Phyre^2

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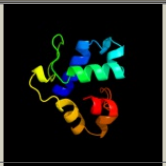
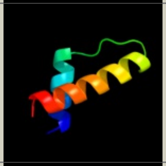
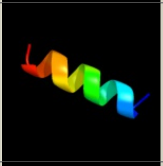
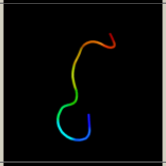
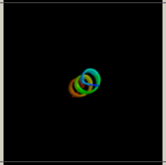
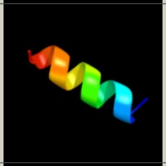
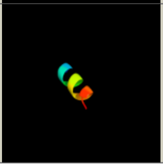
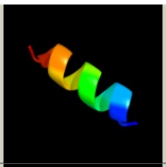
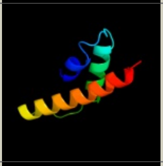
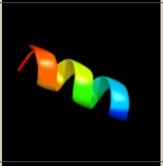
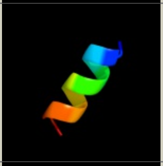
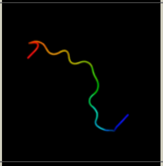
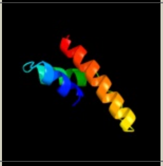
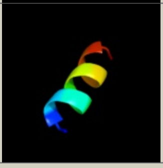
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c37B_	Alignment		97.4	41	**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	c3dtkA_	Alignment		91.3	32	**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
3	c3cqbB_	Alignment		69.2	28	**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
4	c3k7lA_	Alignment		36.1	29	**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
5	c2e3xA_	Alignment		35.0	40	**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
6	c2erpA_	Alignment		34.3	29	**PDB header:**toxin **Chain:** A: **PDB Molecule:**vascular apoptosis-inducing protein 1; **PDBTitle:** crystal structure of vascular apoptosis-inducing protein-1(inhibitor-2 bound form)
7	c2l0rA_	Alignment		32.3	40	**PDB header:**hydrolase,toxin **Chain:** A: **PDB Molecule:**lethal factor; **PDBTitle:** conformational dynamics of the anthrax lethal factor catalytic center
8	d4aiga_	Alignment		31.1	31	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
9	d1atla_	Alignment		31.0	23	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
10	c2dw1B_	Alignment		31.0	36	**PDB header:**apoptosis, toxin **Chain:** B: **PDB Molecule:**catrocollastatin; **PDBTitle:** crystal structure of vap2 from crotalus atrox venom (form 2-2 crystal)
11	c2rjpC_	Alignment		27.1	33	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**adamts-4; **PDBTitle:** crystal structure of adamts4 with inhibitor bound

12	d1r55a_	Alignment		27.0	38	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
13	d1q0qa1	Alignment		26.7	19	**Fold:**Left-handed superhelix **Superfamily:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain **Family:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain
14	c2v4bB_	Alignment		25.3	42	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adamts-1; **PDBTitle:** crystal structure of human adamts-1 catalytic domain and2 cysteine-rich domain (apo-form)
15	c3b8zB_	Alignment		25.1	42	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein adamts-5; **PDBTitle:** high resolution crystal structure of the catalytic domain2 of adamts-5 (aggrecanase-2)
16	d1quaa_	Alignment		24.1	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
17	d1vpra1	Alignment		23.7	25	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Dinoflagellate luciferase repeat
18	d1r0ka1	Alignment		23.5	22	**Fold:**Left-handed superhelix **Superfamily:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain **Family:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain
19	c2rjqA_	Alignment		22.7	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adamts-5; **PDBTitle:** crystal structure of adamts5 with inhibitor bound
20	c1yp1A_	Alignment		22.5	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fii; **PDBTitle:** crystal structure of a non-hemorrhagic fibrin(ogen)olytic2 metalloproteinase from venom of agkistrodon acutus
21	d1hfca_	Alignment	not modelled	22.5	30	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
22	d1eaka2	Alignment	not modelled	22.3	27	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
23	d1j7na2	Alignment	not modelled	22.2	16	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Anthrax toxin lethal factor, N- and C-terminal domains
24	d1nd1a_	Alignment	not modelled	22.0	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
25	d1bswa_	Alignment	not modelled	21.9	38	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
26	d1wnia_	Alignment	not modelled	21.7	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
27	d2i47a1	Alignment	not modelled	21.6	21	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TNF-alpha converting enzyme, TACE, catalytic domain
28	d1qiba_	Alignment	not modelled	21.3	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
29	d1cxva_	Alignment	not modelled	21.2	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain

						Family: Matrix metalloproteases, catalytic domain
30	d1y93a1	Alignment	not modelled	21.2	44	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
31	d1cgla_	Alignment	not modelled	20.7	30	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
32	c2i47A_	Alignment	not modelled	20.7	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adam 17; **PDBTitle:** crystal structure of catalytic domain of tace with inhibitor
33	d1hova_	Alignment	not modelled	19.9	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
34	c2xs4A_	Alignment	not modelled	19.9	44	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**karilysin protease; **PDBTitle:** structure of karilysin catalytic mmp domain in complex with2 magnesium
35	d1xuca1	Alignment	not modelled	19.8	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
36	d1g9ka2	Alignment	not modelled	19.4	50	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
37	d1hy7a_	Alignment	not modelled	19.3	44	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
38	d1i76a_	Alignment	not modelled	19.1	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
39	d1kufa_	Alignment	not modelled	18.9	27	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
40	d1hv5a_	Alignment	not modelled	18.8	44	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
41	c3k7nA_	Alignment	not modelled	18.6	27	**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
42	d1k7ia2	Alignment	not modelled	18.3	40	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
43	d2ovxa1	Alignment	not modelled	18.1	22	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
44	d1mmqa_	Alignment	not modelled	17.9	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
45	d1t3ta7	Alignment	not modelled	17.7	10	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
46	d1sata2	Alignment	not modelled	17.5	40	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
47	d1fbla2	Alignment	not modelled	17.2	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
48	d1bqqm_	Alignment	not modelled	17.2	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
49	c3b4rB_	Alignment	not modelled	17.1	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative zinc metalloprotease mj0392; **PDBTitle:** site-2 protease from methanocaldococcus jannaschii
50	c2jsdA_	Alignment	not modelled	17.0	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-20; **PDBTitle:** solution structure of mmp20 complexed with nngh
51	d1rm8a_	Alignment	not modelled	17.0	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
52	d1q3aa_	Alignment	not modelled	15.9	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
53	c3sksA_	Alignment	not modelled	15.7	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative oligoendopeptidase f; **PDBTitle:** crystal structure of a putative oligoendopeptidase f from bacillus2 anthracis str. ames
54	c1slmA_	Alignment	not modelled	15.3	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**stromelysin-1; **PDBTitle:** crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
55	c2h1jA_	Alignment	not modelled	15.1	36	**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
						PDB header:sugar binding protein **Chain:** A: **PDB Molecule:**ricin b-related lectin;

56	c3phzA_	Alignment	not modelled	14.6	29	**PDBTitle:** crystal structure analysis of polyporus squamosus lectin bound to2 human-type influenza-binding epitope neu5aca2-6galb1-4glcnac
57	c3ce2A_	Alignment	not modelled	14.6	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative peptidase; **PDBTitle:** crystal structure of putative peptidase from chlamydophila abortus
58	c3g5cA_	Alignment	not modelled	14.0	25	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**adam 22; **PDBTitle:** structural and biochemical studies on the ectodomain of human adam22
59	d1kapp2	Alignment	not modelled	13.5	50	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
60	c2vqxA_	Alignment	not modelled	12.4	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metalloproteinase; **PDBTitle:** precursor of protealysin, metalloproteinase from serratia2 proteamaculans.
61	d1npca_	Alignment	not modelled	12.3	29	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
62	c1y791_	Alignment	not modelled	11.7	36	**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
63	d2ilxa1	Alignment	not modelled	11.7	24	**Fold:**LigT-like **Superfamily:**LigT-like **Family:**2',3'-cyclic nucleotide 3'-phosphodiesterase, catalytic domain
64	c3nqxA_	Alignment	not modelled	11.7	29	**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
65	c3dl1A_	Alignment	not modelled	11.0	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative metal-dependent hydrolase; **PDBTitle:** crystal structure of a putative metal-dependent hydrolase2 (yp_001336084.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 2.20 a resolution
66	d1kjpa_	Alignment	not modelled	10.4	29	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
67	c1jiwP_	Alignment	not modelled	10.4	50	**PDB header:**hydrolase/hyrolase inhibitor **Chain:** P: **PDB Molecule:**alkaline metalloproteinase; **PDBTitle:** crystal structure of the apr-aprin complex
68	d1bqba_	Alignment	not modelled	10.3	43	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
69	c3ac6A_	Alignment	not modelled	9.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase 2; **PDBTitle:** crystal structure of purl from thermus thermophilus
70	c3nqzB_	Alignment	not modelled	8.6	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**secreted metalloprotease mcp02; **PDBTitle:** crystal structure of the autoprocessed vibriolysin mcp-02 with e369a2 mutation
71	c3ba0A_	Alignment	not modelled	8.6	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**macrophage metalloelastase; **PDBTitle:** crystal structure of full-length human mmp-12
72	c2cltB_	Alignment	not modelled	8.5	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**interstitial collagenase; **PDBTitle:** crystal structure of the active form (full-length) of human2 fibroblast collagenase.
73	d1pyta_	Alignment	not modelled	8.2	14	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
74	d1t1ra3	Alignment	not modelled	8.0	33	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
75	d1i1ip_	Alignment	not modelled	8.0	40	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
76	d2ejqa1	Alignment	not modelled	7.9	38	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like
77	d1tx3a1	Alignment	not modelled	7.8	21	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease HincII
78	d1c7ka_	Alignment	not modelled	7.6	44	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Zinc protease
79	d1x7va_	Alignment	not modelled	7.3	15	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PA3566-like
80	c2fb0A_	Alignment	not modelled	7.2	0	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of conserved protein of unknown function from2 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution, possible3 oxidoreductase
81	d1jqga2	Alignment	not modelled	7.1	7	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
						Fold:alpha-alpha superhelix

82	d1t06a_	Alignment	not modelled	6.7	28	**Superfamily:**ARM repeat **Family:**BC3264-like
83	d1ayea2	Alignment	not modelled	6.6	18	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
84	d2boaa2	Alignment	not modelled	6.6	14	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
85	d1u4ga_	Alignment	not modelled	6.5	29	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
86	d1o6xa_	Alignment	not modelled	6.4	18	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
87	d1nsaa2	Alignment	not modelled	6.3	11	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
88	c1l6jA_	Alignment	not modelled	6.1	54	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-9; **PDBTitle:** crystal structure of human matrix metalloproteinase mmp92 (gelatinase b).
89	d1s4bp_	Alignment	not modelled	6.0	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
90	d1v54m_	Alignment	not modelled	6.0	28	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX) **Family:**Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX)
91	c2omoC_	Alignment	not modelled	5.9	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**duf176; **PDBTitle:** putative antibiotic biosynthesis monooxygenase from nitrosomonas2 europaea
92	d1pbaa_	Alignment	not modelled	5.9	11	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
93	d2ajfa1	Alignment	not modelled	5.8	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
94	c3p1vB_	Alignment	not modelled	5.7	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**metallo-endopeptidase; **PDBTitle:** crystal structure of a metallo-endopeptidases (bacova_00663) from2 bacteroides ovatus at 1.93 a resolution
95	c1su3A_	Alignment	not modelled	5.6	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**interstitial collagenase; **PDBTitle:** x-ray structure of human prommp-1: new insights into2 collagenase action
96	d2ihoa2	Alignment	not modelled	5.6	9	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**MOA C-terminal domain-like
97	c1om8A_	Alignment	not modelled	5.5	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serralysin; **PDBTitle:** crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallyzed with 10 mm edta
98	d1kwma2	Alignment	not modelled	5.5	11	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
99	d2cpwa1	Alignment	not modelled	5.1	33	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain