








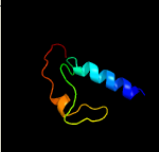





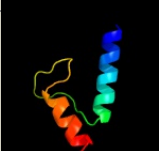
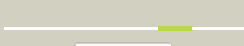
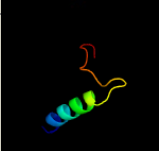



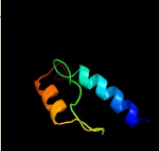


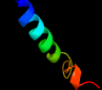
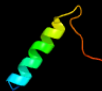


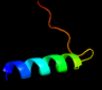




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0198c (- )_234516_236507
Date	Tue Jul 23 14:50:25 BST 2019
Unique Job ID	5f5f4f430c0b6dbf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3zukB_</a>	 Alignment		100.0	100	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> endopeptidase, peptidase family m13; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis zinc metalloprotease2 zmp1 in complex with inhibitor
2	<a href="#">d1dmta_</a>	 Alignment		100.0	32	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Neutral endopeptidase (neprilysin)
3	<a href="#">c3dwbA_</a>	 Alignment		100.0	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endothelin-converting enzyme 1; <b>PDBTitle:</b> structure of human ece-1 complexed with phosphoramidon
4	<a href="#">c4iuwA_</a>	 Alignment		100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> neutral endopeptidase; <b>PDBTitle:</b> crystal structure of pepo from lactobacillus rhamnosis hn001 (dr20)
5	<a href="#">d1bswa_</a>	 Alignment		83.2	22	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like
6	<a href="#">d1wnia_</a>	 Alignment		82.1	19	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like
7	<a href="#">c3k7IA_</a>	 Alignment		82.0	16	<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
8	<a href="#">c2dw1B_</a>	 Alignment		67.2	16	<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)
9	<a href="#">d1r55a_</a>	 Alignment		66.0	42	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like
10	<a href="#">d1atla_</a>	 Alignment		66.0	32	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like
11	<a href="#">c1yp1A_</a>	 Alignment		64.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> fii; <b>PDBTitle:</b> crystal structure of a non-hemorrhagic fibrin(ogen)olytic 2 metalloproteinase from venom of agkistrodon acutus

12	<a href="#">d1nd1a_</a>	Alignment		64.9	28	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like
13	<a href="#">d1kufa_</a>	Alignment		62.5	20	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like
14	<a href="#">c4dd8B_</a>	Alignment		59.3	31	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> disintegrin and metalloproteinase domain-containing protein <b>PDBTitle:</b> adam-8 metalloproteinase domain with bound batimastat
15	<a href="#">c6be6D_</a>	Alignment		57.9	23	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> disintegrin and metalloproteinase domain-containing protein <b>PDBTitle:</b> adam10 extracellular domain
16	<a href="#">d4aiga_</a>	Alignment		57.3	28	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like
17	<a href="#">c3cqbB_</a>	Alignment		55.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable protease htpx homolog; <b>PDBTitle:</b> crystal structure of heat shock protein htpx domain from vibrio2 paraahaemolyticus rimd 2210633
18	<a href="#">d2i47a1</a>	Alignment		55.8	44	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> TNF-alpha converting enzyme, TACE, catalytic domain
19	<a href="#">c3k7nA_</a>	Alignment		54.5	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> k-like; <b>PDBTitle:</b> structures of two elapid snake venom metalloproteases with2 distinct activities highlight the disulfide patterns in the3 d domain of adamalysin family proteins
20	<a href="#">c2e3xA_</a>	Alignment		54.0	14	<b>PDB header:</b> hydrolase, blood clotting, toxin <b>Chain:</b> A: <b>PDB Molecule:</b> coagulation factor x-activating enzyme heavy chain; <b>PDBTitle:</b> crystal structure of russell's viper venom metalloproteinase
21	<a href="#">c2i47A_</a>	Alignment	not modelled	52.9	44	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adam 17; <b>PDBTitle:</b> crystal structure of catalytic domain of tace with inhibitor
22	<a href="#">c3nqzB_</a>	Alignment	not modelled	52.5	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> secreted metalloprotease mcp02; <b>PDBTitle:</b> crystal structure of the autoprocessed vibriolysin mcp-02 with e369a2 mutation
23	<a href="#">c3nqxA_</a>	Alignment	not modelled	48.7	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> secreted metalloprotease mcp02; <b>PDBTitle:</b> crystal structure of vibriolysin mcp-02 mature enzyme, a zinc2 metalloprotease from m4 family
24	<a href="#">c2erpA_</a>	Alignment	not modelled	43.8	13	<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)
25	<a href="#">c2vqxA_</a>	Alignment	not modelled	40.7	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metalloproteinase; <b>PDBTitle:</b> precursor of protealysin, metalloproteinase from serratia2 proteamaculans.
26	<a href="#">d1quaa_</a>	Alignment	not modelled	38.9	20	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like
27	<a href="#">d1u4ga_</a>	Alignment	not modelled	38.6	26	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Thermolysin-like
28	<a href="#">c3b8zB_</a>	Alignment	not modelled	37.3	42	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein adams-5; <b>PDBTitle:</b> high resolution crystal structure of the catalytic domain of adams-52 (aggrecanase-2) <b>PDB header:</b> hydrolase

29	<a href="#">c2v4bB_</a>	Alignment	not modelled	36.9	36	<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)
30	<a href="#">d1npca_</a>	Alignment	not modelled	28.1	60	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Thermolysin-like
31	<a href="#">d1bqba_</a>	Alignment	not modelled	26.5	54	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Thermolysin-like
32	<a href="#">c4gerB_</a>	Alignment	not modelled	26.2	60	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> gentlyase metalloprotease; <b>PDBTitle:</b> crystal structure of gentlyase, the neutral metalloprotease of2 paenibacillus polymyxa
33	<a href="#">c2rjpC_</a>	Alignment	not modelled	26.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> adamts-4; <b>PDBTitle:</b> crystal structure of adamts4 with inhibitor bound
34	<a href="#">d1kjpA_</a>	Alignment	not modelled	25.7	36	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Thermolysin-like
35	<a href="#">c3c37B_</a>	Alignment	not modelled	23.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> peptidase, m48 family; <b>PDBTitle:</b> x-ray structure of the putative zn-dependent peptidase q74d82 at the2 resolution 1.7 a. northeast structural genomics consortium target3 gsr143a
36	<a href="#">c1vzmB_</a>	Alignment	not modelled	19.4	27	<b>PDB header:</b> calcium-binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> osteocalcin; <b>PDBTitle:</b> osteocalcin from fish argyrosomus regius
37	<a href="#">c2qr4B_</a>	Alignment	not modelled	18.1	36	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> peptidase m3b, oligoendopeptidase f; <b>PDBTitle:</b> crystal structure of oligoendopeptidase-f from enterococcus faecium
38	<a href="#">c3g5cA_</a>	Alignment	not modelled	17.2	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> adam 22; <b>PDBTitle:</b> structural and biochemical studies on the ectodomain of human adam22
39	<a href="#">d1k9xa_</a>	Alignment	not modelled	16.7	15	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Neurolysin-like
40	<a href="#">c5zjIA_</a>	Alignment	not modelled	15.8	15	<b>PDB header:</b> allergen <b>Chain:</b> A; <b>PDB Molecule:</b> der f 23 allergen; <b>PDBTitle:</b> crystal structure of the dust mite allergen der f 23 from2 dermatophagoides farinae
41	<a href="#">c4k90A_</a>	Alignment	not modelled	15.4	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> extracellular metalloproteinase mep; <b>PDBTitle:</b> extracellular metalloproteinase from aspergillus
42	<a href="#">d1d0gr3</a>	Alignment	not modelled	14.8	6	<b>Fold:</b> TNF receptor-like <b>Superfamily:</b> TNF receptor-like <b>Family:</b> TNF receptor-like
43	<a href="#">d1mmqa_</a>	Alignment	not modelled	14.7	31	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
44	<a href="#">d1y93a1</a>	Alignment	not modelled	14.4	45	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
45	<a href="#">d1cxva_</a>	Alignment	not modelled	14.4	45	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
46	<a href="#">c5tzqD_</a>	Alignment	not modelled	14.3	15	<b>PDB header:</b> apoptosis <b>Chain:</b> D; <b>PDB Molecule:</b> bcl-2-modifying factor; <b>PDBTitle:</b> crystal structure of fpv039:bmf bh3 complex
47	<a href="#">d1xuca1</a>	Alignment	not modelled	14.1	45	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
48	<a href="#">c3sksA_</a>	Alignment	not modelled	13.6	55	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative oligoendopeptidase f; <b>PDBTitle:</b> crystal structure of a putative oligoendopeptidase f from bacillus2 anthracis str. ames
49	<a href="#">d1i76a_</a>	Alignment	not modelled	13.4	45	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
50	<a href="#">c2xs4A_</a>	Alignment	not modelled	13.3	55	<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
51	<a href="#">c2j83B_</a>	Alignment	not modelled	13.0	46	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> ulilyisin; <b>PDBTitle:</b> ulilyisin metalloprotease in complex with batimastat.
52	<a href="#">d2g7oa1</a>	Alignment	not modelled	12.8	13	<b>Fold:</b> TraM-like <b>Superfamily:</b> TraM-like <b>Family:</b> TraM-like
53	<a href="#">d1tuza_</a>	Alignment	not modelled	12.6	6	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> EF-hand modules in multidomain proteins
54	<a href="#">c4fcaA_</a>	Alignment	not modelled	12.5	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> conserved domain protein; <b>PDBTitle:</b> the crystal structure of a functionally unknown conserved protein from2 bacillus anthracis str. ames.
55	<a href="#">d1eaka2</a>	Alignment	not modelled	12.5	23	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain

56	<a href="#">d2ovxa1</a>	Alignment	not modelled	12.3	36	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
57	<a href="#">d1rh7a_</a>	Alignment	not modelled	12.0	43	<b>Fold:</b> Resistin <b>Superfamily:</b> Resistin <b>Family:</b> Resistin
58	<a href="#">c4wwxB_</a>	Alignment	not modelled	11.9	18	<b>PDB header:</b> hydrolase, ligase <b>Chain:</b> B: <b>PDB Molecule:</b> v(d)j recombination-activating protein 1; <b>PDBTitle:</b> crystal structure of the core rag1/2 recombinase
59	<a href="#">c5ebzF_</a>	Alignment	not modelled	11.9	24	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> F: <b>PDB Molecule:</b> inhibitor of nuclear factor kappa-b kinase subunit alpha; <b>PDBTitle:</b> crystal structure of human ikk1
60	<a href="#">c5tzqC_</a>	Alignment	not modelled	11.8	16	<b>PDB header:</b> apoptosis <b>Chain:</b> C: <b>PDB Molecule:</b> bcl-2-modifying factor; <b>PDBTitle:</b> crystal structure of fpv039:bmf bh3 complex
61	<a href="#">d1bqqm_</a>	Alignment	not modelled	11.7	45	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
62	<a href="#">c4on1B_</a>	Alignment	not modelled	11.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative metalloprotease ii; <b>PDBTitle:</b> crystal structure of metalloproteinase-ii from bacteroides fragilis
63	<a href="#">c4aw6B_</a>	Alignment	not modelled	11.6	64	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> caax prenyl protease 1 homolog; <b>PDBTitle:</b> crystal structure of the human nuclear membrane zinc metalloprotease2 zmpste24 (face1)
64	<a href="#">d1hova_</a>	Alignment	not modelled	11.5	45	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
65	<a href="#">c1wgzC_</a>	Alignment	not modelled	11.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> carboxypeptidase 1; <b>PDBTitle:</b> crystal structure of carboxypeptidase 1 from thermus thermophilus
66	<a href="#">c5xknE_</a>	Alignment	not modelled	11.3	23	<b>PDB header:</b> transferase/signaling protein <b>Chain:</b> E: <b>PDB Molecule:</b> epidermal patterning factor-like protein 4; <b>PDBTitle:</b> crystal structure of plant receptor erl2 in complexe with epfl4
67	<a href="#">c5xknF_</a>	Alignment	not modelled	11.3	23	<b>PDB header:</b> transferase/signaling protein <b>Chain:</b> F: <b>PDB Molecule:</b> epidermal patterning factor-like protein 4; <b>PDBTitle:</b> crystal structure of plant receptor erl2 in complexe with epfl4
68	<a href="#">c1rgxC_</a>	Alignment	not modelled	11.2	43	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> C: <b>PDB Molecule:</b> resistin; <b>PDBTitle:</b> crystal structure of resisitn
69	<a href="#">c3s2xB_</a>	Alignment	not modelled	11.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa synthase subunit alpha; <b>PDBTitle:</b> structure of acetyl-coenzyme a synthase alpha subunit c-terminal2 domain
70	<a href="#">d1dlca3</a>	Alignment	not modelled	11.0	19	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> delta-Endotoxin (insectocide), N-terminal domain <b>Family:</b> delta-Endotoxin (insectocide), N-terminal domain
71	<a href="#">c3t76A_</a>	Alignment	not modelled	10.8	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator vanug; <b>PDBTitle:</b> crystal structure of transcriptional regulator vanug, form ii
72	<a href="#">d1qjba_</a>	Alignment	not modelled	10.8	38	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
73	<a href="#">c2jsdA_</a>	Alignment	not modelled	10.8	38	<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
74	<a href="#">c6aitD_</a>	Alignment	not modelled	10.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-barrel assembly-enhancing protease; <b>PDBTitle:</b> crystal structure of e. coli bepa
75	<a href="#">d1hfca_</a>	Alignment	not modelled	10.5	45	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
76	<a href="#">c3p24C_</a>	Alignment	not modelled	10.5	29	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> bft-3; <b>PDBTitle:</b> structure of profragilysin-3 from bacteroides fragilis
77	<a href="#">d1cgla_</a>	Alignment	not modelled	10.4	38	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
78	<a href="#">c3ce2A_</a>	Alignment	not modelled	10.4	55	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative peptidase; <b>PDBTitle:</b> crystal structure of putative peptidase from chlamydomphila abortus
79	<a href="#">d1hv5a_</a>	Alignment	not modelled	10.3	45	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
80	<a href="#">c2h1jA_</a>	Alignment	not modelled	10.3	55	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oligoendopeptidase f; <b>PDBTitle:</b> 3.1 a x-ray structure of putative oligoendopeptidase f: crystals grown2 by microfluidic seeding
81	<a href="#">d1hy7a_</a>	Alignment	not modelled	10.2	55	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
82	<a href="#">d1rm8a_</a>	Alignment	not modelled	10.2	38	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain

83	<a href="#">c5zihA_</a>	Alignment	not modelled	10.1	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> sensory opsin a,chromson; <b>PDBTitle:</b> crystal structure of the red light-activated channelrhodopsin2 chromson.
84	<a href="#">d1fbla2</a>	Alignment	not modelled	10.1	45	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
85	<a href="#">c2k3jA_</a>	Alignment	not modelled	10.1	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial intermembrane space import and <b>PDBTitle:</b> the solution structure of human mia40
86	<a href="#">c3dtkA_</a>	Alignment	not modelled	10.0	27	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> irre protein; <b>PDBTitle:</b> crystal structure of the irre protein, a central regulator2 of dna damage repair in deinococcaceae
87	<a href="#">d1q3aa_</a>	Alignment	not modelled	9.7	45	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
88	<a href="#">c2rjqA_</a>	Alignment	not modelled	9.7	20	<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
89	<a href="#">c4il3B_</a>	Alignment	not modelled	9.4	67	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ste24p; <b>PDBTitle:</b> crystal structure of s. mikatae ste24p
90	<a href="#">d1sata2</a>	Alignment	not modelled	9.3	45	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal) domain
91	<a href="#">c5sujB_</a>	Alignment	not modelled	9.2	14	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein lpg2148 from legionella2 pneumophila
92	<a href="#">d1rfxa_</a>	Alignment	not modelled	9.0	43	<b>Fold:</b> Resistin <b>Superfamily:</b> Resistin <b>Family:</b> Resistin
93	<a href="#">d1g9ka2</a>	Alignment	not modelled	8.9	45	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal) domain
94	<a href="#">c1dlcA_</a>	Alignment	not modelled	8.8	19	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> delta-endotoxin cryiia; <b>PDBTitle:</b> crystal structure of insecticidal delta-endotoxin from2 bacillus thuringiensis at 2.5 angstroms resolution
95	<a href="#">c1fwoA_</a>	Alignment	not modelled	8.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oryzain beta chain; <b>PDBTitle:</b> the solution structure of a 35-residue fragment from the2 granulin/epithelin-like subdomain of rice oryzain beta3 (rob 382-416 (c398s,c399s,c407s,c413s))
96	<a href="#">c2vogB_</a>	Alignment	not modelled	8.5	16	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bcl-2-modifying factor; <b>PDBTitle:</b> structure of mouse a1 bound to the bmf bh3-domain
97	<a href="#">c6etxR_</a>	Alignment	not modelled	8.4	7	<b>PDB header:</b> dna binding protein <b>Chain:</b> R: <b>PDB Molecule:</b> ino80 complex subunit b; <b>PDBTitle:</b> cryo-em structure of the human ino80 complex bound to nucleosome
98	<a href="#">c6mdxA_</a>	Alignment	not modelled	8.2	30	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> spirt-like domain-containing protein spartan; <b>PDBTitle:</b> mechanism of protease dependent dpc repair
99	<a href="#">c5th6D_</a>	Alignment	not modelled	8.2	38	<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)