

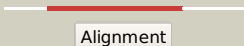

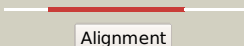



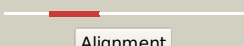

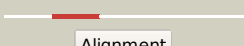

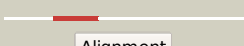













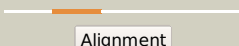

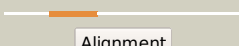

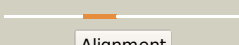

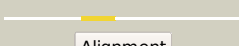
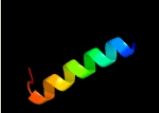






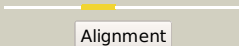
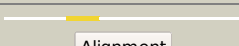
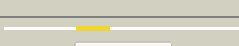

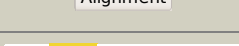
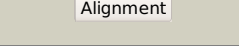
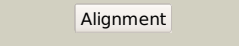

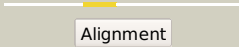


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1977 (-)_2219762_2220808
Date	Mon Aug 5 13:25:07 BST 2019
Unique Job ID	d2af9d865fa45c3f

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c37B_	 Alignment		100.0	18	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
2	c4il3B_	 Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: ste24p; PDBTitle: crystal structure of s. mikatae ste24p
3	c4aw6B_	 Alignment		100.0	20	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	c6aitD_	 Alignment		99.9	20	PDB header: hydrolase Chain: D: PDB Molecule: beta-barrel assembly-enhancing protease; PDBTitle: crystal structure of e. coli bepa
5	c3cqbB_	 Alignment		99.8	22	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		98.7	10	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		96.7	17	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		96.5	19	PDB header: dna binding protein/dna Chain: A: PDB Molecule: spirt-like domain-containing protein spartan; PDBTitle: mechanism of protease dependent dpc repair
10	c6cz6D_	 Alignment		94.8	8	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator prpr; PDBTitle: mycobacterium tuberculosis transcriptional regulator
11	c3sksA_	 Alignment		94.2	20	PDB header: hydrolase Chain: A: PDB Molecule: putative oligoendopeptidase f; PDBTitle: crystal structure of a putative oligoendopeptidase f from bacillus2 anthracis str. ames

12	c2h1jA_	 Alignment		93.2	19	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
13	c3ce2A_	 Alignment		91.0	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative peptidase; PDBTitle: crystal structure of putative peptidase from chlamydomophila abortus
14	d2ajfa1	 Alignment		82.9	17	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
15	c4fgmA_	 Alignment		82.0	10	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase n family protein; PDBTitle: crystal structure of the aminopeptidase n family protein q5qy1 from2 idiomarina loihiensis. northeast structural genomics consortium3 target ilr60.
16	c2xs4A_	 Alignment		80.7	43	PDB header: hydrolase Chain: A: PDB Molecule: karilysin protease; PDBTitle: structure of karilysin catalytic mmp domain in complex with magnesium
17	c5xbvA_	 Alignment		78.7	29	PDB header: hydrolase Chain: A: PDB Molecule: wss1p; PDBTitle: crystal structure of wss1 mutant from saccharomyces cerevisiae
18	c1wgzC_	 Alignment		78.2	19	PDB header: hydrolase Chain: C: PDB Molecule: carboxypeptidase 1; PDBTitle: crystal structure of carboxypeptidase 1 from thermus thermophilus
19	d1c7ka_	 Alignment		78.0	24	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Zinc protease
20	d1k9xa_	 Alignment		77.6	20	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
21	d1r55a_	 Alignment	not modelled	77.5	33	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
22	c1y791_	 Alignment	not modelled	77.1	20	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
23	d2i47a1	 Alignment	not modelled	76.9	28	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: TNF-alpha converting enzyme, TACE, catalytic domain
24	d1atla_	 Alignment	not modelled	76.9	57	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
25	c5zi7A_	 Alignment	not modelled	76.8	13	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase n; PDBTitle: crystal structure of legionella pneumophila aminopeptidase a in2 complex with glutamic acid
26	d1bqqm_	 Alignment	not modelled	76.7	57	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
27	d2ovxa1	 Alignment	not modelled	76.6	43	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
28	d1rm8a_	 Alignment	not modelled	76.6	57	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
29	c2ztaA_	 Alignment	not modelled	76.5	11	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase n;

29	c2gtuA	Alignment	not modelled	76.5	11	PDBTitle: crystal structure of aminopeptidase n from human pathogen neisseria2 meningitidis PDB header: toxin
30	c2erpA	Alignment	not modelled	76.4	39	Chain: A: PDB Molecule: vascular apoptosis-inducing protein 1; PDBTitle: crystal structure of vascular apoptosis-inducing protein-1(inhibitor-2 bound form)
31	d1qjba	Alignment	not modelled	76.0	43	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
32	c3p24C	Alignment	not modelled	75.9	67	PDB header: hydrolase Chain: C: PDB Molecule: bft-3; PDBTitle: structure of profragilysin-3 from bacteroides fragilis
33	c3k7IA	Alignment	not modelled	75.9	43	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
34	c2i47A	Alignment	not modelled	75.8	39	PDB header: hydrolase Chain: A: PDB Molecule: adam 17; PDBTitle: crystal structure of catalytic domain of tace with inhibitor
35	d1cxva	Alignment	not modelled	75.3	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
36	d1y93a1	Alignment	not modelled	75.2	36	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
37	c2dw1B	Alignment	not modelled	74.9	43	PDB header: apoptosis, toxin Chain: B: PDB Molecule: catrocollastatin; PDBTitle: crystal structure of vap2 from crotalus atrox venom (form 2-2 crystal)
38	d1hv5a	Alignment	not modelled	74.9	43	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
39	d1i76a	Alignment	not modelled	74.9	43	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
40	c5dIIA	Alignment	not modelled	74.7	13	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase n; PDBTitle: aminopeptidase n (pepn) from francisella tularensis subsp. tularensis2 schu s4
41	d1xuca1	Alignment	not modelled	74.4	43	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
42	d1hfca	Alignment	not modelled	74.4	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
43	d1hy7a	Alignment	not modelled	73.7	43	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
44	c6be6D	Alignment	not modelled	73.5	27	PDB header: membrane protein Chain: D: PDB Molecule: disintegrin and metalloproteinase domain-containing protein PDBTitle: adam10 extracellular domain
45	c2e3xA	Alignment	not modelled	73.4	43	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	c4on1B	Alignment	not modelled	72.9	42	PDB header: hydrolase Chain: B: PDB Molecule: putative metalloprotease ii; PDBTitle: crystal structure of metalloproteinase-ii from bacteroides fragilis
47	d4aiga	Alignment	not modelled	72.8	54	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
48	d1mmqa	Alignment	not modelled	72.5	43	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
49	c2jsdA	Alignment	not modelled	72.5	50	PDB header: hydrolase Chain: A: PDB Molecule: matrix metalloproteinase-20; PDBTitle: solution structure of mmp20 complexed with nngh
50	c3ebhA	Alignment	not modelled	72.1	13	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: m1 family aminopeptidase; PDBTitle: structure of the m1 alanylaminopeptidase from malaria complexed with2 bestatin
51	c3b7uX	Alignment	not modelled	71.8	17	PDB header: hydrolase Chain: X: PDB Molecule: leukotriene a-4 hydrolase; PDBTitle: leukotriene a4 hydrolase complexed with kelatorphan
52	c4dd8B	Alignment	not modelled	71.4	33	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: disintegrin and metalloproteinase domain-containing protein PDBTitle: adam-8 metalloproteinase domain with bound batimastat
53	c5I43B	Alignment	not modelled	71.3	31	PDB header: hydrolase Chain: B: PDB Molecule: k-26 dipeptidyl carboxypeptidase; PDBTitle: structure of k26-dcp
54	d1cgla	Alignment	not modelled	71.0	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
55	d1hova	Alignment	not modelled	70.9	43	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain

56	c3k7nA	Alignment	not modelled	70.8	32	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
57	d1bswa	Alignment	not modelled	70.8	22	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
58	c3qnfA	Alignment	not modelled	70.6	16	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
59	d1q3aa	Alignment	not modelled	70.6	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
60	c3g5cA	Alignment	not modelled	70.5	21	PDB header: membrane protein Chain: A: PDB Molecule: adam 22; PDBTitle: structural and biochemical studies on the ectodomain of human adam22
61	c1slmA	Alignment	not modelled	70.2	43	PDB header: hydrolase Chain: A: PDB Molecule: stromelysin-1; PDBTitle: crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
62	d1fbla2	Alignment	not modelled	68.8	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
63	c5th6D	Alignment	not modelled	68.6	50	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)
64	d1quaa	Alignment	not modelled	68.3	44	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
65	c2cltB	Alignment	not modelled	68.2	43	PDB header: hydrolase Chain: B: PDB Molecule: interstitial collagenase; PDBTitle: crystal structure of the active form (full-length) of human2 fibroblast collagenase.
66	d1kufa	Alignment	not modelled	67.7	39	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
67	d1eaka2	Alignment	not modelled	67.3	36	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
68	d1uzea	Alignment	not modelled	67.3	15	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
69	d1j36a	Alignment	not modelled	67.2	19	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
70	d1wnia	Alignment	not modelled	67.1	54	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
71	c1yp1A	Alignment	not modelled	66.8	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
72	d1nd1a	Alignment	not modelled	66.6	54	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
73	c4g0dD	Alignment	not modelled	66.6	36	PDB header: hydrolase Chain: D: PDB Molecule: collagenase 3; PDBTitle: human collagenase 3 (mmp-13) full form with peptides from pro-domain
74	c2v4bB	Alignment	not modelled	66.5	46	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)
75	c4wz9A	Alignment	not modelled	66.1	17	PDB header: hydrolase Chain: A: PDB Molecule: agap004809-pa; PDBTitle: apn1 from anopheles gambiae
76	d3b7sa3	Alignment	not modelled	66.0	16	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Leukotriene A4 hydrolase catalytic domain
77	c3ciaA	Alignment	not modelled	65.8	17	PDB header: hydrolase Chain: A: PDB Molecule: cold-active aminopeptidase; PDBTitle: crystal structure of cold-aminopeptidase from colwellia2 psychrerythraea
78	c3b8zB	Alignment	not modelled	65.3	46	PDB header: hydrolase Chain: B: PDB Molecule: protein adamts-5; PDBTitle: high resolution crystal structure of the catalytic domain of adamts-52 (aggrecanase-2)
79	c2mzeA	Alignment	not modelled	64.7	36	PDB header: hydrolase Chain: A: PDB Molecule: matrilysin; PDBTitle: nmr solution structure of the pro form of human matrilysin (prommp-7)
80	c2rjqA	Alignment	not modelled	62.6	46	PDB header: hydrolase Chain: A: PDB Molecule: adamts-5; PDBTitle: crystal structure of adamts5 with inhibitor bound
81	c5ln5A	Alignment	not modelled	62.5	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

82	c3qnfC	Alignment	not modelled	62.3	16	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
83	c2rjpC	Alignment	not modelled	62.2	38	PDB header: hydrolase Chain: C: PDB Molecule: adamts-4; PDBTitle: crystal structure of adamts4 with inhibitor bound
84	c4kxdA	Alignment	not modelled	61.4	16	PDB header: hydrolase Chain: A: PDB Molecule: glutamyl aminopeptidase; PDBTitle: crystal structure of human aminopeptidase a complexed with glutamate2 and calcium
85	d1u4ga	Alignment	not modelled	61.0	24	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
86	c4yu5A	Alignment	not modelled	60.6	42	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
87	c2c6nA	Alignment	not modelled	60.1	18	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
88	c5czwA	Alignment	not modelled	59.9	39	PDB header: hydrolase Chain: A: PDB Molecule: myrolysin; PDBTitle: crystal structure of myrolysin
89	c1su3A	Alignment	not modelled	59.8	50	PDB header: hydrolase Chain: A: PDB Molecule: interstitial collagenase; PDBTitle: x-ray structure of human prommp-1: new insights into2 collagenase action
90	d1npca	Alignment	not modelled	59.1	75	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
91	c2xhqA	Alignment	not modelled	58.6	23	PDB header: hydrolase Chain: A: PDB Molecule: archaemetzincin; PDBTitle: crystal structure of archaemetzincin (amza) from archaeoglobus2 fulgidus at 1.45 a resolution
92	d1bqba	Alignment	not modelled	58.6	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
93	c3ba0A	Alignment	not modelled	58.3	36	PDB header: hydrolase Chain: A: PDB Molecule: macrophage metalloelastase; PDBTitle: crystal structure of full-length human mmp-12
94	c3nqzB	Alignment	not modelled	58.3	50	PDB header: hydrolase Chain: B: PDB Molecule: secreted metalloprotease mcp02; PDBTitle: crystal structure of the autoprocessed vibriolysin mcp-02 with e369a2 mutation
95	d1kjpA	Alignment	not modelled	58.0	63	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
96	c2vqxA	Alignment	not modelled	57.8	63	PDB header: hydrolase Chain: A: PDB Molecule: metalloproteinase; PDBTitle: precursor of protealysin, metalloproteinase from serratia2 proteamaculans.
97	c4gaaA	Alignment	not modelled	56.7	17	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: mgc78867 protein; PDBTitle: structure of leukotriene a4 hydrolase from xenopus laevis complexed2 with inhibitor bestatin
98	d1k7ia2	Alignment	not modelled	56.4	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain
99	d1sata2	Alignment	not modelled	56.2	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain
100	d1kapp2	Alignment	not modelled	55.2	43	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain
101	c4k90A	Alignment	not modelled	53.7	30	PDB header: hydrolase Chain: A: PDB Molecule: extracellular metalloproteinase mep; PDBTitle: extracellular metalloproteinase from aspergillus
102	c4pj6B	Alignment	not modelled	53.5	17	PDB header: hydrolase Chain: B: PDB Molecule: leucyl-cystinyl aminopeptidase; PDBTitle: crystal structure of human insulin regulated aminopeptidase with2 lysine in active site
103	d1g9ka2	Alignment	not modelled	52.8	43	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain
104	c3b37A	Alignment	not modelled	52.4	10	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase n; PDBTitle: crystal structure of e. coli aminopeptidase n in complex with tyrosine
105	c3nqxA	Alignment	not modelled	49.8	25	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
106	c1eakA	Alignment	not modelled	48.9	36	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: 72 kda type iv collagenase; PDBTitle: catalytic domain of prommp-2 e404q mutant
107	c6o38A	Alignment	not modelled	47.9	44	PDB header: sugar binding protein Chain: A: PDB Molecule: acinetobacter secreted protease cpaa; PDBTitle: structure of a chaperone-substrate complex
						PDB header: hydrolase

108	c2qr4B_	Alignment	not modelled	47.8	18	Chain: B: PDB Molecule: peptidase m3b, oligoendopeptidase f; PDBTitle: crystal structure of oligoendopeptidase-f from enterococcus faecium
109	c4fytA_	Alignment	not modelled	47.6	18	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: aminopeptidase n; PDBTitle: human aminopeptidase n (cd13) in complex with amastatin
110	c4gerB_	Alignment	not modelled	45.4	19	PDB header: hydrolase Chain: B: PDB Molecule: gentiyase metalloprotease; PDBTitle: crystal structure of gentiyase, the neutral metalloprotease of <i>f2 paenibacillus polymyxa</i>
111	c1z5hB_	Alignment	not modelled	45.4	11	PDB header: hydrolase Chain: B: PDB Molecule: tricorn protease interacting factor f3; PDBTitle: crystal structures of the tricorn interacting factor f3 from <i>2 thermoplasma acidophilum</i>
112	c4f5cA_	Alignment	not modelled	45.3	18	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
113	d1lmla_	Alignment	not modelled	44.1	23	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Leishmanolysin
114	c1jiwP_	Alignment	not modelled	41.2	44	PDB header: hydrolase/hydrolase inhibitor Chain: P: PDB Molecule: alkaline metalloproteinase; PDBTitle: crystal structure of the apr-aprin complex
115	c2j83B_	Alignment	not modelled	39.1	45	PDB header: hydrolase Chain: B: PDB Molecule: ulilysin; PDBTitle: ulilysin metalloprotease in complex with batimastat.
116	d1s4bp_	Alignment	not modelled	37.2	33	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
117	c2xpyA_	Alignment	not modelled	37.0	13	PDB header: hydrolase Chain: A: PDB Molecule: leukotriene a-4 hydrolase; PDBTitle: structure of native leukotriene a4 hydrolase from <i>saccharomyces2 cerevisiae</i>
118	c2xdtA_	Alignment	not modelled	36.2	16	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
119	c3dwbA_	Alignment	not modelled	35.5	23	PDB header: hydrolase Chain: A: PDB Molecule: endothelin-converting enzyme 1; PDBTitle: structure of human ece-1 complexed with phosphoramidon
120	d3e11a1	Alignment	not modelled	35.2	26	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: TTHA0227-like