
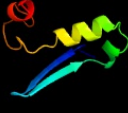





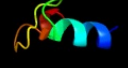















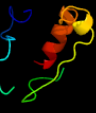




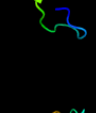

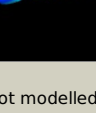


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0185 (-) _215713_216222
Date	Tue Jul 23 14:50:23 BST 2019
Unique Job ID	4bfe98c69fa01379

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6mdxA_</a>	 Alignment		93.0	23	<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
2	<a href="#">c5xbvA_</a>	 Alignment		91.1	23	<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
3	<a href="#">d2ejqa1</a>	 Alignment		86.0	60	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> TTHA0227-like
4	<a href="#">c4jiuA_</a>	 Alignment		84.7	29	<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
5	<a href="#">c4jixB_</a>	 Alignment		80.3	25	<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
6	<a href="#">d3e11a1</a>	 Alignment		68.6	60	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> TTHA0227-like
7	<a href="#">c5a0sA_</a>	 Alignment		65.2	15	<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
8	<a href="#">c6fpcA_</a>	 Alignment		63.1	11	<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
9	<a href="#">c2i0rA_</a>	 Alignment		57.9	23	<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
10	<a href="#">c3dl1A_</a>	 Alignment		57.4	64	<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
11	<a href="#">c5ln5A_</a>	 Alignment		46.5	22	<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

12	<a href="#">d1j7na2</a>	Alignment		35.0	27	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Anthrax toxin lethal factor, N- and C-terminal domains
13	<a href="#">c3vtgA</a>	Alignment		33.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> high choriolytic enzyme 1; <b>PDBTitle:</b> high choriolytic enzyme 1 (hce-1), a hatching enzyme zinc-protease2 from oryzias latipes (medaka fish)
14	<a href="#">c2i47A</a>	Alignment		32.1	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adam 17; <b>PDBTitle:</b> crystal structure of catalytic domain of tace with inhibitor
15	<a href="#">c3kf8D</a>	Alignment		31.6	40	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> protein ten1; <b>PDBTitle:</b> crystal structure of c. tropicalis stn1-ten1 complex
16	<a href="#">c4igjB</a>	Alignment		27.0	20	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> maleylacetoacetate isomerase; <b>PDBTitle:</b> crystal structure of maleylacetoacetate isomerase from2 anaeromyxobacter dehalogenans 2cp-1, target efi-507175
17	<a href="#">d1hfca</a>	Alignment		24.6	38	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
18	<a href="#">d1eb6a</a>	Alignment		24.4	24	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Fungal zinc peptidase
19	<a href="#">d1asta</a>	Alignment		24.2	16	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Astacin
20	<a href="#">d1hv5a</a>	Alignment		23.8	42	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
21	<a href="#">c5y7iB</a>	Alignment	not modelled	23.5	23	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> chloride intracellular channel protein 2; <b>PDBTitle:</b> structure of tilapia fish clic2
22	<a href="#">d1rm8a</a>	Alignment	not modelled	22.2	50	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
23	<a href="#">d1q3aa</a>	Alignment	not modelled	22.1	46	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
24	<a href="#">d1hova</a>	Alignment	not modelled	21.7	42	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
25	<a href="#">d1i76a</a>	Alignment	not modelled	21.2	50	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
26	<a href="#">d1cxva</a>	Alignment	not modelled	21.0	42	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
27	<a href="#">c6jwkB</a>	Alignment	not modelled	20.9	24	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> probable glutathione s-transferase; <b>PDBTitle:</b> crystal structure of maleylpyruvate isomerase from pseudomonas2 aeruginosa pao1
28	<a href="#">c3b4rA</a>	Alignment	not modelled	20.9	67	<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
29	<a href="#">d1cglA</a>	Alignment	not modelled	20.1	42	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain

						<b>Family:</b> Matrix metalloproteases, catalytic domain
30	<a href="#">c5dqsD</a>	Alignment	not modelled	20.0	13	<b>PDB header:</b> translation <b>Chain:</b> D: <b>PDB Molecule:</b> elongation factor 1-beta; <b>PDBTitle:</b> complex structure of human elongation factor 1b alpha and gamma gst-2 like domains
31	<a href="#">d1g12a</a>	Alignment	not modelled	19.2	32	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Fungal zinc peptidase
32	<a href="#">d1eaka2</a>	Alignment	not modelled	18.9	33	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
33	<a href="#">c3cqbB</a>	Alignment	not modelled	18.9	60	<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
34	<a href="#">d1xuca1</a>	Alignment	not modelled	18.9	50	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
35	<a href="#">d1hy7a</a>	Alignment	not modelled	17.5	50	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
36	<a href="#">d1bqqm</a>	Alignment	not modelled	17.5	50	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
37	<a href="#">d2ovxa1</a>	Alignment	not modelled	17.4	42	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
38	<a href="#">c3t6gB</a>	Alignment	not modelled	17.3	28	<b>PDB header:</b> signaling protein, cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> breast cancer anti-estrogen resistance protein 1; <b>PDBTitle:</b> structure of the complex between nsp3 (shep1) and p130cas
39	<a href="#">d1y93a1</a>	Alignment	not modelled	17.2	38	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
40	<a href="#">c3b4rB</a>	Alignment	not modelled	17.1	67	<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
41	<a href="#">c3dtkA</a>	Alignment	not modelled	17.0	16	<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
42	<a href="#">d1fbla2</a>	Alignment	not modelled	17.0	38	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
43	<a href="#">d1smye</a>	Alignment	not modelled	16.5	46	<b>Fold:</b> RPB6/omega subunit-like <b>Superfamily:</b> RPB6/omega subunit-like <b>Family:</b> RNA polymerase omega subunit
44	<a href="#">d1g9ka2</a>	Alignment	not modelled	16.3	36	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal) domain
45	<a href="#">d1fw1a1</a>	Alignment	not modelled	14.9	20	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
46	<a href="#">c2xs4A</a>	Alignment	not modelled	14.7	42	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> kariysin protease; <b>PDBTitle:</b> structure of kariysin catalytic mmp domain in complex with magnesium
47	<a href="#">c5czwA</a>	Alignment	not modelled	14.5	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> myroilysin; <b>PDBTitle:</b> crystal structure of myroilysin
48	<a href="#">c3lqbA</a>	Alignment	not modelled	14.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> loc792177 protein; <b>PDBTitle:</b> crystal structure of the hatching enzyme zhe1 from the zebrafish danio2 rerio
49	<a href="#">d1qjba</a>	Alignment	not modelled	14.3	42	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
50	<a href="#">c3edhA</a>	Alignment	not modelled	14.1	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bone morphogenetic protein 1; <b>PDBTitle:</b> crystal structure of bone morphogenetic protein 1 protease2 domain in complex with partially bound dmso
51	<a href="#">c2v4jA</a>	Alignment	not modelled	12.8	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit <b>PDBTitle:</b> the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration
52	<a href="#">c3lq0A</a>	Alignment	not modelled	12.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> proastacin; <b>PDBTitle:</b> zymogen structure of crayfish astacin metallopeptidase
53	<a href="#">d1ynjk1</a>	Alignment	not modelled	12.6	46	<b>Fold:</b> RPB6/omega subunit-like <b>Superfamily:</b> RPB6/omega subunit-like <b>Family:</b> RNA polymerase omega subunit
54	<a href="#">d1mmqa</a>	Alignment	not modelled	12.5	33	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
55	<a href="#">d1k7ia2</a>	Alignment	not modelled	12.3	36	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal)

						domain
56	<a href="#">c3touB_</a>	Alignment	not modelled	12.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione s-transferase protein; <b>PDBTitle:</b> crystal structure of glutathione transferase (target efi-501058) from2 ralstonia solanacearum gmi1000 with gsh bound
57	<a href="#">d1dp7p_</a>	Alignment	not modelled	11.5	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> P4 origin-binding domain-like
58	<a href="#">d2i47a1</a>	Alignment	not modelled	11.4	24	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> TNF-alpha converting enzyme, TACE, catalytic domain
59	<a href="#">d1sata2</a>	Alignment	not modelled	11.0	36	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal) domain
60	<a href="#">c4l7aB_</a>	Alignment	not modelled	11.0	47	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative zinc-binding metallo-peptidase2 (baccac_01431) from bacteroides caccae atcc 43185 at 2.10 a3 resolution
61	<a href="#">c2j14A_</a>	Alignment	not modelled	10.5	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> maleylpyruvate isomerase; <b>PDBTitle:</b> holo structure of maleyl pyruvate isomerase, a bacterial2 glutathione-s-transferase in zeta class
62	<a href="#">d2h7ca1</a>	Alignment	not modelled	10.3	50	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
63	<a href="#">d3c7ba2</a>	Alignment	not modelled	10.3	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> DsrA/DsrB N-terminal-domain-like
64	<a href="#">d1gz7a_</a>	Alignment	not modelled	10.3	33	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
65	<a href="#">c2pm8A_</a>	Alignment	not modelled	10.2	50	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cholinesterase; <b>PDBTitle:</b> crystal structure of recombinant full length human2 butyrylcholinesterase
66	<a href="#">d1kapp2</a>	Alignment	not modelled	10.2	36	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal) domain
67	<a href="#">c1slmA_</a>	Alignment	not modelled	10.2	50	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> stromelysin-1; <b>PDBTitle:</b> crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
68	<a href="#">c2x3bB_</a>	Alignment	not modelled	10.1	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
69	<a href="#">c4fg5B_</a>	Alignment	not modelled	10.1	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> e3 alpha-esterase-7 coxylesterase; <b>PDBTitle:</b> crystal structure of the alpha-esterase-7 coxylesterase, e3, from2 lucilia cuprina
70	<a href="#">c2j83B_</a>	Alignment	not modelled	9.8	40	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ulilysin; <b>PDBTitle:</b> ulilysin metalloprotease in complex with batimastat.
71	<a href="#">c2jsdA_</a>	Alignment	not modelled	9.7	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 nngh
72	<a href="#">c4pdnA_</a>	Alignment	not modelled	9.6	50	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of e. coli yfcm
73	<a href="#">c2gtqA_</a>	Alignment	not modelled	9.4	50	<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
74	<a href="#">c2qiyC_</a>	Alignment	not modelled	9.3	100	<b>PDB header:</b> signaling protein/hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> ubiquitin carboxyl-terminal hydrolase 3; <b>PDBTitle:</b> yeast deubiquitinase ubp3 and bre5 cofactor complex
75	<a href="#">c2qiyD_</a>	Alignment	not modelled	9.3	100	<b>PDB header:</b> signaling protein/hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> ubiquitin carboxyl-terminal hydrolase 3; <b>PDBTitle:</b> yeast deubiquitinase ubp3 and bre5 cofactor complex
76	<a href="#">c4ke3D_</a>	Alignment	not modelled	9.3	16	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glutathione s-transferase domain; <b>PDBTitle:</b> crystal structure of a glutathione transferase family member from2 burkholderia graminis, target efi-507264, no gsh, disordered domains,3 space group p21, form(2)
77	<a href="#">d2gpfa1</a>	Alignment	not modelled	9.2	21	<b>Fold:</b> Mbth/L9 domain-like <b>Superfamily:</b> Mbth-like <b>Family:</b> Mbth-like
78	<a href="#">d1ukca_</a>	Alignment	not modelled	9.1	29	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
79	<a href="#">c5x61A_</a>	Alignment	not modelled	9.1	50	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acetylcholinesterase; <b>PDBTitle:</b> crystal structure of acetylcholinesterase catalytic subunit of the2 malaria vector anopheles gambiae, 3.4 a
80	<a href="#">c6i2tC_</a>	Alignment	not modelled	8.9	50	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> cholinesterase; <b>PDBTitle:</b> cryoem reconstruction of full-length, fully-glycosylated human2 butyrylcholinesterase tetramer
81	<a href="#">d2ha2a1</a>	Alignment	not modelled	8.8	38	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like

82	<a href="#">c4bdtA</a>	Alignment	not modelled	8.8	50	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> acetylcholinesterase; <b>PDBTitle:</b> human acetylcholinesterase in complex with huprine w and fasciculin 2
83	<a href="#">c3c37B</a>	Alignment	not modelled	8.8	22	<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
84	<a href="#">c1su3A</a>	Alignment	not modelled	8.6	42	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> interstitial collagenase; <b>PDBTitle:</b> x-ray structure of human prommp-1: new insights into2 collagenase action
85	<a href="#">c2mzeA</a>	Alignment	not modelled	8.6	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> matrilysin; <b>PDBTitle:</b> nmr solution structure of the pro form of human matrilysin (prommp-7)
86	<a href="#">c5a2gB</a>	Alignment	not modelled	8.6	50	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> carboxylic ester hydrolase; <b>PDBTitle:</b> an esterase from anaerobic clostridium hathewayi can2 hydrolyze aliphatic aromatic polyesters
87	<a href="#">c3k7IA</a>	Alignment	not modelled	8.3	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atragin; <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
88	<a href="#">c6be6D</a>	Alignment	not modelled	8.3	15	<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
89	<a href="#">c4gerB</a>	Alignment	not modelled	8.3	33	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> gentiylase metalloprotease; <b>PDBTitle:</b> crystal structure of gentiylase, the neutral metalloprotease of2 paenibacillus polymyxa
90	<a href="#">d1dx4a</a>	Alignment	not modelled	8.2	24	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
91	<a href="#">c5w1uA</a>	Alignment	not modelled	8.1	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxylic ester hydrolase; <b>PDBTitle:</b> culex quinquefasciatus carboxylesterase b2
92	<a href="#">c2xpyA</a>	Alignment	not modelled	8.1	56	<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
93	<a href="#">c2voiB</a>	Alignment	not modelled	8.1	45	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bh3-interacting domain death agonist p13; <b>PDBTitle:</b> structure of mouse a1 bound to the bid bh3-domain
94	<a href="#">c5zi7A</a>	Alignment	not modelled	7.9	42	<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
95	<a href="#">d1npca</a>	Alignment	not modelled	7.9	33	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Thermolysin-like
96	<a href="#">c3biwD</a>	Alignment	not modelled	7.8	29	<b>PDB header:</b> cell adhesion/cell adhesion <b>Chain:</b> D: <b>PDB Molecule:</b> neuroligin-1; <b>PDBTitle:</b> crystal structure of the neuroligin-1/neurexin-1beta synaptic adhesion2 complex
97	<a href="#">d1lfa</a>	Alignment	not modelled	7.8	29	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
98	<a href="#">d2v4ja2</a>	Alignment	not modelled	7.7	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> DsrA/DsrB N-terminal-domain-like
99	<a href="#">c5dlIA</a>	Alignment	not modelled	7.7	45	<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