Phyre2

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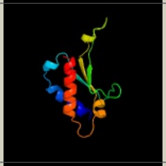
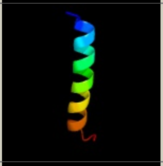
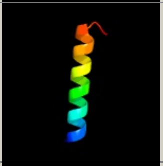
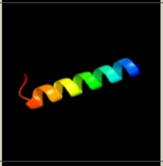
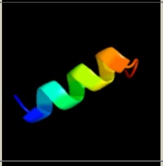
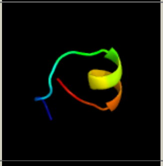
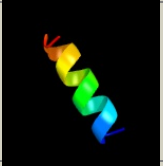
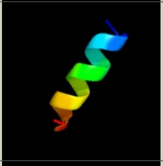
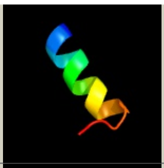
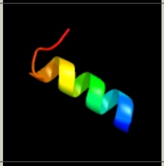
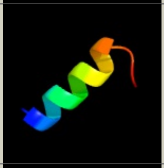
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3e11a1	Alignment		100.0	55	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like
2	d2ejqa1	Alignment		100.0	21	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like
3	c2j83B_	Alignment		95.1	31	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ulilysin; **PDBTitle:** ulilysin metalloprotease in complex with batimastat.
4	c3lmcA_	Alignment		93.4	24	**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
5	c2xhqA_	Alignment		93.2	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**archaemetzincin; **PDBTitle:** crystal structure of archaemetzincin (amza) from archaeoglobus2 fulgidus at 1.45 a resolution
6	c2x7mA_	Alignment		92.4	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**archaemetzincin; **PDBTitle:** crystal structure of archaemetzincin (amza) from methanopyrus2 kandleri at 1.5 a resolution
7	d1y93a1	Alignment		92.2	31	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
8	d1bqqm_	Alignment		91.9	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
9	d2ovxa1	Alignment		91.9	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
10	d1qiba_	Alignment		91.8	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
11	c2xs4A_	Alignment		91.7	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**karilysin protease; **PDBTitle:** structure of karilysin catalytic mmp domain in complex with magnesium

12	d1rm8a_	Alignment		91.6	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
13	d1hv5a_	Alignment		91.6	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
14	d1eaka2	Alignment		91.2	19	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
15	d1hova_	Alignment		91.2	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
16	d1cgla_	Alignment		91.1	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
17	d1mmqa_	Alignment		91.1	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
18	d1g9ka2	Alignment		90.7	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
19	d1hy7a_	Alignment		90.5	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
20	d1q3aa_	Alignment		90.3	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
21	d1i76a_	Alignment	not modelled	90.3	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
22	d1hfca_	Alignment	not modelled	90.1	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
23	d1k7ia2	Alignment	not modelled	90.0	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
24	c2jsdA_	Alignment	not modelled	89.8	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-20; **PDBTitle:** solution structure of mmp20 complexed with nngh
25	d1xuca1	Alignment	not modelled	89.6	31	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
26	d1cxva_	Alignment	not modelled	89.2	38	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
27	c1slmA_	Alignment	not modelled	89.1	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**stromelysin-1; **PDBTitle:** crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
28	c2mzeA_	Alignment	not modelled	88.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrilysin; **PDBTitle:** nmr solution structure of the pro form of human matrilysin (prommp-7)
29	d1kapp2	Alignment	not modelled	88.8	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain

29	d1kapp2	Alignment	not modelled	88.8	33	**Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
30	d1sata2	Alignment	not modelled	88.7	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
31	c5th6D_	Alignment	not modelled	88.1	31	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** D: **PDB Molecule:**matrix metalloproteinase-9,matrix metalloproteinase-9; **PDBTitle:** structure determination of a potent, selective antibody inhibitor of2 human mmp9 (apo mmp9)
32	d1fbla2	Alignment	not modelled	87.7	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
33	c4g0dD_	Alignment	not modelled	87.3	25	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**collagenase 3; **PDBTitle:** human collagenase 3 (mmp-13) full form with peptides from pro-domain
34	c1su3A_	Alignment	not modelled	86.8	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**interstitial collagenase; **PDBTitle:** x-ray structure of human prommp-1: new insights into2 collagenase action
35	c2cltB_	Alignment	not modelled	85.7	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**interstitial collagenase; **PDBTitle:** crystal structure of the active form (full-length) of human2 fibroblast collagenase.
36	c1om8A_	Alignment	not modelled	84.9	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
37	c1jiwP_	Alignment	not modelled	84.7	33	**PDB header:**hydrolase/hyrolase inhibitor **Chain:** P: **PDB Molecule:**alkaline metalloproteinase; **PDBTitle:** crystal structure of the apr-aprin complex
38	c3ba0A_	Alignment	not modelled	84.2	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**macrophage metalloelastase; **PDBTitle:** crystal structure of full-length human mmp-12
39	c3b8zB_	Alignment	not modelled	81.4	43	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein adamts-5; **PDBTitle:** high resolution crystal structure of the catalytic domain of adamts-52 (aggrecanase-2)
40	c5czwA_	Alignment	not modelled	80.4	37	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**myroilysin; **PDBTitle:** crystal structure of myroilysin
41	c4dd8B_	Alignment	not modelled	79.1	32	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**disintegrin and metalloproteinase domain-containing protein **PDBTitle:** adam-8 metalloproteinase domain with bound batimastat
42	d1atla_	Alignment	not modelled	78.0	31	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
43	c6o38A_	Alignment	not modelled	77.9	27	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**acinetobacter secreted protease cpaa; **PDBTitle:** structure of a chaperone-substrate complex
44	c3k7lA_	Alignment	not modelled	77.4	47	**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
45	d1kufa_	Alignment	not modelled	77.0	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
46	c2i47A_	Alignment	not modelled	75.8	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adam 17; **PDBTitle:** crystal structure of catalytic domain of tace with inhibitor
47	d2i47a1	Alignment	not modelled	75.6	31	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TNF-alpha converting enzyme, TACE, catalytic domain
48	c2rjqA_	Alignment	not modelled	75.5	41	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adamts-5; **PDBTitle:** crystal structure of adamts5 with inhibitor bound
49	d1nd1a_	Alignment	not modelled	75.3	56	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
50	d4aiga_	Alignment	not modelled	75.2	44	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
51	d1quaa_	Alignment	not modelled	74.3	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
52	c2e3xA_	Alignment	not modelled	73.9	26	**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
53	c1yp1A_	Alignment	not modelled	73.8	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fii; **PDBTitle:** crystal structure of a non-hemorrhagic fibrin(ogen)olytic2 metalloproteinase from venom of agkistrodon acutus
54	c4yu5A_	Alignment	not modelled	73.6	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**immune inhibitor a, metalloprotease; **PDBTitle:** crystal structure of selenomethionine variant of bacillus anthracis2 immune inhibitor a2 peptidase zymogen
						Fold: Zincin-like

55	d1r55a_	Alignment	not modelled	73.0	40	**Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
56	c6be6D_	Alignment	not modelled	72.8	42	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**disintegrin and metalloproteinase domain-containing protein **PDBTitle:** adam10 extracellular domain
57	c2dw1B_	Alignment	not modelled	72.7	41	**PDB header:**apoptosis, toxin **Chain:** B: **PDB Molecule:**catrocollastatin; **PDBTitle:** crystal structure of vap2 from crotalus atrox venom (form 2-2 crystal)
58	d1wnia_	Alignment	not modelled	72.2	35	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
59	c2erpA_	Alignment	not modelled	71.8	47	**PDB header:**toxin **Chain:** A: **PDB Molecule:**vascular apoptosis-inducing protein 1; **PDBTitle:** crystal structure of vascular apoptosis-inducing protein-1(inhibitor-2 bound form)
60	d1bswa_	Alignment	not modelled	71.6	47	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
61	c3g5cA_	Alignment	not modelled	70.5	35	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**adam 22; **PDBTitle:** structural and biochemical studies on the ectodomain of human adam22
62	c3p1vB_	Alignment	not modelled	70.5	41	**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
63	c2v4bB_	Alignment	not modelled	70.4	33	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adamts-1; **PDBTitle:** crystal structure of human adamts-1 catalytic domain and cysteine-2 rich domain (apo-form)
64	c3k7nA_	Alignment	not modelled	69.7	42	**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
65	c2rjpC_	Alignment	not modelled	69.3	28	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**adamts-4; **PDBTitle:** crystal structure of adamts4 with inhibitor bound
66	c4jixB_	Alignment	not modelled	68.9	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**projannalysin; **PDBTitle:** crystal structure of the metallopeptidase zymogen of2 methanocaldococcus jannaschii jannalysin
67	c3cqbB_	Alignment	not modelled	66.2	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
68	c4l6tA_	Alignment	not modelled	65.4	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ecxa; **PDBTitle:** gm1 bound form of the ecx ab5 holotoxin
69	c3edhA_	Alignment	not modelled	62.7	36	**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
70	c4aw6B_	Alignment	not modelled	62.4	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**caax prenyl protease 1 homolog; **PDBTitle:** crystal structure of the human nuclear membrane zinc metalloprotease2 zmpste24 (face1)
71	c1satA_	Alignment	not modelled	62.2	33	**PDB header:**hydrolase (serine protease) **Chain:** A: **PDB Molecule:**serratia protease; **PDBTitle:** crystal structure of the 50 kda metallo protease from s.2 marcescens
72	c1eakA_	Alignment	not modelled	62.2	21	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**72 kda type iv collagenase; **PDBTitle:** catalytic domain of prommp-2 e404q mutant
73	d1c7ka_	Alignment	not modelled	62.1	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Zinc protease
74	c3vtgA_	Alignment	not modelled	61.2	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**high choriolytic enzyme 1; **PDBTitle:** high choriolytic enzyme 1 (hce-1), a hatching enzyme zinc-protease2 from oryzias latipes (medaka fish)
75	c3lqbA_	Alignment	not modelled	60.4	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**loc792177 protein; **PDBTitle:** crystal structure of the hatching enzyme zhe1 from the zebrafish danio2 rerio
76	d1asta_	Alignment	not modelled	59.9	43	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Astacin
77	c3ujzA_	Alignment	not modelled	57.5	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metalloprotease stce; **PDBTitle:** crystal structure of enterohemorrhagic e. coli stce
78	d1lmla_	Alignment	not modelled	55.9	32	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Leishmanolysin
79	c2x4kB_	Alignment	not modelled	52.3	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; **PDBTitle:** crystal structure of sar1376, a putative 4-oxalocrotonate2 tautomerase from the methicillin-resistant staphylococcus3 aureus (mrsa)
80	c4jiuA_	Alignment	not modelled	51.9	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proabylysin; **PDBTitle:** crystal structure of the metallopeptidase zymogen of pyrococcus abyssi2 abylysin
						Fold:IF3-like

81	d1whra_	Alignment	not modelled	50.6	40	**Superfamily:**R3H domain **Family:**R3H domain
82	c2op8A_	Alignment	not modelled	47.5	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable tautomerase ywhb; **PDBTitle:** crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
83	d1otfa_	Alignment	not modelled	47.0	17	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
84	c5xbvA_	Alignment	not modelled	44.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**wss1p; **PDBTitle:** crystal structure of wss1 mutant from saccharomyces cerevisiae
85	c3mb2G_	Alignment	not modelled	44.9	15	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**4-oxalocrotonate tautomerase family enzyme - alpha subunit; **PDBTitle:** kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
86	c3lq0A_	Alignment	not modelled	43.9	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proastacin; **PDBTitle:** zymogen structure of crayfish astacin metallopeptidase
87	c5ln5A_	Alignment	not modelled	43.0	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin and wlm domain-containing metalloprotease **PDBTitle:** crystal structure of the wss1 e203q mutant from s. pombe
88	c3p24C_	Alignment	not modelled	43.0	36	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**bft-3; **PDBTitle:** structure of profragilysin-3 from bacteroides fragilis
89	c2l0rA_	Alignment	not modelled	41.4	33	**PDB header:**hydrolase,toxin **Chain:** A: **PDB Molecule:**lethal factor; **PDBTitle:** conformational dynamics of the anthrax lethal factor catalytic center
90	c3abfB_	Alignment	not modelled	39.8	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; **PDBTitle:** crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)
91	c4on1B_	Alignment	not modelled	39.4	45	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative metalloprotease ii; **PDBTitle:** crystal structure of metalloproteinase-ii from bacteroides fragilis
92	c6eomA_	Alignment	not modelled	38.4	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** structure of dpp iii from caldithrix abyssi
93	c3ry0A_	Alignment	not modelled	37.5	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tautomerase; **PDBTitle:** crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway
94	c3pvpA_	Alignment	not modelled	36.4	28	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** structure of mycobacterium tuberculosis dnaa-dbd in complex with box22 dna
95	c4gwmA_	Alignment	not modelled	36.4	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**meprin a subunit beta; **PDBTitle:** crystal structure of human promeprin beta
96	d1gyxa_	Alignment	not modelled	35.7	20	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
97	c4fdxB_	Alignment	not modelled	35.5	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-oxalocrotonase tautomerase isozyme; **PDBTitle:** kinetic and structural characterization of the 4-oxalocrotonate2 tautomerase isozymes from methylibium petroleiphilum
98	d2ou3a1	Alignment	not modelled	34.8	38	**Fold:**TerB-like **Superfamily:**TerB-like **Family:**COG3793-like
99	d1j1va_	Alignment	not modelled	34.0	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Chromosomal replication initiation factor DnaA C-terminal domain IV
100	c4l7aB_	Alignment	not modelled	33.8	26	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative zinc-binding metallo-peptidase2 (baccac_01431) from bacteroides caccae atcc 43185 at 2.10 a3 resolution
101	c2ormA_	Alignment	not modelled	33.4	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable tautomerase hp0924; **PDBTitle:** crystal structure of the 4-oxalocrotonate tautomerase homologue dmpi2 from helicobacter pylori.
102	d1rp3a1	Alignment	not modelled	32.9	39	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma3 domain
103	d1j7na2	Alignment	not modelled	32.5	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Anthrax toxin lethal factor, N- and C-terminal domains
104	c4gwnA_	Alignment	not modelled	32.5	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**meprin a subunit beta; **PDBTitle:** crystal structure of human mature meprin beta
105	d1bjpa_	Alignment	not modelled	32.1	16	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
						PDB header:hydrolase

106	c1z5hB_	Alignment	not modelled	31.7	29	**Chain:** B: **PDB Molecule:**tricorn protease interacting factor f3; **PDBTitle:** crystal structures of the tricorn interacting factor f3 from2 thermoplasma acidophilum
107	c1gxdA_	Alignment	not modelled	30.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**72 kda type iv collagenase; **PDBTitle:** prommp-2/timp-2 complex
108	c1mszA_	Alignment	not modelled	28.5	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding protein smubp-2; **PDBTitle:** solution structure of the r3h domain from human smubp-2
109	d1msza_	Alignment	not modelled	28.5	25	**Fold:**IF3-like **Superfamily:**R3H domain **Family:**R3H domain
110	d1tvia_	Alignment	not modelled	27.6	21	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Predicted metal-dependent hydrolase
111	c1l6jA_	Alignment	not modelled	27.3	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-9; **PDBTitle:** crystal structure of human matrix metalloproteinase mmp92 (gelatinase b).
112	c5zumB_	Alignment	not modelled	26.9	33	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dipeptidyl-peptidase iii; **PDBTitle:** structure of dipeptidyl-peptidase iii from corallococcus sp. strain2 egb
113	c5un4C_	Alignment	not modelled	25.8	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**4-oxalocrotonate tautomerase; **PDBTitle:** crystal structure of native fused 4-ot
114	d1ew4a_	Alignment	not modelled	25.2	18	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
115	d1xm5a_	Alignment	not modelled	24.9	21	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Predicted metal-dependent hydrolase
116	d1z67a1	Alignment	not modelled	23.7	11	**Fold:**YidB-like **Superfamily:**YidB-like **Family:**YidB-like
117	c6mdxA_	Alignment	not modelled	23.6	25	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**sprt-like domain-containing protein spartan; **PDBTitle:** mechanism of protease dependent dpc repair
118	c4wz9A_	Alignment	not modelled	23.6	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**agap004809-pa; **PDBTitle:** apn1 from anopheles gambiae
119	c4kxdA_	Alignment	not modelled	22.7	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutamyl aminopeptidase; **PDBTitle:** crystal structure of human aminopeptidase a complexed with glutamate2 and calcium
120	d1oz9a_	Alignment	not modelled	22.6	18	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Predicted metal-dependent hydrolase