Phyre^2

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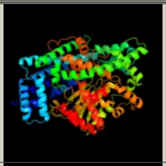
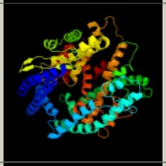
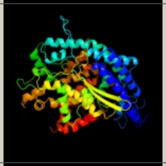
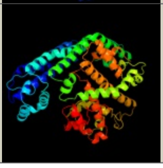
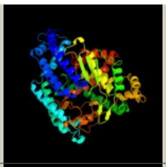
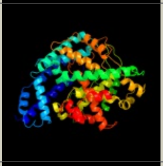
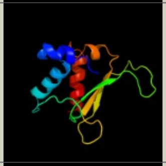
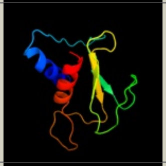
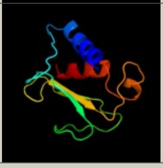
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1y79l_	Alignment		100.0	32	**PDB header:**hydrolase **Chain:** 1: **PDB Molecule:**peptidyl-dipeptidase dcp; **PDBTitle:** crystal structure of the e.coli dipeptidyl carboxypeptidase2 dcp in complex with a peptidic inhibitor
2	d1s4bp_	Alignment		100.0	31	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
3	d1i1ip_	Alignment		100.0	30	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
4	c3ce2A_	Alignment		100.0	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative peptidase; **PDBTitle:** crystal structure of putative peptidase from chlamydophila abortus
5	c2h1jA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligoendopeptidase f; **PDBTitle:** 3.1 a x-ray structure of putative oligoendopeptidase f: crystals grown2 by microfluidic seeding
6	c3sksA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative oligoendopeptidase f; **PDBTitle:** crystal structure of a putative oligoendopeptidase f from bacillus2 anthracis str. ames
7	d2ajfa1	Alignment		100.0	14	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
8	d1uzea_	Alignment		100.0	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
9	c2c6nA_	Alignment		100.0	16	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**angiotensin-converting enzyme, somatic isoform; **PDBTitle:** structure of human somatic angiontensin-i converting enzyme n domain2 with lisinopril
10	d1j36a_	Alignment		100.0	17	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
11	c2qr4B_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase m3b, oligoendopeptidase f; **PDBTitle:** crystal structure of oligoendopeptidase-f from enterococcus faecium

12	d1k9xa_	Alignment		100.0	15	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
13	c1wgzC_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**carboxypeptidase 1; **PDBTitle:** crystal structure of carboxypeptidase 1 from thermus thermophilus
14	c3dwcA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallocarboxypeptidase; **PDBTitle:** trypanosoma cruzi metallocarboxypeptidase 1
15	c3hq2A_	Alignment		100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**bacillus subtilis m32 carboxypeptidase; **PDBTitle:** bsucp crystal structure
16	d1g9ka2	Alignment		96.0	23	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
17	d1kapp2	Alignment		95.9	21	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
18	d1k7ia2	Alignment		95.6	19	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
19	d1qiba_	Alignment		95.5	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
20	d1y93a1	Alignment		95.4	14	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
21	d1hfca_	Alignment	not modelled	95.4	15	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
22	d2ovxa1	Alignment	not modelled	95.3	14	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
23	d1cgla_	Alignment	not modelled	95.3	16	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
24	d1hv5a_	Alignment	not modelled	95.0	15	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
25	d1j7na2	Alignment	not modelled	94.8	14	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Anthrax toxin lethal factor, N- and C-terminal domains
26	c1om8A_	Alignment	not modelled	94.7	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serralysin; **PDBTitle:** crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallyzed with 10 mm edta
27	d1xuca1	Alignment	not modelled	94.1	15	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
28	c2xs4A_	Alignment	not modelled	94.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**karilysin protease; **PDBTitle:** structure of karilysin catalytic mmp domain in complex with2 magnesium
29	d1mmqa_	Alignment	not modelled	94.0	10	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain

						Family: Matrix metalloproteases, catalytic domain
30	d1sata2	Alignment	not modelled	93.9	16	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
31	c2cltB_	Alignment	not modelled	93.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**interstitial collagenase; **PDBTitle:** crystal structure of the active form (full-length) of human2 fibroblast collagenase.
32	c2jsdA_	Alignment	not modelled	93.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-20; **PDBTitle:** solution structure of mmp20 complexed with nngh
33	c2l0rA_	Alignment	not modelled	93.6	14	**PDB header:**hydrolase,toxin **Chain:** A: **PDB Molecule:**lethal factor; **PDBTitle:** conformational dynamics of the anthrax lethal factor catalytic center
34	d1hova_	Alignment	not modelled	93.5	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
35	c1jiwP_	Alignment	not modelled	93.5	20	**PDB header:**hydrolase/hyrolase inhibitor **Chain:** P: **PDB Molecule:**alkaline metalloproteinase; **PDBTitle:** crystal structure of the apr-aprin complex
36	c3g5cA_	Alignment	not modelled	93.4	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**adam 22; **PDBTitle:** structural and biochemical studies on the ectodomain of human adam22
37	d1q3aa_	Alignment	not modelled	93.3	9	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
38	c3edhA_	Alignment	not modelled	93.1	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**bone morphogenetic protein 1; **PDBTitle:** crystal structure of bone morphogenetic protein 1 protease2 domain in complex with partially bound dmso
39	c2xhqA_	Alignment	not modelled	93.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**archaemetzincin; **PDBTitle:** crystal structure of archaemetzincin (amza) from archaeoglobus2 fulgidus at 1.45 a resolution
40	c1slmA_	Alignment	not modelled	93.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**stromelysin-1; **PDBTitle:** crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
41	c3p24C_	Alignment	not modelled	92.9	26	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**bft-3; **PDBTitle:** structure of profragilysin-3 from bacteroides fragilis
42	d1bqqm_	Alignment	not modelled	92.8	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
43	d1eaka2	Alignment	not modelled	92.5	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
44	d1fbla2	Alignment	not modelled	92.4	12	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
45	d1i76a_	Alignment	not modelled	92.3	12	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
46	c3dtkA_	Alignment	not modelled	92.2	16	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**irre protein; **PDBTitle:** crystal structure of the irre protein, a central regulator2 of dna damage repair in deinococcaceae
47	d1rm8a_	Alignment	not modelled	92.0	12	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
48	c3k7lA_	Alignment	not modelled	91.9	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atragin; **PDBTitle:** structures of two elapid snake venom metalloproteases with2 distinct activities highlight the disulfide patterns in the3 d domain of adamalysin family proteins
49	d1cxva_	Alignment	not modelled	91.6	15	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
50	c1yqyA_	Alignment	not modelled	91.5	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lethal factor; **PDBTitle:** structure of b. anthrax lethal factor in complex with a2 hydroxamate inhibitor
51	c1su3A_	Alignment	not modelled	91.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**interstitial collagenase; **PDBTitle:** x-ray structure of human prommp-1: new insights into2 collagenase action
52	d1hy7a_	Alignment	not modelled	91.4	14	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
53	c3ba0A_	Alignment	not modelled	91.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**macrophage metalloelastase; **PDBTitle:** crystal structure of full-length human mmp-12
54	d1asta_	Alignment	not modelled	91.1	23	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Astacin
55	c3o0yC_	Alignment	not modelled	90.9	13	**PDB header:**lipid binding protein **Chain:** C: **PDB Molecule:**lipoprotein; **PDBTitle:** the crystal structure of the putative lipoprotein from colwellia2 psychrerythraea
						PDB header:hydrolase

56	c3lqbA_	Alignment	not modelled	90.9	24	**Chain:** A: **PDB Molecule:**loc792177 protein; **PDBTitle:** crystal structure of the hatching enzyme zhe1 from the zebrafish danio2 rerio
57	c3lq0A_	Alignment	not modelled	89.4	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proastacin; **PDBTitle:** zymogen structure of crayfish astacin metallopeptidase
58	c1pwqA_	Alignment	not modelled	89.2	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lethal factor; **PDBTitle:** crystal structure of anthrax lethal factor complexed with2 thioacetyl-tyr-pro-met-amide, a metal-chelating peptidyl3 small molecule inhibitor
59	c2erpA_	Alignment	not modelled	88.9	19	**PDB header:**toxin **Chain:** A: **PDB Molecule:**vascular apoptosis-inducing protein 1; **PDBTitle:** crystal structure of vascular apoptosis-inducing protein-1(inhibitor-2 bound form)
60	d1quaa_	Alignment	not modelled	88.6	21	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
61	d1atla_	Alignment	not modelled	88.5	19	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
62	d4aiga_	Alignment	not modelled	88.1	21	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
63	c1yp1A_	Alignment	not modelled	87.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fii; **PDBTitle:** crystal structure of a non-hemorrhagic fibrin(ogen)olytic2 metalloproteinase from venom of agkistrodon acutus
64	d1kufa_	Alignment	not modelled	86.8	26	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
65	d1nd1a_	Alignment	not modelled	86.6	24	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
66	d2i47a1	Alignment	not modelled	86.6	27	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TNF-alpha converting enzyme, TACE, catalytic domain
67	c3nqzB_	Alignment	not modelled	86.5	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**secreted metalloprotease mcp02; **PDBTitle:** crystal structure of the autoprocessed vibriolysin mcp-02 with e369a2 mutation
68	c2i47A_	Alignment	not modelled	86.4	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adam 17; **PDBTitle:** crystal structure of catalytic domain of tace with inhibitor
69	d1r55a_	Alignment	not modelled	85.7	20	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
70	c1satA_	Alignment	not modelled	85.5	16	**PDB header:**hydrolase (serine protease) **Chain:** A: **PDB Molecule:**serratia protease; **PDBTitle:** crystal structure of the 50 kda metallo protease from s.2 marcescens
71	c2fpqA_	Alignment	not modelled	85.5	47	**PDB header:**toxin **Chain:** A: **PDB Molecule:**botulinum neurotoxin d light chain; **PDBTitle:** crystal structure of botulinum neurotoxin type d light chain
72	d1wnia_	Alignment	not modelled	85.4	24	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
73	d1bswa_	Alignment	not modelled	85.2	23	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
74	c1zb7A_	Alignment	not modelled	84.5	41	**PDB header:**toxin **Chain:** A: **PDB Molecule:**neurotoxin; **PDBTitle:** crystal structure of botulinum neurotoxin type g light chain
75	d1epwa3	Alignment	not modelled	84.2	35	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Clostridium neurotoxins, catalytic domain
76	c1z7hA_	Alignment	not modelled	84.1	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tetanus toxin light chain; **PDBTitle:** 2.3 angstrom crystal structure of tetanus neurotoxin light2 chain
77	d1f83a_	Alignment	not modelled	84.1	35	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Clostridium neurotoxins, catalytic domain
78	c3k3qB_	Alignment	not modelled	84.0	35	**PDB header:**immune system **Chain:** B: **PDB Molecule:**botulinum neurotoxin type a; **PDBTitle:** crystal structure of a llama antibody complexed with the c.2 botulinum neurotoxin serotype a catalytic domain
79	c2qn0A_	Alignment	not modelled	84.0	29	**PDB header:**toxin **Chain:** A: **PDB Molecule:**neurotoxin; **PDBTitle:** structure of botulinum neurotoxin serotype c1 light chain2 protease
80	d3bona1	Alignment	not modelled	83.9	35	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Clostridium neurotoxins, catalytic domain
81	c2vqxA_	Alignment	not modelled	83.9	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metalloproteinase; **PDBTitle:** precursor of protealysin, metalloproteinase from serratia2 proteamaculans.
82	d1kjpa_	Alignment	not modelled	83.9	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain

						Family: Thermolysin-like
83	c2dw1B_	Alignment	not modelled	83.8	33	**PDB header:**apoptosis, toxin **Chain:** B: **PDB Molecule:**catrocollastatin; **PDBTitle:** crystal structure of vap2 from crotalus atrox venom (form 2-2 crystal)
84	c1e1hC_	Alignment	not modelled	83.7	35	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**botulinum neurotoxin type a light chain; **PDBTitle:** crystal structure of recombinant botulinum neurotoxin type2 a light chain, self-inhibiting zn endopeptidase.
85	d1u4ga_	Alignment	not modelled	83.5	18	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
86	d1npca_	Alignment	not modelled	83.5	20	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
87	c3k7nA_	Alignment	not modelled	83.5	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**k-like; **PDBTitle:** structures of two elapid snake venom metalloproteases with2 distinct activities highlight the disulfide patterns in the3 d domain of adamalysin family proteins
88	c3nqxA_	Alignment	not modelled	83.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**secreted metalloprotease mcp02; **PDBTitle:** crystal structure of vibriolysin mcp-02 mature enzyme, a zinc2 metalloprotease from m4 family
89	d3btaa3	Alignment	not modelled	83.4	35	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Clostridium neurotoxins, catalytic domain
90	d1t3ca_	Alignment	not modelled	83.3	35	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Clostridium neurotoxins, catalytic domain
91	c2ilpA_	Alignment	not modelled	83.3	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**botulinum neurotoxin a light-chain; **PDBTitle:** clostridium botulinum serotype a light chain inhibited by 4-2 chlorocinnamic hydroxamate
92	c2a97B_	Alignment	not modelled	83.1	41	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**botulinum neurotoxin type f; **PDBTitle:** crystal structure of catalytic domain of clostridium2 botulinum neurotoxin serotype f
93	c3b8zB_	Alignment	not modelled	83.0	46	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein adamts-5; **PDBTitle:** high resolution crystal structure of the catalytic domain2 of adamts-5 (aggrecanase-2)
94	c2xhlA_	Alignment	not modelled	82.5	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**botulinum neurotoxin b light chain; **PDBTitle:** structure of a functional derivative of clostridium2 botulinum neurotoxin type b
95	c2x7mA_	Alignment	not modelled	81.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**archaemetzincin; **PDBTitle:** crystal structure of archaemetzincin (amza) from methanopyrus2 kandleri at 1.5 a resolution
96	c3zuqA_	Alignment	not modelled	80.8	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**botulinum neurotoxin type b; **PDBTitle:** crystal structure of an engineered botulinum neurotoxin2 type b-derivative, lc-b-gs-hn-b
97	c3zusD_	Alignment	not modelled	80.7	35	**PDB header:**hydrolase/signaling protein **Chain:** D: **PDB Molecule:**botulinum neurotoxin type a, synaptosomal-associated **PDBTitle:** crystal structure of an engineered botulinum neurotoxin2 type a-snare23 derivative, lc-a-snap23-hn-a
98	c2e3xA_	Alignment	not modelled	80.7	23	**PDB header:**hydrolase, blood clotting, toxin **Chain:** A: **PDB Molecule:**coagulation factor x-activating enzyme heavy chain; **PDBTitle:** crystal structure of russell's viper venom metalloproteinase
99	c2rjqA_	Alignment	not modelled	80.6	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adamts-5; **PDBTitle:** crystal structure of adamts5 with inhibitor bound
100	c3ffzA_	Alignment	not modelled	80.4	41	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**botulinum neurotoxin type e; **PDBTitle:** domain organization in clostridium butulinum neurotoxin2 type e is unique: its implication in faster translocation
101	c2j83B_	Alignment	not modelled	80.0	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ulilysin; **PDBTitle:** ulilysin metalloprotease in complex with batimastat.
102	d1bqba_	Alignment	not modelled	79.7	24	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
103	c2rjpC_	Alignment	not modelled	79.1	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**adamts-4; **PDBTitle:** crystal structure of adamts4 with inhibitor bound
104	c3b4rB_	Alignment	not modelled	79.1	42	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative zinc metalloprotease mj0392; **PDBTitle:** site-2 protease from methanocaldococcus jannaschii
105	d2ejqa1	Alignment	not modelled	78.9	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like
106	c2nyyA_	Alignment	not modelled	78.3	35	**PDB header:**toxin/immune system **Chain:** A: **PDB Molecule:**botulinum neurotoxin type a; **PDBTitle:** crystal structure of botulinum neurotoxin type a complexed with2 monoclonal antibody cr1
107	c1s0bA_	Alignment	not modelled	77.9	35	**PDB header:**toxin, hydrolase **Chain:** A: **PDB Molecule:**botulinum neurotoxin type b; **PDBTitle:** crystal structure of botulinum neurotoxin type b at ph 4.0
108	c2v4bB_	Alignment	not modelled	77.1	31	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adamts-1;

108	c2v4bB_	Alignment	not modelled	77.1	31	**PDBTitle:** crystal structure of human adamts-1 catalytic domain and2 cysteine-rich domain (apo-form)
109	c3zurA_	Alignment	not modelled	76.5	24	**PDB header:**hydrolase/signaling protein **Chain:** A: **PDB Molecule:**botulinum neurotoxin type a, synaptosomal-associated **PDBTitle:** crystal structure of an engineered botulinum neurotoxin2 type a-snare23 derivative, lc0-a-snap25-hn-a
110	c1eakA_	Alignment	not modelled	70.2	33	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**72 kda type iv collagenase; **PDBTitle:** catalytic domain of prommp-2 e404q mutant
111	c3cqbB_	Alignment	not modelled	70.1	33	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable protease htpx homolog; **PDBTitle:** crystal structure of heat shock protein htpx domain from vibrio2 parahaemolyticus rimd 2210633
112	c3dl1A_	Alignment	not modelled	70.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative metal-dependent hydrolase; **PDBTitle:** crystal structure of a putative metal-dependent hydrolase2 (yp_001336084.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 2.20 a resolution
113	d1c7ka_	Alignment	not modelled	66.8	40	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Zinc protease
114	c3iukB_	Alignment	not modelled	66.8	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of putative bacterial protein of unknown function2 (duf885, pf05960.1,) from arthrobacter aurescens tc1, reveals fold3 similar to that of m32 carboxypeptidases
115	c3p1vB_	Alignment	not modelled	65.7	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**metallo-endopeptidase; **PDBTitle:** crystal structure of a metallo-endopeptidases (bacova_00663) from2 bacteroides ovatus at 1.93 a resolution
116	c3c37B_	Alignment	not modelled	64.8	31	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase, m48 family; **PDBTitle:** x-ray structure of the putative zn-dependent peptidase q74d82 at the2 resolution 1.7 a. northeast structural genomics consortium target3 gsr143a
117	c1l6jA_	Alignment	not modelled	60.6	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-9; **PDBTitle:** crystal structure of human matrix metalloproteinase mmp92 (gelatinase b).
118	c1gxdA_	Alignment	not modelled	54.1	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**72 kda type iv collagenase; **PDBTitle:** prommp-2/timp-2 complex
119	d1lmla_	Alignment	not modelled	51.7	12	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Leishmanolysin
120	c3cskA_	Alignment	not modelled	47.8	58	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable dipeptidyl-peptidase 3; **PDBTitle:** structure of dpp iii from saccharomyces cerevisiae