Phyre^2

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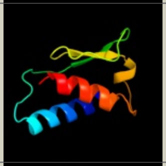
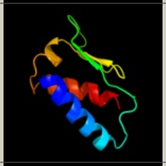
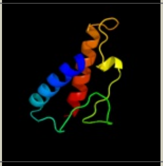
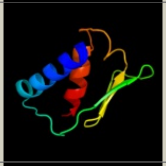
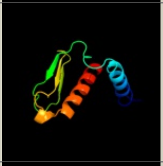
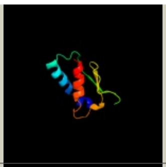
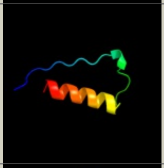
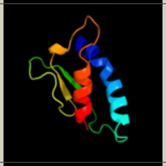
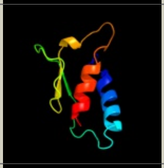
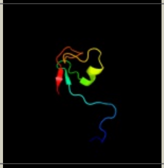
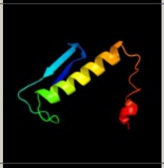
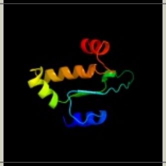
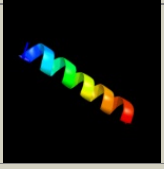
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cqbB_	Alignment		96.9	18	**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
2	c2xdtA_	Alignment		96.1	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoplasmic reticulum aminopeptidase 1; **PDBTitle:** crystal structure of the soluble domain of human2 endoplasmic reticulum aminopeptidase 1 erap1
3	c3mdjB_	Alignment		96.0	26	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**endoplasmic reticulum aminopeptidase 1; **PDBTitle:** er aminopeptidase, erap1, bound to the zinc aminopeptidase inhibitor,2 bestatin
4	c3qnfA_	Alignment		96.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoplasmic reticulum aminopeptidase 1; **PDBTitle:** crystal structure of the open state of human endoplasmic reticulum2 aminopeptidase 1 erap1
5	c3b37A_	Alignment		95.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase n; **PDBTitle:** crystal structure of e. coli aminopeptidase n in complex with tyrosine
6	c3se6A_	Alignment		95.5	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoplasmic reticulum aminopeptidase 2; **PDBTitle:** crystal structure of the human endoplasmic reticulum aminopeptidase 2
7	c2gtqA_	Alignment		95.4	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase n; **PDBTitle:** crystal structure of aminopeptidase n from human pathogen neisseria2 meningitidis
8	c3ebhA_	Alignment		95.4	25	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**m1 family aminopeptidase; **PDBTitle:** structure of the m1 alanylaminopeptidase from malaria complexed with2 bestatin
9	c1z5hB_	Alignment		95.1	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**tricorn protease interacting factor f3; **PDBTitle:** crystal structures of the tricorn interacting factor f32 from thermoplasma acidophilum
10	c3dtkA_	Alignment		94.7	24	**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
11	c3c37B_	Alignment		94.5	14	**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

12	c3ciaA_	Alignment		93.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cold-active aminopeptidase; **PDBTitle:** crystal structure of cold-aminopeptidase from colwellia2 psychrerythraea
13	c2xpyA_	Alignment		92.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leukotriene a-4 hydrolase; **PDBTitle:** structure of native leukotriene a4 hydrolase from saccharomyces2 cerevisiae
14	d1lmla_	Alignment		91.5	24	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Leishmanolysin
15	c3b7uX_	Alignment		91.3	15	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**leukotriene a-4 hydrolase; **PDBTitle:** leukotriene a4 hydrolase complexed with kelatorphan
16	d3b7sa3	Alignment		90.2	16	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Leukotriene A4 hydrolase catalytic domain
17	c2lcqA_	Alignment		85.2	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative toxin vapc6; **PDBTitle:** solution structure of the endonuclease nob1 from p.horikoshii
18	d1j7na2	Alignment		83.6	18	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Anthrax toxin lethal factor, N- and C-terminal domains
19	d1oz9a_	Alignment		76.6	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Predicted metal-dependent hydrolase
20	d2ejqa1	Alignment		72.9	38	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like
21	d1mmqa_	Alignment	not modelled	72.1	15	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
22	d1p3ja2	Alignment	not modelled	71.0	18	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
23	d2ak3a2	Alignment	not modelled	70.8	15	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
24	d1zina2	Alignment	not modelled	70.7	24	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
25	d1s3ga2	Alignment	not modelled	70.0	18	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
26	d1e4va2	Alignment	not modelled	68.5	15	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
27	c2jsdA_	Alignment	not modelled	66.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-20; **PDBTitle:** solution structure of mmp20 complexed with nngh

28	c2l0rA_	Alignment	not modelled	66.0	24	**PDB header:**hydrolase,toxin **Chain:** A: **PDB Molecule:**lethal factor; **PDBTitle:** conformational dynamics of the anthrax lethal factor catalytic center
29	d1vd4a_	Alignment	not modelled	65.5	18	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
30	c2vqxA_	Alignment	not modelled	63.3	39	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metalloproteinase; **PDBTitle:** precursor of protealysin, metalloproteinase from serratia2 proteamaculans.
31	d1akya2	Alignment	not modelled	62.1	15	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
32	d1kjpa_	Alignment	not modelled	61.5	39	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
33	d1npca_	Alignment	not modelled	61.1	28	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
34	d3e11a1	Alignment	not modelled	61.1	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like
35	d1bqba_	Alignment	not modelled	60.6	28	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
36	c1slmA_	Alignment	not modelled	60.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**stromelysin-1; **PDBTitle:** crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
37	c3nqxA_	Alignment	not modelled	58.1	28	**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
38	c1f2iI_	Alignment	not modelled	57.8	25	**PDB header:**transcription/dna **Chain:** I: **PDB Molecule:**fusion of n-terminal 17-mer peptide extension to **PDBTitle:** cocrystal structure of selected zinc finger dimer bound to2 dna
39	d1m2ka_	Alignment	not modelled	57.7	14	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
40	d1xm5a_	Alignment	not modelled	57.4	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Predicted metal-dependent hydrolase
41	c3nqzB_	Alignment	not modelled	56.5	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**secreted metalloprotease mcp02; **PDBTitle:** crystal structure of the autoprocessed vibriolysin mcp-02 with e369a2 mutation
42	c3dl1A_	Alignment	not modelled	56.5	27	**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
43	c2eprA_	Alignment	not modelled	55.9	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**poz-, at hook-, and zinc finger-containing **PDBTitle:** solution structure of the secound zinc finger domain of2 zinc finger protein 278
44	d1eaka2	Alignment	not modelled	54.9	12	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
45	c1su3A_	Alignment	not modelled	54.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**interstitial collagenase; **PDBTitle:** x-ray structure of human prommp-1: new insights into2 collagenase action
46	c3edhA_	Alignment	not modelled	53.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**bone morphogenetic protein 1; **PDBTitle:** crystal structure of bone morphogenetic protein 1 protease2 domain in complex with partially bound dmso
47	d1sata2	Alignment	not modelled	51.2	16	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
48	d1u4ga_	Alignment	not modelled	49.3	28	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
49	d1eb6a_	Alignment	not modelled	48.4	19	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Fungal zinc peptidase
50	d2csha1	Alignment	not modelled	46.2	29	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
51	d1cgla_	Alignment	not modelled	45.5	46	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
52	d1cxva_	Alignment	not modelled	45.0	46	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
53	d2qtva5	Alignment	not modelled	44.1	9	**Fold:**Rubredoxin-like **Superfamily:**Zn-finger domain of Sec23/24 **Family:**Zn-finger domain of Sec23/24

54	c1xaxA_	Alignment	not modelled	43.8	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0054 protein hi0004; **PDBTitle:** nmr structure of hi0004, a putative essential gene product2 from haemophilus influenzae
55	d1hfca_	Alignment	not modelled	43.5	46	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
56	c3pkiF_	Alignment	not modelled	43.4	17	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** human sirt6 crystal structure in complex with adp ribose
57	d1xuca1	Alignment	not modelled	43.3	38	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
58	d1rm8a_	Alignment	not modelled	43.1	46	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
59	c2xs4A_	Alignment	not modelled	42.8	46	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**karilysin protease; **PDBTitle:** structure of karilysin catalytic mmp domain in complex with2 magnesium
60	d1q3aa_	Alignment	not modelled	42.0	46	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
61	c2c6nA_	Alignment	not modelled	41.7	12	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**angiotensin-converting enzyme, somatic isoform; **PDBTitle:** structure of human somatic angiontensin-i converting enzyme n domain2 with lisinopril
62	d1hv5a_	Alignment	not modelled	41.5	38	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
63	d1qiba_	Alignment	not modelled	40.6	31	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
64	d1i76a_	Alignment	not modelled	40.3	38	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
65	c2adrA_	Alignment	not modelled	40.1	28	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**adr1; **PDBTitle:** adr1 dna-binding domain from saccharomyces cerevisiae, nmr,2 25 structures
66	d1g9ka2	Alignment	not modelled	39.8	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
67	c3ba0A_	Alignment	not modelled	39.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**macrophage metalloelastase; **PDBTitle:** crystal structure of full-length human mmp-12
68	d1y93a1	Alignment	not modelled	39.7	31	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
69	d1hy7a_	Alignment	not modelled	39.4	38	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
70	c3h0gL_	Alignment	not modelled	39.4	23	**PDB header:**transcription **Chain:** L: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
71	c2ja6L_	Alignment	not modelled	38.9	23	**PDB header:**transferase **Chain:** L: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii 7.7 **PDBTitle:** cpd lesion containing rna polymerase ii elongation complex2 b
72	c2ythA_	Alignment	not modelled	38.7	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 224; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 479-2 511) of human zinc finger protein 224
73	c2ytjA_	Alignment	not modelled	38.1	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 484; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 771-2 803) of human zinc finger protein 484
74	c3b4rB_	Alignment	not modelled	37.5	45	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative zinc metalloprotease mj0392; **PDBTitle:** site-2 protease from methanocaldococcus jannaschii
75	c2kdxA_	Alignment	not modelled	37.5	16	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
76	c3lq0A_	Alignment	not modelled	36.8	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proastacin; **PDBTitle:** zymogen structure of crayfish astacin metallopeptidase
77	d2ovxa1	Alignment	not modelled	36.5	31	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
78	c3glsC_	Alignment	not modelled	36.5	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nad-dependent deacetylase sirtuin-3, **PDBTitle:** crystal structure of human sirt3
79	d1x6ma_	Alignment	not modelled	36.3	16	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**Glutathione-dependent formaldehyde-activating enzyme, Gfa
						PDB header:hydrolase **Chain:** A: **PDB Molecule:**atragin;

80	c3k7lA_	Alignment	not modelled	36.2	22	**PDBTitle:** structures of two elapid snake venom metalloproteases with2 distinct activities highlight the disulfide patterns in the3 d domain of adamalysin family proteins
81	d1g12a_	Alignment	not modelled	35.4	30	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Fungal zinc peptidase
82	d1asta_	Alignment	not modelled	35.4	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Astacin
83	d1hova_	Alignment	not modelled	35.1	31	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
84	c2i47A_	Alignment	not modelled	35.1	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adam 17; **PDBTitle:** crystal structure of catalytic domain of tace with inhibitor
85	d2gmga1	Alignment	not modelled	34.8	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF0610-like
86	d1kapp2	Alignment	not modelled	34.7	29	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
87	d1bqqm_	Alignment	not modelled	34.5	54	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
88	c2drpD_	Alignment	not modelled	34.0	25	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**protein (tramtrack dna-binding domain); **PDBTitle:** the crystal structure of a two zinc-finger peptide reveals2 an extension to the rules for zinc-finger/dna recognition
89	d2i47a1	Alignment	not modelled	33.8	29	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TNF-alpha converting enzyme, TACE, catalytic domain
90	c1g2dC_	Alignment	not modelled	33.8	21	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**tata box zinc finger protein; **PDBTitle:** structure of a cys2his2 zinc finger/tata box complex (clone2 #2)
91	c3lqbA_	Alignment	not modelled	33.6	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**loc792177 protein; **PDBTitle:** crystal structure of the hatching enzyme zhe1 from the zebrafish danio2 rerio
92	c1q14A_	Alignment	not modelled	33.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hst2 protein; **PDBTitle:** structure and autoregulation of the yeast hst2 homolog of sir2
93	d3cmna1	Alignment	not modelled	32.7	26	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Caur0242-like
94	c3cmnA_	Alignment	not modelled	32.7	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of a putative hydrolase with a novel fold2 from chloroflexus aurantiacus
95	c2dlkA_	Alignment	not modelled	32.3	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**novel protein; **PDBTitle:** solution structure of the first and the second zf-c2h22 domains of zinc finger protein 692
96	c1m2oA_	Alignment	not modelled	32.3	9	**PDB header:**protein transport/signaling protein **Chain:** A: **PDB Molecule:**protein transport protein sec23; **PDBTitle:** crystal structure of the sec23-sar1 complex
97	d1fx7a3	Alignment	not modelled	32.2	56	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
98	c2em3A_	Alignment	not modelled	32.1	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 28 homolog; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 640-2 672) of human zinc finger protein 28 homolog
99	c3sksA_	Alignment	not modelled	32.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative oligoendopeptidase f; **PDBTitle:** crystal structure of a putative oligoendopeptidase f from bacillus2 anthracis str. ames
100	c1x5wA_	Alignment	not modelled	31.8	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 64, isoforms 1; **PDBTitle:** solution structure of the c2h2 type zinc-binding domain of2 human zinc finger protein 64, isoforms 1 and 2
101	c2epsA_	Alignment	not modelled	31.2	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**poz-, at hook-, and zinc finger-containing **PDBTitle:** solution structure of the 4th zinc finger domain of zinc2 finger protein 278
102	d1fbla2	Alignment	not modelled	31.1	46	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
103	c3b8zB_	Alignment	not modelled	31.1	55	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein adamts-5; **PDBTitle:** high resolution crystal structure of the catalytic domain2 of adamts-5 (aggrecanase-2)
104	c1un6D_	Alignment	not modelled	30.4	23	**PDB header:**rna-binding protein/rna **Chain:** D: **PDB Molecule:**transcription factor iiia; **PDBTitle:** the crystal structure of a zinc finger - rna complex2 reveals two modes of molecular recognition
105	c2ktvA_	Alignment	not modelled	30.4	11	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic peptide chain release factor subunit 1; **PDBTitle:** human erf1 c-domain, "open" conformer
106	c2xhqA_	Alignment	not modelled	29.9	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**archaemetzincin; **PDBTitle:** crystal structure of archaemetzincin (amza) from

						archaeoglobus2 fulgidus at 1.45 a resolution
107	c2v4bB_	Alignment	not modelled	29.4	40	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adamts-1; **PDBTitle:** crystal structure of human adamts-1 catalytic domain and2 cysteine-rich domain (apo-form)
108	c2emlA_	Alignment	not modelled	29.4	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 28 homolog; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 752-2 784) of human zinc finger protein 28 homolog
109	d1r55a_	Alignment	not modelled	29.4	40	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
110	d6rxna_	Alignment	not modelled	29.3	16	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
111	d1s24a_	Alignment	not modelled	29.3	16	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
112	c1s24A_	Alignment	not modelled	29.3	16	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubredoxin 2; **PDBTitle:** rubredoxin domain ii from pseudomonas oleovorans
113	d1x3za1	Alignment	not modelled	29.3	21	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
114	c2eozA_	Alignment	not modelled	29.2	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 473; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 809-2 841) of human zinc finger protein 473
115	d4rxna_	Alignment	not modelled	29.2	13	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
116	d1iu5a_	Alignment	not modelled	29.2	13	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
117	c2emwA_	Alignment	not modelled	28.9	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 268; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 301-2 331) of human zinc finger protein 268
118	d1q1aa_	Alignment	not modelled	28.8	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
119	d1j36a_	Alignment	not modelled	28.8	15	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
120	d1rb9a_	Alignment	not modelled	28.6	16	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin