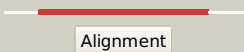

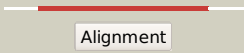



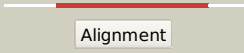

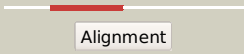



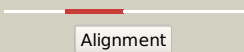

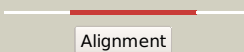

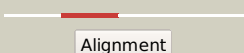








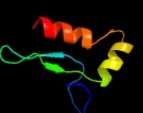
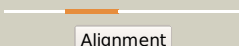

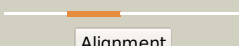

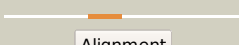

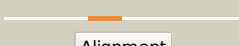
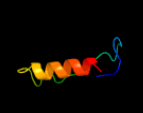

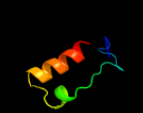




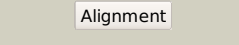


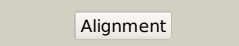
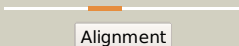
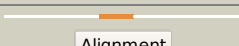




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0563_(htpX)_653882_654742
 Date Fri Jul 26 01:50:11 BST 2019
 Unique Job ID 4f4fb488d49023c9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4aw6B_	 Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: caax prenyl protease 1 homolog; PDBTitle: crystal structure of the human nuclear membrane zinc metalloprotease2 zmpste24 (face1)
2	c4il3B_	 Alignment		100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: ste24p; PDBTitle: crystal structure of s. mikatae ste24p
3	c3c37B_	 Alignment		99.9	29	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
4	c6aitD_	 Alignment		99.8	27	PDB header: hydrolase Chain: D: PDB Molecule: beta-barrel assembly-enhancing protease; PDBTitle: crystal structure of e. coli bepa
5	c3cqbB_	 Alignment		99.8	34	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
6	c4jixB_	 Alignment		98.2	17	PDB header: hydrolase Chain: B: PDB Molecule: projannalysin; PDBTitle: crystal structure of the metallopeptidase zymogen of2 methanocaldococcus jannaschii jannalysin
7	c4jiuA_	 Alignment		97.1	18	PDB header: hydrolase Chain: A: PDB Molecule: proabylysin; PDBTitle: crystal structure of the metallopeptidase zymogen of pyrococcus abyssi2 abylysin
8	c3dtkA_	 Alignment		97.0	16	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
9	c6mdxA_	 Alignment		96.1	13	PDB header: dna binding protein/dna Chain: A: PDB Molecule: sprrt-like domain-containing protein spartan; PDBTitle: mechanism of protease dependent dpc repair
10	c6cz6D_	 Alignment		94.0	14	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator prpr; PDBTitle: mycobacterium tuberculosis transcriptional regulator
11	c3skSA_	 Alignment		93.4	13	PDB header: hydrolase Chain: A: PDB Molecule: putative oligoendopeptidase f; PDBTitle: crystal structure of a putative oligoendopeptidase f from bacillus2 anthracis str. ames

12	c5xbvA_	 Alignment		90.7	13	PDB header: hydrolase Chain: A: PDB Molecule: wss1p; PDBTitle: crystal structure of wss1 mutant from saccharomyces cerevisiae
13	c3ce2A_	 Alignment		89.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative peptidase; PDBTitle: crystal structure of putative peptidase from chlamydomonada abortus
14	c2gtqA_	 Alignment		88.9	15	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase n; PDBTitle: crystal structure of aminopeptidase n from human pathogen neisseria meningitidis
15	c2h1jA_	 Alignment		88.9	13	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
16	d1r55a_	 Alignment		87.6	19	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
17	c3k7nA_	 Alignment		87.5	19	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
18	c1yp1A_	 Alignment		86.5	19	PDB header: hydrolase Chain: A: PDB Molecule: fii; PDBTitle: crystal structure of a non-hemorrhagic fibrin(ogen)olytic2 metalloproteinase from venom of agkistrodon acutus
19	d1bswa_	 Alignment		86.2	19	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
20	c5zi7A_	 Alignment		86.0	12	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase n; PDBTitle: crystal structure of legionella pneumophila aminopeptidase a in2 complex with glutamic acid
21	c2xs4A_	 Alignment	not modelled	86.0	42	PDB header: hydrolase Chain: A: PDB Molecule: karilysin protease; PDBTitle: structure of karilysin catalytic mmp domain in complex with magnesium
22	c3k71A_	 Alignment	not modelled	85.4	14	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
23	c3b7uX_	 Alignment	not modelled	85.2	20	PDB header: hydrolase Chain: X: PDB Molecule: leukotriene a-4 hydrolase; PDBTitle: leukotriene a4 hydrolase complexed with kelatorphan
24	c2erpA_	 Alignment	not modelled	84.9	11	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)
25	d1atla_	 Alignment	not modelled	84.3	14	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
26	d1bqqm_	 Alignment	not modelled	84.0	45	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
27	d1rm8a_	 Alignment	not modelled	83.8	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
28	c5dlla_	 Alignment	not modelled	83.7	17	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase n; PDBTitle: aminopeptidase n (pepn) from francisella tularensis subsp. tularensis2 schu s4

29	d1k9xa_	Alignment	not modelled	83.6	24	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
30	d4aiga_	Alignment	not modelled	83.6	16	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
31	c4dd8B_	Alignment	not modelled	83.3	14	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: disintegrin and metalloproteinase domain-containing protein PDBTitle: adam-8 metalloproteinase domain with bound batimastat
32	d2ovxa1	Alignment	not modelled	83.2	33	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
33	c3ebhA_	Alignment	not modelled	83.1	17	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: m1 family aminopeptidase; PDBTitle: structure of the m1 alanylaminopeptidase from malaria complexed with2 bestatin
34	d1cxva_	Alignment	not modelled	82.9	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
35	d1qjba_	Alignment	not modelled	82.8	42	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
36	c2dw1B_	Alignment	not modelled	82.7	11	PDB header: apoptosis, toxin Chain: B: PDB Molecule: catrocollastatin; PDBTitle: crystal structure of vap2 from crotalus atrox venom (form 2-2 crystal)
37	c4gaaA_	Alignment	not modelled	82.6	23	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: mgc78867 protein; PDBTitle: structure of leukotriene a4 hydrolase from xenopus laevis complexed2 with inhibitor bestatin
38	d1u4ga_	Alignment	not modelled	82.6	18	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
39	d1xuca1	Alignment	not modelled	82.4	42	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
40	d1y93a1	Alignment	not modelled	82.4	33	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
41	c2i47A_	Alignment	not modelled	82.2	38	PDB header: hydrolase Chain: A: PDB Molecule: adam 17; PDBTitle: crystal structure of catalytic domain of tace with inhibitor
42	d1i76a_	Alignment	not modelled	82.2	42	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
43	d2i47a1	Alignment	not modelled	82.1	38	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: TNF-alpha converting enzyme, TACE, catalytic domain
44	c1wgzC_	Alignment	not modelled	81.9	24	PDB header: hydrolase Chain: C: PDB Molecule: carboxypeptidase 1; PDBTitle: crystal structure of carboxypeptidase 1 from thermus thermophilus
45	c2e3xA_	Alignment	not modelled	81.8	22	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
46	d1hv5a_	Alignment	not modelled	81.5	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
47	d1wnia_	Alignment	not modelled	81.3	22	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
48	d1hfca_	Alignment	not modelled	81.2	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
49	c3b37A_	Alignment	not modelled	81.1	14	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase n; PDBTitle: crystal structure of e. coli aminopeptidase n in complex with tyrosine
50	d1mmqa_	Alignment	not modelled	80.9	33	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
51	d1hy7a_	Alignment	not modelled	80.8	42	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
52	d1hova_	Alignment	not modelled	80.7	42	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
53	c3qnfA_	Alignment	not modelled	80.4	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
54	d1cgla_	Alignment	not modelled	80.1	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
55	c3p24C_	Alignment	not modelled	79.8	56	PDB header: hydrolase Chain: C: PDB Molecule: bft-3; PDBTitle: structure of profragilysin-3 from bacteroides fragilis

56	d1q3aa_	Alignment	not modelled	79.6	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
57	c2jsdA_	Alignment	not modelled	79.5	42	PDB header: hydrolase Chain: A: PDB Molecule: matrix metalloproteinase-20; PDBTitle: solution structure of mmp20 complexed with nngh
58	c1slmA_	Alignment	not modelled	79.4	42	PDB header: hydrolase Chain: A: PDB Molecule: stromelysin-1; PDBTitle: crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
59	c2cltB_	Alignment	not modelled	79.4	42	PDB header: hydrolase Chain: B: PDB Molecule: interstitial collagenase; PDBTitle: crystal structure of the active form (full-length) of human2 fibroblast collagenase.
60	c1y791_	Alignment	not modelled	79.3	18	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
61	c5ln5A_	Alignment	not modelled	79.2	19	PDB header: hydrolase Chain: A: PDB Molecule: ubiquitin and wlm domain-containing metalloprotease PDBTitle: crystal structure of the wss1 e203q mutant from s. pombe
62	d1eaka2	Alignment	not modelled	78.0	33	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
63	c3ciaA_	Alignment	not modelled	78.0	14	PDB header: hydrolase Chain: A: PDB Molecule: cold-active aminopeptidase; PDBTitle: crystal structure of cold-aminopeptidase from colwellia2 psychrerythraea
64	c5th6D_	Alignment	not modelled	77.7	42	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)
65	d1quaa_	Alignment	not modelled	77.6	27	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
66	c4on1B_	Alignment	not modelled	77.5	44	PDB header: hydrolase Chain: B: PDB Molecule: putative metalloprotease ii; PDBTitle: crystal structure of metalloproteinase-ii from bacteroides fragilis
67	c4g0dD_	Alignment	not modelled	77.3	33	PDB header: hydrolase Chain: D: PDB Molecule: collagenase 3; PDBTitle: human collagenase 3 (mmp-13) full form with peptides from pro-domain
68	d1kufa_	Alignment	not modelled	77.1	27	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
69	c3g5cA_	Alignment	not modelled	77.1	15	PDB header: membrane protein Chain: A: PDB Molecule: adam 22; PDBTitle: structural and biochemical studies on the ectodomain of human adam22
70	d1fbla2	Alignment	not modelled	77.1	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
71	c5czwA_	Alignment	not modelled	76.9	27	PDB header: hydrolase Chain: A: PDB Molecule: myroilysin; PDBTitle: crystal structure of myroilysin
72	c6be6D_	Alignment	not modelled	76.4	19	PDB header: membrane protein Chain: D: PDB Molecule: disintegrin and metalloproteinase domain-containing protein PDBTitle: adam10 extracellular domain
73	c4wz9A_	Alignment	not modelled	76.0	22	PDB header: hydrolase Chain: A: PDB Molecule: agap004809-pa; PDBTitle: apn1 from anopheles gambiae
74	d1nd1a_	Alignment	not modelled	76.0	44	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
75	d1c7ka_	Alignment	not modelled	75.2	16	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Zinc protease
76	c2mzeA_	Alignment	not modelled	75.0	25	PDB header: hydrolase Chain: A: PDB Molecule: matrilysin; PDBTitle: nmr solution structure of the pro form of human matrilysin (prommp-7)
77	c3b8zB_	Alignment	not modelled	75.0	33	PDB header: hydrolase Chain: B: PDB Molecule: protein adams-5; PDBTitle: high resolution crystal structure of the catalytic domain of adams-52 (aggrecanase-2)
78	c3qnfC_	Alignment	not modelled	75.0	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
79	c5l43B_	Alignment	not modelled	74.8	16	PDB header: hydrolase Chain: B: PDB Molecule: k-26 dipeptidyl carboxypeptidase; PDBTitle: structure of k26-dcp
80	c4pj6B_	Alignment	not modelled	73.9	15	PDB header: hydrolase Chain: B: PDB Molecule: leucyl-cystinyl aminopeptidase; PDBTitle: crystal structure of human insulin regulated aminopeptidase with2 lysine in active site
81	c3hq2A_	Alignment	not modelled	73.6	18	PDB header: hydrolase Chain: A: PDB Molecule: bacillus subtilis m32 carboxypeptidase; PDBTitle: bsucp crystal structure
						PDB header: hydrolase

82	c2v4bB	Alignment	not modelled	73.2	56	Chain: B: PDB Molecule: adams-1; PDBTitle: crystal structure of human adams-1 catalytic domain and cysteine-2 rich domain (apo-form)
83	c1su3A	Alignment	not modelled	73.1	50	PDB header: hydrolase Chain: A: PDB Molecule: interstitial collagenase; PDBTitle: x-ray structure of human prommp-1: new insights into2 collagenase action
84	c2rjpC	Alignment	not modelled	72.3	38	PDB header: hydrolase Chain: C: PDB Molecule: adams-4; PDBTitle: crystal structure of adams4 with inhibitor bound
85	c2rjqA	Alignment	not modelled	71.6	38	PDB header: hydrolase Chain: A: PDB Molecule: adams-5; PDBTitle: crystal structure of adams5 with inhibitor bound
86	c3ba0A	Alignment	not modelled	70.9	36	PDB header: hydrolase Chain: A: PDB Molecule: macrophage metalloelastase; PDBTitle: crystal structure of full-length human mmp-12
87	c4k90A	Alignment	not modelled	70.6	33	PDB header: hydrolase Chain: A: PDB Molecule: extracellular metalloproteinase mep; PDBTitle: extracellular metalloproteinase from aspergillus
88	d2ejqa1	Alignment	not modelled	70.4	40	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: TTHA0227-like
89	c4yu5A	Alignment	not modelled	70.4	33	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
90	c3mdjB	Alignment	not modelled	70.2	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
91	c4kxdA	Alignment	not modelled	69.9	17	PDB header: hydrolase Chain: A: PDB Molecule: glutamyl aminopeptidase; PDBTitle: crystal structure of human aminopeptidase a complexed with glutamate2 and calcium
92	d2ajfa1	Alignment	not modelled	69.9	11	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
93	c2j83B	Alignment	not modelled	69.8	33	PDB header: hydrolase Chain: B: PDB Molecule: ulilysin; PDBTitle: ulilysin metalloprotease in complex with batimastat.
94	d1npca	Alignment	not modelled	69.7	75	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
95	c5e3xA	Alignment	not modelled	68.5	10	PDB header: hydrolase Chain: A: PDB Molecule: thermostable carboxypeptidase 1; PDBTitle: crystal structure of thermostable carboxypeptidase (fiscp) from2 fervidobacterium islandicum aw-1
96	c3nqxA	Alignment	not modelled	68.5	63	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
97	d1kjpA	Alignment	not modelled	68.5	63	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
98	d1bqba	Alignment	not modelled	68.4	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
99	c4gerB	Alignment	not modelled	67.9	75	PDB header: hydrolase Chain: B: PDB Molecule: gentlyase metalloprotease; PDBTitle: crystal structure of gentlyase, the neutral metalloprotease of2 paenibacillus polymyxa
100	c3nqzB	Alignment	not modelled	67.9	63	PDB header: hydrolase Chain: B: PDB Molecule: secreted metalloprotease mcp02; PDBTitle: crystal structure of the autoprocessed vibriolysin mcp-02 with e369a2 mutation
101	c2xpyA	Alignment	not modelled	67.0	15	PDB header: hydrolase Chain: A: PDB Molecule: leukotriene a-4 hydrolase; PDBTitle: structure of native leukotriene a4 hydrolase from saccharomyces2 cerevisiae
102	c2vqxA	Alignment	not modelled	66.2	63	PDB header: hydrolase Chain: A: PDB Molecule: metalloproteinase; PDBTitle: precursor of protealysin, metalloproteinase from serratia2 proteamaculans.
103	c2xdtA	Alignment	not modelled	66.1	17	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
104	d1kapp2	Alignment	not modelled	65.4	45	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain
105	c1eakA	Alignment	not modelled	65.3	33	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: 72 kda type iv collagenase; PDBTitle: catalytic domain of prommp-2 e404q mutant
106	c2c6nA	Alignment	not modelled	64.7	17	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
107	d3b7sa3	Alignment	not modelled	64.7	16	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Leukotriene A4 hydrolase catalytic domain
108	d1sata2	Alignment	not modelled	64.4	33	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal)

					domain
109	d1k7ia2	Alignment	not modelled	63.5	33 Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain
110	d1g9ka2	Alignment	not modelled	63.3	50 Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain
111	c2xhqA	Alignment	not modelled	63.3	24 PDB header: hydrolase Chain: A: PDB Molecule: archaemetzincin; PDBTitle: crystal structure of archaemetzincin (amza) from archaeoglobus2 fulgidus at 1.45 a resolution
112	c4fytA	Alignment	not modelled	62.8	22 PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: aminopeptidase n; PDBTitle: human aminopeptidase n (cd13) in complex with amastatin
113	c1z5hB	Alignment	not modelled	62.4	17 PDB header: hydrolase Chain: B: PDB Molecule: tricorn protease interacting factor f3; PDBTitle: crystal structures of the tricorn interacting factor f3 from2 thermoplasma acidophilum
114	d1s4bp	Alignment	not modelled	60.7	33 Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
115	d2di4a1	Alignment	not modelled	60.3	24 Fold: FtsH protease domain-like Superfamily: FtsH protease domain-like Family: FtsH protease domain-like
116	c4f5cA	Alignment	not modelled	60.3	25 PDB header: hydrolase/viral protein Chain: A: PDB Molecule: aminopeptidase n; PDBTitle: crystal structure of the spike receptor binding domain of a porcine2 respiratory coronavirus in complex with the pig aminopeptidase n3 ectodomain
117	c3b4rA	Alignment	not modelled	60.3	45 PDB header: hydrolase Chain: A: PDB Molecule: putative zinc metalloprotease mj0392; PDBTitle: site-2 protease from methanocaldococcus jannaschii
118	c3b4rB	Alignment	not modelled	58.8	45 PDB header: hydrolase Chain: B: PDB Molecule: putative zinc metalloprotease mj0392; PDBTitle: site-2 protease from methanocaldococcus jannaschii
119	c5givD	Alignment	not modelled	58.0	10 PDB header: hydrolase Chain: D: PDB Molecule: carboxypeptidase 1; PDBTitle: crystal structure of m32 carboxypeptidase from deinococcus radiodurans2 r1
120	d2ce7a1	Alignment	not modelled	57.2	31 Fold: FtsH protease domain-like Superfamily: FtsH protease domain-like Family: FtsH protease domain-like