Phyre^2

Email	l.a.kelley@imperial.ac.uk
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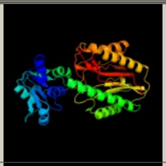
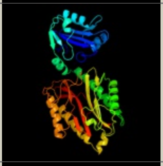
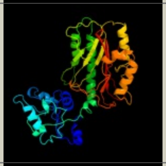
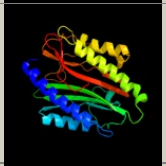
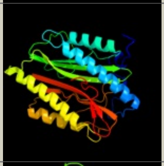
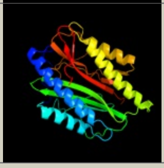
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3q6dA_	Alignment		100.0	44	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**proline dipeptidase; **PDBTitle:** xaa-pro dipeptidase from bacillus anthracis.
2	c1wy2B_	Alignment		100.0	39	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**xaa-pro dipeptidase; **PDBTitle:** crystal structure of the prolidase from pyrococcus horikoshii ot3
3	c2howB_	Alignment		100.0	32	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**356aa long hypothetical dipeptidase; **PDBTitle:** dipeptidase (ph0974) from pyrococcus horikoshii ot3
4	c2zsgB_	Alignment		100.0	37	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminopeptidase p, putative; **PDBTitle:** crystal structure of x-pro aminopeptidase from thermotoga maritima2 msb8
5	c1chmA_	Alignment		100.0	23	**PDB header:**creatinase **Chain:** A: **PDB Molecule:**creatine amidinohydrolase; **PDBTitle:** enzymatic mechanism of creatine amidinohydrolase as deduced2 from crystal structures
6	c3ctzA_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**xaa-pro aminopeptidase 1; **PDBTitle:** structure of human cytosolic x-prolyl aminopeptidase
7	c1w7vD_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**xaa-pro aminopeptidase; **PDBTitle:** znmg substituted aminopeptidase p from e. coli
8	c2oknB_	Alignment		100.0	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**xaa-pro dipeptidase; **PDBTitle:** crystal strcture of human prolidase
9	c3cb5A_	Alignment		100.0	19	**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)
10	c3ig4E_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**xaa-pro aminopeptidase; **PDBTitle:** structure of a putative aminopeptidase p from bacillus anthracis
11	c3l24A_	Alignment		100.0	24	**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

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	c1kp0B_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**creatine amidinohydrolase; **PDBTitle:** the crystal structure analysis of creatine amidinohydrolase2 from actinobacillus
14	d1pv9a2	Alignment		100.0	51	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
15	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
16	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
17	c3s6bA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** crystal structure of methionine aminopeptidase 1b from plasmodium2 falciparum, pf10_0150
18	c3mx6A_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** crystal structure of methionine aminopeptidase from rickettsia2 prowazekii bound to methionine
19	d1chma2	Alignment		100.0	28	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
20	c1yj3A_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** crystal structure analysis of product bound methionine2 aminopeptidase type 1c from mycobacterium tuberculosis
21	d2gg2a1	Alignment	not modelled	100.0	25	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
22	c3tavA_	Alignment	not modelled	100.0	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** crystal structure of a methionine aminopeptidase from mycobacterium2 abscessus
23	d2v3za2	Alignment	not modelled	100.0	33	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
24	d1o0xa_	Alignment	not modelled	100.0	27	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
25	d1qxya_	Alignment	not modelled	100.0	25	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
26	d1b6aa2	Alignment	not modelled	100.0	18	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
27	c2v6cA_	Alignment	not modelled	100.0	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**proliferation-associated protein 2g4; **PDBTitle:** crystal structure of erbb3 binding protein 1 (ebp1)
28	d1xgsa2	Alignment	not modelled	100.0	24	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
29	c2q8kA_	Alignment	not modelled	100.0	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**proliferation-associated protein 2g4;

						PDBTitle: the crystal structure of ebp1
30	c1xgnB_	Alignment	not modelled	100.0	26	**PDB header:**aminopeptidase **Chain:** B: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** methionine aminopeptidase from hyperthermophile pyrococcus2 furiosus
31	d1kp0a2	Alignment	not modelled	100.0	27	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
32	c1b6aA_	Alignment	not modelled	100.0	26	**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	20	**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	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase 2; **PDBTitle:** h-metap2 complexed with a444148
35	c3pn9C_	Alignment	not modelled	99.7	10	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**proline dipeptidase; **PDBTitle:** crystal structure of a proline dipeptidase from streptococcus2 pneumoniae tigr4
36	c3ovkD_	Alignment	not modelled	99.7	24	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**aminopeptidase p, xaa-pro dipeptidase; **PDBTitle:** crystal structure of an xxa-pro aminopeptidase from streptococcus2 pyogenes
37	c3il0B_	Alignment	not modelled	99.7	21	**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
38	c3oooA_	Alignment	not modelled	99.7	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proline dipeptidase; **PDBTitle:** the structure of a proline dipeptidase from streptococcus agalactiae2 2603v
39	d1chma1	Alignment	not modelled	99.6	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Creatinase/prolidase N-terminal domain **Family:**Creatinase/prolidase N-terminal domain
40	c3i7mA_	Alignment	not modelled	99.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**xaa-pro dipeptidase; **PDBTitle:** n-terminal domain of xaa-pro dipeptidase from lactobacillus brevis.
41	c3o5vA_	Alignment	not modelled	99.6	9	**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
42	c3qocD_	Alignment	not modelled	99.6	18	**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
43	d1pv9a1	Alignment	not modelled	99.5	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Creatinase/prolidase N-terminal domain **Family:**Creatinase/prolidase N-terminal domain
44	d1kp0a1	Alignment	not modelled	98.3	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Creatinase/prolidase N-terminal domain **Family:**Creatinase/prolidase N-terminal domain
45	d2v3za1	Alignment	not modelled	97.8	8	**Fold:**Ribonuclease H-like motif **Superfamily:**Creatinase/prolidase N-terminal domain **Family:**Creatinase/prolidase N-terminal domain
46	c2y0oA_	Alignment	not modelled	53.5	13	**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
47	c3mpbA_	Alignment	not modelled	41.9	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar isomerase; **PDBTitle:** z5688 from e. coli o157:h7 bound to fructose
48	d1rp1a2	Alignment	not modelled	27.3	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
49	c3prdA_	Alignment	not modelled	26.7	27	**PDB header:**chaperone, isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase; **PDBTitle:** structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
50	c2pplA_	Alignment	not modelled	26.1	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pancreatic lipase-related protein 1; **PDBTitle:** human pancreatic lipase-related protein 1
51	d1hpla2	Alignment	not modelled	25.9	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
52	d1l1pa_	Alignment	not modelled	25.6	38	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
53	d1e4cp_	Alignment	not modelled	25.5	25	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
54	d1etha2	Alignment	not modelled	24.2	23	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
						PDB header:structural genomics,unknown function

55	c2c5qE_	Alignment	not modelled	23.1	17	**Chain:** E: **PDB Molecule:**rraa-like protein yer010c; **PDBTitle:** crystal structure of yeast yer010cp
56	d1lpbb2	Alignment	not modelled	22.4	23	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
57	c2pvsB_	Alignment	not modelled	22.1	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**pancreatic lipase-related protein 2; **PDBTitle:** structure of human pancreatic lipase related protein 22 mutant n336q
58	d1gpla2	Alignment	not modelled	21.8	23	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
59	c1hplB_	Alignment	not modelled	21.0	20	**PDB header:**hydrolase(carboxylic esterase) **Chain:** B: **PDB Molecule:**lipase; **PDBTitle:** horse pancreatic lipase. the crystal structure at 2.32 angstroms resolution
60	d1t11a3	Alignment	not modelled	21.0	29	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
61	d1bu8a2	Alignment	not modelled	20.8	27	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
62	c1rp1A_	Alignment	not modelled	20.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pancreatic lipase related protein 1; **PDBTitle:** dog pancreatic lipase related protein 1
63	c1gplA_	Alignment	not modelled	18.8	23	**PDB header:**serine esterase **Chain:** A: **PDB Molecule:**rp2 lipase; **PDBTitle:** rp2 lipase
64	c2opiB_	Alignment	not modelled	15.5	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**l-fuculose-1-phosphate aldolase; **PDBTitle:** crystal structure of l-fuculose-1-phosphate aldolase from bacteroides2 thetaiotaomicron
65	c2gezE_	Alignment	not modelled	15.1	12	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**l-asparaginase alpha subunit; **PDBTitle:** crystal structure of potassium-independent plant asparaginase
66	c1htrP_	Alignment	not modelled	14.9	25	**PDB header:**aspartyl protease **Chain:** P: **PDB Molecule:**progastricsin (pro segment); **PDBTitle:** crystal and molecular structures of human progastricsin at 1.622 angstroms resolution
67	d1b25a2	Alignment	not modelled	14.8	20	**Fold:**Aldehyde ferredoxin oxidoreductase, N-terminal domain **Superfamily:**Aldehyde ferredoxin oxidoreductase, N-terminal domain **Family:**Aldehyde ferredoxin oxidoreductase, N-terminal domain
68	c2kw0A_	Alignment	not modelled	14.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ccmh protein; **PDBTitle:** solution structure of n-terminal domain of ccmh from escherichia.coli
69	d1rm4a1	Alignment	not modelled	14.3	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
70	d1aora2	Alignment	not modelled	14.0	26	**Fold:**Aldehyde ferredoxin oxidoreductase, N-terminal domain **Superfamily:**Aldehyde ferredoxin oxidoreductase, N-terminal domain **Family:**Aldehyde ferredoxin oxidoreductase, N-terminal domain
71	c3a9lB_	Alignment	not modelled	13.8	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**poly-gamma-glutamate hydrolase; **PDBTitle:** structure of bacteriophage poly-gamma-glutamate hydrolase
72	c2gacA_	Alignment	not modelled	13.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosylasparaginase; **PDBTitle:** t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum
73	c1avfQ_	Alignment	not modelled	12.7	25	**PDB header:**aspartyl protease **Chain:** Q: **PDB Molecule:**gastricsin; **PDBTitle:** activation intermediate 2 of human gastricsin from human2 stomach
74	c2zakB_	Alignment	not modelled	12.5	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**l-asparaginase precursor; **PDBTitle:** orthorhombic crystal structure of precursor e. coli isoaspartyl2 peptidase/l-asparaginase (ecaiii) with active-site t179a mutation
75	c3ds8A_	Alignment	not modelled	11.3	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2722 protein; **PDBTitle:** the crysatl structure of the gene lin2722 products from listeria2 innocua
76	c2a8lB_	Alignment	not modelled	11.1	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**threonine aspartase 1; **PDBTitle:** crystal structure of human taspase1 (t234a mutant)
77	d1hq0a_	Alignment	not modelled	10.9	14	**Fold:**CNF1/YfiH-like putative cysteine hydrolases **Superfamily:**CNF1/YfiH-like putative cysteine hydrolases **Family:**Type 1 cytotoxic necrotizing factor, catalytic domain
78	d1eaka2	Alignment	not modelled	10.7	60	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
79	d1ex9a_	Alignment	not modelled	10.6	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
80	d1bqqm_	Alignment	not modelled	10.1	60	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
81	c3edhA_	Alignment	not modelled	10.0	46	**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
82	d1lgya_	Alignment	not modelled	10.0	22	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
83	d3tgla_	Alignment	not modelled	10.0	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
84	d1tiba_	Alignment	not modelled	9.9	26	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
85	c2b76N_	Alignment	not modelled	9.9	16	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**fumarate reductase iron-sulfur protein; **PDBTitle:** e. coli quinol fumarate reductase frda e49q mutation
86	d1tiaa_	Alignment	not modelled	9.9	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
87	c3lqbA_	Alignment	not modelled	9.7	46	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**loc792177 protein; **PDBTitle:** crystal structure of the hatching enzyme zhe1 from the zebrafish danio2 rerio
88	c2hl7A_	Alignment	not modelled	9.6	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c-type biogenesis protein ccmh; **PDBTitle:** crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
89	d2ovxa1	Alignment	not modelled	9.5	50	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
90	c1slmA_	Alignment	not modelled	9.5	40	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**stromelysin-1; **PDBTitle:** crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
91	d1rm8a_	Alignment	not modelled	9.5	60	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
92	d1hova_	Alignment	not modelled	9.4	60	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
93	c3re1B_	Alignment	not modelled	9.3	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen-iii synthetase; **PDBTitle:** crystal structure of uroporphyrinogen iii synthase from pseudomonas2 syringae pv. tomato dc3000
94	c2kxxA_	Alignment	not modelled	9.3	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**small protein a; **PDBTitle:** nmr structure of escherichia coli bame, a lipoprotein component of the2 beta-barrel assembly machinery complex
95	c3nr7A_	Alignment	not modelled	9.2	33	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding protein h-ns; **PDBTitle:** crystal structure of s. typhimurium h-ns 1-83
96	d1q3aa_	Alignment	not modelled	9.2	40	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
97	c3o0dF_	Alignment	not modelled	9.1	33	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**triacylglycerol lipase; **PDBTitle:** crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
98	d1w26a3	Alignment	not modelled	9.0	37	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
99	d1cgla_	Alignment	not modelled	9.0	40	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain