

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3io1B_	 Alignment		100.0	65	PDB header: hydrolase Chain: B: PDB Molecule: aminobenzoyl-glutamate utilization protein; PDBTitle: crystal structure of aminobenzoyl-glutamate utilization2 protein from klebsiella pneumoniae
2	c3ramC_	 Alignment		100.0	22	PDB header: hydrolase Chain: C: PDB Molecule: hmra protein; PDBTitle: crystal structure of hmra
3	c3pfoB_	 Alignment		100.0	14	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	c1ysjB_	 Alignment		100.0	28	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
5	c2zogA_	 Alignment		100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: cytosolic non-specific dipeptidase; PDBTitle: crystal structure of mouse carnosinase cn2 complexed with zn and2 bestatin
6	c3dljB_	 Alignment		100.0	12	PDB header: hydrolase Chain: B: PDB Molecule: beta-ala-his dipeptidase; PDBTitle: crystal structure of human carnosine dipeptidase 1
7	c2pokB_	 Alignment		100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: peptidase, m20/m25/m40 family; PDBTitle: crystal structure of a m20 family metallo peptidase from streptococcus2 pneumoniae
8	c2q43A_	 Alignment		100.0	23	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
9	c1cg2D_	 Alignment		100.0	20	PDB header: metallo carboxypeptidase Chain: D: PDB Molecule: carboxypeptidase g2; PDBTitle: carboxypeptidase g2
10	c3pfeA_	 Alignment		100.0	10	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
11	c1lfwA_	 Alignment		100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: pepv; PDBTitle: crystal structure of pepv

12	c1vgyB_	Alignment		100.0	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: succinyl-diaminopimelate desuccinylase; PDBTitle: crystal structure of succinyl diaminopimelate desuccinylase
13	c3gb0A_	Alignment		100.0	18	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
14	c2v8gD_	Alignment		100.0	19	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
15	c3ic1A_	Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: succinyl-diaminopimelate desuccinylase; PDBTitle: crystal structure of zinc-bound succinyl-diaminopimelate desuccinylase2 from haemophilus influenzae
16	c3rzaA_	Alignment		100.0	16	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
17	c2rb7A_	Alignment		100.0	18	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
18	c3ifeA_	Alignment		100.0	16	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'.
19	c3mrub_	Alignment		100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: aminoacyl-histidine dipeptidase; PDBTitle: crystal structure of aminoacylhistidine dipeptidase from vibrio2 alginolyticus
20	c3khzA_	Alignment		100.0	15	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
21	c2imoA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: allantoate amidohydrolase; PDBTitle: crystal structure of allantoate amidohydrolase from escherichia coli2 at ph 4.6
22	c3n5fB_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: n-carbamoyl-l-amino acid hydrolase; PDBTitle: crystal structure of l-n-carbamoylase from geobacillus2 stearothermophilus cect43
23	c1vixA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: peptidase t; PDBTitle: crystal structure of a putative peptidase t
24	c2f7vA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: acetylglutamine deacetylase; PDBTitle: structure of acetylglutamine deacetylase complexed with2 one co
25	c3ct9B_	Alignment	not modelled	100.0	17	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
26	c2qyvB_	Alignment	not modelled	100.0	14	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
27	c3bx8A_	Alignment	not modelled	100.0	13	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
						Fold: Phosphorylase/hydrolase-like

28	d1xmba1	Alignment	not modelled	100.0	38	Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
29	d1ysja1	Alignment	not modelled	100.0	34	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
30	c1vheA	Alignment	not modelled	100.0	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: aminopeptidase/glucanase homolog; PDBTitle: crystal structure of a aminopeptidase/glucanase homolog
31	d1lfwa1	Alignment	not modelled	100.0	14	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
32	c3isxA	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase; PDBTitle: crystal structure of endoglucanase (tm1050) from thermotoga2 maritima at 1.40 a resolution
33	c1yloA	Alignment	not modelled	100.0	15	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
34	d1z2la1	Alignment	not modelled	100.0	19	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
35	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
36	c2cf4A	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: protein ph0519; PDBTitle: pyrococcus horikoshii tet1 peptidase can assemble into a2 tetrahedron or a large octahedral shell
37	c3kl9F	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: F: PDB Molecule: glutamyl aminopeptidase; PDBTitle: crystal structure of pepa from streptococcus pneumoniae
38	d1cg2a1	Alignment	not modelled	100.0	23	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
39	c2pe3A	Alignment	not modelled	100.0	11	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
40	c1vhoA	Alignment	not modelled	100.0	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: endoglucanase; PDBTitle: crystal structure of a putative peptidase/endoglucanase
41	d1vgya1	Alignment	not modelled	100.0	17	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
42	c2fvga	Alignment	not modelled	100.0	9	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase; PDBTitle: crystal structure of endoglucanase (tm1049) from thermotoga maritima2 at 2.01 a resolution
43	c3t6mA	Alignment	not modelled	100.0	20	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
44	d1vixa1	Alignment	not modelled	100.0	28	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
45	d1r3na1	Alignment	not modelled	100.0	23	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
46	c3cpxC	Alignment	not modelled	100.0	13	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
47	d1fnoa4	Alignment	not modelled	100.0	19	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
48	c1q7IA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: aminoacylase-1; PDBTitle: zn-binding domain of the t347g mutant of human aminoacylase-2 i
49	d1vhea2	Alignment	not modelled	99.9	16	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
50	d1yloa2	Alignment	not modelled	99.9	23	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
51	d1vhoo2	Alignment	not modelled	99.9	17	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
52	d1xfoa2	Alignment	not modelled	99.9	16	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
53	c2greC	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: C: PDB Molecule: deblocking aminopeptidase; PDBTitle: crystal structure of deblocking aminopeptidase from bacillus cereus
						Fold: Phosphorylase/hydrolase-like

54	d2grea2	Alignment	not modelled	99.9	15	Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
55	d1z2la2	Alignment	not modelled	99.8	13	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
56	d1cg2a2	Alignment	not modelled	99.8	28	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
57	d2fvga2	Alignment	not modelled	99.8	12	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
58	d1r3na2	Alignment	not modelled	99.7	19	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
59	d1vgya2	Alignment	not modelled	99.7	18	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
60	d1ysja2	Alignment	not modelled	99.6	23	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
61	d1tkja1	Alignment	not modelled	99.6	21	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
62	d1rtqa_	Alignment	not modelled	99.5	15	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
63	c3pb6X_	Alignment	not modelled	99.4	19	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
64	c3tc8A_	Alignment	not modelled	99.3	16	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
65	d1lfwa2	Alignment	not modelled	99.2	19	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
66	d1xmba2	Alignment	not modelled	99.2	23	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
67	c1q7lB_	Alignment	not modelled	99.1	13	PDB header: hydrolase Chain: B: PDB Molecule: aminoacylase-1; PDBTitle: zn-binding domain of the t347g mutant of human aminoacylase-2 i
68	c3iibA_	Alignment	not modelled	99.0	14	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
69	d2afwa1	Alignment	not modelled	99.0	16	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Glutaminyl-peptide cyclotransferase-like
70	c3guxA_	Alignment	not modelled	99.0	12	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
71	d3bi1a3	Alignment	not modelled	98.9	14	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: FolH catalytic domain-like
72	c2ek8A_	Alignment	not modelled	98.8	17	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: aminopeptidase from aneurinibacillus sp. strain am-1
73	d1y0ya2	Alignment	not modelled	98.6	19	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
74	d1de4c3	Alignment	not modelled	98.4	17	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: FolH catalytic domain-like
75	d1fnoa3	Alignment	not modelled	98.0	11	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
76	c3rbuA_	Alignment	not modelled	97.9	17	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-prnpa
77	c2ootA_	Alignment	not modelled	97.9	17	PDB header: hydrolase Chain: A: PDB Molecule: glutamate carboxypeptidase 2; PDBTitle: a high resolution structure of ligand-free human glutamate2 carboxypeptidase ii
78	c1cx8F_	Alignment	not modelled	97.8	18	PDB header: metal transport Chain: F: PDB Molecule: transferrin receptor protein; PDBTitle: crytal structure of the ectodomain of human transferrin receptor
79	d1y7ea2	Alignment	not modelled	96.7	12	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
						PDB header: hydrolase

80	c2hc9A_	Alignment	not modelled	96.6	11	Chain: A: PDB Molecule: leucine aminopeptidase 1; PDBTitle: structure of caenorhabditis elegans leucine aminopeptidase-zinc2 complex (lap1)
81	c3jruB_	Alignment	not modelled	96.2	12	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
82	c2ijzF_	Alignment	not modelled	95.8	12	PDB header: hydrolase Chain: F: PDB Molecule: probable m18-family aminopeptidase 2; PDBTitle: crystal structure of aminopeptidase
83	c3l6sA_	Alignment	not modelled	95.6	11	PDB header: hydrolase Chain: A: PDB Molecule: aspartyl aminopeptidase; PDBTitle: crystal structure of human aspartyl aminopeptidase (dnpep),2 in complex with aspartic acid hydroxamate
84	c3kzwD_	Alignment	not modelled	95.4	12	PDB header: hydrolase Chain: D: PDB Molecule: cytosol aminopeptidase; PDBTitle: crystal structure of cytosol aminopeptidase from staphylococcus aureus2 col
85	c2glfB_	Alignment	not modelled	94.7	13	PDB header: hydrolase Chain: B: PDB Molecule: probable m18-family aminopeptidase 1; PDBTitle: crystal structure of aminopeptidase (m18 family) from thermotoga2 maritima
86	d1lama1	Alignment	not modelled	94.7	11	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Leucine aminopeptidase, C-terminal domain
87	c3kr5E_	Alignment	not modelled	94.3	11	PDB header: hydrolase Chain: E: PDB Molecule: m17 leucyl aminopeptidase; PDBTitle: structure of a protease 4
88	c3h8gC_	Alignment	not modelled	94.0	12	PDB header: hydrolase Chain: C: PDB Molecule: cytosol aminopeptidase; PDBTitle: bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida
89	d1gyta2	Alignment	not modelled	93.9	7	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Leucine aminopeptidase, C-terminal domain
90	c1y7eA_	Alignment	not modelled	92.4	9	PDB header: hydrolase Chain: A: PDB Molecule: probable m18-family aminopeptidase 1; PDBTitle: the crystal structure of aminopeptidase i from borrelia burgdorferi2 b31
91	c1lanA_	Alignment	not modelled	92.4	11	PDB header: hydrolase (alpha-aminoacyl peptide) Chain: A: PDB Molecule: leucine aminopeptidase; PDBTitle: leucine aminopeptidase complex with l-leucinal
92	c3ij3A_	Alignment	not modelled	91.8	14	PDB header: hydrolase Chain: A: PDB Molecule: cytosol aminopeptidase; PDBTitle: 1.8 angstrom resolution crystal structure of cytosol aminopeptidase2 from coxiella burnetii
93	c1gytG_	Alignment	not modelled	91.7	8	PDB header: hydrolase Chain: G: PDB Molecule: cytosol aminopeptidase; PDBTitle: e. coli aminopeptidase a (pepa)
94	c3peiA_	Alignment	not modelled	90.6	10	PDB header: hydrolase Chain: A: PDB Molecule: cytosol aminopeptidase; PDBTitle: crystal structure of cytosol aminopeptidase from francisella2 tularensis
95	c2gljR_	Alignment	not modelled	89.7	16	PDB header: hydrolase Chain: R: PDB Molecule: PDBTitle: crystal structure of aminopeptidase i from clostridium2 acetobutylicum
96	c3k9tA_	Alignment	not modelled	82.2	12	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
97	c3chgB_	Alignment	not modelled	50.2	18	PDB header: ligand binding protein Chain: B: PDB Molecule: glycine betaine-binding protein; PDBTitle: the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
98	c2wwbB_	Alignment	not modelled	41.0	18	PDB header: ribosome Chain: B: PDB Molecule: protein transport protein sec61 subunit gamma; PDBTitle: cryo-em structure of the mammalian sec61 complex bound to the2 actively translating wheat germ 80s ribosome
99	c2wamB_	Alignment	not modelled	27.5	15	PDB header: unknown function Chain: B: PDB Molecule: conserved hypothetical alanine and leucine rich PDBTitle: crystal structure of mycobacterium tuberculosis unknown2 function protein rv2714
100	c3pn1A_	Alignment	not modelled	26.8	16	PDB header: ligase/ligase inhibitor Chain: A: PDB Molecule: dna ligase; PDBTitle: novel bacterial nad+-dependent dna ligase inhibitors with broad2 spectrum potency and antibacterial efficacy in vivo
101	c3fayA_	Alignment	not modelled	26.1	11	PDB header: membrane protein Chain: A: PDB Molecule: ras gtpase-activating-like protein iqgap1; PDBTitle: crystal structure of the gap-related domain of iqgap1
102	d2p90a1	Alignment	not modelled	25.5	10	Fold: Phosphorylase/hydrolase-like Superfamily: Cgl1923-like Family: Cgl1923-like