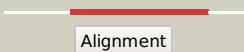

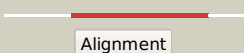

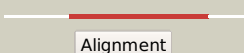

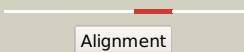

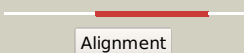

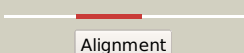
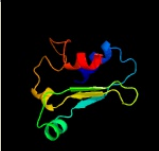






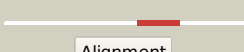





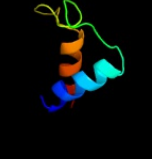

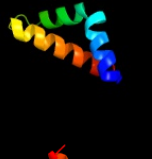
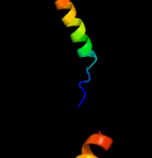
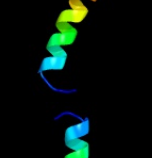

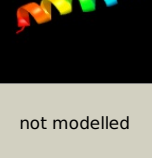


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2575_(-)_2899349_2900230
Date	Wed Aug 7 12:50:21 BST 2019
Unique Job ID	cbdd29cc1c059563

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4il3B_	 Alignment		98.0	22	PDB header: hydrolase Chain: B: PDB Molecule: ste24p; PDBTitle: crystal structure of s. mikatae ste24p
2	c3c37B_	 Alignment		97.9	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	c4aw6B_	 Alignment		97.5	22	PDB header: hydrolase Chain: B: PDB Molecule: caax prenyl protease 1 homolog; PDBTitle: crystal structure of the human nuclear membrane zinc metalloprotease2 zmpste24 (face1)
4	c3dtkA_	 Alignment		97.0	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
5	c6aitD_	 Alignment		96.7	22	PDB header: hydrolase Chain: D: PDB Molecule: beta-barrel assembly-enhancing protease; PDBTitle: crystal structure of e. coli bepa
6	c3cqbB_	 Alignment		94.7	17	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
7	c4k90A_	 Alignment		92.6	50	PDB header: hydrolase Chain: A: PDB Molecule: extracellular metalloproteinase mep; PDBTitle: extracellular metalloproteinase from aspergillus
8	d1kjpA_	 Alignment		92.5	30	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
9	c3sksA_	 Alignment		92.4	32	PDB header: hydrolase Chain: A: PDB Molecule: putative oligoendopeptidase f; PDBTitle: crystal structure of a putative oligoendopeptidase f from bacillus2 anthracis str. ames
10	d1npca_	 Alignment		92.2	23	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
11	d1bqba_	 Alignment		91.4	32	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like

12	c2vqxA_	Alignment		91.1	20	PDB header: hydrolase Chain: A: PDB Molecule: metalloproteinase; PDBTitle: precursor of protealysin, metalloproteinase from serratia2 proteamaculans.
13	c3ce2A_	Alignment		90.6	32	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative peptidase; PDBTitle: crystal structure of putative peptidase from chlamydomophila abortus
14	c4gerB_	Alignment		90.5	29	PDB header: hydrolase Chain: B: PDB Molecule: gentiyase metalloprotease; PDBTitle: crystal structure of gentiyase, the neutral metalloprotease of2 paenibacillus polymyxa
15	c3nqzB_	Alignment		90.4	23	PDB header: hydrolase Chain: B: PDB Molecule: secreted metalloprotease mcp02; PDBTitle: crystal structure of the autoprocessed vibriolysin mcp-02 with e369a2 mutation
16	c6cz6D_	Alignment		90.0	18	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator prpr; PDBTitle: mycobacterium tuberculosis transcriptional regulator
17	d1s4bp_	Alignment		90.0	28	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
18	c2h1jA_	Alignment		89.9	32	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
19	c5l43B_	Alignment		89.6	33	PDB header: hydrolase Chain: B: PDB Molecule: k-26 dipeptidyl carboxypeptidase; PDBTitle: structure of k26-dcp
20	c1y791_	Alignment		89.6	26	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
21	c3nqxA_	Alignment	not modelled	88.8	21	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
22	c4ka8A_	Alignment	not modelled	88.2	47	PDB header: hydrolase Chain: A: PDB Molecule: oligopeptidase a; PDBTitle: structure of organellar oligopeptidase
23	d1l1ip_	Alignment	not modelled	88.1	25	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
24	d2ejqa1	Alignment	not modelled	86.9	40	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: TTHA0227-like
25	d1u4ga_	Alignment	not modelled	85.9	28	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
26	c2qr4B_	Alignment	not modelled	85.8	25	PDB header: hydrolase Chain: B: PDB Molecule: peptidase m3b, oligoendopeptidase f; PDBTitle: crystal structure of oligoendopeptidase-f from enterococcus faecium
27	c3k7lA_	Alignment	not modelled	84.3	36	PDB header: hydrolase Chain: A: PDB Molecule: atrugin; PDBTitle: structures of two elapid snake venom metalloproteases with2 distinct activities highlight the disulfide patterns in the3 d domain of adamalysin family proteins
28	d2i47a1	Alignment	not modelled	84.2	30	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: TNF-alpha converting enzyme, TACE, catalytic domain

29	d1r55a_	Alignment	not modelled	83.6	43	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
30	c2i47A_	Alignment	not modelled	82.5	30	PDB header: hydrolase Chain: A: PDB Molecule: adam 17; PDBTitle: crystal structure of catalytic domain of tace with inhibitor
31	c2dw1B_	Alignment	not modelled	82.4	36	PDB header: apoptosis, toxin Chain: B: PDB Molecule: catrocollastatin; PDBTitle: crystal structure of vap2 from crotalus atrox venom (form 2-2 crystal)
32	c2e3xA_	Alignment	not modelled	82.0	36	PDB header: hydrolase, blood clotting, toxin Chain: A: PDB Molecule: coagulation factor x-activating enzyme heavy chain; PDBTitle: crystal structure of russell's viper venom metalloproteinase
33	c3k7nA_	Alignment	not modelled	81.7	29	PDB header: hydrolase Chain: A: PDB Molecule: k-like; PDBTitle: structures of two elapid snake venom metalloproteases with 2 distinct activities highlight the disulfide patterns in the 3 d domain of adamalysin family proteins
34	c2erpA_	Alignment	not modelled	81.7	38	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)
35	c3dwbA_	Alignment	not modelled	81.6	20	PDB header: hydrolase Chain: A: PDB Molecule: endothelin-converting enzyme 1; PDBTitle: structure of human ece-1 complexed with phosphoramidon
36	c6be6D_	Alignment	not modelled	81.6	40	PDB header: membrane protein Chain: D: PDB Molecule: disintegrin and metalloproteinase domain-containing protein PDBTitle: adam10 extracellular domain
37	d1quaa_	Alignment	not modelled	81.3	43	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
38	d2ajfa1	Alignment	not modelled	80.4	19	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
39	d1atla_	Alignment	not modelled	80.3	36	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
40	d4aiga_	Alignment	not modelled	80.3	36	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
41	d1wnia_	Alignment	not modelled	80.0	36	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
42	c1eakA_	Alignment	not modelled	79.9	23	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: 72 kda type iv collagenase; PDBTitle: catalytic domain of prommp-2 e404q mutant
43	d1nd1a_	Alignment	not modelled	79.9	38	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
44	d1uzea_	Alignment	not modelled	79.4	22	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
45	c4iuwA_	Alignment	not modelled	79.2	14	PDB header: hydrolase Chain: A: PDB Molecule: neutral endopeptidase; PDBTitle: crystal structure of pepo from lactobacillus rhamnosis hn001 (dr20)
46	d1kufa_	Alignment	not modelled	78.6	36	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
47	c5kdiA_	Alignment	not modelled	78.1	60	PDB header: hydrolase Chain: A: PDB Molecule: f5/8 type c domain protein; PDBTitle: zmpb metallopeptidase from clostridium perfringens
48	c2c6nA_	Alignment	not modelled	78.0	29	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: angiotensin-converting enzyme, somatic isoform; PDBTitle: structure of human somatic angiotensin-i converting enzyme n domain2 with lisinopril
49	c2rjpC_	Alignment	not modelled	76.7	31	PDB header: hydrolase Chain: C: PDB Molecule: adamts-4; PDBTitle: crystal structure of adamts4 with inhibitor bound
50	d1j36a_	Alignment	not modelled	76.5	29	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
51	c4dd8B_	Alignment	not modelled	76.4	43	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: disintegrin and metalloproteinase domain-containing protein PDBTitle: adam-8 metalloproteinase domain with bound batimastat
52	c4fcaA_	Alignment	not modelled	76.2	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of a functionally unknown conserved protein from2 bacillus anthracis str. ames.
53	c3g5cA_	Alignment	not modelled	76.1	17	PDB header: membrane protein Chain: A: PDB Molecule: adam 22; PDBTitle: structural and biochemical studies on the ectodomain of human adam22
54	c2xs4A_	Alignment	not modelled	75.7	46	PDB header: hydrolase Chain: A: PDB Molecule: karilysin protease; PDBTitle: structure of karilysin catalytic mmp domain in complex with magnesium

55	d1bswa_	Alignment	not modelled	75.7	31	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
56	c2v4bB_	Alignment	not modelled	75.5	38	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)
57	c1yp1A_	Alignment	not modelled	75.4	50	PDB header: hydrolase Chain: A: PDB Molecule: ffii; PDBTitle: crystal structure of a non-hemorrhagic fibrin(ogen)olytic2 metalloproteinase from venom of agkistrodon acutus
58	c2rjqA_	Alignment	not modelled	75.2	46	PDB header: hydrolase Chain: A: PDB Molecule: adamts-5; PDBTitle: crystal structure of adamts5 with inhibitor bound
59	c4yu5A_	Alignment	not modelled	74.0	50	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
60	c3b8zB_	Alignment	not modelled	73.5	38	PDB header: hydrolase Chain: B: PDB Molecule: protein adamts-5; PDBTitle: high resolution crystal structure of the catalytic domain of adamts-52 (aggrecanase-2)
61	d1xuca1	Alignment	not modelled	73.3	46	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
62	d1dmta_	Alignment	not modelled	72.8	17	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neutral endopeptidase (neprilysin)
63	c5kd2A_	Alignment	not modelled	72.8	50	PDB header: hydrolase Chain: A: PDB Molecule: metallopeptidase; PDBTitle: bt_4244 metallopeptidase from bacteroides thetaiotaomicron
64	d1y93a1	Alignment	not modelled	72.7	31	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
65	d1cxva_	Alignment	not modelled	71.9	46	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
66	c3o0yC_	Alignment	not modelled	71.3	14	PDB header: lipid binding protein Chain: C: PDB Molecule: lipoprotein; PDBTitle: the crystal structure of the putative lipoprotein from colwellia2 psychrerythraea
67	d1q3aa_	Alignment	not modelled	71.1	46	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
68	d1rm8a_	Alignment	not modelled	71.0	38	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
69	d1sata2	Alignment	not modelled	70.8	33	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain
70	c2jsdA_	Alignment	not modelled	70.8	46	PDB header: hydrolase Chain: A: PDB Molecule: matrix metalloproteinase-20; PDBTitle: solution structure of mmp20 complexed with nngh
71	c2cltB_	Alignment	not modelled	70.6	38	PDB header: hydrolase Chain: B: PDB Molecule: interstitial collagenase; PDBTitle: crystal structure of the active form (full-length) of human2 fibroblast collagenase.
72	d1mmqa_	Alignment	not modelled	70.5	38	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
73	d1g9ka2	Alignment	not modelled	70.5	33	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain
74	c2j83B_	Alignment	not modelled	70.3	40	PDB header: hydrolase Chain: B: PDB Molecule: ulilysin; PDBTitle: ulilysin metalloprotease in complex with batimastat.
75	d1i76a_	Alignment	not modelled	70.2	46	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
76	d1hv5a_	Alignment	not modelled	70.1	46	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
77	d1bqqm_	Alignment	not modelled	69.9	38	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
78	d1hfca_	Alignment	not modelled	69.8	46	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
79	d2ovxa1	Alignment	not modelled	67.8	38	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
80	d1k7ia2	Alignment	not modelled	67.3	33	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain
81	d1qiba_	Alignment	not modelled	67.0	46	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain

82	d1hy7a_	Alignment	not modelled	67.0	46	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
83	c4g0dD_	Alignment	not modelled	66.9	38	PDB header: hydrolase Chain: D: PDB Molecule: collagenase 3; PDBTitle: human collagenase 3 (mmp-13) full form with peptides from pro-domain
84	c1wgzC_	Alignment	not modelled	65.6	21	PDB header: hydrolase Chain: C: PDB Molecule: carboxypeptidase 1; PDBTitle: crystal structure of carboxypeptidase 1 from thermus thermophilus
85	d1cglA_	Alignment	not modelled	65.6	46	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
86	c5th6D_	Alignment	not modelled	65.5	46	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)
87	c3ba0A_	Alignment	not modelled	64.9	36	PDB header: hydrolase Chain: A: PDB Molecule: macrophage metalloelastase; PDBTitle: crystal structure of full-length human mmp-12
88	c1slmA_	Alignment	not modelled	64.7	46	PDB header: hydrolase Chain: A: PDB Molecule: stromelysin-1; PDBTitle: crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
89	c2mzeA_	Alignment	not modelled	64.5	31	PDB header: hydrolase Chain: A: PDB Molecule: matrilysin; PDBTitle: nmr solution structure of the pro form of human matrilysin (prommp-7)
90	c2l0rA_	Alignment	not modelled	64.0	40	PDB header: hydrolase,toxin Chain: A: PDB Molecule: lethal factor; PDBTitle: conformational dynamics of the anthrax lethal factor catalytic center
91	c5kdvA_	Alignment	not modelled	64.0	50	PDB header: hydrolase Chain: A: PDB Molecule: metallopeptidase; PDBTitle: impa metallopeptidase from pseudomonas aeruginosa
92	d1kapp2	Alignment	not modelled	63.6	33	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain
93	c3zukB_	Alignment	not modelled	62.6	15	PDB header: hydrolase/inhibitor Chain: B: PDB Molecule: endopeptidase, peptidase family m13; PDBTitle: crystal structure of mycobacterium tuberculosis zinc metalloprotease2 zmp1 in complex with inhibitor
94	c1su3A_	Alignment	not modelled	61.7	50	PDB header: hydrolase Chain: A: PDB Molecule: interstitial collagenase; PDBTitle: x-ray structure of human prommp-1: new insights into2 collagenase action
95	c1jiwP_	Alignment	not modelled	61.2	33	PDB header: hydrolase/hydrolase inhibitor Chain: P: PDB Molecule: alkaline metalloproteinase; PDBTitle: crystal structure of the apr-aprin complex
96	d1k9xa_	Alignment	not modelled	60.7	26	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
97	c5e3xA_	Alignment	not modelled	60.3	24	PDB header: hydrolase Chain: A: PDB Molecule: thermostable carboxypeptidase 1; PDBTitle: crystal structure of thermostable carboxypeptidase (fiscp) from2 fervidobacterium islandicum aw-1
98	c5czwA_	Alignment	not modelled	59.8	50	PDB header: hydrolase Chain: A: PDB Molecule: myroilysin; PDBTitle: crystal structure of myroilysin
99	c3p24C_	Alignment	not modelled	59.4	67	PDB header: hydrolase Chain: C: PDB Molecule: bft-3; PDBTitle: structure of profragilysin-3 from bacteroides fragilis
100	d1hova_	Alignment	not modelled	59.3	46	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
101	c5b42A_	Alignment	not modelled	58.5	19	PDB header: dna binding protein Chain: A: PDB Molecule: dna mismatch repair protein muti; PDBTitle: crystal structure of the c-terminal endonuclease domain of aquifex2 aeolicus mutl.
102	d1eaka2	Alignment	not modelled	56.8	38	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
103	c4on1B_	Alignment	not modelled	56.6	67	PDB header: hydrolase Chain: B: PDB Molecule: putative metalloprotease ii; PDBTitle: crystal structure of metalloproteinase-ii from bacteroides fragilis
104	d1fbla2	Alignment	not modelled	56.6	46	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
105	c6h56A_	Alignment	not modelled	56.1	22	PDB header: metal binding protein Chain: A: PDB Molecule: effector domain of pseudomonas aeruginosa vgrg2b; PDBTitle: effector domain of pseudomonas aeruginosa vgrg2b
106	c3qnfC_	Alignment	not modelled	55.3	15	PDB header: hydrolase Chain: C: PDB Molecule: endoplasmic reticulum aminopeptidase 1; PDBTitle: crystal structure of the open state of human endoplasmic reticulum2 aminopeptidase 1 erap1
107	c3dwcA_	Alignment	not modelled	54.9	16	PDB header: hydrolase Chain: A: PDB Molecule: metallocarboxypeptidase; PDBTitle: trypanosoma cruzi metallocarboxypeptidase 1
						Fold: Zincin-like

108	d1j7na2	Alignment	not modelled	54.5	38	Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Anthrax toxin lethal factor, N- and C-terminal domains
109	c1l6jA_	Alignment	not modelled	54.1	50	PDB header: hydrolase Chain: A: PDB Molecule: matrix metalloproteinase-9; PDBTitle: crystal structure of human matrix metalloproteinase mmp92 (gelatinase b).
110	d1c7ka_	Alignment	not modelled	53.9	30	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Zinc protease
111	c4jixB_	Alignment	not modelled	53.9	14	PDB header: hydrolase Chain: B: PDB Molecule: projannalysin; PDBTitle: crystal structure of the metallopeptidase zymogen of2 methanocaldococcus jannaschii jannalysin
112	c1om8A_	Alignment	not modelled	50.3	33	PDB header: hydrolase Chain: A: PDB Molecule: serralysin; PDBTitle: crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallized with 10 mm edta
113	c5givD_	Alignment	not modelled	50.3	26	PDB header: hydrolase Chain: D: PDB Molecule: carboxypeptidase 1; PDBTitle: crystal structure of m32 carboxypeptidase from deinococcus radiodurans2 r1
114	c6o38A_	Alignment	not modelled	49.2	40	PDB header: sugar binding protein Chain: A: PDB Molecule: acinetobacter secreted protease cpaa; PDBTitle: structure of a chaperone-substrate complex
115	c3qnfA_	Alignment	not modelled	48.7	15	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
116	d1asta_	Alignment	not modelled	48.2	30	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Astacin
117	c4jiuA_	Alignment	not modelled	47.8	44	PDB header: hydrolase Chain: A: PDB Molecule: proabylysin; PDBTitle: crystal structure of the metallopeptidase zymogen of pyrococcus abyssi2 abylysin
118	c4fgmA_	Alignment	not modelled	45.4	10	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase n family protein; PDBTitle: crystal structure of the aminopeptidase n family protein q5qty1 from2 idiomarina loihiensis. northeast structural genomics consortium3 target ilr60.
119	c3iukB_	Alignment	not modelled	45.4	12	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
120	c3lqbA_	Alignment	not modelled	45.3	25	PDB header: hydrolase Chain: A: PDB Molecule: loc792177 protein; PDBTitle: crystal structure of the hatching enzyme zhe1 from the zebrafish danio2 rerio