



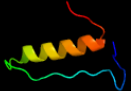

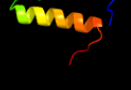
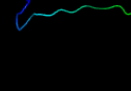




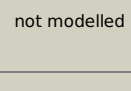
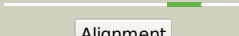

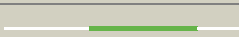




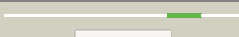
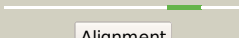
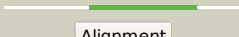

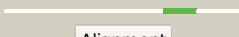
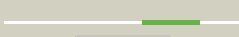

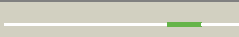
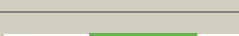

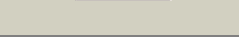
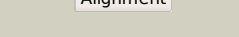

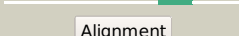
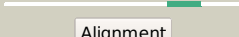


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3dtkA_</a>	 Alignment		91.5	22	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> irre protein; <b>PDBTitle:</b> crystal structure of the irre protein, a central regulator2 of dna damage repair in deinococcaceae <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
2	<a href="#">c4jiuA_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> proabylysin; <b>PDBTitle:</b> crystal structure of the metallopeptidase zymogen of pyrococcus abyssi2 abylysin <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
3	<a href="#">c6aitD_</a>	 Alignment		90.4	18	<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 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
4	<a href="#">c3c37B_</a>	 Alignment		95.0	15	<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 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
5	<a href="#">c4jixB_</a>	 Alignment		99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> projannalysin; <b>PDBTitle:</b> crystal structure of the metallopeptidase zymogen of2 methanocaldococcus jannaschii jannalysin <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
6	<a href="#">c6mdxA_</a>	 Alignment		98.8	18	<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 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
7	<a href="#">c5xbvA_</a>	 Alignment		99.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> wss1p; <b>PDBTitle:</b> crystal structure of wss1 mutant from saccharomyces cerevisiae <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
8	<a href="#">c5ln5A_</a>	 Alignment		97.7	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin and wlm domain-containing metalloprotease <b>PDBTitle:</b> crystal structure of the wss1 e203q mutant from s. pombe <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
9	<a href="#">c4il3B_</a>	 Alignment		91.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ste24p; <b>PDBTitle:</b> crystal structure of s. mikatae ste24p <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
10	<a href="#">c3cqbB_</a>	 Alignment		95.5	13	<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 parahaemolyticus rimd 2210633 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
11	<a href="#">c4aw6B_</a>	 Alignment		89.9	26	<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) <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>

12	<a href="#">d1bswa_</a>	Alignment		86.5	18	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
13	<a href="#">d1atla_</a>	Alignment		85.8	23	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
14	<a href="#">d1quaa_</a>	Alignment		83.4	20	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
15	<a href="#">d1r55a_</a>	Alignment		80.7	20	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
16	<a href="#">d1ndla_</a>	Alignment		80.5	20	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
17	<a href="#">c6oiuD_</a>	Alignment		80.4	11	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> aminopeptidase n; <b>PDBTitle:</b> x-ray crystal structure of the ectodomain of the toxoplasma gondii2 me49 aminopeptidase n (tgme49_224350) <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
18	<a href="#">d4aiga_</a>	Alignment		79.5	15	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
19	<a href="#">c1yp1A_</a>	Alignment		79.4	23	<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)olytic2 metalloproteinase from venom of agkistrodon acutus <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
20	<a href="#">c3b37A_</a>	Alignment		78.2	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase n; <b>PDBTitle:</b> crystal structure of e. coli aminopeptidase n in complex with tyrosine <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
21	<a href="#">c5zi7A_</a>	Alignment	not modelled	77.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase n; <b>PDBTitle:</b> crystal structure of legionella pneumophila aminopeptidase a in2 complex with glutamic acid <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
22	<a href="#">d1kufa_</a>	Alignment	not modelled	77.4	23	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
23	<a href="#">c5dlla_</a>	Alignment	not modelled	77.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase n; <b>PDBTitle:</b> aminopeptidase n (pepn) from francisella tularensis subsp. tularensis2 schu s4 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
24	<a href="#">c3ebhA_</a>	Alignment	not modelled	76.5	12	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> m1 family aminopeptidase; <b>PDBTitle:</b> structure of the m1 alanylaminopeptidase from malaria complexed with2 bestatin <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
25	<a href="#">c3k7lA_</a>	Alignment	not modelled	76.4	18	<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 distinct2 activities highlight the disulfide patterns in the d domain of3 adamalysin family proteins <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
26	<a href="#">c2gtqA_</a>	Alignment	not modelled	75.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase n; <b>PDBTitle:</b> crystal structure of aminopeptidase n from human pathogen neisseria2 meningitidis <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
27	<a href="#">d1wnia_</a>	Alignment	not modelled	73.9	20	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain

27	<a href="#">c1w1nA_</a>	Alignment	not modelled	73.9	20	<b>Family:</b> Reprolysin-like <b>PDB entry:</b> <a href="#">PDBe RCSB PDBj</a>
28	<a href="#">c2xdtA_</a>	Alignment	not modelled	73.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoplasmic reticulum aminopeptidase 1; <b>PDBTitle:</b> crystal structure of the soluble domain of human2 endoplasmic reticulum aminopeptidase 1 erap1 <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
29	<a href="#">c2e3xA_</a>	Alignment	not modelled	72.4	20	<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 <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
30	<a href="#">c4dd8B_</a>	Alignment	not modelled	70.2	13	<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 <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
31	<a href="#">c4kxdA_</a>	Alignment	not modelled	70.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl aminopeptidase; <b>PDBTitle:</b> crystal structure of human aminopeptidase a complexed with glutamate2 and calcium <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
32	<a href="#">c2i47A_</a>	Alignment	not modelled	69.0	26	<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 <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
33	<a href="#">c1eakA_</a>	Alignment	not modelled	68.5	24	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> 72 kda type iv collagenase; <b>PDBTitle:</b> catalytic domain of prommp-2 e404q mutant <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
34	<a href="#">d2i47a1</a>	Alignment	not modelled	68.0	26	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> TNF-alpha converting enzyme, TACE, catalytic domain <b>PDB entry:</b> <a href="#">PDBe RCSB PDBj</a>
35	<a href="#">c2erpA_</a>	Alignment	not modelled	67.9	15	<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) <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
36	<a href="#">c3k7nA_</a>	Alignment	not modelled	67.8	18	<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 with distinct2 activities highlight the disulfide patterns in the d domain of3 adamalysin family proteins <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
37	<a href="#">c3dl1A_</a>	Alignment	not modelled	67.1	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative metal-dependent hydrolase; <b>PDBTitle:</b> crystal structure of a putative metal-dependent hydrolase2 (yp_001336084.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 2.20 a resolution <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
38	<a href="#">c3g5cA_</a>	Alignment	not modelled	66.2	23	<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 <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
39	<a href="#">c2rjqA_</a>	Alignment	not modelled	65.6	22	<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 <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
40	<a href="#">c6be6D_</a>	Alignment	not modelled	65.5	27	<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 <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
41	<a href="#">c4fytA_</a>	Alignment	not modelled	63.2	15	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase n; <b>PDBTitle:</b> human aminopeptidase n (cd13) in complex with amastatin <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
42	<a href="#">c5czwA_</a>	Alignment	not modelled	61.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> myroilysin; <b>PDBTitle:</b> crystal structure of myroilysin <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
43	<a href="#">c4wz9A_</a>	Alignment	not modelled	59.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> agap004809-pa; <b>PDBTitle:</b> apn1 from anopheles gambiae <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
44	<a href="#">c4pj6B_</a>	Alignment	not modelled	59.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> leucyl-cystinyl aminopeptidase; <b>PDBTitle:</b> crystal structure of human insulin regulated aminopeptidase with2 lysine in active site <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
45	<a href="#">c2dw1B_</a>	Alignment	not modelled	58.7	18	<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) <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
46	<a href="#">c3cmnA_</a>	Alignment	not modelled	57.5	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> crystal structure of a putative hydrolase with a novel fold from2 chloroflexus aurantiacus <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
47	<a href="#">d3cmna1</a>	Alignment	not modelled	57.1	30	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Caur0242-like <b>PDB entry:</b> <a href="#">PDBe RCSB PDBj</a>
48	<a href="#">c6qigA_</a>	Alignment	not modelled	56.8	25	<b>PDB header:</b> blood clotting <b>Chain:</b> A: <b>PDB Molecule:</b> a disintegrin and metalloproteinase with thrombospondin <b>PDBTitle:</b> metalloproteinase <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>

49	<a href="#">c2v4bB_</a>	 Alignment	not modelled	55.0	31	<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) <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
50	<a href="#">c6i89A_</a>	 Alignment	not modelled	55.0	10	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ardc protein; <b>PDBTitle:</b> crystal structure of antirestriction ard protein from r388 plasmid.2 metal-free structure. <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
51	<a href="#">c3qnfC_</a>	 Alignment	not modelled	54.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> endoplasmic reticulum aminopeptidase 1; <b>PDBTitle:</b> crystal structure of the open state of human endoplasmic reticulum2 aminopeptidase 1 erap1 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
52	<a href="#">c2l0rA_</a>	 Alignment	not modelled	54.4	23	<b>PDB header:</b> hydrolase,toxin <b>Chain:</b> A: <b>PDB Molecule:</b> lethal factor; <b>PDBTitle:</b> conformational dynamics of the anthrax lethal factor catalytic center <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
53	<a href="#">d1rm8a_</a>	 Alignment	not modelled	54.1	44	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
54	<a href="#">c2rjpC_</a>	 Alignment	not modelled	53.9	25	<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 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
55	<a href="#">d3e11a1</a>	 Alignment	not modelled	53.8	44	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> TTHA0227-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
56	<a href="#">d1bqqm_</a>	 Alignment	not modelled	53.4	39	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
57	<a href="#">d1hv5a_</a>	 Alignment	not modelled	52.8	28	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
58	<a href="#">c3qnfA_</a>	 Alignment	not modelled	52.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoplasmic reticulum aminopeptidase 1; <b>PDBTitle:</b> crystal structure of the open state of human endoplasmic reticulum2 aminopeptidase 1 erap1 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
59	<a href="#">d1xuca1</a>	 Alignment	not modelled	52.6	28	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
60	<a href="#">c5a0sA_</a>	 Alignment	not modelled	52.5	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> zinc metalloprotease zmp1; <b>PDBTitle:</b> apo-structure of metalloprotease zmp1 variant e143a from clostridium2 difficile <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
61	<a href="#">d1k7ia2</a>	 Alignment	not modelled	51.2	18	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal) domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
62	<a href="#">d1lmla_</a>	 Alignment	not modelled	50.9	21	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Leishmanolysin <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
63	<a href="#">c3b8zB_</a>	 Alignment	not modelled	50.9	38	<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) <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
64	<a href="#">c3mdjB_</a>	 Alignment	not modelled	50.3	19	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> endoplasmic reticulum aminopeptidase 1; <b>PDBTitle:</b> er aminopeptidase, erap1, bound to the zinc aminopeptidase inhibitor,2 bestatin <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
65	<a href="#">d1sata2</a>	 Alignment	not modelled	48.7	14	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal) domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
66	<a href="#">c6fpcA_</a>	 Alignment	not modelled	48.6	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pro-pro endopeptidase; <b>PDBTitle:</b> structure of the pro-pro endopeptidase (ppep-2) from paenibacillus2 alvei <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
67	<a href="#">c4f5cA_</a>	 Alignment	not modelled	48.3	15	<b>PDB header:</b> hydrolase/viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase n; <b>PDBTitle:</b> crystal structure of the spike receptor binding domain of a porcine2 respiratory coronavirus in complex with the pig aminopeptidase n3 ectodomain <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
68	<a href="#">d1npca_</a>	 Alignment	not modelled	47.8	50	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Thermolysin-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
69	<a href="#">c1slmA_</a>	 Alignment	not modelled	47.7	28	<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 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
70	<a href="#">d1qiba_</a>	 Alignment	not modelled	47.5	33	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
						<b>PDB header:</b> hydrolase

71	<a href="#">c1l6jA_</a>	Alignment	not modelled	47.4	25	<b>Chain:</b> A: <b>PDB Molecule:</b> matrix metalloproteinase-9; <b>PDBTitle:</b> crystal structure of human matrix metalloproteinase mmp92 (gelatinase b). <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
72	<a href="#">c6a8zB_</a>	Alignment	not modelled	47.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> zinc metalloprotease, putative; <b>PDBTitle:</b> crystal structure of m1 zinc metalloproteinase from deinococcus2 radiodurans <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
73	<a href="#">c2xs4A_</a>	Alignment	not modelled	46.8	39	<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 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
74	<a href="#">d1kjpA_</a>	Alignment	not modelled	46.1	63	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Thermolysin-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
75	<a href="#">c2mzeA_</a>	Alignment	not modelled	45.6	22	<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) <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
76	<a href="#">c1z5hB_</a>	Alignment	not modelled	44.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> tricorn protease interacting factor f3; <b>PDBTitle:</b> crystal structures of the tricorn interacting factor f3 from2 thermoplasma acidophilum <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
77	<a href="#">d1hfca_</a>	Alignment	not modelled	44.4	33	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
78	<a href="#">d1q3aa_</a>	Alignment	not modelled	44.4	33	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
79	<a href="#">d1hova_</a>	Alignment	not modelled	44.2	33	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
80	<a href="#">d1bqba_</a>	Alignment	not modelled	44.0	50	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Thermolysin-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
81	<a href="#">c4gerB_</a>	Alignment	not modelled	44.0	63	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> gentiyase metalloprotease; <b>PDBTitle:</b> crystal structure of gentiyase, the neutral metalloprotease of2 paenibacillus polymyxa <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
82	<a href="#">c2xhqA_</a>	Alignment	not modelled	44.0	23	<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 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
83	<a href="#">d2ovxa1</a>	Alignment	not modelled	43.8	22	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
84	<a href="#">d1mmqa_</a>	Alignment	not modelled	43.5	28	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
85	<a href="#">c3nqxA_</a>	Alignment	not modelled	43.1	38	<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 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
86	<a href="#">d1y93a1</a>	Alignment	not modelled	43.0	33	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
87	<a href="#">c3nqzB_</a>	Alignment	not modelled	42.7	38	<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 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
88	<a href="#">c3se6A_</a>	Alignment	not modelled	42.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoplasmic reticulum aminopeptidase 2; <b>PDBTitle:</b> crystal structure of the human endoplasmic reticulum aminopeptidase 2 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
89	<a href="#">d1i76a_</a>	Alignment	not modelled	42.6	28	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
90	<a href="#">c2vqxA_</a>	Alignment	not modelled	42.3	63	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metalloproteinase; <b>PDBTitle:</b> precursor of protealysin, metalloproteinase from serratia2 proteamaculans. <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
91	<a href="#">d1cgla_</a>	Alignment	not modelled	42.2	33	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
92	<a href="#">d1hy7a_</a>	Alignment	not modelled	42.1	28	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
93	<a href="#">c2jsdA_</a>	Alignment	not modelled	41.7	28	<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 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
						<b>PDB header:</b> hydrolase



94	<a href="#">c4k90A</a>	Alignment	not modelled	41.7	63	<b>Chain:</b> A: <b>PDB Molecule:</b> extracellular metalloproteinase mep; <b>PDBTitle:</b> extracellular metalloproteinase from aspergillus <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
95	<a href="#">d2ejqa1</a>	Alignment	not modelled	41.6	29	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> TTHA0227-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
96	<a href="#">d1cxva</a>	Alignment	not modelled	40.7	33	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
97	<a href="#">c4gaaA</a>	Alignment	not modelled	40.4	23	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> mgc78867 protein; <b>PDBTitle:</b> structure of leukotriene a4 hydrolase from xenopus laevis complexed2 with inhibitor bestatin <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
98	<a href="#">d1eb6a</a>	Alignment	not modelled	40.3	33	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Fungal zinc peptidase <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
99	<a href="#">c6h56A</a>	Alignment	not modelled	39.8	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> effector domain of pseudomonas aeruginosa vgrg2b; <b>PDBTitle:</b> effector domain of pseudomonas aeruginosa vgrg2b <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
100	<a href="#">c5th6D</a>	Alignment	not modelled	39.1	28	<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) <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
101	<a href="#">d1u4ga</a>	Alignment	not modelled	38.1	38	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Thermolysin-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
102	<a href="#">c1su3A</a>	Alignment	not modelled	37.9	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> interstitial collagenase; <b>PDBTitle:</b> x-ray structure of human prommp-1: new insights into2 collagenase action <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
103	<a href="#">d1kapp2</a>	Alignment	not modelled	37.2	27	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal) domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
104	<a href="#">c3p24C</a>	Alignment	not modelled	36.3	33	<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 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
105	<a href="#">d1eaka2</a>	Alignment	not modelled	36.3	28	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
106	<a href="#">c6yzeA</a>	Alignment	not modelled	35.9	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> zinc metalloproteinase; <b>PDBTitle:</b> zinc metalloprotease proa from native source <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
107	<a href="#">d3b7sa3</a>	Alignment	not modelled	35.9	19	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Leukotriene A4 hydrolase catalytic domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
108	<a href="#">c2xpyA</a>	Alignment	not modelled	35.4	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> leukotriene a-4 hydrolase; <b>PDBTitle:</b> structure of native leukotriene a4 hydrolase from saccharomyces2 cerevisiae <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
109	<a href="#">d1g9ka2</a>	Alignment	not modelled	34.7	25	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal) domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
110	<a href="#">c6s1za</a>	Alignment	not modelled	34.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> angiotensin-converting enzyme; <b>PDBTitle:</b> crystal structure of anopheles gambiae anoace2 in complex with2 fosinoprilat <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
111	<a href="#">c4fgmA</a>	Alignment	not modelled	34.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase n family protein; <b>PDBTitle:</b> crystal structure of the aminopeptidase n family protein q5qty1 from2 idiomarina loihiensis. northeast structural genomics consortium3 target ilr60. <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
112	<a href="#">c2cltB</a>	Alignment	not modelled	34.0	28	<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. <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
113	<a href="#">c4g0dD</a>	Alignment	not modelled	33.6	22	<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 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
114	<a href="#">c2x7mA</a>	Alignment	not modelled	33.6	36	<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 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
115	<a href="#">c3ciaA</a>	Alignment	not modelled	33.5	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cold-active aminopeptidase; <b>PDBTitle:</b> crystal structure of cold-aminopeptidase from colwellia2 psychrerythraea <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
						<b>PDB header:</b> hydrolase

116	<a href="#">c3b7uX_</a>	Alignment	not modelled	33.3	23	<b>Chain:</b> X: <b>PDB Molecule:</b> leukotriene a-4 hydrolase; <b>PDBTitle:</b> leukotriene a4 hydrolase complexed with kelatorphan <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
117	<a href="#">c3edhA_</a>	Alignment	not modelled	33.3	57	<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 dms0 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
118	<a href="#">d1fbla2</a>	Alignment	not modelled	32.7	33	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
119	<a href="#">c1qxdA_</a>	Alignment	not modelled	32.7	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 72 kda type iv collagenase; <b>PDBTitle:</b> prommp-2/timp-2 complex <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
120	<a href="#">c3b4rA_</a>	Alignment	not modelled	31.7	63	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative zinc metalloprotease mj0392; <b>PDBTitle:</b> site-2 protease from methanocaldococcus jannaschii <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>