Phyre2

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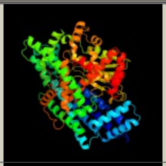
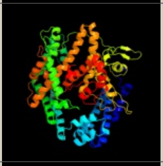
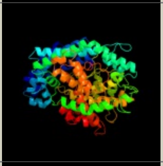
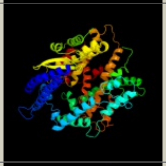
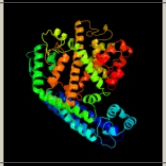
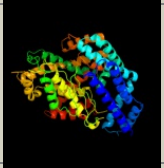
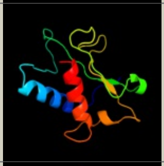
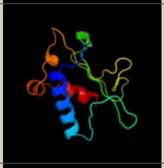
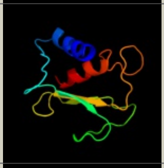
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1y791_	Alignment		100.0	100	**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
2	d1i1ip_	Alignment		100.0	24	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
3	d1s4bp_	Alignment		100.0	27	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
4	c3ce2A_	Alignment		100.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative peptidase; **PDBTitle:** crystal structure of putative peptidase from chlamydophila abortus
5	c2h1jA_	Alignment		100.0	15	**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
6	c3sksA_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative oligoendopeptidase f; **PDBTitle:** crystal structure of a putative oligoendopeptidase f from bacillus2 anthracis str. ames
7	d2ajfa1	Alignment		100.0	12	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
8	d1uzea_	Alignment		100.0	11	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
9	c2c6nA_	Alignment		100.0	12	**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
10	c2qr4B_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase m3b, oligoendopeptidase f; **PDBTitle:** crystal structure of oligoendopeptidase-f from enterococcus faecium
11	d1j36a_	Alignment		100.0	15	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like

12	c1wgzC_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**carboxypeptidase 1; **PDBTitle:** crystal structure of carboxypeptidase 1 from thermus thermophilus
13	d1k9xa_	Alignment		100.0	15	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
14	c3dwcA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallocarboxypeptidase; **PDBTitle:** trypanosoma cruzi metallocarboxypeptidase 1
15	c3hq2A_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**bacillus subtilis m32 carboxypeptidase; **PDBTitle:** bsucp crystal structure
16	d1g9ka2	Alignment		96.3	20	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
17	d1kapp2	Alignment		96.1	23	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
18	c1om8A_	Alignment		95.5	19	**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
19	d1cgla_	Alignment		95.5	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
20	d1j7na2	Alignment		95.4	23	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Anthrax toxin lethal factor, N- and C-terminal domains
21	d1k7ia2	Alignment	not modelled	95.4	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
22	c1jiwP_	Alignment	not modelled	95.3	21	**PDB header:**hydrolase/hyrolase inhibitor **Chain:** P: **PDB Molecule:**alkaline metalloproteinase; **PDBTitle:** crystal structure of the apr-aprin complex
23	d1hfca_	Alignment	not modelled	94.9	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
24	d2ovxa1	Alignment	not modelled	94.8	10	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
25	d1hv5a_	Alignment	not modelled	94.7	17	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
26	c1pwqA_	Alignment	not modelled	94.6	22	**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
27	d1sata2	Alignment	not modelled	94.4	12	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
28	d1hova_	Alignment	not modelled	94.4	15	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
						PDB header:hydrolase

29	c1yqyA_	Alignment	not modelled	94.3	32	**Chain:** A: **PDB Molecule:**lethal factor; **PDBTitle:** structure of b. anthrax lethal factor in complex with a2 hydroxamate inhibitor
30	d1bqqm_	Alignment	not modelled	93.9	14	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
31	d1hy7a_	Alignment	not modelled	93.9	12	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
32	d1cxva_	Alignment	not modelled	93.8	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
33	d1mmqa_	Alignment	not modelled	93.8	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
34	d1q3aa_	Alignment	not modelled	93.5	11	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
35	c3edhA_	Alignment	not modelled	93.5	17	**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
36	d1qiba_	Alignment	not modelled	93.5	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
37	d1y93a1	Alignment	not modelled	93.5	14	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
38	c1su3A_	Alignment	not modelled	93.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**interstitial collagenase; **PDBTitle:** x-ray structure of human prommp-1: new insights into2 collagenase action
39	d1xuca1	Alignment	not modelled	93.1	12	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
40	c2l0rA_	Alignment	not modelled	92.9	35	**PDB header:**hydrolase,toxin **Chain:** A: **PDB Molecule:**lethal factor; **PDBTitle:** conformational dynamics of the anthrax lethal factor catalytic center
41	c2xhqA_	Alignment	not modelled	92.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**archaemetzincin; **PDBTitle:** crystal structure of archaemetzincin (amza) from archaeoglobus2 fulgidus at 1.45 a resolution
42	d1i76a_	Alignment	not modelled	92.7	15	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
43	d1rm8a_	Alignment	not modelled	92.3	15	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
44	d1asta_	Alignment	not modelled	92.3	16	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Astacin
45	c3dtkA_	Alignment	not modelled	92.0	41	**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
46	d1fbla2	Alignment	not modelled	91.6	14	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
47	c2cltB_	Alignment	not modelled	91.2	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**interstitial collagenase; **PDBTitle:** crystal structure of the active form (full-length) of human2 fibroblast collagenase.
48	c3lq0A_	Alignment	not modelled	91.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proastacin; **PDBTitle:** zymogen structure of crayfish astacin metallopeptidase
49	c2xs4A_	Alignment	not modelled	91.1	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**karilysin protease; **PDBTitle:** structure of karilysin catalytic mmp domain in complex with2 magnesium
50	c2jsdA_	Alignment	not modelled	91.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-20; **PDBTitle:** solution structure of mmp20 complexed with nngh
51	c3k7lA_	Alignment	not modelled	90.5	25	**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
52	c3lqbA_	Alignment	not modelled	90.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**loc792177 protein; **PDBTitle:** crystal structure of the hatching enzyme zhe1 from the zebrafish danio2 rerio
53	c3o0yC_	Alignment	not modelled	90.4	13	**PDB header:**lipid binding protein **Chain:** C: **PDB Molecule:**lipoprotein; **PDBTitle:** the crystal structure of the putative lipoprotein from colwellia2 psychrerythraea
54	d1kufa_	Alignment	not modelled	89.5	24	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
55	d1quaa_	Alignment	not modelled	89.5	15	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like

56	c3nqzB_	Alignment	not modelled	89.2	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**secreted metalloprotease mcp02; **PDBTitle:** crystal structure of the autoprocessed vibriolysin mcp-02 with e369a2 mutation
57	d1eaka2	Alignment	not modelled	88.8	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
58	d1atla_	Alignment	not modelled	88.8	24	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
59	d2i47a1	Alignment	not modelled	88.2	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TNF-alpha converting enzyme, TACE, catalytic domain
60	d1nd1a_	Alignment	not modelled	88.2	24	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
61	c2i47A_	Alignment	not modelled	88.1	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adam 17; **PDBTitle:** crystal structure of catalytic domain of tace with inhibitor
62	c1zb7A_	Alignment	not modelled	87.9	31	**PDB header:**toxin **Chain:** A: **PDB Molecule:**neurotoxin; **PDBTitle:** crystal structure of botulinum neurotoxin type g light chain
63	d1kjpa_	Alignment	not modelled	87.9	19	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
64	c2erpA_	Alignment	not modelled	87.8	23	**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)
65	c1yp1A_	Alignment	not modelled	87.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fii; **PDBTitle:** crystal structure of a non-hemorrhagic fibrin(ogen)olytic2 metalloproteinase from venom of agkistrodon acutus
66	c2vqxA_	Alignment	not modelled	87.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metalloproteinase; **PDBTitle:** precursor of protealysin, metalloproteinase from serratia2 proteamaculans.
67	d4aiga_	Alignment	not modelled	87.4	17	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
68	c1satA_	Alignment	not modelled	87.3	12	**PDB header:**hydrolase (serine protease) **Chain:** A: **PDB Molecule:**serratia protease; **PDBTitle:** crystal structure of the 50 kda metallo protease from s.2 marcescens
69	d1r55a_	Alignment	not modelled	87.3	16	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
70	c3ba0A_	Alignment	not modelled	87.0	55	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**macrophage metalloelastase; **PDBTitle:** crystal structure of full-length human mmp-12
71	d1bswa_	Alignment	not modelled	86.4	20	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
72	c1slmA_	Alignment	not modelled	86.3	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**stromelysin-1; **PDBTitle:** crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
73	d1npca_	Alignment	not modelled	86.3	15	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
74	c2dw1B_	Alignment	not modelled	85.7	33	**PDB header:**apoptosis, toxin **Chain:** B: **PDB Molecule:**catrocollastatin; **PDBTitle:** crystal structure of vap2 from crotalus atrox venom (form 2-2 crystal)
75	c3nqxA_	Alignment	not modelled	85.6	15	**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
76	d1u4ga_	Alignment	not modelled	85.4	16	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
77	c3b8zB_	Alignment	not modelled	85.0	46	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein adamts-5; **PDBTitle:** high resolution crystal structure of the catalytic domain2 of adamts-5 (aggrecanase-2)
78	d1wnia_	Alignment	not modelled	85.0	40	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
79	c3k7nA_	Alignment	not modelled	84.4	23	**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
80	c3g5cA_	Alignment	not modelled	84.4	23	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**adam 22; **PDBTitle:** structural and biochemical studies on the ectodomain of human adam22
81	c2fpqA_	Alignment	not modelled	83.4	22	**PDB header:**toxin **Chain:** A: **PDB Molecule:**botulinum neurotoxin d light chain; **PDBTitle:** crystal structure of botulinum neurotoxin type d light chain
						PDB header:hydrolase

82	c2rjqA_	Alignment	not modelled	82.8	38	**Chain:** A: **PDB Molecule:**adamts-5; **PDBTitle:** crystal structure of adamts5 with inhibitor bound
83	d1epwa3	Alignment	not modelled	82.3	50	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Clostridium neurotoxins, catalytic domain
84	c3k3qB_	Alignment	not modelled	82.2	44	**PDB header:**immune system **Chain:** B: **PDB Molecule:**botulinum neurotoxin type a; **PDBTitle:** crystal structure of a llama antibody complexed with the c.2 botulinum neurotoxin serotype a catalytic domain
85	c1z7hA_	Alignment	not modelled	82.1	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tetanus toxin light chain; **PDBTitle:** 2.3 angstrom crystal structure of tetanus neurotoxin light2 chain
86	d1f83a_	Alignment	not modelled	82.1	50	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Clostridium neurotoxins, catalytic domain
87	c1e1hC_	Alignment	not modelled	82.0	44	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**botulinum neurotoxin type a light chain; **PDBTitle:** crystal structure of recombinant botulinum neurotoxin type2 a light chain, self-inhibiting zn endopeptidase.
88	c2e3xA_	Alignment	not modelled	82.0	19	**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
89	c2qn0A_	Alignment	not modelled	81.9	38	**PDB header:**toxin **Chain:** A: **PDB Molecule:**neurotoxin; **PDBTitle:** structure of botulinum neurotoxin serotype c1 light chain2 protease
90	d3bona1	Alignment	not modelled	81.8	44	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Clostridium neurotoxins, catalytic domain
91	d3btaa3	Alignment	not modelled	81.2	44	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Clostridium neurotoxins, catalytic domain
92	d1t3ca_	Alignment	not modelled	81.1	50	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Clostridium neurotoxins, catalytic domain
93	c2a97B_	Alignment	not modelled	81.0	56	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**botulinum neurotoxin type f; **PDBTitle:** crystal structure of catalytic domain of clostridium2 botulinum neurotoxin serotype f
94	c2ilpA_	Alignment	not modelled	81.0	44	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**botulinum neurotoxin a light-chain; **PDBTitle:** clostridium botulinum serotype a light chain inhibited by 4-2 chlorocinnamic hydroxamate
95	c2rjpC_	Alignment	not modelled	80.8	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**adamts-4; **PDBTitle:** crystal structure of adamts4 with inhibitor bound
96	c2xhlA_	Alignment	not modelled	80.2	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**botulinum neurotoxin b light chain; **PDBTitle:** structure of a functional derivative of clostridium2 botulinum neurotoxin type b
97	c2j83B_	Alignment	not modelled	80.2	56	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ulilysin; **PDBTitle:** ulilysin metalloprotease in complex with batimastat.
98	c2x7mA_	Alignment	not modelled	79.8	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**archaemetzincin; **PDBTitle:** crystal structure of archaemetzincin (amza) from methanopyrus2 kandleri at 1.5 a resolution
99	c3b4rB_	Alignment	not modelled	79.3	42	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative zinc metalloprotease mj0392; **PDBTitle:** site-2 protease from methanocaldococcus jannaschii
100	c2v4bB_	Alignment	not modelled	79.2	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)
101	c3zuqA_	Alignment	not modelled	78.3	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**botulinum neurotoxin type b; **PDBTitle:** crystal structure of an engineered botulinum neurotoxin2 type b-derivative, lc-b-gs-hn-b
102	c3zusD_	Alignment	not modelled	78.3	44	**PDB header:**hydrolase/signaling protein **Chain:** D: **PDB Molecule:**botulinum neurotoxin type a, synaptosomal-associated **PDBTitle:** crystal structure of an engineered botulinum neurotoxin2 type a-snare23 derivative, lc-a-snap23-hn-a
103	c3ffzA_	Alignment	not modelled	77.5	56	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**botulinum neurotoxin type e; **PDBTitle:** domain organization in clostridium butulinum neurotoxin2 type e is unique: its implication in faster translocation
104	c3p24C_	Alignment	not modelled	77.1	50	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**bft-3; **PDBTitle:** structure of profragilysin-3 from bacteroides fragilis
105	d2ejqa1	Alignment	not modelled	76.8	39	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like
106	d1bqba_	Alignment	not modelled	76.4	22	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
107	c3cqbB_	Alignment	not modelled	75.1	33	**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
108	c2nvyA	Alignment	not modelled	74.9	44	**PDB header:**toxin/immune system **Chain:** A: **PDB Molecule:**botulinum neurotoxin type a;

108	c2nyyA_	Alignment	not modelled	74.9	44	**PDBTitle:** crystal structure of botulinum neurotoxin type a complexed with2 monoclonal antibody cr1
109	c1s0bA_	Alignment	not modelled	74.5	50	**PDB header:**toxin, hydrolase **Chain:** A: **PDB Molecule:**botulinum neurotoxin type b; **PDBTitle:** crystal structure of botulinum neurotoxin type b at ph 4.0
110	c3zurA_	Alignment	not modelled	72.8	31	**PDB header:**hydrolase/signaling protein **Chain:** A: **PDB Molecule:**botulinum neurotoxin type a, synaptosomal-associated **PDBTitle:** crystal structure of an engineered botulinum neurotoxin2 type a-snare23 derivative, lc0-a-snap25-hn-a
111	c3dl1A_	Alignment	not modelled	71.5	20	**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
112	c1eakA_	Alignment	not modelled	71.1	33	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**72 kda type iv collagenase; **PDBTitle:** catalytic domain of prommp-2 e404q mutant
113	c3c37B_	Alignment	not modelled	70.1	33	**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
114	d1lmla_	Alignment	not modelled	69.9	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Leishmanolysin
115	d1c7ka_	Alignment	not modelled	65.9	40	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Zinc protease
116	c3p1vB_	Alignment	not modelled	64.3	50	**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
117	c1l6jA_	Alignment	not modelled	58.6	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-9; **PDBTitle:** crystal structure of human matrix metalloproteinase mmp92 (gelatinase b).
118	c1gxdA_	Alignment	not modelled	53.8	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**72 kda type iv collagenase; **PDBTitle:** prommp-2/timp-2 complex
119	c3lmcA_	Alignment	not modelled	50.4	26	**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
120	c3cskA_	Alignment	not modelled	45.0	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable dipeptidyl-peptidase 3; **PDBTitle:** structure of dpp iii from saccharomyces cerevisiae