Phyre^{2}

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Description	P64429
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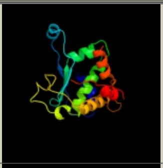
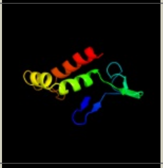
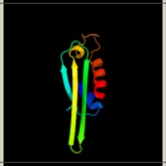
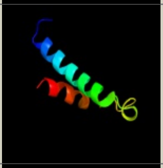
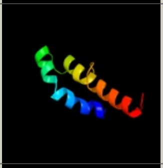
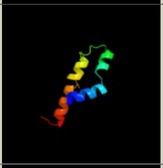
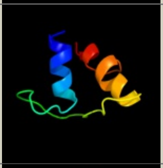
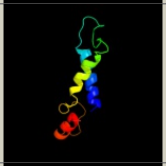
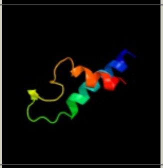
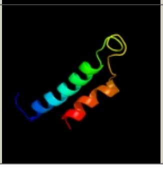
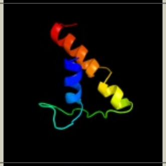
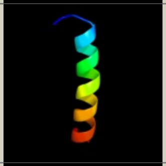
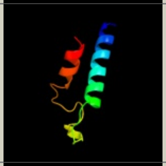
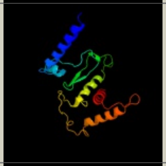
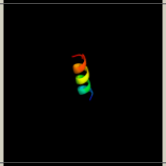
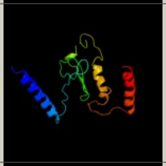
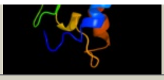
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c37B_	Alignment		98.2	18	**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	c3dtkA_	Alignment		96.7	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
3	c3cqbB_	Alignment		95.6	24	**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
4	c3sksA_	Alignment		91.6	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative oligoendopeptidase f; **PDBTitle:** crystal structure of a putative oligoendopeptidase f from bacillus2 anthracis str. ames
5	c2vqxA_	Alignment		90.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metalloproteinase; **PDBTitle:** precursor of protealysin, metalloproteinase from serratia2 proteamaculans.
6	d1kjpa_	Alignment		90.2	24	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
7	d1npca_	Alignment		90.2	27	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
8	d1bqba_	Alignment		89.7	31	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
9	d1i1ip_	Alignment		89.6	16	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
10	c1y791_	Alignment		89.6	20	**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
11	c3ce2A_	Alignment		89.5	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative peptidase; **PDBTitle:** crystal structure of putative peptidase from chlamydophila abortus

12	c3nqzB_	Alignment		88.7	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**secreted metalloprotease mcp02; **PDBTitle:** crystal structure of the autoprocessed vibriolysin mcp-02 with e369a2 mutation
13	c3nqxA_	Alignment		88.1	24	**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
14	c2h1jA_	Alignment		87.9	32	**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
15	d1s4bp_	Alignment		86.9	17	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
16	c3dwbA_	Alignment		85.1	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endothelin-converting enzyme 1; **PDBTitle:** structure of human ece-1 complexed with phosphoramidon
17	d2ejqa1	Alignment		84.7	40	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like
18	d1dmta_	Alignment		84.2	16	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neutral endopeptidase (neprilysin)
19	d1r55a_	Alignment		83.8	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
20	c3k7lA_	Alignment		83.7	36	**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
21	d1u4ga_	Alignment	not modelled	83.7	43	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
22	c2dw1B_	Alignment	not modelled	82.6	36	**PDB header:**apoptosis, toxin **Chain:** B: **PDB Molecule:**catrocollastatin; **PDBTitle:** crystal structure of vap2 from crotalus atrox venom (form 2-2 crystal)
23	d1k7ia2	Alignment	not modelled	82.4	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
24	d2i47a1	Alignment	not modelled	82.2	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TNF-alpha converting enzyme, TACE, catalytic domain
25	c2erpA_	Alignment	not modelled	81.6	36	**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)
26	c2e3xA_	Alignment	not modelled	81.5	36	**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
27	d1bqqm_	Alignment	not modelled	81.4	15	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
28	d4aiga_	Alignment	not modelled	81.0	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like

29	c3k7nA_	Alignment	not modelled	81.0	36	**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
30	d1quaa_	Alignment	not modelled	80.7	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
31	d1atla_	Alignment	not modelled	80.6	43	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
32	c2i47A_	Alignment	not modelled	80.4	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adam 17; **PDBTitle:** crystal structure of catalytic domain of tace with inhibitor
33	c2jsdA_	Alignment	not modelled	80.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-20; **PDBTitle:** solution structure of mmp20 complexed with nngh
34	d1wnia_	Alignment	not modelled	80.1	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
35	c1eakA_	Alignment	not modelled	80.1	22	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**72 kda type iv collagenase; **PDBTitle:** catalytic domain of prommp-2 e404q mutant
36	c2qr4B_	Alignment	not modelled	79.8	38	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase m3b, oligoendopeptidase f; **PDBTitle:** crystal structure of oligoendopeptidase-f from enterococcus faecium
37	d1nd1a_	Alignment	not modelled	79.4	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
38	d1kufa_	Alignment	not modelled	78.6	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
39	c2xs4A_	Alignment	not modelled	77.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**karilysin protease; **PDBTitle:** structure of karilysin catalytic mmp domain in complex with2 magnesium
40	d1j36a_	Alignment	not modelled	77.3	16	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
41	c1yp1A_	Alignment	not modelled	76.5	43	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fii; **PDBTitle:** crystal structure of a non-hemorrhagic fibrin(ogen)olytic2 metalloproteinase from venom of agkistrodon acutus
42	c3g5cA_	Alignment	not modelled	76.4	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**adam 22; **PDBTitle:** structural and biochemical studies on the ectodomain of human adam22
43	d1c7ka_	Alignment	not modelled	76.1	32	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Zinc protease
44	c2rjpC_	Alignment	not modelled	76.0	31	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**adamts-4; **PDBTitle:** crystal structure of adamts4 with inhibitor bound
45	d2ajfa1	Alignment	not modelled	75.6	18	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
46	d1bswa_	Alignment	not modelled	75.4	31	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
47	c2rjqA_	Alignment	not modelled	75.1	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adamts-5; **PDBTitle:** crystal structure of adamts5 with inhibitor bound
48	c2v4bB_	Alignment	not modelled	74.2	38	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adamts-1; **PDBTitle:** crystal structure of human adamts-1 catalytic domain and2 cysteine-rich domain (apo-form)
49	d1uzea_	Alignment	not modelled	73.9	22	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
50	c3zukB_	Alignment	not modelled	73.0	12	**PDB header:**hydrolase/inhibitor **Chain:** B: **PDB Molecule:**endopeptidase, peptidase family m13; **PDBTitle:** crystal structure of mycobacterium tuberculosis zinc metalloprotease2 zmp1 in complex with inhibitor
51	c3p24C_	Alignment	not modelled	72.7	53	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**bft-3; **PDBTitle:** structure of profragilysin-3 from bacteroides fragilis
52	c2c6nA_	Alignment	not modelled	72.5	27	**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
53	c3b8zB_	Alignment	not modelled	72.3	38	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein adamts-5; **PDBTitle:** high resolution crystal structure of the catalytic domain2 of adamts-5 (aggrecanase-2)
54	c3mdjB_	Alignment		71.3	20	**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
55	c3qnfA_	Alignment	not modelled	71.0	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
56	d1xuca1	Alignment	not modelled	69.3	46	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
57	c2gtqA_	Alignment	not modelled	68.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase n; **PDBTitle:** crystal structure of aminopeptidase n from human pathogen neisseria2 meningitidis
58	c2j83B_	Alignment	not modelled	68.7	40	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ulilysin; **PDBTitle:** ulilysin metalloprotease in complex with batimastat.
59	d1cxva_	Alignment	not modelled	68.5	46	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
60	c3o0yC_	Alignment	not modelled	68.4	27	**PDB header:**lipid binding protein **Chain:** C: **PDB Molecule:**lipoprotein; **PDBTitle:** the crystal structure of the putative lipoprotein from colwellia2 psychrerythraea
61	d1rm8a_	Alignment	not modelled	68.2	38	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
62	d1y93a1	Alignment	not modelled	67.9	31	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
63	d1q3aa_	Alignment	not modelled	66.7	46	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
64	c2cltB_	Alignment	not modelled	66.7	38	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**interstitial collagenase; **PDBTitle:** crystal structure of the active form (full-length) of human2 fibroblast collagenase.
65	d1i76a_	Alignment	not modelled	66.6	46	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
66	d1sata2	Alignment	not modelled	66.5	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
67	d1mmqa_	Alignment	not modelled	66.1	38	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
68	c3se6A_	Alignment	not modelled	66.1	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoplasmic reticulum aminopeptidase 2; **PDBTitle:** crystal structure of the human endoplasmic reticulum aminopeptidase 2
69	c1slmA_	Alignment	not modelled	66.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**stromelysin-1; **PDBTitle:** crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
70	d1g9ka2	Alignment	not modelled	65.9	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
71	d1hfca_	Alignment	not modelled	65.5	46	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
72	c1pwqA_	Alignment	not modelled	65.3	21	**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
73	c1wgzC_	Alignment	not modelled	65.0	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**carboxypeptidase 1; **PDBTitle:** crystal structure of carboxypeptidase 1 from thermus thermophilus
74	d1hv5a_	Alignment	not modelled	64.8	55	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
75	d1hy7a_	Alignment	not modelled	63.1	46	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
76	d2ovxa1	Alignment	not modelled	63.1	38	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
77	d1qiba_	Alignment	not modelled	62.2	46	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
78	d1cgla_	Alignment	not modelled	61.6	46	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
79	c3ba0A_	Alignment	not modelled	61.5	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**macrophage metalloelastase; **PDBTitle:** crystal structure of full-length human mmp-12
						PDB header:hydrolase,toxin

80	c2l0rA_	Alignment	not modelled	59.1	40	**Chain:** A: **PDB Molecule:**lethal factor; **PDBTitle:** conformational dynamics of the anthrax lethal factor catalytic center
81	d1kapp2	Alignment	not modelled	59.1	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
82	c1su3A_	Alignment	not modelled	57.6	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**interstitial collagenase; **PDBTitle:** x-ray structure of human prommp-1: new insights into2 collagenase action
83	c1jiwP_	Alignment	not modelled	56.4	33	**PDB header:**hydrolase/hyrolase inhibitor **Chain:** P: **PDB Molecule:**alkaline metalloproteinase; **PDBTitle:** crystal structure of the apr-aprin complex
84	d1hova_	Alignment	not modelled	56.2	46	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
85	d1eaka2	Alignment	not modelled	54.7	38	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
86	c3hq2A_	Alignment	not modelled	53.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**bacillus subtilis m32 carboxypeptidase; **PDBTitle:** bsucp crystal structure
87	c3iukB_	Alignment	not modelled	53.2	11	**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
88	d1k9xa_	Alignment	not modelled	53.2	20	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
89	d1j7na2	Alignment	not modelled	53.2	38	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Anthrax toxin lethal factor, N- and C-terminal domains
90	d1fbla2	Alignment	not modelled	52.8	46	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
91	c2xdtA_	Alignment	not modelled	51.6	16	**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
92	c3b37A_	Alignment	not modelled	51.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase n; **PDBTitle:** crystal structure of e. coli aminopeptidase n in complex with tyrosine
93	c1l6jA_	Alignment	not modelled	51.3	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-9; **PDBTitle:** crystal structure of human matrix metalloproteinase mmp92 (gelatinase b).
94	c1gxdA_	Alignment	not modelled	48.6	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**72 kda type iv collagenase; **PDBTitle:** prommp-2/timp-2 complex
95	c3gabC_	Alignment	not modelled	46.6	29	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dna mismatch repair protein mutl; **PDBTitle:** c-terminal domain of bacillus subtilis mutl crystal form i
96	c1om8A_	Alignment	not modelled	46.6	33	**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	d1asta_	Alignment	not modelled	43.1	40	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Astacin
98	c3iabA_	Alignment	not modelled	39.9	46	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**ribonucleases p/mrp protein subunit pop6; **PDBTitle:** crystal structure of rnase p /rnase mrp proteins pop6, pop72 in a complex with the p3 domain of rnase mrp rna
99	c3lqbA_	Alignment	not modelled	39.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**loc792177 protein; **PDBTitle:** crystal structure of the hatching enzyme zhe1 from the zebrafish danio2 rerio
100	c1yqyA_	Alignment	not modelled	37.6	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lethal factor; **PDBTitle:** structure of b. anthrax lethal factor in complex with a2 hydroxamate inhibitor
101	c1satA_	Alignment	not modelled	36.7	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
102	c3edhA_	Alignment	not modelled	36.6	50	**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
103	c3dwcA_	Alignment	not modelled	32.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallocarboxypeptidase; **PDBTitle:** trypanosoma cruzi metallocarboxypeptidase 1
104	c3p1vB_	Alignment	not modelled	32.3	38	**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
105	c3ncvB_	Alignment	not modelled	32.1	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dna mismatch repair protein mutl; **PDBTitle:** ngol
						PDB header:hydrolase inhibitor

106	c3ebhA_	Alignment	not modelled	32.0	36	**Chain:** A: **PDB Molecule:**m1 family aminopeptidase; **PDBTitle:** structure of the m1 alanylaminopeptidase from malaria complexed with2 bestatin
107	c3lq0A_	Alignment	not modelled	28.5	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proastacin; **PDBTitle:** zymogen structure of crayfish astacin metallopeptidase
108	c1z5hB_	Alignment	not modelled	27.9	40	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**tricorn protease interacting factor f3; **PDBTitle:** crystal structures of the tricorn interacting factor f32 from thermoplasma acidophilum
109	c3b7uX_	Alignment	not modelled	27.8	21	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**leukotriene a-4 hydrolase; **PDBTitle:** leukotriene a4 hydrolase complexed with kelatorphan
110	c3b4rB_	Alignment	not modelled	26.8	33	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative zinc metalloprotease mj0392; **PDBTitle:** site-2 protease from methanocaldococcus jannaschii
111	c3ciaA_	Alignment	not modelled	26.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cold-active aminopeptidase; **PDBTitle:** crystal structure of cold-aminopeptidase from colwellia2 psychrerythraea
112	d3e11a1	Alignment	not modelled	23.9	44	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like