

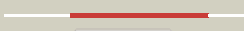








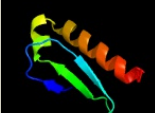










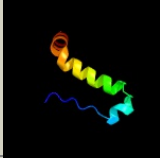
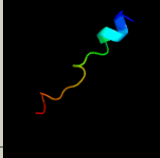
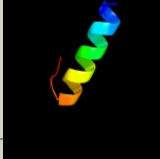
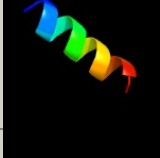
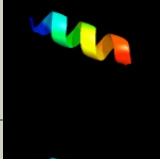

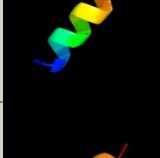
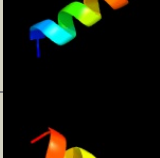
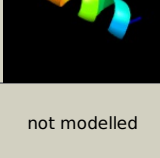


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1845c (-) _2095225_2096175
Date	Fri Aug 2 13:30:45 BST 2019
Unique Job ID	2748537a85926f80

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4il3B_</a>	 Alignment		99.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ste24p; <b>PDBTitle:</b> crystal structure of s. mikatae ste24p
2	<a href="#">c4aw6B_</a>	 Alignment		99.7	18	<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)
3	<a href="#">c3c37B_</a>	 Alignment		99.4	26	<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
4	<a href="#">c3cqbB_</a>	 Alignment		99.3	22	<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
5	<a href="#">c4jixB_</a>	 Alignment		98.8	10	<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
6	<a href="#">c6aitD_</a>	 Alignment		98.5	20	<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
7	<a href="#">c4jiuA_</a>	 Alignment		95.5	29	<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
8	<a href="#">c5xbvA_</a>	 Alignment		94.0	16	<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
9	<a href="#">c6mdxA_</a>	 Alignment		93.0	16	<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
10	<a href="#">c3dtkA_</a>	 Alignment		84.6	15	<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
11	<a href="#">c5ln5A_</a>	 Alignment		84.1	18	<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

12	<a href="#">c6cz6D</a>	Alignment		77.8	13	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> hth-type transcriptional regulator prpr; <b>PDBTitle:</b> mycobacterium tuberculosis transcriptional regulator
13	<a href="#">d2ejqa1</a>	Alignment		74.9	47	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> TTHA0227-like
14	<a href="#">d3e11a1</a>	Alignment		61.8	35	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> TTHA0227-like
15	<a href="#">c3qnfC</a>	Alignment		50.7	27	<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
16	<a href="#">c6h56A</a>	Alignment		50.3	23	<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
17	<a href="#">d1cxva</a>	Alignment		45.9	25	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
18	<a href="#">c4wz9A</a>	Alignment		45.6	43	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> agap004809-pa; <b>PDBTitle:</b> apn1 from anopheles gambiae
19	<a href="#">c3qnfA</a>	Alignment		45.5	29	<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
20	<a href="#">c2gtqA</a>	Alignment		45.0	23	<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
21	<a href="#">c4gaaA</a>	Alignment	not modelled	44.9	31	<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
22	<a href="#">c3k7nA</a>	Alignment	not modelled	43.8	38	<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
23	<a href="#">c5dllA</a>	Alignment	not modelled	43.7	31	<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
24	<a href="#">c4dd8B</a>	Alignment	not modelled	43.7	33	<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
25	<a href="#">c3b7uX</a>	Alignment	not modelled	43.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> leukotriene a-4 hydrolase; <b>PDBTitle:</b> leukotriene a4 hydrolase complexed with kelatorphan
26	<a href="#">c3b37A</a>	Alignment	not modelled	43.4	23	<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
27	<a href="#">d3b7sa3</a>	Alignment	not modelled	42.8	19	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Leukotriene A4 hydrolase catalytic domain
28	<a href="#">d1npca</a>	Alignment	not modelled	42.4	38	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Thermolysin-like

29	<a href="#">d1quaa_</a>	Alignment	not modelled	42.4	27	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like
30	<a href="#">c1yp1A_</a>	Alignment	not modelled	42.3	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ffii; <b>PDBTitle:</b> crystal structure of a non-hemorrhagic fibrin(ogen)olytic2 metalloproteinase from venom of agkistrodon acutus
31	<a href="#">c3sksA_</a>	Alignment	not modelled	42.2	21	<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
32	<a href="#">c2l0rA_</a>	Alignment	not modelled	41.9	33	<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
33	<a href="#">c3ebhA_</a>	Alignment	not modelled	40.4	31	<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
34	<a href="#">c5zi7A_</a>	Alignment	not modelled	39.9	31	<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
35	<a href="#">c2erpA_</a>	Alignment	not modelled	39.9	31	<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)
36	<a href="#">d1bqba_</a>	Alignment	not modelled	39.5	38	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Thermolysin-like
37	<a href="#">c4fgmA_</a>	Alignment	not modelled	39.2	23	<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.
38	<a href="#">d1kjpA_</a>	Alignment	not modelled	39.2	38	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Thermolysin-like
39	<a href="#">c4gerB_</a>	Alignment	not modelled	38.9	38	<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
40	<a href="#">c3ciaA_</a>	Alignment	not modelled	38.9	31	<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
41	<a href="#">c3nqxA_</a>	Alignment	not modelled	38.8	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
42	<a href="#">c3nqzB_</a>	Alignment	not modelled	38.7	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
43	<a href="#">c1z5hB_</a>	Alignment	not modelled	38.6	36	<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
44	<a href="#">c3k71A_</a>	Alignment	not modelled	38.5	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atragin; <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
45	<a href="#">c4k90A_</a>	Alignment	not modelled	38.4	50	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular metalloproteinase mep; <b>PDBTitle:</b> extracellular metalloproteinase from aspergillus
46	<a href="#">d1u4ga_</a>	Alignment	not modelled	38.4	38	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Thermolysin-like
47	<a href="#">c2rjpC_</a>	Alignment	not modelled	38.0	22	<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
48	<a href="#">c2vqxA_</a>	Alignment	not modelled	37.1	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metalloproteinase; <b>PDBTitle:</b> precursor of protealysin, metalloproteinase from serratia2 proteamaculans.
49	<a href="#">c3mdjB_</a>	Alignment	not modelled	37.1	29	<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
50	<a href="#">c2xpyA_</a>	Alignment	not modelled	36.3	50	<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
51	<a href="#">d1bqqm_</a>	Alignment	not modelled	35.7	18	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
52	<a href="#">c2xs4A_</a>	Alignment	not modelled	35.6	24	<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
53	<a href="#">c4kxdA_</a>	Alignment	not modelled	35.5	36	<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
54	<a href="#">c2e3xA_</a>	Alignment	not modelled	35.1	33	<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
55	<a href="#">c4fytA_</a>	Alignment	not modelled	34.2	36	<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
56	<a href="#">d1nd1a_</a>	Alignment	not modelled	34.1	31	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like
57	<a href="#">c3b4rA_</a>	Alignment	not modelled	34.1	30	<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
58	<a href="#">d1hova_</a>	Alignment	not modelled	33.5	17	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
59	<a href="#">c2xdtA_</a>	Alignment	not modelled	32.9	29	<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
60	<a href="#">c3b4rB_</a>	Alignment	not modelled	32.2	30	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative zinc metalloprotease mj0392; <b>PDBTitle:</b> site-2 protease from methanocaldococcus jannaschii
61	<a href="#">d1rm8a_</a>	Alignment	not modelled	32.1	18	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
62	<a href="#">d4aiga_</a>	Alignment	not modelled	31.8	21	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like
63	<a href="#">d2ovxa1</a>	Alignment	not modelled	31.2	12	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
64	<a href="#">c4f5cA_</a>	Alignment	not modelled	31.2	36	<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
65	<a href="#">d1qiba_</a>	Alignment	not modelled	30.9	18	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
66	<a href="#">c4pj6B_</a>	Alignment	not modelled	30.7	43	<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
67	<a href="#">d1wnia_</a>	Alignment	not modelled	29.9	38	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like
68	<a href="#">c3se6A_</a>	Alignment	not modelled	28.8	36	<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
69	<a href="#">c5a0sA_</a>	Alignment	not modelled	28.5	38	<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
70	<a href="#">c6fpcA_</a>	Alignment	not modelled	28.4	38	<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
71	<a href="#">c3p24C_</a>	Alignment	not modelled	28.0	21	<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
72	<a href="#">d1r55a_</a>	Alignment	not modelled	27.6	24	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like
73	<a href="#">d1hv5a_</a>	Alignment	not modelled	26.0	18	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
74	<a href="#">d1lmla_</a>	Alignment	not modelled	25.3	24	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Leishmanolysin
75	<a href="#">d1y93a1</a>	Alignment	not modelled	25.2	18	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
76	<a href="#">d1c7ka_</a>	Alignment	not modelled	25.1	14	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Zinc protease
77	<a href="#">d1mmqa_</a>	Alignment	not modelled	24.6	24	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
78	<a href="#">d1xuca1</a>	Alignment	not modelled	24.3	18	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
79	<a href="#">d1cgla_</a>	Alignment	not modelled	23.9	18	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
80	<a href="#">c3g5cA_</a>	Alignment	not modelled	23.9	21	<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>Fold:</b> Zincin-like

81	<a href="#">d1g12a_</a>	Alignment	not modelled	23.9	23	<b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Fungal zinc peptidase
82	<a href="#">c3b8zB_</a>	Alignment	not modelled	23.6	29	<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)
83	<a href="#">c4on1B_</a>	Alignment	not modelled	23.4	36	<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
84	<a href="#">c4g0dD_</a>	Alignment	not modelled	22.6	12	<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
85	<a href="#">d1hfca_</a>	Alignment	not modelled	22.5	18	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
86	<a href="#">d1eb6a_</a>	Alignment	not modelled	22.2	31	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Fungal zinc peptidase
87	<a href="#">d1eaka2</a>	Alignment	not modelled	22.2	12	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
88	<a href="#">c5furl_</a>	Alignment	not modelled	21.6	17	<b>PDB header:</b> transcription <b>Chain:</b> I: <b>PDB Molecule:</b> transcription initiation factor tfiid subunit 2; <b>PDBTitle:</b> structure of human tfiid-ii bound to core promoter dna
89	<a href="#">d1atla_</a>	Alignment	not modelled	21.5	14	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like
90	<a href="#">c2v4bB_</a>	Alignment	not modelled	21.2	20	<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)
91	<a href="#">c2x3bB_</a>	Alignment	not modelled	21.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> toxic extracellular endopeptidase; <b>PDBTitle:</b> asap1 inactive mutant e294a, an extracellular toxic zinc2 metalloendopeptidase
92	<a href="#">d2di4a1</a>	Alignment	not modelled	20.6	31	<b>Fold:</b> FtsH protease domain-like <b>Superfamily:</b> FtsH protease domain-like <b>Family:</b> FtsH protease domain-like
93	<a href="#">d1bswa_</a>	Alignment	not modelled	20.1	33	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like
94	<a href="#">d1hy7a_</a>	Alignment	not modelled	19.9	18	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
95	<a href="#">c2jsdA_</a>	Alignment	not modelled	19.7	18	<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
96	<a href="#">d1i76a_</a>	Alignment	not modelled	19.4	18	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
97	<a href="#">d1q3aa_</a>	Alignment	not modelled	19.1	18	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
98	<a href="#">d2i47a1</a>	Alignment	not modelled	18.5	23	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> TNF-alpha converting enzyme, TACE, catalytic domain
99	<a href="#">c6be6D_</a>	Alignment	not modelled	18.4	14	<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