Phyre^2

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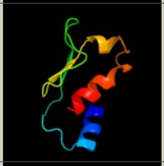
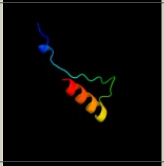
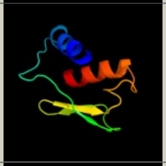
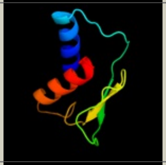
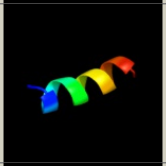
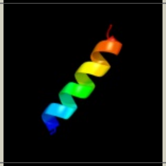
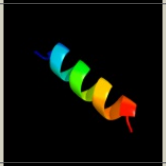
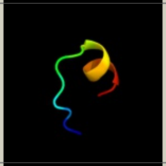
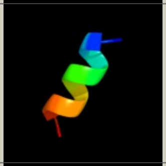
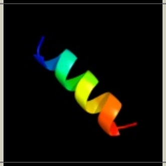
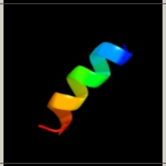
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c37B_	Alignment		100.0	26	**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	26	**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		97.4	17	**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	c3b7uX_	Alignment		91.3	22	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**leukotriene a-4 hydrolase; **PDBTitle:** leukotriene a4 hydrolase complexed with kelatorphan
5	d2ejqa1	Alignment		89.3	19	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like
6	c3ciaA_	Alignment		87.3	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cold-active aminopeptidase; **PDBTitle:** crystal structure of cold-aminopeptidase from colwellia2 psychrerythraea
7	c2gtqA_	Alignment		86.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase n; **PDBTitle:** crystal structure of aminopeptidase n from human pathogen neisseria2 meningitidis
8	d1r55a_	Alignment		86.7	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
9	c3ebhA_	Alignment		86.2	19	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**m1 family aminopeptidase; **PDBTitle:** structure of the m1 alanylaminopeptidase from malaria complexed with2 bestatin
10	c2xs4A_	Alignment		86.1	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**karilysin protease; **PDBTitle:** structure of karilysin catalytic mmp domain in complex with2 magnesium
11	d1atla_	Alignment		84.7	28	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like

12	c3b37A_	Alignment		84.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase n; **PDBTitle:** crystal structure of e. coli aminopeptidase n in complex with tyrosine
13	d2i47a1	Alignment		84.4	39	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TNF-alpha converting enzyme, TACE, catalytic domain
14	c2i47A_	Alignment		84.4	44	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adam 17; **PDBTitle:** crystal structure of catalytic domain of tace with inhibitor
15	c3k7lA_	Alignment		84.2	33	**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
16	d1bqqm_	Alignment		83.8	50	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
17	c2dw1B_	Alignment		83.6	33	**PDB header:**apoptosis, toxin **Chain:** B: **PDB Molecule:**catrocollastatin; **PDBTitle:** crystal structure of vap2 from crotalus atrox venom (form 2-2 crystal)
18	d1bswa_	Alignment		83.5	27	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
19	d1rm8a_	Alignment		83.4	43	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
20	c2erpA_	Alignment		83.4	22	**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)
21	d2ovxa1	Alignment	not modelled	83.3	29	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
22	d1y93a1	Alignment	not modelled	82.9	29	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
23	d1u4ga_	Alignment	not modelled	82.8	23	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
24	c3sksA_	Alignment	not modelled	82.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative oligoendopeptidase f; **PDBTitle:** crystal structure of a putative oligoendopeptidase f from bacillus2 anthracis str. ames
25	c3nqxA_	Alignment	not modelled	82.5	22	**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
26	d1qiba_	Alignment	not modelled	82.4	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
27	d1cxva_	Alignment	not modelled	82.3	43	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
28	d1xuca1	Alignment	not modelled	82.2	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
						PDB header:hydrolase **Chain:** A: **PDB Molecule:**k-like;

29	c3k7nA_	Alignment	not modelled	82.1	31	**PDBTitle:** structures of two elapid snake venom metalloproteases with2 distinct activities highlight the disulfide patterns in the3 d domain of adamalysin family proteins
30	c2e3xA_	Alignment	not modelled	81.9	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
31	d1hv5a_	Alignment	not modelled	81.8	43	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
32	d1i76a_	Alignment	not modelled	81.7	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
33	c3qnfA_	Alignment	not modelled	81.6	14	**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
34	d4aiga_	Alignment	not modelled	81.4	31	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
35	d1hfca_	Alignment	not modelled	81.3	43	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
36	d1hy7a_	Alignment	not modelled	81.1	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
37	c3p24C_	Alignment	not modelled	81.0	58	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**bft-3; **PDBTitle:** structure of profragilysin-3 from bacteroides fragilis
38	d1mmqa_	Alignment	not modelled	81.0	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
39	c2cltB_	Alignment	not modelled	80.7	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**interstitial collagenase; **PDBTitle:** crystal structure of the active form (full-length) of human2 fibroblast collagenase.
40	c1yp1A_	Alignment	not modelled	80.3	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fii; **PDBTitle:** crystal structure of a non-hemorrhagic fibrin(ogen)olytic2 metalloproteinase from venom of agkistrodon acutus
41	c2xpyA_	Alignment	not modelled	80.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leukotriene a-4 hydrolase; **PDBTitle:** structure of native leukotriene a4 hydrolase from saccharomyces2 cerevisiae
42	d1quaa_	Alignment	not modelled	79.8	31	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
43	d1hova_	Alignment	not modelled	79.7	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
44	c3mdjB_	Alignment	not modelled	79.7	13	**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
45	c2jsdA_	Alignment	not modelled	79.6	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-20; **PDBTitle:** solution structure of mmp20 complexed with nngh
46	c1slmA_	Alignment	not modelled	79.4	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**stromelysin-1; **PDBTitle:** crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
47	d1q3aa_	Alignment	not modelled	79.4	43	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
48	d1cgla_	Alignment	not modelled	78.6	43	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
49	c2v4bB_	Alignment	not modelled	78.6	55	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adamts-1; **PDBTitle:** crystal structure of human adamts-1 catalytic domain and2 cysteine-rich domain (apo-form)
50	d1kufa_	Alignment	not modelled	78.5	31	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
51	d1wnia_	Alignment	not modelled	78.3	38	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
52	c1z5hB_	Alignment	not modelled	78.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**tricorn protease interacting factor f3; **PDBTitle:** crystal structures of the tricorn interacting factor f32 from thermoplasma acidophilum
53	c3g5cA_	Alignment	not modelled	78.0	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**adam 22; **PDBTitle:** structural and biochemical studies on the ectodomain of human adam22
54	d1lmla_	Alignment	not modelled	77.8	22	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Leishmanolysin
						PDB header:hydrolase

55	c3b8zB_	Alignment	not modelled	77.6	36	**Chain:** B: **PDB Molecule:**protein adamts-5; **PDBTitle:** high resolution crystal structure of the catalytic domain2 of adamts-5 (aggrecanase-2)
56	d1nd1a_	Alignment	not modelled	77.4	45	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
57	d3b7sa3	Alignment	not modelled	76.8	21	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Leukotriene A4 hydrolase catalytic domain
58	d1eaka2	Alignment	not modelled	76.7	29	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
59	d1fbla2	Alignment	not modelled	76.7	43	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
60	d1bqba_	Alignment	not modelled	76.6	18	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
61	d1kjpa_	Alignment	not modelled	76.5	23	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
62	c2xdtA_	Alignment	not modelled	75.2	13	**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
63	c2rjqA_	Alignment	not modelled	75.0	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adamts-5; **PDBTitle:** crystal structure of adamts5 with inhibitor bound
64	c2rjpC_	Alignment	not modelled	75.0	45	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**adamts-4; **PDBTitle:** crystal structure of adamts4 with inhibitor bound
65	c3se6A_	Alignment	not modelled	74.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoplasmic reticulum aminopeptidase 2; **PDBTitle:** crystal structure of the human endoplasmic reticulum aminopeptidase 2
66	d1c7ka_	Alignment	not modelled	74.5	55	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Zinc protease
67	c3ba0A_	Alignment	not modelled	73.6	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**macrophage metalloelastase; **PDBTitle:** crystal structure of full-length human mmp-12
68	d3e11a1	Alignment	not modelled	73.5	19	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like
69	d1npca_	Alignment	not modelled	73.2	22	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
70	c1su3A_	Alignment	not modelled	73.1	43	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**interstitial collagenase; **PDBTitle:** x-ray structure of human prommp-1: new insights into2 collagenase action
71	c3nqzB_	Alignment	not modelled	72.9	50	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**secreted metalloprotease mcp02; **PDBTitle:** crystal structure of the autoprocessed vibriolysin mcp-02 with e369a2 mutation
72	c2qr4B_	Alignment	not modelled	72.3	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase m3b, oligoendopeptidase f; **PDBTitle:** crystal structure of oligoendopeptidase-f from enterococcus faecium
73	d2ajfa1	Alignment	not modelled	72.2	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
74	c2h1jA_	Alignment	not modelled	71.1	55	**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
75	c2vqxA_	Alignment	not modelled	69.0	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metalloproteinase; **PDBTitle:** precursor of protealysin, metalloproteinase from serratia2 proteamaculans.
76	c3ce2A_	Alignment	not modelled	68.4	42	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative peptidase; **PDBTitle:** crystal structure of putative peptidase from chlamydophila abortus
77	c1eakA_	Alignment	not modelled	67.3	29	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**72 kda type iv collagenase; **PDBTitle:** catalytic domain of prommp-2 e404q mutant
78	c2xhqA_	Alignment	not modelled	65.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**archaemetzincin; **PDBTitle:** crystal structure of archaemetzincin (amza) from archaeoglobus2 fulgidus at 1.45 a resolution
79	c1y791_	Alignment	not modelled	65.1	45	**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
80	c2j83B_	Alignment	not modelled	65.0	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ulilysin; **PDBTitle:** ulilysin metalloprotease in complex with batimastat.
81	d1sata2	Alignment	not modelled	64.8	29	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain

81	d1sata2	Alignment	not modelled	64.8	29	**Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
82	d1kapp2	Alignment	not modelled	64.0	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
83	d1k7ia2	Alignment	not modelled	63.2	22	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
84	d1g9ka2	Alignment	not modelled	63.2	45	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
85	d1s4bp_	Alignment	not modelled	60.8	42	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
86	d1i1ip_	Alignment	not modelled	57.8	42	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
87	c2c6nA_	Alignment	not modelled	50.6	36	**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
88	c1jiwP_	Alignment	not modelled	50.1	54	**PDB header:**hydrolase/hyrolase inhibitor **Chain:** P: **PDB Molecule:**alkaline metalloproteinase; **PDBTitle:** crystal structure of the apr-aprin complex
89	c1l6jA_	Alignment	not modelled	49.5	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-9; **PDBTitle:** crystal structure of human matrix metalloproteinase mmp92 (gelatinase b).
90	c3b4rB_	Alignment	not modelled	48.8	50	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative zinc metalloprotease mj0392; **PDBTitle:** site-2 protease from methanocaldococcus jannaschii
91	c3zukB_	Alignment	not modelled	48.8	32	**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
92	d1k9xa_	Alignment	not modelled	48.1	10	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
93	c3lqbA_	Alignment	not modelled	47.8	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**loc792177 protein; **PDBTitle:** crystal structure of the hatching enzyme zhe1 from the zebrafish danio2 rerio
94	c3dwbA_	Alignment	not modelled	45.3	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endothelin-converting enzyme 1; **PDBTitle:** structure of human ece-1 complexed with phosphoramidon
95	d1j36a_	Alignment	not modelled	44.4	45	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
96	c2x3bB_	Alignment	not modelled	44.2	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**toxic extracellular endopeptidase; **PDBTitle:** asap1 inactive mutant e294a, an extracellular toxic zinc2 metalloendopeptidase
97	d1asta_	Alignment	not modelled	43.9	42	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Astacin
98	c3edhA_	Alignment	not modelled	43.1	54	**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
99	c1gxdA_	Alignment	not modelled	41.6	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**72 kda type iv collagenase; **PDBTitle:** prommp-2/timp-2 complex
100	c1om8A_	Alignment	not modelled	41.2	50	**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
101	c3lq0A_	Alignment	not modelled	39.0	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proastacin; **PDBTitle:** zymogen structure of crayfish astacin metallopeptidase
102	c2l0rA_	Alignment	not modelled	38.2	40	**PDB header:**hydrolase,toxin **Chain:** A: **PDB Molecule:**lethal factor; **PDBTitle:** conformational dynamics of the anthrax lethal factor catalytic center
103	d1dmta_	Alignment	not modelled	33.3	23	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neutral endopeptidase (neprilysin)
104	d1uzea_	Alignment	not modelled	31.6	45	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
105	d1saza1	Alignment	not modelled	31.4	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
106	d1j7na2	Alignment	not modelled	27.7	29	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Anthrax toxin lethal factor, N- and C-terminal domains
107	d2di4a1	Alignment	not modelled	26.2	33	**Fold:**FtsH protease domain-like **Superfamily:**FtsH protease domain-like **Family:**FtsH protease domain-like

108	c1wgzC_	Alignment	not modelled	25.2	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**carboxypeptidase 1; **PDBTitle:** crystal structure of carboxypeptidase 1 from thermus thermophilus
109	d2ce7a1	Alignment	not modelled	23.6	28	**Fold:**FtsH protease domain-like **Superfamily:**FtsH protease domain-like **Family:**FtsH protease domain-like
110	d1np3a1	Alignment	not modelled	23.0	29	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Acetohydroxy acid isomeroreductase (ketol-acid reductoisomerase, KARI)