	not modelled	5.2	25	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> TTHA0227-like