



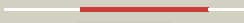







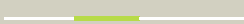

















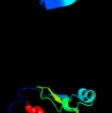


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3dl1A_</a>	 Alignment		100.0	80	<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
2	<a href="#">c2l0rA_</a>	 Alignment		99.8	18	<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
3	<a href="#">dlj7na2</a>	 Alignment		99.8	16	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Anthrax toxin lethal factor, N- and C-terminal domains
4	<a href="#">c1yqyA_</a>	 Alignment		97.2	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lethal factor; <b>PDBTitle:</b> structure of b. anthrax lethal factor in complex with a2 hydroxamate inhibitor
5	<a href="#">c1pwqA_</a>	 Alignment		97.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lethal factor; <b>PDBTitle:</b> crystal structure of anthrax lethal factor complexed with2 thioacetyl-tyr-pro-met-amide, a metal-chelating peptidyl3 small molecule inhibitor
6	<a href="#">d2ejqa1</a>	 Alignment		84.6	13	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> TTHA0227-like
7	<a href="#">c2xpyA_</a>	 Alignment		64.6	17	<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
8	<a href="#">c3lq0A_</a>	 Alignment		59.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> proastacin; <b>PDBTitle:</b> zymogen structure of crayfish astacin metallopeptidase
9	<a href="#">d1hv5a_</a>	 Alignment		57.3	29	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
10	<a href="#">d1qiba_</a>	 Alignment		55.8	36	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
11	<a href="#">d1i76a_</a>	 Alignment		53.6	42	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain

12	<a href="#">dlk7ia2</a>	Alignment		53.2	23	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal) domain
13	<a href="#">dlhfca_</a>	Alignment		53.1	33	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
14	<a href="#">dlkapp2</a>	Alignment		52.4	31	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal) domain
15	<a href="#">dlq3aa_</a>	Alignment		52.2	42	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
16	<a href="#">dlasta_</a>	Alignment		51.5	50	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Astacin
17	<a href="#">dlmmqa_</a>	Alignment		51.2	29	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
18	<a href="#">dlcxva_</a>	Alignment		50.4	36	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
19	<a href="#">c3edhA_</a>	Alignment		50.3	30	<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
20	<a href="#">c3ciaA_</a>	Alignment		48.9	30	<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
21	<a href="#">dlcgla_</a>	Alignment	not modelled	48.5	36	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
22	<a href="#">dl93a1</a>	Alignment	not modelled	48.0	36	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
23	<a href="#">d2ixoa1</a>	Alignment	not modelled	48.0	15	<b>Fold:</b> PTPA-like <b>Superfamily:</b> PTPA-like <b>Family:</b> PTPA-like
24	<a href="#">dlg9ka2</a>	Alignment	not modelled	47.8	22	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal) domain
25	<a href="#">c3lqbA_</a>	Alignment	not modelled	47.4	40	<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
26	<a href="#">dlhy7a_</a>	Alignment	not modelled	47.3	36	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
27	<a href="#">dlbqqm_</a>	Alignment	not modelled	46.4	36	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
28	<a href="#">dlfbla2</a>	Alignment	not modelled	45.6	28	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
29	<a href="#">c2xs4A</a>	Alignment	not modelled	45.6	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> karilysin protease;

29	<a href="#">c4a94A</a>	Alignment	not modelled	43.0	33	<b>PDBTitle:</b> structure of karilysin catalytic mmp domain in complex with2 magnesium
30	<a href="#">d1eaka2</a>	Alignment	not modelled	45.5	15	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
31	<a href="#">c2jsdA</a>	Alignment	not modelled	44.9	42	<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
32	<a href="#">d1xuca1</a>	Alignment	not modelled	44.8	42	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
33	<a href="#">d1hova</a>	Alignment	not modelled	44.6	19	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
34	<a href="#">d1rm8a</a>	Alignment	not modelled	44.6	36	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
35	<a href="#">d2ovxa1</a>	Alignment	not modelled	44.4	36	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
36	<a href="#">c1su3A</a>	Alignment	not modelled	41.5	33	<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
37	<a href="#">d1sata2</a>	Alignment	not modelled	41.3	17	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal) domain
38	<a href="#">c3ba0A</a>	Alignment	not modelled	40.3	36	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> macrophage metalloelastase; <b>PDBTitle:</b> crystal structure of full-length human mmp-12
39	<a href="#">c3b4rB</a>	Alignment	not modelled	40.2	30	<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
40	<a href="#">c1slmA</a>	Alignment	not modelled	39.7	42	<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
41	<a href="#">d2ixna1</a>	Alignment	not modelled	36.7	16	<b>Fold:</b> PTPA-like <b>Superfamily:</b> PTPA-like <b>Family:</b> PTPA-like
42	<a href="#">c1jiwP</a>	Alignment	not modelled	36.3	22	<b>PDB header:</b> hydrolase/hyrolase inhibitor <b>Chain:</b> P: <b>PDB Molecule:</b> alkaline metalloproteinase; <b>PDBTitle:</b> crystal structure of the apr-aprin complex
43	<a href="#">c3d7iB</a>	Alignment	not modelled	35.2	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> carboxymuconolactone decarboxylase family protein; <b>PDBTitle:</b> crystal structure of carboxymuconolactone decarboxylase family protein2 possibly involved in oxygen detoxification (1591455) from3 methanococcus jannaschii at 1.75 a resolution
44	<a href="#">d1kjpA</a>	Alignment	not modelled	34.6	27	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Thermolysin-like
45	<a href="#">d1lm1a</a>	Alignment	not modelled	33.9	42	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Leishmanolysin
46	<a href="#">c2cltB</a>	Alignment	not modelled	33.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> interstitial collagenase; <b>PDBTitle:</b> crystal structure of the active form (full-length) of human2 fibroblast collagenase.
47	<a href="#">d1bqba</a>	Alignment	not modelled	33.3	18	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Thermolysin-like
48	<a href="#">c1y791</a>	Alignment	not modelled	32.8	27	<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
49	<a href="#">c1eakA</a>	Alignment	not modelled	32.6	10	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> 72 kda type iv collagenase; <b>PDBTitle:</b> catalytic domain of prommp-2 e404q mutant
50	<a href="#">d3e11a1</a>	Alignment	not modelled	29.3	33	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> TTHA0227-like
51	<a href="#">c3b7uX</a>	Alignment	not modelled	29.0	32	<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
52	<a href="#">c1l6jA</a>	Alignment	not modelled	23.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> matrix metalloproteinase-9; <b>PDBTitle:</b> crystal structure of human matrix metalloproteinase mmp92 (gelatinase b).
53	<a href="#">c1om8A</a>	Alignment	not modelled	23.6	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serralysin; <b>PDBTitle:</b> crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallized with 10 mm edta
54	<a href="#">d1neka3</a>	Alignment	not modelled	23.1	24	<b>Fold:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
						<b>PDB header:</b> hydrolase

55	<a href="#">c2j83B_</a>	Alignment	not modelled	22.5	18	<b>Chain:</b> B: <b>PDB Molecule:</b> ulilysin; <b>PDBTitle:</b> ulilysin metalloprotease in complex with batimastat.
56	<a href="#">c3c0hB_</a>	Alignment	not modelled	21.4	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> peripheral plasma membrane protein cask; <b>PDBTitle:</b> cask cam-kinase domain- amppnp complex, p1 form
57	<a href="#">c1satA_</a>	Alignment	not modelled	20.8	17	<b>PDB header:</b> hydrolase (serine protease) <b>Chain:</b> A: <b>PDB Molecule:</b> serratia protease; <b>PDBTitle:</b> crystal structure of the 50 kda metallo protease from s.2 marcescens
58	<a href="#">d3b7sa3</a>	Alignment	not modelled	20.0	40	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Leukotriene A4 hydrolase catalytic domain
59	<a href="#">c2oqjL_</a>	Alignment	not modelled	19.0	50	<b>PDB header:</b> immune system <b>Chain:</b> L: <b>PDB Molecule:</b> peptide 2g12.1 (acppshvldmrsgtclaaegk); <b>PDBTitle:</b> crystal structure analysis of fab 2g12 in complex with peptide 2g12.1
60	<a href="#">c2oqjC_</a>	Alignment	not modelled	18.9	50	<b>PDB header:</b> immune system <b>Chain:</b> C: <b>PDB Molecule:</b> peptide 2g12.1 (acppshvldmrsgtclaaegk); <b>PDBTitle:</b> crystal structure analysis of fab 2g12 in complex with peptide 2g12.1
61	<a href="#">d1kufa_</a>	Alignment	not modelled	18.8	23	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like
62	<a href="#">c2oqjI_</a>	Alignment	not modelled	18.7	50	<b>PDB header:</b> immune system <b>Chain:</b> I: <b>PDB Molecule:</b> peptide 2g12.1 (acppshvldmrsgtclaaegk); <b>PDBTitle:</b> crystal structure analysis of fab 2g12 in complex with peptide 2g12.1
63	<a href="#">c3k7lA_</a>	Alignment	not modelled	17.9	29	<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
64	<a href="#">d2ixma1</a>	Alignment	not modelled	17.8	18	<b>Fold:</b> PTPA-like <b>Superfamily:</b> PTPA-like <b>Family:</b> PTPA-like
65	<a href="#">c2gtqA_</a>	Alignment	not modelled	17.7	30	<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
66	<a href="#">d1npca_</a>	Alignment	not modelled	16.7	20	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Thermolysin-like
67	<a href="#">c2g62A_</a>	Alignment	not modelled	16.4	22	<b>PDB header:</b> hydrolase activator <b>Chain:</b> A: <b>PDB Molecule:</b> protein phosphatase 2a, regulatory subunit b' (pr 53); <b>PDBTitle:</b> crystal structure of human ptpa
68	<a href="#">c2oqjF_</a>	Alignment	not modelled	15.7	50	<b>PDB header:</b> immune system <b>Chain:</b> F: <b>PDB Molecule:</b> peptide 2g12.1 (acppshvldmrsgtclaaegk); <b>PDBTitle:</b> crystal structure analysis of fab 2g12 in complex with peptide 2g12.1
69	<a href="#">c2erpA_</a>	Alignment	not modelled	15.4	29	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> vascular apoptosis-inducing protein 1; <b>PDBTitle:</b> crystal structure of vascular apoptosis-inducing protein-1(inhibitor-2 bound form)
70	<a href="#">c3k7nA_</a>	Alignment	not modelled	15.3	36	<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
71	<a href="#">c3ebhA_</a>	Alignment	not modelled	14.9	30	<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
72	<a href="#">d1wlfa2</a>	Alignment	not modelled	14.8	27	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Cdc48 N-terminal domain-like
73	<a href="#">c2c1iA_</a>	Alignment	not modelled	14.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan glcnac deacetylase; <b>PDBTitle:</b> structure of streptococcus pneumoniae peptidoglycan2 deacetylase (sppgda) d 275 n mutant.
74	<a href="#">c2i47A_</a>	Alignment	not modelled	14.7	21	<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
75	<a href="#">c1wgzC_</a>	Alignment	not modelled	14.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> carboxypeptidase 1; <b>PDBTitle:</b> crystal structure of carboxypeptidase 1 from thermus thermophilus
76	<a href="#">c2c30A_</a>	Alignment	not modelled	14.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase pak 6; <b>PDBTitle:</b> crystal structure of the human p21-activated kinase 6
77	<a href="#">c3b37A_</a>	Alignment	not modelled	13.9	40	<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
78	<a href="#">d2i47a1</a>	Alignment	not modelled	13.6	21	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> TNF-alpha converting enzyme, TACE, catalytic domain
79	<a href="#">c3ppuB_</a>	Alignment	not modelled	13.2	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione-s-transferase; <b>PDBTitle:</b> crystal structure of the glutathione-s-transferase xi from2 phanerochaete chrysosporium
80	<a href="#">c1yp1A_</a>	Alignment	not modelled	13.1	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> fii; <b>PDBTitle:</b> crystal structure of a non-hemorrhagic fibrin(ogen)olytic2 metalloproteinase from venom of agkistrodon acutus

81	<a href="#">d2ajfa1</a>	Alignment	not modelled	12.9	11	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Neurolysin-like
82	<a href="#">d1nd1a_</a>	Alignment	not modelled	12.9	29	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like
83	<a href="#">c3famA</a>	Alignment	not modelled	12.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> carbon catabolite-derepressing protein kinase; <b>PDBTitle:</b> crystal structure of the protein kinase domain of yeast amp-2 activated protein kinase snf1
84	<a href="#">c1yyeA_</a>	Alignment	not modelled	12.8	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> estrogen receptor beta; <b>PDBTitle:</b> crystal structure of estrogen receptor beta complexed with2 way-202196
85	<a href="#">d1eb6a_</a>	Alignment	not modelled	12.5	16	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Fungal zinc peptidase
86	<a href="#">c1z5hB_</a>	Alignment	not modelled	12.4	60	<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 f32 from thermoplasma acidophilum
87	<a href="#">c2v4bB_</a>	Alignment	not modelled	12.3	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> adamts-1; <b>PDBTitle:</b> crystal structure of human adamts-1 catalytic domain and2 cysteine-rich domain (apo-form)
88	<a href="#">c3cqB_</a>	Alignment	not modelled	12.2	15	<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
89	<a href="#">d1phka_</a>	Alignment	not modelled	12.2	9	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
90	<a href="#">c2e3xA_</a>	Alignment	not modelled	12.2	29	<b>PDB header:</b> hydrolase, blood clotting, toxin <b>Chain:</b> A: <b>PDB Molecule:</b> coagulation factor x-activating enzyme heavy chain; <b>PDBTitle:</b> crystal structure of russell's viper venom metalloproteinase
91	<a href="#">c3g5cA_</a>	Alignment	not modelled	12.1	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> adam 22; <b>PDBTitle:</b> structural and biochemical studies on the ectodomain of human adam22
92	<a href="#">c3nqzB_</a>	Alignment	not modelled	11.9	20	<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
93	<a href="#">d1atla_</a>	Alignment	not modelled	11.9	29	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Reprolysin-like
94	<a href="#">c3b8zB_</a>	Alignment	not modelled	11.8	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein adamts-5; <b>PDBTitle:</b> high resolution crystal structure of the catalytic domain2 of adamts-5 (aggrecanase-2)
95	<a href="#">d1chua3</a>	Alignment	not modelled	11.8	14	<b>Fold:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
96	<a href="#">c3ce2A_</a>	Alignment	not modelled	11.7	36	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative peptidase; <b>PDBTitle:</b> crystal structure of putative peptidase from chlamydomonada abortus
97	<a href="#">c2rjpC_</a>	Alignment	not modelled	11.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> adamts-4; <b>PDBTitle:</b> crystal structure of adamts4 with inhibitor bound
98	<a href="#">c2rjqA_</a>	Alignment	not modelled	11.3	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adamts-5; <b>PDBTitle:</b> crystal structure of adamts5 with inhibitor bound
99	<a href="#">c2dw1B_</a>	Alignment	not modelled	11.3	29	<b>PDB header:</b> apoptosis, toxin <b>Chain:</b> B: <b>PDB Molecule:</b> catrocollastatin; <b>PDBTitle:</b> crystal structure of vap2 from crotalus atrox venom (form 2-2 crystal)