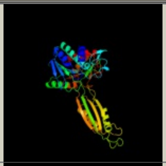
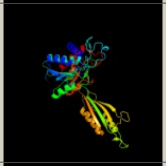
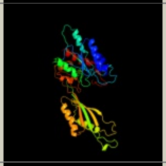
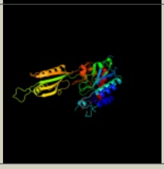
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0AED7
Date	Thu Jan 5 11:23:04 GMT 2012
Unique Job ID	2cd4e38e85ffa5c8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1vgyB_	Alignment		100.0	56	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of succinyl diaminopimelate desuccinylase
2	c3ic1A_	Alignment		100.0	60	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of zinc-bound succinyl-diaminopimelate desuccinylase2 from haemophilus influenzae
3	c3pfoB_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative acetylornithine deacetylase; **PDBTitle:** crystal structure of a putative acetylornithine deacetylase (rpa2325)2 from rhodopseudomonas palustris cga009 at 1.90 a resolution
4	c2zogA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosolic non-specific dipeptidase; **PDBTitle:** crystal structure of mouse carnosinase cn2 complexed with zn and2 bestatin
5	c2pokB_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase, m20/m25/m40 family; **PDBTitle:** crystal structure of a m20 family metallo peptidase from streptococcus2 pneumoniae
6	c3dljB_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-ala-his dipeptidase; **PDBTitle:** crystal structure of human carnosine dipeptidase 1
7	c2rb7A_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase, m20/m25/m40 family; **PDBTitle:** crystal structure of co-catalytic metallopeptidase (yp_387682.1) from2 desulfovibrio desulfuricans g20 at 1.60 a resolution
8	c3mruB_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminoacyl-histidine dipeptidase; **PDBTitle:** crystal structure of aminoacylhistidine dipeptidase from vibrio2 alginolyticus
9	c1cg2D_	Alignment		100.0	22	**PDB header:**metallocarboxypeptidase **Chain:** D: **PDB Molecule:**carboxypeptidase g2; **PDBTitle:** carboxypeptidase g2
10	c3rzaA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tripeptidase; **PDBTitle:** crystal structure of a tripeptidase (sav1512) from staphylococcus2 aureus subsp. aureus mu50 at 2.10 a resolution
11	c3pfeA_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of a m20a metallo peptidase (dape, lpg0809) from2 legionella pneumophila subsp. pneumophila str. philadelphia 1 at 1.503 a resolution

12	c3gb0A_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase t; **PDBTitle:** crystal structure of aminopeptidase pept (np_980509.1) from bacillus2 cereus atcc 10987 at 2.04 a resolution
13	c3tx8A_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of a succinyl-diaminopimelate desuccinylase (arge)2 from corynebacterium glutamicum atcc 13032 at 2.97 a resolution
14	c3ct9B_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acetylornithine deacetylase; **PDBTitle:** crystal structure of a putative zinc peptidase (np_812461.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.31 a resolution
15	c2f7vA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aectylcitrulline deacetylase; **PDBTitle:** structure of acetylcitrulline deacetylase complexed with2 one co
16	c2qyvB_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**xaa-his dipeptidase; **PDBTitle:** crystal structure of putative xaa-his dipeptidase (yp_718209.1) from2 haemophilus somnus 129pt at 2.11 a resolution
17	c3ifeA_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase t; **PDBTitle:** 1.55 angstrom resolution crystal structure of peptidase t (pept-1)2 from bacillus anthracis str. 'ames ancestor'.
18	c1lfwA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pepv; **PDBTitle:** crystal structure of pepv
19	c3ramC_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**hmra protein; **PDBTitle:** crystal structure of hmra
20	c1vixA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase t; **PDBTitle:** crystal structure of a putative peptidase t
21	c3n5fB_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**n-carbamoyl-l-amino acid hydrolase; **PDBTitle:** crystal structure of l-n-carbamoylase from geobacillus2 stearothermophilus cect43
22	c2v8gD_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-alanine synthase; **PDBTitle:** crystal structure of beta-alanine synthase from2 saccharomyces kluyveri in complex with the product beta-3 alanine
23	c3khzA_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative dipeptidase sacol1801; **PDBTitle:** crystal structure of r350a mutant of staphylococcus aureus2 metallopeptidase (sapep/dape) in the apo-form
24	c2imoA_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**allantoate amidohydrolase; **PDBTitle:** crystal structure of allantoate amidohydrolase from escherichia coli2 at ph 4.6
25	c1ysjB_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein yxep; **PDBTitle:** crystal structure of bacillus subtilis yxep protein (apc1829), a2 dinuclear metal binding peptidase from m20 family
26	c2q43A_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**iaa-amino acid hydrolase ilr1-like 2; **PDBTitle:** ensemble refinement of the protein crystal structure of iaa-aminoacid2 hydrolase from arabidopsis thaliana gene at5g56660
27	c3io1B_	Alignment	not modelled	100.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminobenzoyl-glutamate utilization protein; **PDBTitle:** crystal structure of aminobenzoyl-glutamate utilization2 protein from klebsiella pneumoniae
28	c1vheA_	Alignment	not modelled	100.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**aminopeptidase/glucanase homolog;

28	c1vheA_	Alignment	not modelled	100.0	[illegible]	**PDBTitle:** crystal structure of a aminopeptidase/glucanase homolog
29	c3t6mA_	Alignment	not modelled	100.0	68	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of the catalytic domain of dape protein from2 v.cholerea in the zn bound form
30	c1yloA_	Alignment	not modelled	100.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein sf2450; **PDBTitle:** crystal structure of protein of unknown function (possible2 aminopeptidase) s2589 from shigella flexneri 2a str. 2457t
31	c2cf4A_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein ph0519; **PDBTitle:** pyrococcus horikoshii tet1 peptidase can assemble into a2 tetrahedron or a large octahedral shell
32	c3isxA_	Alignment	not modelled	100.0	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of endoglucanase (tm1050) from thermotoga2 maritima at 1.40 a resolution
33	c1vhoA_	Alignment	not modelled	100.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of a putative peptidase/endoglucanase
34	c1y0yA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**frv operon protein frvx; **PDBTitle:** crystal structure of tetrahedral aminopeptidase from p. horikoshii in2 complex with amastatin
35	c3kl9F_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**glutamyl aminopeptidase; **PDBTitle:** crystal structure of pepa from streptococcus pneumoniae
36	c2pe3A_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**354aa long hypothetical operon protein frv; **PDBTitle:** crystal structure of frv operon protein frvx (ph1821)from pyrococcus2 horikoshii ot3
37	d1lfwa1	Alignment	not modelled	100.0	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
38	d1vixa1	Alignment	not modelled	100.0	21	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
39	d1z2la1	Alignment	not modelled	100.0	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
40	d1cg2a1	Alignment	not modelled	100.0	28	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
41	d1fnoa4	Alignment	not modelled	100.0	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
42	c2fvgA_	Alignment	not modelled	100.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of endoglucanase (tm1049) from thermotoga maritima2 at 2.01 a resolution
43	d1vgya1	Alignment	not modelled	100.0	43	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
44	d1vhea2	Alignment	not modelled	100.0	18	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
45	c3cpxC_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**aminopeptidase, m42 family; **PDBTitle:** crystal structure of putative m42 glutamyl aminopeptidase2 (yp_676701.1) from cytophaga hutchinsonii atcc 33406 at 2.39 a3 resolution
46	d1yloa2	Alignment	not modelled	100.0	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
47	d1xfoa2	Alignment	not modelled	100.0	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
48	d1xmba1	Alignment	not modelled	100.0	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
49	d1vhoa2	Alignment	not modelled	100.0	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
50	d1r3na1	Alignment	not modelled	100.0	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
51	c2greC_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**deblocking aminopeptidase; **PDBTitle:** crystal structure of deblocking aminopeptidase from bacillus cereus
52	c1q7lA_	Alignment	not modelled	99.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminoacylase-1; **PDBTitle:** zn-binding domain of the t347g mutant of human aminoacylase-2 i
53	d1ysja1	Alignment	not modelled	99.9	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
54	d2fvga2	Alignment	not modelled	99.9	16	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases

						Family: Bacterial dinuclear zinc exopeptidases
55	d2grea2	Alignment	not modelled	99.9	18	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
56	d1tkja1	Alignment	not modelled	99.7	22	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
57	d1vgya2	Alignment	not modelled	99.6	61	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
58	d1rtqa_	Alignment	not modelled	99.6	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
59	c3tc8A_	Alignment	not modelled	99.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leucine aminopeptidase; **PDBTitle:** crystal structure of a hypothetical zn-dependent exopeptidase2 (bdi_3547) from parabacteroides distasonis atcc 8503 at 1.06 a3 resolution
60	d1z2la2	Alignment	not modelled	99.4	16	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
61	d1cg2a2	Alignment	not modelled	99.4	16	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
62	c2glfB_	Alignment	not modelled	99.4	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable m18-family aminopeptidase 1; **PDBTitle:** crystal structure of aminipeptidase (m18 family) from thermotoga2 maritima
63	d1y0ya2	Alignment	not modelled	99.3	18	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
64	c3pb6X_	Alignment	not modelled	99.3	21	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glutaminyl-peptide cyclotransferase-like protein; **PDBTitle:** crystal structure of the catalytic domain of human golgi-resident2 glutaminyl cyclase at ph 6.5
65	c1q7lB_	Alignment	not modelled	99.3	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminoacylase-1; **PDBTitle:** zn-binding domain of the t347g mutant of human aminoacylase-2 i
66	c3l6sA_	Alignment	not modelled	99.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aspartyl aminopeptidase; **PDBTitle:** crystal structure of human aspartyl aminopeptidase (dnpep),2 in complex with aspartic acid hydroxamate
67	d2afwa1	Alignment	not modelled	99.3	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Glutaminyl-peptide cyclotransferase-like
68	d1r3na2	Alignment	not modelled	99.3	21	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
69	c3guxA_	Alignment	not modelled	99.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative zn-dependent exopeptidase; **PDBTitle:** crystal structure of a putative zn-dependent exopeptidase (bvu_1317)2 from bacteroides vulgatus atcc 8482 at 1.80 a resolution
70	d1ysja2	Alignment	not modelled	99.0	20	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
71	d1y7ea2	Alignment	not modelled	98.9	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
72	c2ek8A_	Alignment	not modelled	98.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase; **PDBTitle:** aminopeptidase from aneurinibacillus sp. strain am-1
73	d1lfwa2	Alignment	not modelled	98.8	14	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
74	c3iibA_	Alignment	not modelled	98.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase m28; **PDBTitle:** crystal structure of peptidase m28 precursor (yp_926796.1) from2 shewanella amazonensis sb2b at 1.70 a resolution
75	d3bi1a3	Alignment	not modelled	98.6	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**FolH catalytic domain-like
76	c1y7eA_	Alignment	not modelled	98.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable m18-family aminopeptidase 1; **PDBTitle:** the crystal structure of aminopeptidase i from borrelia burgdorferi2 b31
77	d1de4c3	Alignment	not modelled	98.6	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**FolH catalytic domain-like
78	d1xmba2	Alignment	not modelled	98.5	17	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
79	c2gljR_	Alignment	not modelled	98.4	18	**PDB header:**hydrolase **Chain:** R: **PDB Molecule:** **PDBTitle:** crystal structure of aminopeptidase i from clostridium2 acetobutylicum
80	c2ijzF_	Alignment	not modelled	98.4	19	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**probable m18-family aminopeptidase 2;

						PDBTitle: crystal structure of aminopeptidase
81	c2ootA_	Alignment	not modelled	97.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutamate carboxypeptidase 2; **PDBTitle:** a high resolution structure of ligand-free human glutamate2 carboxypeptidase ii
82	c3rbuA_	Alignment	not modelled	97.6	16	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**glutamate carboxypeptidase 2; **PDBTitle:** n-terminally avitev-tagged human glutamate carboxypeptidase ii in2 complex with 2-pmpa
83	c1cx8F_	Alignment	not modelled	97.5	12	**PDB header:**metal transport **Chain:** F: **PDB Molecule:**transferrin receptor protein; **PDBTitle:** crytal structure of the ectodomain of human transferrin receptor
84	d1fnoa3	Alignment	not modelled	92.4	18	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
85	c3k9tA_	Alignment	not modelled	75.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative peptidase; **PDBTitle:** crystal structure of putative peptidase (np_348812.1) from clostridium2 acetobutylicum at 2.37 a resolution
86	d1lama1	Alignment	not modelled	67.7	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Leucine aminopeptidase, C-terminal domain
87	c3kzwD_	Alignment	not modelled	55.7	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** crystal structure of cytosol aminopeptidase from staphylococcus aureus2 col
88	c3ij3A_	Alignment	not modelled	47.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** 1.8 angstrom resolution crystal structure of cytosol aminopeptidase2 from coxiella burnetii
89	c1lanA_	Alignment	not modelled	47.4	15	**PDB header:**hydrolase (alpha-aminoacylpeptide) **Chain:** A: **PDB Molecule:**leucine aminopeptidase; **PDBTitle:** leucine aminopeptidase complex with l-leucinal
90	c2hc9A_	Alignment	not modelled	45.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leucine aminopeptidase 1; **PDBTitle:** structure of caenorhabditis elegans leucine aminopeptidase-zinc2 complex (lap1)
91	c3jruB_	Alignment	not modelled	42.4	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable cytosol aminopeptidase; **PDBTitle:** crystal structure of leucyl aminopeptidase (pepa) from xoo0834,2 xanthomonas oryzae pv. oryzae kacc10331
92	c3h8gC_	Alignment	not modelled	40.2	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida
93	d1bvyf_	Alignment	not modelled	34.4	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
94	c1bvyF_	Alignment	not modelled	34.4	17	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**protein (cytochrome p450 bm-3); **PDBTitle:** complex of the heme and fmn-binding domains of the2 cytochrome p450(bm-3)
95	d1gyta2	Alignment	not modelled	32.0	10	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Leucine aminopeptidase, C-terminal domain
96	c1gytG_	Alignment	not modelled	31.2	10	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** e. coli aminopeptidase a (pepa)
97	c3peiA_	Alignment	not modelled	18.5	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** crystal structure of cytosol aminopeptidase from francisella2 tularensis
98	d1x87a_	Alignment	not modelled	18.2	12	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
99	c3hlyA_	Alignment	not modelled	18.0	19	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavodoxin-like domain; **PDBTitle:** crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.