Phyre2

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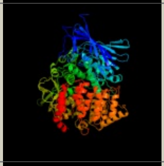
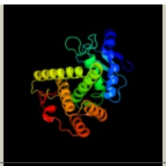
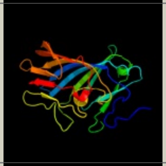
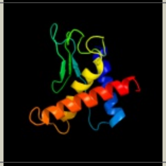
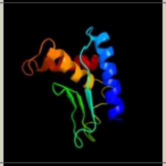
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3b37A_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase n; **PDBTitle:** crystal structure of e. coli aminopeptidase n in complex with tyrosine
2	c3ebhA_	Alignment		100.0	35	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**m1 family aminopeptidase; **PDBTitle:** structure of the m1 alanylaminopeptidase from malaria complexed with2 bestatin
3	c2gtqA_	Alignment		100.0	47	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase n; **PDBTitle:** crystal structure of aminopeptidase n from human pathogen neisseria2 meningitidis
4	c3se6A_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoplasmic reticulum aminopeptidase 2; **PDBTitle:** crystal structure of the human endoplasmic reticulum aminopeptidase 2
5	c2xdtA_	Alignment		100.0	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
6	c3mdjB_	Alignment		100.0	17	**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
7	c1z5hB_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**tricorn protease interacting factor f3; **PDBTitle:** crystal structures of the tricorn interacting factor f32 from thermoplasma acidophilum
8	c3qnfA_	Alignment		100.0	17	**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
9	c3b7uX_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**leukotriene a-4 hydrolase; **PDBTitle:** leukotriene a4 hydrolase complexed with kelatorphan
10	c3ciaA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cold-active aminopeptidase; **PDBTitle:** crystal structure of cold-aminopeptidase from colwellia2 psychrerythraea
11	c2xpyA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leukotriene a-4 hydrolase; **PDBTitle:** structure of native leukotriene a4 hydrolase from saccharomyces2 cerevisiae

12	d3b7sa3	Alignment		100.0	24	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Leukotriene A4 hydrolase catalytic domain
13	d3b7sa2	Alignment		100.0	23	**Fold:**Leukotriene A4 hydrolase N-terminal domain **Superfamily:**Leukotriene A4 hydrolase N-terminal domain **Family:**Leukotriene A4 hydrolase N-terminal domain
14	c3rjoA_	Alignment		99.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoplasmic reticulum aminopeptidase 1; **PDBTitle:** crystal structure of erap1 peptide binding domain
15	c2vqxA_	Alignment		95.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metalloproteinase; **PDBTitle:** precursor of protealysin, metalloproteinase from serratia2 proteamaculans.
16	d1u4ga_	Alignment		95.1	11	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
17	d1npca_	Alignment		93.7	17	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
18	c3cqbB_	Alignment		93.3	20	**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
19	c3nqzB_	Alignment		91.8	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**secreted metalloprotease mcp02; **PDBTitle:** crystal structure of the autoprocessed vibriolysin mcp-02 with e369a2 mutation
20	c3nqxA_	Alignment		91.1	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
21	c3k7nA_	Alignment	not modelled	89.3	20	**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
22	d1bqba_	Alignment	not modelled	88.6	17	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
23	c3k7lA_	Alignment	not modelled	88.3	16	**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
24	c2dw1B_	Alignment	not modelled	87.5	19	**PDB header:**apoptosis, toxin **Chain:** B: **PDB Molecule:**catrocollastatin; **PDBTitle:** crystal structure of vap2 from crotalus atrox venom (form 2-2 crystal)
25	c2erpA_	Alignment	not modelled	86.1	17	**PDB header:**toxin **Chain:** A: **PDB Molecule:**vascular apoptosis-inducing protein 1; **PDBTitle:** crystal structure of vascular apoptosis-inducing protein-1(inhibitor-2 bound form)
26	d1kjpa_	Alignment	not modelled	86.0	14	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
27	d1r55a_	Alignment	not modelled	84.4	14	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
28	c3c37B_	Alignment	not modelled	83.9	15	**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
29	d4aiga_	Alignment	not modelled	83.8	14	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
30	c3g5cA_	Alignment	not modelled	82.1	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**adam 22; **PDBTitle:** structural and biochemical studies on the ectodomain of human adam22
31	c2e3xA_	Alignment	not modelled	82.1	15	**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
32	d1nd1a_	Alignment	not modelled	79.4	16	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
33	c2rjpC_	Alignment	not modelled	78.5	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**adamts-4; **PDBTitle:** crystal structure of adamts4 with inhibitor bound
34	d1quaa_	Alignment	not modelled	78.1	16	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
35	d1kufa_	Alignment	not modelled	77.7	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
36	d1atla_	Alignment	not modelled	77.5	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
37	d1bswa_	Alignment	not modelled	77.3	16	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
38	c2rjqA_	Alignment	not modelled	76.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adamts-5; **PDBTitle:** crystal structure of adamts5 with inhibitor bound
39	c2y50A_	Alignment	not modelled	75.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**collagenase; **PDBTitle:** crystal structure of collagenase g from clostridium2 histolyticum at 2.80 angstrom resolution
40	d1wnia_	Alignment	not modelled	73.4	11	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
41	c2j83B_	Alignment	not modelled	71.8	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ulilysin; **PDBTitle:** ulilysin metalloprotease in complex with batimastat.
42	c1yp1A_	Alignment	not modelled	70.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fii; **PDBTitle:** crystal structure of a non-hemorrhagic fibrin(ogen)olytic2 metalloproteinase from venom of agkistrodon acutus
43	c3iukB_	Alignment	not modelled	70.2	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of putative bacterial protein of unknown function2 (duf885, pf05960.1,) from arthrobacter aurescens tc1, reveals fold3 similar to that of m32 carboxypeptidases
44	c2v4bB_	Alignment	not modelled	69.1	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adamts-1; **PDBTitle:** crystal structure of human adamts-1 catalytic domain and2 cysteine-rich domain (apo-form)
45	c3dtkA_	Alignment	not modelled	68.7	15	**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	c3o0yC_	Alignment	not modelled	67.4	10	**PDB header:**lipid binding protein **Chain:** C: **PDB Molecule:**lipoprotein; **PDBTitle:** the crystal structure of the putative lipoprotein from colwellia2 psychrerythraea
47	c2i47A_	Alignment	not modelled	61.9	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adam 17; **PDBTitle:** crystal structure of catalytic domain of tace with inhibitor
48	c3lmcA_	Alignment	not modelled	61.5	19	**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
49	c3b8zB_	Alignment	not modelled	61.1	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein adamts-5; **PDBTitle:** high resolution crystal structure of the catalytic domain2 of adamts-5 (aggrecanase-2)
50	d2i47a1	Alignment	not modelled	60.7	38	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TNF-alpha converting enzyme, TACE, catalytic domain
51	c2qn0A_	Alignment	not modelled	59.2	21	**PDB header:**toxin **Chain:** A: **PDB Molecule:**neurotoxin; **PDBTitle:** structure of botulinum neurotoxin serotype c1 light chain2 protease
52	c2xhqA_	Alignment	not modelled	57.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**archaemetzincin; **PDBTitle:** crystal structure of archaemetzincin (amza) from archaeoglobus2 fulgidus at 1.45 a resolution
53	c1z7hA_	Alignment	not modelled	57.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tetanus toxin light chain; **PDBTitle:** 2.3 angstrom crystal structure of tetanus neurotoxin light2 chain

54	d1f83a_	Alignment	not modelled	56.8	26	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Clostridium neurotoxins, catalytic domain
55	d3btaa3	Alignment	not modelled	56.4	18	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Clostridium neurotoxins, catalytic domain
56	c3hjlA_	Alignment	not modelled	54.0	15	**PDB header:**proton transport **Chain:** A: **PDB Molecule:**flagellar motor switch protein flig; **PDBTitle:** the structure of full-length flig from aquifex aeolicus
57	d1k9xa_	Alignment	not modelled	53.9	10	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
58	c3ka1A_	Alignment	not modelled	53.4	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**rbcx protein; **PDBTitle:** crystal structure of rbcx from thermosynechococcus elongatus
59	d1epwa3	Alignment	not modelled	52.9	26	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Clostridium neurotoxins, catalytic domain
60	d2ejqa1	Alignment	not modelled	49.4	6	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like
61	c2o0cB_	Alignment	not modelled	49.4	18	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**alr2278 protein; **PDBTitle:** crystal structure of the h-nox domain from nostoc sp. pcc 71202 complexed to no
62	c3zusD_	Alignment	not modelled	49.0	18	**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
63	c2nyyA_	Alignment	not modelled	48.9	18	**PDB header:**toxin/immune system **Chain:** A: **PDB Molecule:**botulinum neurotoxin type a; **PDBTitle:** crystal structure of botulinum neurotoxin type a complexed with2 monoclonal antibody cr1
64	d3bona1	Alignment	not modelled	47.4	18	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Clostridium neurotoxins, catalytic domain
65	c3deeA_	Alignment	not modelled	47.4	0	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative regulatory protein; **PDBTitle:** crystal structure of a putative regulatory protein involved in2 transcription (ngo1945) from neisseria gonorrhoeae fa 1090 at 2.25 a3 resolution
66	d1j7na2	Alignment	not modelled	47.4	17	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Anthrax toxin lethal factor, N- and C-terminal domains
67	c3zuqA_	Alignment	not modelled	46.9	26	**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
68	d2f22a1	Alignment	not modelled	46.3	36	**Fold:**DinB/YfiT-like putative metalloenzymes **Superfamily:**DinB/YfiT-like putative metalloenzymes **Family:**DinB-like
69	c1s0bA_	Alignment	not modelled	45.0	26	**PDB header:**toxin, hydrolase **Chain:** A: **PDB Molecule:**botulinum neurotoxin type b; **PDBTitle:** crystal structure of botulinum neurotoxin type b at ph 4.0
70	c3pl4A_	Alignment	not modelled	44.7	12	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**flagellar motor switch protein; **PDBTitle:** crystal structure of flig (residue 116-343) from h. pylori
71	c3zurA_	Alignment	not modelled	43.8	13	**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
72	c3dl1A_	Alignment	not modelled	39.0	12	**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
73	c2y0oA_	Alignment	not modelled	38.9	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable d-lyxose ketol-isomerase; **PDBTitle:** the structure of a d-lyxose isomerase from the sigmab2 regulon of bacillus subtilis
74	c2l0rA_	Alignment	not modelled	38.7	15	**PDB header:**hydrolase,toxin **Chain:** A: **PDB Molecule:**lethal factor; **PDBTitle:** conformational dynamics of the anthrax lethal factor catalytic center
75	d1lmla_	Alignment	not modelled	38.4	19	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Leishmanolysin
76	c3sohB_	Alignment	not modelled	36.4	26	**PDB header:**motor protein **Chain:** B: **PDB Molecule:**flagellar motor switch protein flig; **PDBTitle:** architecture of the flagellar rotor
77	d1bqqm_	Alignment	not modelled	35.5	45	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
78	d2a1jb1	Alignment	not modelled	34.8	20	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
79	d1rm8a_	Alignment	not modelled	32.3	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain

80	c2xs4A_	Alignment	not modelled	32.1	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**karilysin protease; **PDBTitle:** structure of karilysin catalytic mmp domain in complex with2 magnesium
81	d1hv5a_	Alignment	not modelled	32.0	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
82	c2x7mA_	Alignment	not modelled	31.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**archaemetzincin; **PDBTitle:** crystal structure of archaemetzincin (amza) from methanopyrus2 kandleri at 1.5 a resolution
83	d1cxva_	Alignment	not modelled	30.2	19	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
84	d1i76a_	Alignment	not modelled	29.7	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
85	d1hfca_	Alignment	not modelled	28.9	45	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
86	d1mmqa_	Alignment	not modelled	28.5	27	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
87	d1xuca1	Alignment	not modelled	28.5	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
88	c2k9mA_	Alignment	not modelled	28.2	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** structure of the core binding domain of sigma54
89	d1qiba_	Alignment	not modelled	27.9	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
90	d1y93a1	Alignment	not modelled	27.9	27	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
91	d1q3aa_	Alignment	not modelled	27.5	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
92	d1hy7a_	Alignment	not modelled	27.5	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
93	d2ovxa1	Alignment	not modelled	27.4	27	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
94	d1cgla_	Alignment	not modelled	27.3	45	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
95	d1lsha1	Alignment	not modelled	25.9	13	**Fold:**alpha-alpha superhelix **Superfamily:**Lipovitellin-phosvitin complex, superhelical domain **Family:**Lipovitellin-phosvitin complex, superhelical domain
96	d1s5qb_	Alignment	not modelled	25.7	11	**Fold:**PAH2 domain **Superfamily:**PAH2 domain **Family:**PAH2 domain
97	c2py8B_	Alignment	not modelled	25.4	20	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**hypothetical protein rbcx; **PDBTitle:** rbcx
98	c2jsdA_	Alignment	not modelled	25.0	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-20; **PDBTitle:** solution structure of mmp20 complexed with nngh
99	d1vh8a_	Alignment	not modelled	24.8	10	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
100	d1x2ia1	Alignment	not modelled	24.8	15	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
101	d1hova_	Alignment	not modelled	24.8	23	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
102	d1kfta_	Alignment	not modelled	23.5	24	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Excinuclease UvrC C-terminal domain
103	c1kftA_	Alignment	not modelled	23.5	24	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**excinuclease abc subunit c; **PDBTitle:** solution structure of the c-terminal domain of uvrc from e-2 coli
104	d1st6a5	Alignment	not modelled	23.3	14	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
105	d2py8a1	Alignment	not modelled	23.0	22	**Fold:**RbcX-like **Superfamily:**RbcX-like **Family:**RbcX-like
106	c2veeC_	Alignment	not modelled	22.6	8	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**protoglobin; **PDBTitle:** structure of protoglobin from methanosarcina acetivorans2 c2a
107	d1eaka2	Alignment	not modelled	22.5	27	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain

						Family: Matrix metalloproteases, catalytic domain
108	d2vv5a2	Alignment	not modelled	21.9	11	**Fold:**Ferredoxin-like **Superfamily:**Mechanosensitive channel protein MscS (YggB), C-terminal domain **Family:**Mechanosensitive channel protein MscS (YggB), C-terminal domain
109	c2z0uB_	Alignment	not modelled	21.7	10	**PDB header:**lipid binding protein **Chain:** B: **PDB Molecule:**ww domain-containing protein 1; **PDBTitle:** crystal structure of c2 domain of kibra protein
110	c3pkrA_	Alignment	not modelled	21.7	12	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**flagellar motor switch protein; **PDBTitle:** crystal structure of flig (residue 86-343) from h. pylori
111	d1fbla2	Alignment	not modelled	21.4	45	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
112	d1j9ia_	Alignment	not modelled	20.6	22	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Terminase gpNU1 subunit domain
113	d1c7ka_	Alignment	not modelled	20.3	56	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Zinc protease
114	c2cltB_	Alignment	not modelled	20.1	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**interstitial collagenase; **PDBTitle:** crystal structure of the active form (full-length) of human2 fibroblast collagenase.