Phyre^2

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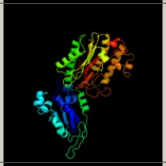
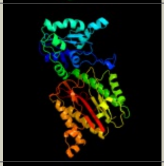
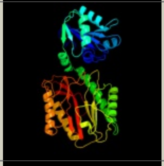
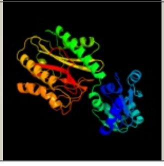
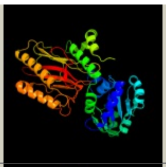
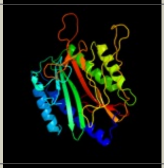
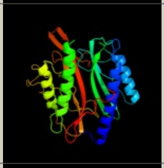
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3l24A_	Alignment		100.0	51	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**xaa-pro dipeptidase; **PDBTitle:** crystal structure of the nerve agent degrading2 organophosphate anhydrolase/prolidase in complex with3 inhibitors
2	c2oknB_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**xaa-pro dipeptidase; **PDBTitle:** crystal strcture of human prolidase
3	c1w7vD_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**xaa-pro aminopeptidase; **PDBTitle:** znmg substituted aminopeptidase p from e. coli
4	c3ig4E_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**xaa-pro aminopeptidase; **PDBTitle:** structure of a putative aminopeptidase p from bacillus anthracis
5	c3cb5A_	Alignment		100.0	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fact complex subunit spt16; **PDBTitle:** crystal structure of the s. pombe peptidase homology domain of fact2 complex subunit spt16 (form a)
6	c1chmA_	Alignment		100.0	21	**PDB header:**creatinase **Chain:** A: **PDB Molecule:**creatine amidinohydrolase; **PDBTitle:** enzymatic mechanism of creatine amidinohydrolase as deduced2 from crystal structures
7	c3ctzA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**xaa-pro aminopeptidase 1; **PDBTitle:** structure of human cytosolic x-prolyl aminopeptidase
8	c2howB_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**356aa long hypothetical dipeptidase; **PDBTitle:** dipeptidase (ph0974) from pyrococcus horikoshii ot3
9	c1wy2B_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**xaa-pro dipeptidase; **PDBTitle:** crystal structure of the prolidase from pyrococcus horikoshii ot3
10	c2zsgB_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminopeptidase p, putative; **PDBTitle:** crystal structure of x-pro aminopeptidase from thermotoga maritima2 msb8
11	c3q6dA_	Alignment		100.0	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**proline dipeptidase; **PDBTitle:** xaa-pro dipeptidase from bacillus anthracis.

12	c3bitA_	Alignment		100.0	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fact complex subunit spt16; **PDBTitle:** crystal structure of yeast spt16 n-terminal domain
13	c2g6pA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase 1; **PDBTitle:** crystal structure of truncated (delta 1-89) human methionine2 aminopeptidase type 1 in complex with pyridyl pyrimidine derivative
14	c2gz5A_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase 1; **PDBTitle:** human type 1 methionine aminopeptidase in complex with ovalicin at 1.12 ang
15	c3s6bA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** crystal structure of methionine aminopeptidase 1b from plasmodium2 falciparum, pf10_0150
16	c1yj3A_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** crystal structure analysis of product bound methionine2 aminopeptidase type 1c from mycobacterium tuberculosis
17	c3tavA_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** crystal structure of a methionine aminopeptidase from mycobacterium2 abscessus
18	d1o0xa_	Alignment		100.0	20	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
19	d2gg2a1	Alignment		100.0	19	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
20	d2v3za2	Alignment		100.0	33	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
21	c3mx6A_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** crystal structure of methionine aminopeptidase from rickettsia2 prowazekii bound to methionine
22	d1qxya_	Alignment	not modelled	100.0	20	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
23	d1chma2	Alignment	not modelled	100.0	23	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
24	c1kp0B_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**creatine amidinohydrolase; **PDBTitle:** the crystal structure analysis of creatine amidinohydrolase2 from actinobacillus
25	d1pv9a2	Alignment	not modelled	100.0	28	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
26	d1b6aa2	Alignment	not modelled	100.0	14	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
27	d1xgsa2	Alignment	not modelled	100.0	21	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
28	c2v6cA_	Alignment	not modelled	100.0	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**proliferation-associated protein 2g4; **PDBTitle:** crystal structure of erbb3 binding protein 1 (ebp1)
29	c2q8kA_	Alignment	not modelled	100.0	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**proliferation-associated protein 2g4;

						PDBTitle: the crystal structure of ebp1
30	c1xgnB_	Alignment	not modelled	100.0	21	**PDB header:**aminopeptidase **Chain:** B: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** methionine aminopeptidase from hyperthermophile pyrococcus2 furiosus
31	d1kp0a2	Alignment	not modelled	100.0	22	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
32	c1b6aA_	Alignment	not modelled	100.0	16	**PDB header:**angiogenesis inhibitor **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** human methionine aminopeptidase 2 complexed with tnp-470
33	c3fm3B_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**methionine aminopeptidase 2; **PDBTitle:** crystal structure of an encephalitozoon cuniculi methionine2 aminopeptidase type 2
34	c1yw7A_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase 2; **PDBTitle:** h-metap2 complexed with a444148
35	d2v3za1	Alignment	not modelled	99.6	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Creatinase/prolidase N-terminal domain **Family:**Creatinase/prolidase N-terminal domain
36	d1chma1	Alignment	not modelled	99.0	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Creatinase/prolidase N-terminal domain **Family:**Creatinase/prolidase N-terminal domain
37	c3pn9C_	Alignment	not modelled	99.0	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**proline dipeptidase; **PDBTitle:** crystal structure of a proline dipeptidase from streptococcus2 pneumoniae tigr4
38	c3i7mA_	Alignment	not modelled	98.8	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**xaa-pro dipeptidase; **PDBTitle:** n-terminal domain of xaa-pro dipeptidase from lactobacillus brevis.
39	c3il0B_	Alignment	not modelled	98.8	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminopeptidase p; xaa-pro aminopeptidase; **PDBTitle:** the crystal structure of the aminopeptidase p,xaa-pro aminopeptidase2 from streptococcus thermophilus
40	c3oooA_	Alignment	not modelled	98.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proline dipeptidase; **PDBTitle:** the structure of a proline dipeptidase from streptococcus agalactiae2 2603v
41	c3ovkD_	Alignment	not modelled	98.7	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**aminopeptidase p, xaa-pro dipeptidase; **PDBTitle:** crystal structure of an xxa-pro aminopeptidase from streptococcus2 pyogenes
42	c3o5vA_	Alignment	not modelled	98.5	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**x-pro dipeptidase; **PDBTitle:** the crystal structure of the creatinase/prolidase n-terminal domain of2 an x-pro dipeptidase from streptococcus pyogenes to 1.85a
43	d1pv9a1	Alignment	not modelled	98.3	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Creatinase/prolidase N-terminal domain **Family:**Creatinase/prolidase N-terminal domain
44	c3qocD_	Alignment	not modelled	98.2	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative metallopeptidase; **PDBTitle:** crystal structure of n-terminal domain (creatinase/prolidase like2 domain) of putative metallopeptidase from corynebacterium diphtheriae
45	d1kp0a1	Alignment	not modelled	89.8	26	**Fold:**Ribonuclease H-like motif **Superfamily:**Creatinase/prolidase N-terminal domain **Family:**Creatinase/prolidase N-terminal domain
46	d1wsaa_	Alignment	not modelled	63.1	20	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
47	d1o7ja_	Alignment	not modelled	53.8	19	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
48	d1agxa_	Alignment	not modelled	53.8	18	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
49	c3mpbA_	Alignment	not modelled	53.6	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar isomerase; **PDBTitle:** z5688 from e. coli o157:h7 bound to fructose
50	c2wltA_	Alignment	not modelled	48.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**l-asparaginase; **PDBTitle:** the crystal structure of helicobacter pylori l-asparaginase2 at 1.4 a resolution
51	c2d6fA_	Alignment	not modelled	37.1	10	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit d; **PDBTitle:** crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
52	d4pgaa_	Alignment	not modelled	36.9	21	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
53	c1utyA_	Alignment	not modelled	34.3	30	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 2; **PDBTitle:** crystal structure of the rna binding domain of bluetongue2 virus non-structural protein 2(ns2)
54	d1utya_	Alignment	not modelled	34.3	30	**Fold:**BTV NS2-like ssRNA-binding domain **Superfamily:**BTV NS2-like ssRNA-binding domain **Family:**BTV NS2-like ssRNA-binding domain
						PDB header:structural genomics,unknown function

55	c2c5qE_	Alignment	not modelled	33.4	9	**Chain:** E: **PDB Molecule:**rraa-like protein yer010c; **PDBTitle:** crystal structure of yeast yer010cp
56	d2d6fa2	Alignment	not modelled	32.8	11	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
57	d2olra1	Alignment	not modelled	32.1	18	**Fold:**PEP carboxykinase-like **Superfamily:**PEP carboxykinase-like **Family:**PEP carboxykinase C-terminal domain
58	c1zq1B_	Alignment	not modelled	31.5	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit d; **PDBTitle:** structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
59	c3nxkE_	Alignment	not modelled	29.2	16	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**cytoplasmic l-asparaginase; **PDBTitle:** crystal structure of probable cytoplasmic l-asparaginase from2 campylobacter jejuni
60	c2y0oA_	Alignment	not modelled	28.3	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable d-lyxose ketol-isomerase; **PDBTitle:** the structure of a d-lyxose isomerase from the sigmab2 regulon of bacillus subtilis
61	c2nyuA_	Alignment	not modelled	27.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative ribosomal rna methyltransferase 2; **PDBTitle:** crystal structure of human ftsj homolog 2 (e.coli) protein2 in complex with s-adenosylmethionine
62	d1j3ba1	Alignment	not modelled	26.8	25	**Fold:**PEP carboxykinase-like **Superfamily:**PEP carboxykinase-like **Family:**PEP carboxykinase C-terminal domain
63	d1xuca1	Alignment	not modelled	26.5	58	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
64	d1qiba_	Alignment	not modelled	25.5	50	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
65	d1i76a_	Alignment	not modelled	25.4	58	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
66	d1cxva_	Alignment	not modelled	24.9	58	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
67	d1hfca_	Alignment	not modelled	23.2	58	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
68	d1hy7a_	Alignment	not modelled	22.7	57	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
69	c2cltB_	Alignment	not modelled	20.3	64	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**interstitial collagenase; **PDBTitle:** crystal structure of the active form (full-length) of human2 fibroblast collagenase.
70	c3nojA_	Alignment	not modelled	19.2	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate **PDBTitle:** the structure of hmg/cha aldolase from the protocatechuate degradation2 pathway of pseudomonas putida
71	c1ylhA_	Alignment	not modelled	18.0	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate carboxykinase; **PDBTitle:** crystal structure of phosphoenolpyruvate carboxykinase from2 actinobaccilus succinogenes in complex with manganese and3 pyruvate
72	d2i47a1	Alignment	not modelled	16.3	43	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TNF-alpha converting enzyme, TACE, catalytic domain
73	d1eaka2	Alignment	not modelled	16.1	50	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
74	d1rm8a_	Alignment	not modelled	15.9	50	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
75	c2i47A_	Alignment	not modelled	15.5	40	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adam 17; **PDBTitle:** crystal structure of catalytic domain of tace with inhibitor
76	c1yp1A_	Alignment	not modelled	15.2	47	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fii; **PDBTitle:** crystal structure of a non-hemorrhagic fibrin(ogen)olytic2 metalloproteinase from venom of agkistrodon acutus
77	d1bqqm_	Alignment	not modelled	14.5	60	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
78	c3k7lA_	Alignment	not modelled	14.4	47	**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
79	c3edhA_	Alignment	not modelled	14.4	42	**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
80	d1r55a_	Alignment	not modelled	14.2	67	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like

81	d2ovxa1	Alignment	not modelled	14.0	60	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
82	d1q3aa_	Alignment	not modelled	14.0	60	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
83	c2erpA_	Alignment	not modelled	14.0	47	**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)
84	c1slmA_	Alignment	not modelled	13.8	70	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**stromelysin-1; **PDBTitle:** crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
85	c3jr1A_	Alignment	not modelled	13.8	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative fructosamine-3-kinase; **PDBTitle:** crystal structure of putative fructosamine-3-kinase2 (yp_719053.1) from haemophilus somnus 129pt at 2.32 a3 resolution
86	d1wnia_	Alignment	not modelled	13.7	57	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
87	d1atla_	Alignment	not modelled	13.6	50	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
88	d1fbla2	Alignment	not modelled	13.5	60	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
89	c2xs4A_	Alignment	not modelled	13.4	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**karilysin protease; **PDBTitle:** structure of karilysin catalytic mmp domain in complex with2 magnesium
90	c2dw1B_	Alignment	not modelled	13.4	47	**PDB header:**apoptosis, toxin **Chain:** B: **PDB Molecule:**catrocollastatin; **PDBTitle:** crystal structure of vap2 from crotalus atrox venom (form 2-2 crystal)
91	d1nd1a_	Alignment	not modelled	13.4	47	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
92	d1hova_	Alignment	not modelled	13.3	50	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
93	d1cgla_	Alignment	not modelled	13.2	60	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
94	c2rjqA_	Alignment	not modelled	13.2	56	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adamts-5; **PDBTitle:** crystal structure of adamts5 with inhibitor bound
95	c3lqbA_	Alignment	not modelled	13.1	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**loc792177 protein; **PDBTitle:** crystal structure of the hatching enzyme zhe1 from the zebrafish danio2 rerio
96	d1y93a1	Alignment	not modelled	13.0	58	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
97	d1bswa_	Alignment	not modelled	13.0	35	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
98	d4aiga_	Alignment	not modelled	12.8	47	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
99	d1hv5a_	Alignment	not modelled	12.4	70	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain