
















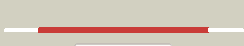














# Phyre2

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Description	RVBD2189c (-) _2451255_2452028
Date	Mon Aug 5 13:25:31 BST 2019
Unique Job ID	60ce826e7f2b3891

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4ar9A_</a>	 Alignment		99.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> collagenase colt; <b>PDBTitle:</b> crystal structure of the peptidase domain of collagenase t2 from clostridium tetani at 1.69 angstrom resolution.
2	<a href="#">c4ar1A_</a>	 Alignment		99.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> colh protein; <b>PDBTitle:</b> crystal structure of the peptidase domain of collagenase h from2 clostridium histolyticum at 2.01 angstrom resolution.
3	<a href="#">c3qnfC_</a>	 Alignment		99.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> endoplasmic reticulum aminopeptidase 1; <b>PDBTitle:</b> crystal structure of the open state of human endoplasmic reticulum2 aminopeptidase 1 erap1
4	<a href="#">c3qnfA_</a>	 Alignment		99.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> endoplasmic reticulum aminopeptidase 1; <b>PDBTitle:</b> crystal structure of the open state of human endoplasmic reticulum2 aminopeptidase 1 erap1
5	<a href="#">c4gaaA_</a>	 Alignment		99.5	12	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A; <b>PDB Molecule:</b> mgc78867 protein; <b>PDBTitle:</b> structure of leukotriene a4 hydrolase from xenopus laevis complexed2 with inhibitor bestatin
6	<a href="#">c4kxdA_</a>	 Alignment		99.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> glutamyl aminopeptidase; <b>PDBTitle:</b> crystal structure of human aminopeptidase a complexed with glutamate2 and calcium
7	<a href="#">c2y50A_</a>	 Alignment		99.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> collagenase; <b>PDBTitle:</b> crystal structure of collagenase g from clostridium2 histolyticum at 2.80 angstrom resolution
8	<a href="#">c2xdtA_</a>	 Alignment		99.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> endoplasmic reticulum aminopeptidase 1; <b>PDBTitle:</b> crystal structure of the soluble domain of human2 endoplasmic reticulum aminopeptidase 1 erap1
9	<a href="#">c3b7uX_</a>	 Alignment		99.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> X; <b>PDB Molecule:</b> leukotriene a-4 hydrolase; <b>PDBTitle:</b> leukotriene a4 hydrolase complexed with kelatorphan
10	<a href="#">c2gtqA_</a>	 Alignment		99.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> aminopeptidase n; <b>PDBTitle:</b> crystal structure of aminopeptidase n from human pathogen neisseria2 meningitidis
11	<a href="#">c3ciaA_</a>	 Alignment		99.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> cold-active aminopeptidase; <b>PDBTitle:</b> crystal structure of cold-aminopeptidase from colwellia2 psychrerythraea

12	<a href="#">c3mdjB_</a>	Alignment		99.4	12	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> endoplasmic reticulum aminopeptidase 1; <b>PDBTitle:</b> er aminopeptidase, erap1, bound to the zinc aminopeptidase inhibitor,2 bestatin
13	<a href="#">c5dlIA_</a>	Alignment		99.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase n; <b>PDBTitle:</b> aminopeptidase n (pepn) from francisella tularensis subsp. tularensis2 schu s4
14	<a href="#">c3b37A_</a>	Alignment		99.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase n; <b>PDBTitle:</b> crystal structure of e. coli aminopeptidase n in complex with tyrosine
15	<a href="#">c5zi7A_</a>	Alignment		99.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase n; <b>PDBTitle:</b> crystal structure of legionella pneumophila aminopeptidase a in2 complex with glutamic acid
16	<a href="#">c5furl_</a>	Alignment		99.4	11	<b>PDB header:</b> transcription <b>Chain:</b> I: <b>PDB Molecule:</b> transcription initiation factor tfiid subunit 2; <b>PDBTitle:</b> structure of human tfiid-iiia bound to core promoter dna
17	<a href="#">d3b7sa3</a>	Alignment		99.3	13	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Leukotriene A4 hydrolase catalytic domain
18	<a href="#">c1z5hB_</a>	Alignment		99.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> tricorn protease interacting factor f3; <b>PDBTitle:</b> crystal structures of the tricorn interacting factor f3 from2 thermoplasma acidophilum
19	<a href="#">c6a8zB_</a>	Alignment		99.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> zinc metalloprotease, putative; <b>PDBTitle:</b> crystal structure of m1 zinc metalloprotease from deinococcus2 radiodurans
20	<a href="#">c3se6A_</a>	Alignment		99.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoplasmic reticulum aminopeptidase 2; <b>PDBTitle:</b> crystal structure of the human endoplasmic reticulum aminopeptidase 2
21	<a href="#">c4pj6B_</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> leucyl-cystinyl aminopeptidase; <b>PDBTitle:</b> crystal structure of human insulin regulated aminopeptidase with2 lysine in active site
22	<a href="#">c6hqaA_</a>	Alignment	not modelled	99.3	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> taf2; <b>PDBTitle:</b> molecular structure of promoter-bound yeast tfiid
23	<a href="#">c3ebhA_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> m1 family aminopeptidase; <b>PDBTitle:</b> structure of the m1 alanylaminopeptidase from malaria complexed with2 bestatin
24	<a href="#">c2xpyA_</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> leukotriene a-4 hydrolase; <b>PDBTitle:</b> structure of native leukotriene a4 hydrolase from saccharomyces2 cerevisiae
25	<a href="#">c4fytA_</a>	Alignment	not modelled	99.3	10	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase n; <b>PDBTitle:</b> human aminopeptidase n (cd13) in complex with amastatin
26	<a href="#">c4wz9A_</a>	Alignment	not modelled	99.2	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> agap004809-pa; <b>PDBTitle:</b> apn1 from anopheles gambiae
27	<a href="#">c4fgmA_</a>	Alignment	not modelled	99.2	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase n family protein; <b>PDBTitle:</b> crystal structure of the aminopeptidase n family protein q5qty1 from2 idiomarina loihiensis. northeast structural genomics consortium3 target ilr60.
28	<a href="#">c4f5cA_</a>	Alignment	not modelled	99.1	15	<b>PDB header:</b> hydrolase/viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase n; <b>PDBTitle:</b> crystal structure of the spike receptor binding domain of a porcine2 respiratory coronavirus in complex with the pig

						aminopeptidase n3 ectodomain <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> secreted metalloprotease mcp02; <b>PDBTitle:</b> crystal structure of vibriolysin mcp-02 mature enzyme, a zinc2 metalloprotease from m4 family
29	<a href="#">c3nqxA_</a>	Alignment	not modelled	93.9	25	
30	<a href="#">c3nqzB_</a>	Alignment	not modelled	93.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> secreted metalloprotease mcp02; <b>PDBTitle:</b> crystal structure of the autoprocessed vibriolysin mcp-02 with e369a2 mutation
31	<a href="#">d1u4ga_</a>	Alignment	not modelled	93.1	23	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Thermolysin-like
32	<a href="#">c2vqxA_</a>	Alignment	not modelled	93.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metalloproteinase; <b>PDBTitle:</b> precursor of protealysin, metalloproteinase from serratia2 proteamaculans.
33	<a href="#">c3c37B_</a>	Alignment	not modelled	92.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peptidase, m48 family; <b>PDBTitle:</b> x-ray structure of the putative zn-dependent peptidase q74d82 at the2 resolution 1.7 a. northeast structural genomics consortium target3 gsr143a
34	<a href="#">d1npca_</a>	Alignment	not modelled	92.2	30	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Thermolysin-like
35	<a href="#">c4gerB_</a>	Alignment	not modelled	92.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> gentlyase metalloprotease; <b>PDBTitle:</b> crystal structure of gentlyase, the neutral metalloprotease of2 paenibacillus polymyxa
36	<a href="#">d1kjpa_</a>	Alignment	not modelled	91.9	24	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Thermolysin-like
37	<a href="#">c3cqbB_</a>	Alignment	not modelled	90.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable protease htpx homolog; <b>PDBTitle:</b> crystal structure of heat shock protein htpx domain from vibrio2 parahaemolyticus rimd 2210633
38	<a href="#">c6h56A_</a>	Alignment	not modelled	90.6	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> effector domain of pseudomonas aeruginosa vgrg2b; <b>PDBTitle:</b> effector domain of pseudomonas aeruginosa vgrg2b
39	<a href="#">d1bqba_</a>	Alignment	not modelled	90.5	24	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Thermolysin-like
40	<a href="#">c6aitD_</a>	Alignment	not modelled	88.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-barrel assembly-enhancing protease; <b>PDBTitle:</b> crystal structure of e. coli bepa
41	<a href="#">c4jixB_</a>	Alignment	not modelled	88.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> projannalysin; <b>PDBTitle:</b> crystal structure of the metallopeptidase zymogen of2 methanocaldococcus jannaschii jannalysin
42	<a href="#">c4jiuA_</a>	Alignment	not modelled	87.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> proabylysin; <b>PDBTitle:</b> crystal structure of the metallopeptidase zymogen of pyrococcus abyssi2 abylysin
43	<a href="#">c5zyoD_</a>	Alignment	not modelled	83.6	19	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> ribosomal rna large subunit methyltransferase h; <b>PDBTitle:</b> crystal structure of domain-swapped circular-permuted ybea (cp74) from2 escherichia coli
44	<a href="#">c4il3B_</a>	Alignment	not modelled	82.8	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ste24p; <b>PDBTitle:</b> crystal structure of s. mikatae ste24p
45	<a href="#">c3o0yC_</a>	Alignment	not modelled	81.6	15	<b>PDB header:</b> lipid binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> lipoprotein; <b>PDBTitle:</b> the crystal structure of the putative lipoprotein from colwellia2 psychrerythraea
46	<a href="#">c4aw6B_</a>	Alignment	not modelled	79.6	30	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> caax prenyl protease 1 homolog; <b>PDBTitle:</b> crystal structure of the human nuclear membrane zinc metalloprotease2 zmpste24 (face1)
47	<a href="#">c6mdxA_</a>	Alignment	not modelled	78.8	21	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> spirt-like domain-containing protein spartan; <b>PDBTitle:</b> mechanism of protease dependent dpc repair
48	<a href="#">c6bdeA_</a>	Alignment	not modelled	75.4	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; <b>PDBTitle:</b> crystal structure of fe(ii) unliganded h-nox protein mutant a71g from2 k. algicida
49	<a href="#">c5a0sA_</a>	Alignment	not modelled	72.4	6	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> zinc metalloprotease zmp1; <b>PDBTitle:</b> apo-structure of metalloprotease zmp1 variant e143a from clostridium2 difficile
50	<a href="#">c2kilA_</a>	Alignment	not modelled	71.6	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> nmr structure of the h103g mutant so2144 h-nox domain from2 shewanella oneidensis in the fe(ii)co ligation state
51	<a href="#">d1j7na2</a>	Alignment	not modelled	68.5	10	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Anthrax toxin lethal factor, N- and C-terminal domains
52	<a href="#">d1u55a_</a>	Alignment	not modelled	66.9	9	<b>Fold:</b> Ligand-binding domain in the NO signalling and Golgi transport <b>Superfamily:</b> Ligand-binding domain in the NO signalling and Golgi transport <b>Family:</b> H-NOX domain
53	<a href="#">c3dl1A_</a>	Alignment	not modelled	66.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative metal-dependent hydrolase; <b>PDBTitle:</b> crystal structure of a putative metal-dependent hydrolase2 (yp_001336084.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 2.20 a resolution

54	<a href="#">c5mnwA_</a>	Alignment	not modelled	65.5	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> guanylate cyclase soluble subunit beta-1; <b>PDBTitle:</b> solution structure of the cinaciguat bound human beta1 h-nox.
55	<a href="#">c3dtkA_</a>	Alignment	not modelled	63.7	26	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> irre protein; <b>PDBTitle:</b> crystal structure of the irre protein, a central regulator2 of dna damage repair in deinococcaceae
56	<a href="#">c5xbvA_</a>	Alignment	not modelled	58.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> wss1p; <b>PDBTitle:</b> crystal structure of wss1 mutant from saccharomyces cerevisiae
57	<a href="#">d2ejqa1</a>	Alignment	not modelled	53.5	15	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> TTHA0227-like
58	<a href="#">c2o0cB_</a>	Alignment	not modelled	51.2	23	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> alr2278 protein; <b>PDBTitle:</b> crystal structure of the h-nox domain from nostoc sp. pcc 71202 complexed to no
59	<a href="#">c2l0rA_</a>	Alignment	not modelled	50.5	30	<b>PDB header:</b> hydrolase,toxin <b>Chain:</b> A: <b>PDB Molecule:</b> lethal factor; <b>PDBTitle:</b> conformational dynamics of the anthrax lethal factor catalytic center
60	<a href="#">c3b4rA_</a>	Alignment	not modelled	49.5	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative zinc metalloprotease mj0392; <b>PDBTitle:</b> site-2 protease from methanocaldococcus jannaschii
61	<a href="#">c4k90A_</a>	Alignment	not modelled	49.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular metalloproteinase mep; <b>PDBTitle:</b> extracellular metalloproteinase from aspergillus
62	<a href="#">d1lmla_</a>	Alignment	not modelled	43.4	17	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Leishmanolysin
63	<a href="#">c6fpcA_</a>	Alignment	not modelled	42.7	6	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pro-pro endopeptidase; <b>PDBTitle:</b> structure of the pro-pro endopeptidase (ppep-2) from paenibacillus2 alvei
64	<a href="#">c3b4rB_</a>	Alignment	not modelled	41.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative zinc metalloprotease mj0392; <b>PDBTitle:</b> site-2 protease from methanocaldococcus jannaschii
65	<a href="#">d1eb6a_</a>	Alignment	not modelled	39.6	27	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Fungal zinc peptidase
66	<a href="#">c2fpgA_</a>	Alignment	not modelled	38.0	20	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> botulinum neurotoxin d light chain; <b>PDBTitle:</b> crystal structure of botulinum neurotoxin type d light chain
67	<a href="#">c5ln5A_</a>	Alignment	not modelled	37.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin and wlm domain-containing metalloprotease <b>PDBTitle:</b> crystal structure of the wss1 e203q mutant from s. pombe
68	<a href="#">d1g12a_</a>	Alignment	not modelled	37.0	36	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Fungal zinc peptidase
69	<a href="#">c1y791_</a>	Alignment	not modelled	36.5	24	<b>PDB header:</b> hydrolase <b>Chain:</b> 1: <b>PDB Molecule:</b> peptidyl-dipeptidase dcp; <b>PDBTitle:</b> crystal structure of the e.coli dipeptidyl carboxypeptidase2 dcp in complex with a peptidic inhibitor
70	<a href="#">c2x3bB_</a>	Alignment	not modelled	35.5	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> toxic extracellular endopeptidase; <b>PDBTitle:</b> asap1 inactive mutant e294a, an extracellular toxic zinc2 metalloendopeptidase
71	<a href="#">d1qjba_</a>	Alignment	not modelled	34.9	36	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
72	<a href="#">c3sksA_</a>	Alignment	not modelled	34.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oligoendopeptidase f; <b>PDBTitle:</b> crystal structure of a putative oligoendopeptidase f from bacillus2 anthracis str. ames
73	<a href="#">c5th6D_</a>	Alignment	not modelled	34.0	16	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> matrix metalloproteinase-9,matrix metalloproteinase-9; <b>PDBTitle:</b> structure determination of a potent, selective antibody inhibitor of2 human mmp9 (apo mmp9)
74	<a href="#">d1hova_</a>	Alignment	not modelled	32.2	29	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
75	<a href="#">d1cglA_</a>	Alignment	not modelled	31.7	16	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
76	<a href="#">d1cxva_</a>	Alignment	not modelled	30.5	50	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
77	<a href="#">c5l43B_</a>	Alignment	not modelled	30.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> k-26 dipeptidyl carboxypeptidase; <b>PDBTitle:</b> structure of k26-dcp
78	<a href="#">d1rm8a_</a>	Alignment	not modelled	29.7	46	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
79	<a href="#">c2xs4A_</a>	Alignment	not modelled	29.6	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> karilysin protease; <b>PDBTitle:</b> structure of karilysin catalytic mmp domain in complex with magnesium <b>PDB header:</b> toxin

80	<a href="#">c6rimB_</a>	Alignment	not modelled	28.2	24	<b>Chain:</b> B: <b>PDB Molecule:</b> putative botulinum-like toxin wo; <b>PDBTitle:</b> crystal structure of the catalytic domain of the weissela oryzae2 botulinum like toxin
81	<a href="#">d1bl0a1</a>	Alignment	not modelled	27.9	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> AraC type transcriptional activator
82	<a href="#">d1hv5a_</a>	Alignment	not modelled	27.1	36	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
83	<a href="#">c4lgiD_</a>	Alignment	not modelled	26.7	24	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> n-terminal truncated nlec structure
84	<a href="#">c1e1hC_</a>	Alignment	not modelled	26.5	25	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> botulinum neurotoxin type a light chain; <b>PDBTitle:</b> crystal structure of recombinant botulinum neurotoxin type a light2 chain, self-inhibiting zn endopeptidase.
85	<a href="#">d1hfca_</a>	Alignment	not modelled	26.0	46	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
86	<a href="#">d1duga2</a>	Alignment	not modelled	25.5	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione S-transferase (GST), N-terminal domain
87	<a href="#">d1li1ip_</a>	Alignment	not modelled	25.4	15	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Neurolysin-like
88	<a href="#">d2ovxa1</a>	Alignment	not modelled	25.3	29	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
89	<a href="#">c3k7nA_</a>	Alignment	not modelled	25.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> k-like; <b>PDBTitle:</b> structures of two elapid snake venom metalloproteases with2 distinct activities highlight the disulfide patterns in the3 d domain of adamalysin family proteins
90	<a href="#">d3e11a1</a>	Alignment	not modelled	24.7	15	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> TTHA0227-like
91	<a href="#">d1hy7a_</a>	Alignment	not modelled	23.7	38	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
92	<a href="#">c1yvga_</a>	Alignment	not modelled	23.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tetanus toxin, light chain; <b>PDBTitle:</b> structural analysis of the catalytic domain of tetanus neurotoxin
93	<a href="#">d1d5ya1</a>	Alignment	not modelled	23.2	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> AraC type transcriptional activator
94	<a href="#">d1q3aa_</a>	Alignment	not modelled	23.1	46	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
95	<a href="#">d1xuca1</a>	Alignment	not modelled	23.0	38	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
96	<a href="#">d1mmqa_</a>	Alignment	not modelled	23.0	29	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
97	<a href="#">d1i76a_</a>	Alignment	not modelled	22.7	16	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
98	<a href="#">c2jsdA_</a>	Alignment	not modelled	22.5	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> matrix metalloproteinase-20; <b>PDBTitle:</b> solution structure of mmp20 complexed with nngn
99	<a href="#">c6be6D_</a>	Alignment	not modelled	22.5	32	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> disintegrin and metalloproteinase domain-containing protein <b>PDBTitle:</b> adam10 extracellular domain
100	<a href="#">c2j83B_</a>	Alignment	not modelled	22.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ulilyisin; <b>PDBTitle:</b> ulilyisin metalloprotease in complex with batimastat.
101	<a href="#">d1y93a1</a>	Alignment	not modelled	22.2	31	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
102	<a href="#">c4on1B_</a>	Alignment	not modelled	21.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative metalloprotease ii; <b>PDBTitle:</b> crystal structure of metalloproteinase-ii from bacteroides fragilis
103	<a href="#">d1fbla2</a>	Alignment	not modelled	21.2	46	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
104	<a href="#">d2fhea2</a>	Alignment	not modelled	21.2	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione S-transferase (GST), N-terminal domain
105	<a href="#">d1oe8a2</a>	Alignment	not modelled	21.1	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione S-transferase (GST), N-terminal domain
106	<a href="#">c6f4eA_</a>	Alignment	not modelled	20.9	31	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> catalytic domain of botulinum neurotoxin x; <b>PDBTitle:</b> crystal structure of the zinc-free catalytic domain of botulinum2 neurotoxin x

107	<a href="#">d1okta2</a>	Alignment	not modelled	20.9	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione S-transferase (GST), N-terminal domain
108	<a href="#">d2fnoa2</a>	Alignment	not modelled	20.8	7	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione S-transferase (GST), N-terminal domain