Phyre^2

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Description	P42597
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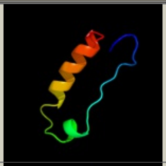
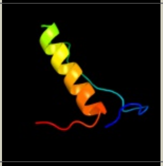
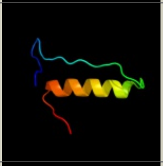
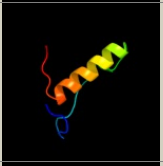
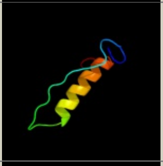
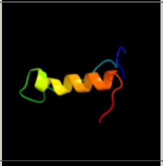
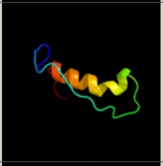
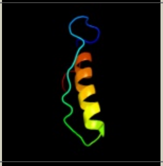
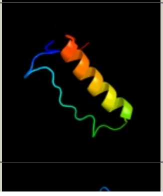
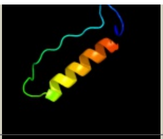
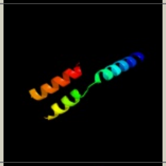
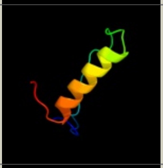
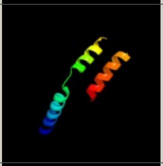
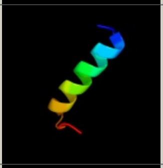
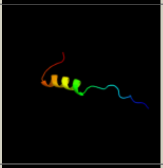
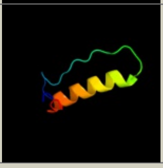
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cqbB_	Alignment		94.8	16	**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
2	c3c37B_	Alignment		94.5	19	**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
3	c3dtkA_	Alignment		92.9	14	**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	d1atla_	Alignment		85.9	23	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
5	d1bswa_	Alignment		85.8	18	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
6	d1quaa_	Alignment		83.4	18	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
7	d1r55a_	Alignment		80.4	20	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
8	d1nd1a_	Alignment		80.4	20	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
9	d4aiga_	Alignment		80.1	15	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
10	c1yp1A_	Alignment		79.6	25	**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	d1kufa_	Alignment		77.1	23	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like

12	c3k7lA_	Alignment		76.8	18	**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
13	c3cmnA_	Alignment		75.4	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of a putative hydrolase with a novel fold2 from chloroflexus aurantiacus
14	c2xdtA_	Alignment		74.2	15	**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
15	d1wnia_	Alignment		73.9	20	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
16	d3cmna1	Alignment		73.6	23	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Caur0242-like
17	c2gtqA_	Alignment		72.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase n; **PDBTitle:** crystal structure of aminopeptidase n from human pathogen neisseria2 meningitidis
18	c2i47A_	Alignment		72.6	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adam 17; **PDBTitle:** crystal structure of catalytic domain of tace with inhibitor
19	c1eakA_	Alignment		72.4	21	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**72 kda type iv collagenase; **PDBTitle:** catalytic domain of prommp-2 e404q mutant
20	c2e3xA_	Alignment		72.1	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
21	d2i47a1	Alignment	not modelled	72.1	26	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TNF-alpha converting enzyme, TACE, catalytic domain
22	c3ebhA_	Alignment	not modelled	71.8	14	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**m1 family aminopeptidase; **PDBTitle:** structure of the m1 alanylaminopeptidase from malaria complexed with2 bestatin
23	c3b37A_	Alignment	not modelled	71.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase n; **PDBTitle:** crystal structure of e. coli aminopeptidase n in complex with tyrosine
24	c3dl1A_	Alignment	not modelled	70.8	40	**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
25	c3g5cA_	Alignment	not modelled	69.5	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**adam 22; **PDBTitle:** structural and biochemical studies on the ectodomain of human adam22
26	c2rjqA_	Alignment	not modelled	68.8	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adamts-5; **PDBTitle:** crystal structure of adamts5 with inhibitor bound
27	c2erpA_	Alignment	not modelled	66.8	15	**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)
28	c3k7nA_	Alignment	not modelled	66.6	18	**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

29	d1rm8a_	Alignment	not modelled	62.4	44	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
30	c3mdjB_	Alignment	not modelled	62.3	16	**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
31	d1xuca1	Alignment	not modelled	61.2	28	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
32	d3e11a1	Alignment	not modelled	60.4	44	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like
33	d1k7ia2	Alignment	not modelled	60.4	18	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
34	c2l0rA_	Alignment	not modelled	59.5	23	**PDB header:**hydrolase,toxin **Chain:** A: **PDB Molecule:**lethal factor; **PDBTitle:** conformational dynamics of the anthrax lethal factor catalytic center
35	d1hv5a_	Alignment	not modelled	59.1	28	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
36	d1bqqm_	Alignment	not modelled	58.8	39	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
37	c2dw1B_	Alignment	not modelled	58.6	18	**PDB header:**apoptosis, toxin **Chain:** B: **PDB Molecule:**catrocollastatin; **PDBTitle:** crystal structure of vap2 from crotalus atrox venom (form 2-2 crystal)
38	d1sata2	Alignment	not modelled	58.1	19	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
39	c2v4bB_	Alignment	not modelled	57.6	31	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adamts-1; **PDBTitle:** crystal structure of human adamts-1 catalytic domain and2 cysteine-rich domain (apo-form)
40	c3qnfA_	Alignment	not modelled	57.2	16	**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
41	d2ejqa1	Alignment	not modelled	56.9	35	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like
42	c1slmA_	Alignment	not modelled	56.3	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**stromelysin-1; **PDBTitle:** crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
43	d1qiba_	Alignment	not modelled	56.2	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
44	c2xs4A_	Alignment	not modelled	55.7	39	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**karilysin protease; **PDBTitle:** structure of karilysin catalytic mmp domain in complex with2 magnesium
45	c2rjpC_	Alignment	not modelled	55.6	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**adamts-4; **PDBTitle:** crystal structure of adamts4 with inhibitor bound
46	c3b8zB_	Alignment	not modelled	54.3	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)
47	d1q3aa_	Alignment	not modelled	53.6	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
48	d1hfca_	Alignment	not modelled	53.5	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
49	d1mmqa_	Alignment	not modelled	52.6	28	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
50	d1lmla_	Alignment	not modelled	52.5	21	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Leishmanolysin
51	d1cgla_	Alignment	not modelled	51.7	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
52	d1i76a_	Alignment	not modelled	51.3	28	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
53	d2ovxa1	Alignment	not modelled	50.9	22	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
54	d1hy7a_	Alignment	not modelled	50.9	28	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
55	c1l6jA	Alignment	not modelled	50.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-9;

55	c1l6jA_	Alignment	not modelled	50.7	21	**PDBTitle:** crystal structure of human matrix metalloproteinase mmp92 (gelatinase b).
56	d1hova_	Alignment	not modelled	50.6	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
57	c2xhqA_	Alignment	not modelled	50.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**archaemetzincin; **PDBTitle:** crystal structure of archaemetzincin (amza) from archaeoglobus2 fulgidus at 1.45 a resolution
58	d1cxva_	Alignment	not modelled	50.3	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
59	d1y93a1	Alignment	not modelled	50.2	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
60	c2jsdA_	Alignment	not modelled	49.7	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-20; **PDBTitle:** solution structure of mmp20 complexed with nngh
61	c1su3A_	Alignment	not modelled	47.3	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**interstitial collagenase; **PDBTitle:** x-ray structure of human prommp-1: new insights into2 collagenase action
62	c3se6A_	Alignment	not modelled	46.3	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoplasmic reticulum aminopeptidase 2; **PDBTitle:** crystal structure of the human endoplasmic reticulum aminopeptidase 2
63	c1z5hB_	Alignment	not modelled	45.6	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**tricorn protease interacting factor f3; **PDBTitle:** crystal structures of the tricorn interacting factor f32 from thermoplasma acidophilum
64	d1npca_	Alignment	not modelled	45.6	50	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
65	d1eaka2	Alignment	not modelled	45.4	28	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
66	d1kjpa_	Alignment	not modelled	43.6	63	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
67	d1kapp2	Alignment	not modelled	43.2	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
68	c2cltB_	Alignment	not modelled	42.8	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**interstitial collagenase; **PDBTitle:** crystal structure of the active form (full-length) of human2 fibroblast collagenase.
69	d1bqba_	Alignment	not modelled	41.7	50	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
70	c3nqxA_	Alignment	not modelled	40.8	38	**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	c3nqzB_	Alignment	not modelled	40.5	38	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**secreted metalloprotease mcp02; **PDBTitle:** crystal structure of the autoprocessed vibriolysin mcp-02 with e369a2 mutation
72	d1g9ka2	Alignment	not modelled	40.3	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
73	c2xpyA_	Alignment	not modelled	40.2	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leukotriene a-4 hydrolase; **PDBTitle:** structure of native leukotriene a4 hydrolase from saccharomyces2 cerevisiae
74	c2vqxA_	Alignment	not modelled	40.1	63	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metalloproteinase; **PDBTitle:** precursor of protealysin, metalloproteinase from serratia2 proteamaculans.
75	d1fbla2	Alignment	not modelled	38.9	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
76	c2x7mA_	Alignment	not modelled	38.3	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**archaemetzincin; **PDBTitle:** crystal structure of archaemetzincin (amza) from methanopyrus2 kandleri at 1.5 a resolution
77	d3b7sa3	Alignment	not modelled	38.3	19	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Leukotriene A4 hydrolase catalytic domain
78	d1eb6a_	Alignment	not modelled	38.2	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Fungal zinc peptidase
79	c3ciaA_	Alignment	not modelled	38.2	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cold-active aminopeptidase; **PDBTitle:** crystal structure of cold-aminopeptidase from colwellia2 psychrerythraea
80	c3b7uX_	Alignment	not modelled	38.1	23	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**leukotriene a-4 hydrolase; **PDBTitle:** leukotriene a4 hydrolase complexed with kelatorphan
81	c3p24C_	Alignment	not modelled	37.8	33	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**bft-3; **PDBTitle:** structure of profragilysin-3 from bacteroides fragilis

82	c3edhA_	Alignment	not modelled	36.7	57	**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
83	c3lmcA_	Alignment	not modelled	35.7	36	**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
84	d1u4ga_	Alignment	not modelled	35.5	38	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
85	c3ba0A_	Alignment	not modelled	31.4	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**macrophage metalloelastase; **PDBTitle:** crystal structure of full-length human mmp-12
86	d1asta_	Alignment	not modelled	30.6	31	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Astacin
87	d1g12a_	Alignment	not modelled	29.6	44	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Fungal zinc peptidase
88	c1jiwP_	Alignment	not modelled	27.7	25	**PDB header:**hydrolase/hyrolase inhibitor **Chain:** P: **PDB Molecule:**alkaline metalloproteinase; **PDBTitle:** crystal structure of the apr-aprin complex
89	c3lq0A_	Alignment	not modelled	26.4	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proastacin; **PDBTitle:** zymogen structure of crayfish astacin metallopeptidase
90	d1j7na2	Alignment	not modelled	26.2	20	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Anthrax toxin lethal factor, N- and C-terminal domains
91	c3lqbA_	Alignment	not modelled	25.2	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**loc792177 protein; **PDBTitle:** crystal structure of the hatching enzyme zhe1 from the zebrafish danio2 rerio
92	c2x3bB_	Alignment	not modelled	24.6	44	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**toxic extracellular endopeptidase; **PDBTitle:** asap1 inactive mutant e294a, an extracellular toxic zinc2 metalloendopeptidase
93	c1om8A_	Alignment	not modelled	24.6	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
94	c3b4rB_	Alignment	not modelled	24.1	50	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative zinc metalloprotease mj0392; **PDBTitle:** site-2 protease from methanocaldococcus jannaschii
95	d1wh4a_	Alignment	not modelled	19.5	13	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
96	c1gxdA_	Alignment	not modelled	18.7	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**72 kda type iv collagenase; **PDBTitle:** prommp-2/timp-2 complex
97	d1oz9a_	Alignment	not modelled	17.7	18	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Predicted metal-dependent hydrolase
98	c1satA_	Alignment	not modelled	13.9	25	**PDB header:**hydrolase (serine protease) **Chain:** A: **PDB Molecule:**serratia protease; **PDBTitle:** crystal structure of the 50 kda metallo protease from s.2 marcescens
99	c2kmgA_	Alignment	not modelled	12.2	17	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**klca; **PDBTitle:** the structure of the klca and ardb proteins show a novel2 fold and antirestriction activity against type i dna3 restriction systems in vivo but not in vitro