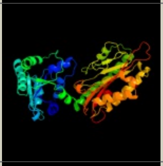
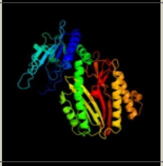
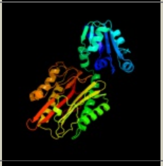
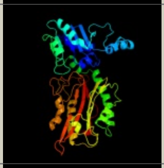
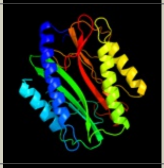
Email	l.a.kelley@imperial.ac.uk
Description	P15034
Date	Thu Jan 5 11:34:21 GMT 2012
Unique Job ID	0bbee394a4875b49

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1w7vD_	Alignment		100.0	99	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**xaa-pro aminopeptidase; **PDBTitle:** znmg substituted aminopeptidase p from e. coli
2	c3ig4E_	Alignment		100.0	31	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**xaa-pro aminopeptidase; **PDBTitle:** structure of a putative aminopeptidase p from bacillus anthracis
3	c2oknB_	Alignment		100.0	35	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**xaa-pro dipeptidase; **PDBTitle:** crystal strcture of human prolidase
4	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)
5	c3l24A_	Alignment		100.0	25	**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
6	c1chmA_	Alignment		100.0	22	**PDB header:**creatinase **Chain:** A: **PDB Molecule:**creatine amidinohydrolase; **PDBTitle:** enzymatic mechanism of creatine amidinohydrolase as deduced2 from crystal structures
7	c3bitA_	Alignment		100.0	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fact complex subunit spt16; **PDBTitle:** crystal structure of yeast spt16 n-terminal domain
8	c1wy2B_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**xaa-pro dipeptidase; **PDBTitle:** crystal structure of the prolidase from pyrococcus horikoshii ot3
9	c2zsgB_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminopeptidase p, putative; **PDBTitle:** crystal structure of x-pro aminopeptidase from thermotoga maritima2 msb8
10	c2howB_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**356aa long hypothetical dipeptidase; **PDBTitle:** dipeptidase (ph0974) from pyrococcus horikoshii ot3
11	c3q6dA_	Alignment		100.0	29	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**proline dipeptidase; **PDBTitle:** xaa-pro dipeptidase from bacillus anthracis.

12	d2v3za2	Alignment		100.0	98	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
13	c3ctzA_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**xaa-pro aminopeptidase 1; **PDBTitle:** structure of human cytosolic x-prolyl aminopeptidase
14	c2g6pA_	Alignment		100.0	19	**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
15	c2gz5A_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase 1; **PDBTitle:** human type 1 methionine aminopeptidase in complex with ovalicin at 1.12 ang
16	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
17	c1yj3A_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** crystal structure analysis of product bound methionine2 aminopeptidase type 1c from mycobacterium tuberculosis
18	c3mx6A_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** crystal structure of methionine aminopeptidase from rickettsia2 prowazekii bound to methionine
19	c3tavA_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** crystal structure of a methionine aminopeptidase from mycobacterium2 abscessus
20	d2gg2a1	Alignment		100.0	27	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
21	d1chma2	Alignment	not modelled	100.0	26	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
22	d1o0xa_	Alignment	not modelled	100.0	24	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
23	d1pv9a2	Alignment	not modelled	100.0	36	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
24	d1qxya_	Alignment	not modelled	100.0	22	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
25	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
26	d1b6aa2	Alignment	not modelled	100.0	17	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
27	c2v6cA_	Alignment	not modelled	100.0	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**proliferation-associated protein 2g4; **PDBTitle:** crystal structure of erbb3 binding protein 1 (ebp1)
28	c2q8kA_	Alignment	not modelled	100.0	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**proliferation-associated protein 2g4; **PDBTitle:** the crystal structure of ebp1
29	d1xgsa2	Alignment	not modelled	100.0	23	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase

						Family: Creatinase/aminopeptidase
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	22	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
32	c1b6aA_	Alignment	not modelled	100.0	19	**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	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase 2; **PDBTitle:** h-metap2 complexed with a444148
35	d2v3za1	Alignment	not modelled	99.9	100	**Fold:**Ribonuclease H-like motif **Superfamily:**Creatinase/prolidase N-terminal domain **Family:**Creatinase/prolidase N-terminal domain
36	d1chma1	Alignment	not modelled	99.4	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Creatinase/prolidase N-terminal domain **Family:**Creatinase/prolidase N-terminal domain
37	c3pn9C_	Alignment	not modelled	99.2	13	**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	99.2	12	**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	99.2	14	**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	c3ovkD_	Alignment	not modelled	99.1	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**aminopeptidase p, xaa-pro dipeptidase; **PDBTitle:** crystal structure of an xxa-pro aminopeptidase from streptococcus2 pyogenes
41	c3oooA_	Alignment	not modelled	99.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proline dipeptidase; **PDBTitle:** the structure of a proline dipeptidase from streptococcus agalactiae2 2603v
42	c3qocD_	Alignment	not modelled	99.0	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
43	c3o5vA_	Alignment	not modelled	98.7	16	**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
44	d1pv9a1	Alignment	not modelled	98.6	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Creatinase/prolidase N-terminal domain **Family:**Creatinase/prolidase N-terminal domain
45	d1kp0a1	Alignment	not modelled	96.0	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Creatinase/prolidase N-terminal domain **Family:**Creatinase/prolidase N-terminal domain
46	c3mpbA_	Alignment	not modelled	67.4	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar isomerase; **PDBTitle:** z5688 from e. coli o157:h7 bound to fructose
47	c2c5qE_	Alignment	not modelled	63.4	10	**PDB header:**structural genomics,unknown function **Chain:** E: **PDB Molecule:**rraa-like protein yer010c; **PDBTitle:** crystal structure of yeast yer010cp
48	d1j3ba1	Alignment	not modelled	45.7	16	**Fold:**PEP carboxykinase-like **Superfamily:**PEP carboxykinase-like **Family:**PEP carboxykinase C-terminal domain
49	c3nojA_	Alignment	not modelled	45.7	12	**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
50	c2fk5B_	Alignment	not modelled	35.6	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fuculose-1-phosphate aldolase; **PDBTitle:** crystal structure of l-fuculose-1-phosphate aldolase from thermus2 thermophilus hb8
51	d1y7ma2	Alignment	not modelled	35.5	21	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
52	d1l1pa_	Alignment	not modelled	35.1	25	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
53	c2xrhA_	Alignment	not modelled	31.2	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein hp0721; **PDBTitle:** crystal structure of the truncated form of hp0721
54	d1t11a3	Alignment	not modelled	30.1	25	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
						PDB header:isomerase

55	c2y0oA_	Alignment	not modelled	29.8	30	**Chain:** A: **PDB Molecule:**probable d-lyxose ketol-isomerase; **PDBTitle:** the structure of a d-lyxose isomerase from the sigmab2 regulon of bacillus subtilis
56	c3k4iC_	Alignment	not modelled	28.5	13	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein pspto_3204 from2 pseudomonas syringae pv. tomato str. dc3000
57	d1e4cp_	Alignment	not modelled	28.5	24	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
58	c3hgkE_	Alignment	not modelled	25.4	19	**PDB header:**transferase **Chain:** E: **PDB Molecule:**effector protein hopab2; **PDBTitle:** crystal structure of effect protein avrptob complexed with2 kinase pto
59	d2olra1	Alignment	not modelled	24.8	15	**Fold:**PEP carboxykinase-like **Superfamily:**PEP carboxykinase-like **Family:**PEP carboxykinase C-terminal domain
60	c2zakB_	Alignment	not modelled	19.9	23	**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
61	c1t3mA_	Alignment	not modelled	18.6	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
62	c2a8lB_	Alignment	not modelled	17.3	5	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**threonine aspartase 1; **PDBTitle:** crystal structure of human taspase1 (t234a mutant)
63	c3prdA_	Alignment	not modelled	17.1	23	**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
64	c2gezE_	Alignment	not modelled	16.4	14	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**l-asparaginase alpha subunit; **PDBTitle:** crystal structure of potassium-independent plant asparaginase
65	c2opiB_	Alignment	not modelled	16.0	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**l-fuculose-1-phosphate aldolase; **PDBTitle:** crystal structure of l-fuculose-1-phosphate aldolase from bacteroides2 thetaiotaomicron
66	d1xuca1	Alignment	not modelled	14.7	58	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
67	d1qiba_	Alignment	not modelled	14.3	42	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
68	c3czqA_	Alignment	not modelled	14.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative polyphosphate kinase 2; **PDBTitle:** crystal structure of putative polyphosphate kinase 2 from2 sinorhizobium meliloti
69	d1i76a_	Alignment	not modelled	13.9	50	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
70	d1cxva_	Alignment	not modelled	13.9	67	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
71	c2nyuA_	Alignment	not modelled	13.9	20	**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
72	d1s1ma2	Alignment	not modelled	13.2	32	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
73	d1vqqa1	Alignment	not modelled	12.7	12	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Penicillin binding protein 2a (PBP2A), N-terminal domain
74	d1vcoa2	Alignment	not modelled	12.5	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
75	c3fmyA_	Alignment	not modelled	12.4	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator mqsa **PDBTitle:** structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
76	d1eaka2	Alignment	not modelled	12.4	40	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
77	c1yvyA_	Alignment	not modelled	12.3	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate carboxykinase [atp]; **PDBTitle:** crystal strucutre of anaerobiospirillum succiniciproducens2 phosphoenolpyruvate carboxykinase
78	d1w26a3	Alignment	not modelled	12.1	25	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
79	d1m1fa_	Alignment	not modelled	11.5	18	**Fold:**SH3-like barrel **Superfamily:**Cell growth inhibitor/plasmid maintenance toxic component **Family:**Kid/PemK
80	d1mlda2	Alignment	not modelled	11.5	19	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain

81	c3nvaB_	Alignment	not modelled	11.4	28	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** dimeric form of ctp synthase from sulfolobus solfataricus
82	d1q5rh_	Alignment	not modelled	11.1	23	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
83	c3jr1A_	Alignment	not modelled	10.2	18	**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
84	c1w26B_	Alignment	not modelled	9.9	22	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**trigger factor; **PDBTitle:** trigger factor in complex with the ribosome forms a2 molecular cradle for nascent proteins
85	d1c3ha_	Alignment	not modelled	9.2	19	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
86	d2ovxa1	Alignment	not modelled	9.2	60	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
87	d1eg7a_	Alignment	not modelled	9.2	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
88	c2kw0A_	Alignment	not modelled	9.1	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ccmh protein; **PDBTitle:** solution structure of n-terminal domain of ccmh from escherichia.coli
89	c2plwA_	Alignment	not modelled	8.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna methyltransferase, putative; **PDBTitle:** crystal structure of a ribosomal rna methyltransferase, putative, from2 plasmodium falciparum (pf13_0052).
90	d1rm8a_	Alignment	not modelled	8.7	60	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
91	d2k57a1	Alignment	not modelled	8.7	15	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**YgdI/YgdR-like
92	c1hxvA_	Alignment	not modelled	8.7	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** ppiase domain of the mycoplasma genitalium trigger factor
93	d1hxva_	Alignment	not modelled	8.7	22	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
94	c1slmA_	Alignment	not modelled	8.7	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**stromelysin-1; **PDBTitle:** crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
95	d1q3aa_	Alignment	not modelled	8.6	60	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
96	c3ocrA_	Alignment	not modelled	8.6	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**class ii aldolase/adducin domain protein; **PDBTitle:** crystal structure of aldolase ii superfamily protein from pseudomonas2 syringae
97	c1qs2A_	Alignment	not modelled	8.4	18	**PDB header:**toxin **Chain:** A: **PDB Molecule:**adp-ribosyltransferase; **PDBTitle:** crystal structure of vip2 with nad
98	c3sviA_	Alignment	not modelled	8.3	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**type iii effector hopab2; **PDBTitle:** structure of the pto-binding domain of hoppmal generated by limited2 thermolysin digestion
99	c2irpA_	Alignment	not modelled	8.2	32	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative aldolase class 2 protein aq_1979; **PDBTitle:** crystal structure of the l-fuculose-1-phosphate aldolase (aq_1979)2 from aquifex aeolicus vf5