Phyre2

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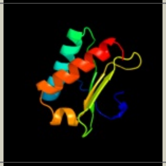
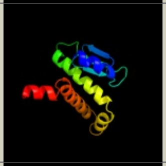
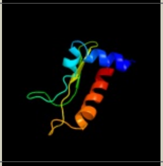
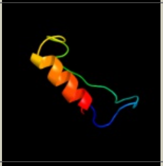
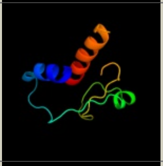
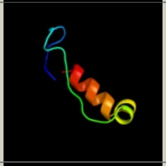
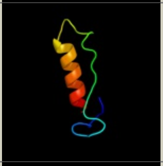
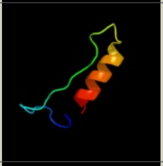
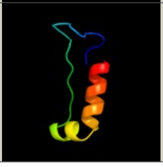
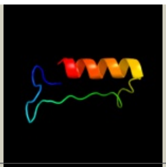
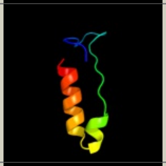
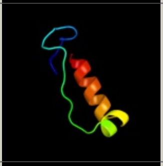
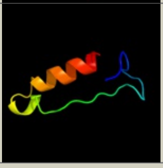
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c37B_	Alignment		99.9	22	**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
2	c3cqbB_	Alignment		99.7	74	**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
3	c3dtkA_	Alignment		97.0	15	**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
4	c3sksA_	Alignment		92.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative oligoendopeptidase f; **PDBTitle:** crystal structure of a putative oligoendopeptidase f from bacillus2 anthracis str. ames
5	c3k7nA_	Alignment		89.0	22	**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
6	c2gtqA_	Alignment		89.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase n; **PDBTitle:** crystal structure of aminopeptidase n from human pathogen neisseria2 meningitidis
7	d1bswa_	Alignment		88.2	19	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
8	c2h1jA_	Alignment		88.0	9	**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
9	d1r55a_	Alignment		87.8	41	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
10	c1yp1A_	Alignment		87.3	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fii; **PDBTitle:** crystal structure of a non-hemorrhagic fibrin(ogen)olytic2 metalloproteinase from venom of agkistrodon acutus
11	c3k7lA_	Alignment		87.1	19	**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

12	d1atla_	Alignment		86.7	14	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
13	c1wgzC_	Alignment		86.4	10	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**carboxypeptidase 1; **PDBTitle:** crystal structure of carboxypeptidase 1 from thermus thermophilus
14	c3ce2A_	Alignment		86.3	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative peptidase; **PDBTitle:** crystal structure of putative peptidase from chlamydophila abortus
15	c2erpA_	Alignment		86.0	14	**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)
16	d4aiga_	Alignment		85.6	19	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
17	c3b7uX_	Alignment		85.6	18	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**leukotriene a-4 hydrolase; **PDBTitle:** leukotriene a4 hydrolase complexed with kelatorphan
18	c2xs4A_	Alignment		85.4	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**karilysin protease; **PDBTitle:** structure of karilysin catalytic mmp domain in complex with2 magnesium
19	c3ebhA_	Alignment		85.2	22	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**m1 family aminopeptidase; **PDBTitle:** structure of the m1 alanylaminopeptidase from malaria complexed with2 bestatin
20	c2e3xA_	Alignment		84.9	25	**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
21	c2dw1B_	Alignment	not modelled	84.9	14	**PDB header:**apoptosis, toxin **Chain:** B: **PDB Molecule:**catrocollastatin; **PDBTitle:** crystal structure of vap2 from crotalus atrox venom (form 2-2 crystal)
22	c3qnfA_	Alignment	not modelled	84.4	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoplasmic reticulum aminopeptidase 1; **PDBTitle:** crystal structure of the open state of human endoplasmic reticulum2 aminopeptidase 1 erap1
23	d1k9xa_	Alignment	not modelled	83.6	12	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
24	d1bqqm_	Alignment	not modelled	83.5	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
25	c3b37A_	Alignment	not modelled	83.5	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase n; **PDBTitle:** crystal structure of e. coli aminopeptidase n in complex with tyrosine
26	d1wnia_	Alignment	not modelled	83.2	17	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
27	d1rm8a_	Alignment	not modelled	83.2	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
28	d2ovxa1	Alignment	not modelled	82.7	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain

29	d1cxva_	Alignment	not modelled	82.6	42	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
30	d1kufa_	Alignment	not modelled	82.6	19	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
31	d1xuca1	Alignment	not modelled	82.5	42	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
32	d1quaa_	Alignment	not modelled	82.5	19	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
33	d1qiba_	Alignment	not modelled	82.3	42	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
34	d1i76a_	Alignment	not modelled	82.3	42	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
35	d1y93a1	Alignment	not modelled	82.1	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
36	d2i47a1	Alignment	not modelled	81.9	38	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TNF-alpha converting enzyme, TACE, catalytic domain
37	c3g5cA_	Alignment	not modelled	81.9	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**adam 22; **PDBTitle:** structural and biochemical studies on the ectodomain of human adam22
38	c2i47A_	Alignment	not modelled	81.7	40	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adam 17; **PDBTitle:** crystal structure of catalytic domain of tace with inhibitor
39	d1hy7a_	Alignment	not modelled	81.1	50	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
40	d1hv5a_	Alignment	not modelled	81.1	42	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
41	d1hfca_	Alignment	not modelled	81.0	42	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
42	d1nd1a_	Alignment	not modelled	80.9	22	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
43	d1mmqa_	Alignment	not modelled	80.9	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
44	d1u4ga_	Alignment	not modelled	79.8	18	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
45	c2jsdA_	Alignment	not modelled	79.7	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-20; **PDBTitle:** solution structure of mmp20 complexed with nngh
46	c2cltB_	Alignment	not modelled	79.6	33	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**interstitial collagenase; **PDBTitle:** crystal structure of the active form (full-length) of human2 fibroblast collagenase.
47	d1cgla_	Alignment	not modelled	79.5	42	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
48	d1hova_	Alignment	not modelled	79.5	42	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
49	d1q3aa_	Alignment	not modelled	79.5	42	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
50	c1slmA_	Alignment	not modelled	79.3	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**stromelysin-1; **PDBTitle:** crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
51	c3ciaA_	Alignment	not modelled	78.4	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cold-active aminopeptidase; **PDBTitle:** crystal structure of cold-aminopeptidase from colwellia2 psychrerythraea
52	d1c7ka_	Alignment	not modelled	78.2	16	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Zinc protease
53	d1fbla2	Alignment	not modelled	77.9	42	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
54	c3p24C_	Alignment	not modelled	77.7	67	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**bft-3; **PDBTitle:** structure of profragilysin-3 from bacteroides fragilis
55	d1eaka2	Alignment	not modelled	77.0	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
56	d2ejqa1	Alignment	not modelled	75.5	18	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain

						Family:TTHA0227-like
57	c3b8zB_	Alignment	not modelled	75.0	56	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein adamts-5; **PDBTitle:** high resolution crystal structure of the catalytic domain2 of adamts-5 (aggrecanase-2)
58	c2v4bB_	Alignment	not modelled	74.1	44	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adamts-1; **PDBTitle:** crystal structure of human adamts-1 catalytic domain and2 cysteine-rich domain (apo-form)
59	c1su3A_	Alignment	not modelled	74.0	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**interstitial collagenase; **PDBTitle:** x-ray structure of human prommp-1: new insights into2 collagenase action
60	c2qr4B_	Alignment	not modelled	73.7	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase m3b, oligoendopeptidase f; **PDBTitle:** crystal structure of oligoendopeptidase-f from enterococcus faecium
61	c1z5hB_	Alignment	not modelled	73.5	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**tricorn protease interacting factor f3; **PDBTitle:** crystal structures of the tricorn interacting factor f32 from thermoplasma acidophilum
62	c2xhqA_	Alignment	not modelled	73.5	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**archaemetzincin; **PDBTitle:** crystal structure of archaemetzincin (amza) from archaeoglobus2 fulgidus at 1.45 a resolution
63	c3hq2A_	Alignment	not modelled	73.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**bacillus subtilis m32 carboxypeptidase; **PDBTitle:** bsucp crystal structure
64	d2ajfa1	Alignment	not modelled	72.8	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
65	c2rjpC_	Alignment	not modelled	72.3	38	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**adamts-4; **PDBTitle:** crystal structure of adamts4 with inhibitor bound
66	c2xdtA_	Alignment	not modelled	72.2	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoplasmic reticulum aminopeptidase 1; **PDBTitle:** crystal structure of the soluble domain of human2 endoplasmic reticulum aminopeptidase 1 erap1
67	c2rjqA_	Alignment	not modelled	71.9	63	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adamts-5; **PDBTitle:** crystal structure of adamts5 with inhibitor bound
68	c3ba0A_	Alignment	not modelled	71.8	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**macrophage metalloelastase; **PDBTitle:** crystal structure of full-length human mmp-12
69	d1npca_	Alignment	not modelled	70.1	63	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
70	c3nqxA_	Alignment	not modelled	69.5	75	**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
71	d1kjpa_	Alignment	not modelled	69.4	63	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
72	d1bqba_	Alignment	not modelled	69.4	75	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
73	c2j83B_	Alignment	not modelled	69.4	44	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ulilysin; **PDBTitle:** ulilysin metalloprotease in complex with batimastat.
74	c2xpyA_	Alignment	not modelled	69.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leukotriene a-4 hydrolase; **PDBTitle:** structure of native leukotriene a4 hydrolase from saccharomyces2 cerevisiae
75	c3nqzB_	Alignment	not modelled	69.0	75	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**secreted metalloprotease mcp02; **PDBTitle:** crystal structure of the autoprocessed vibriolysin mcp-02 with e369a2 mutation
76	c2vqxA_	Alignment	not modelled	67.8	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metalloproteinase; **PDBTitle:** precursor of protealysin, metalloproteinase from serratia2 proteamaculans.
77	c3se6A_	Alignment	not modelled	67.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoplasmic reticulum aminopeptidase 2; **PDBTitle:** crystal structure of the human endoplasmic reticulum aminopeptidase 2
78	d1sata2	Alignment	not modelled	66.7	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
79	d1kapp2	Alignment	not modelled	66.7	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
80	c3mdjB_	Alignment	not modelled	66.4	25	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**endoplasmic reticulum aminopeptidase 1; **PDBTitle:** er aminopeptidase, erap1, bound to the zinc aminopeptidase inhibitor,2 bestatin
81	c3lmcA_	Alignment	not modelled	66.1	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase, zinc-dependent; **PDBTitle:** crystal structure of zinc-dependent peptidase from methanocorpusculum2 labreanum (strain z), northeast structural genomics consortium target3 mur16

82	d1k7ia2	Alignment	not modelled	65.9	31	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
83	c1y791_	Alignment	not modelled	64.4	27	**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
84	c2c6nA_	Alignment	not modelled	64.0	15	**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
85	d1g9ka2	Alignment	not modelled	63.8	50	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
86	d3b7sa3	Alignment	not modelled	62.8	22	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Leukotriene A4 hydrolase catalytic domain
87	c1eakA_	Alignment	not modelled	62.8	33	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**72 kda type iv collagenase; **PDBTitle:** catalytic domain of prommp-2 e404q mutant
88	d1s4bp_	Alignment	not modelled	62.6	27	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
89	c3p1vB_	Alignment	not modelled	61.0	24	**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
90	d1i1ip_	Alignment	not modelled	59.7	27	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
91	d3e11a1	Alignment	not modelled	59.1	21	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like
92	c3b4rB_	Alignment	not modelled	58.1	33	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative zinc metalloprotease mj0392; **PDBTitle:** site-2 protease from methanocaldococcus jannaschii
93	c1jiwP_	Alignment	not modelled	55.4	36	**PDB header:**hydrolase/hyrolase inhibitor **Chain:** P: **PDB Molecule:**alkaline metalloproteinase; **PDBTitle:** crystal structure of the apr-aprin complex
94	c2l0rA_	Alignment	not modelled	54.3	27	**PDB header:**hydrolase,toxin **Chain:** A: **PDB Molecule:**lethal factor; **PDBTitle:** conformational dynamics of the anthrax lethal factor catalytic center
95	d2di4a1	Alignment	not modelled	53.8	41	**Fold:**FtsH protease domain-like **Superfamily:**FtsH protease domain-like **Family:**FtsH protease domain-like
96	c1om8A_	Alignment	not modelled	52.3	40	**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
97	c3lqbA_	Alignment	not modelled	51.9	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**loc792177 protein; **PDBTitle:** crystal structure of the hatching enzyme zhe1 from the zebrafish danio2 rerio
98	d1lmla_	Alignment	not modelled	51.4	12	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Leishmanolysin
99	d1uzea_	Alignment	not modelled	49.6	15	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
100	c3edhA_	Alignment	not modelled	49.2	27	**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
101	d1j7na2	Alignment	not modelled	49.0	21	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Anthrax toxin lethal factor, N- and C-terminal domains
102	d1j36a_	Alignment	not modelled	48.4	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
103	d2ce7a1	Alignment	not modelled	47.9	38	**Fold:**FtsH protease domain-like **Superfamily:**FtsH protease domain-like **Family:**FtsH protease domain-like
104	c1l6jA_	Alignment	not modelled	46.4	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-9; **PDBTitle:** crystal structure of human matrix metalloproteinase mmp92 (gelatinase b).
105	c2di4B_	Alignment	not modelled	45.6	44	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cell division protein ftsh homolog; **PDBTitle:** crystal structure of the ftsh protease domain
106	c1gxdA_	Alignment	not modelled	44.2	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**72 kda type iv collagenase; **PDBTitle:** prommp-2/timp-2 complex
107	c3lq0A_	Alignment	not modelled	43.8	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proastacin; **PDBTitle:** zymogen structure of crayfish astacin metallopeptidase
108	d1asta_	Alignment	not modelled	41.3	15	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Astacin

109	d1saza1	Alignment	not modelled	32.0	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
110	c1satA_	Alignment	not modelled	31.4	50	**PDB header:**hydrolase (serine protease) **Chain:** A: **PDB Molecule:**serratia protease; **PDBTitle:** crystal structure of the 50 kda metallo protease from s.2 marcescens
111	c2x7mA_	Alignment	not modelled	31.1	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**archaemetzincin; **PDBTitle:** crystal structure of archaemetzincin (amza) from methanopyrus2 kandleri at 1.5 a resolution
112	c2x3bB_	Alignment	not modelled	29.0	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**toxic extracellular endopeptidase; **PDBTitle:** asap1 inactive mutant e294a, an extracellular toxic zinc2 metalloendopeptidase
113	d1a6qa2	Alignment	not modelled	25.1	11	**Fold:**PP2C-like **Superfamily:**PP2C-like **Family:**PP2C-like
114	d1eb6a_	Alignment	not modelled	21.2	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Fungal zinc peptidase
115	c2pnqA_	Alignment	not modelled	20.6	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]]-phosphatase **PDBTitle:** crystal structure of pyruvate dehydrogenase phosphatase 12 (pdp1)