



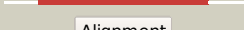

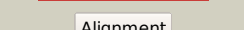

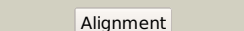


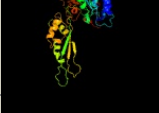


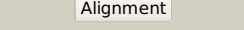
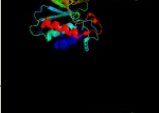
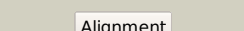

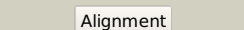


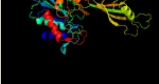


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1202_(dapE)_1345266_1346330
Date	Wed Jul 31 22:05:29 BST 2019
Unique Job ID	201f15f0d4522c3b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3tx8A_	 Alignment		100.0	56	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
2	c2rb7A_	 Alignment		100.0	23	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
3	c3pfoB_	 Alignment		100.0	18	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	c5k8nE_	 Alignment		100.0	20	PDB header: hydrolase Chain: E: PDB Molecule: 5-nitroanthranilic acid aminohydrolase; PDBTitle: 5naa-bound 5-nitroanthranilate aminohydrolase
5	c1vgvB_	 Alignment		100.0	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: succinyl-diaminopimelate desuccinylase; PDBTitle: crystal structure of succinyl diaminopimelate desuccinylase
6	c3ct9B_	 Alignment		100.0	24	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
7	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
8	c2f7vA_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: acetylornithine deacetylase; PDBTitle: structure of acetylornithine deacetylase complexed with2 one co
9	c3ic1A_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: succinyl-diaminopimelate desuccinylase; PDBTitle: crystal structure of zinc-bound succinyl-diaminopimelate desuccinylase2 from haemophilus influenzae
10	c1cg2D_	 Alignment		100.0	23	PDB header: metallocarboxypeptidase Chain: D: PDB Molecule: carboxypeptidase g2; PDBTitle: carboxypeptidase g2
11	c2pokB_	 Alignment		100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: peptidase, m20/m25/m40 family; PDBTitle: crystal structure of a m20 family metallo peptidase from streptococcus2 pneumoniae

12	c4ewtC_	Alignment		100.0	13	PDB header: hydrolase Chain: C: PDB Molecule: peptidase, m20/m25/m40 family; PDBTitle: the crystal structure of a putative aminohydrolase from methicillin2 resistant staphylococcus aureus
13	c3rzaA_	Alignment		100.0	21	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
14	c3mruB_	Alignment		100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: aminoacyl-histidine dipeptidase; PDBTitle: crystal structure of aminoacylhistidine dipeptidase from vibrio2 alginolyticus
15	c3dljB_	Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: beta-ala-his dipeptidase; PDBTitle: crystal structure of human carnosine dipeptidase 1
16	c2zogA_	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: cytosolic non-specific dipeptidase; PDBTitle: crystal structure of mouse carnosinase cn2 complexed with zn and2 bestatin
17	c2qyvB_	Alignment		100.0	21	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
18	c4q7aD_	Alignment		100.0	25	PDB header: hydrolase Chain: D: PDB Molecule: n-acetyl-ornithine/n-acetyl-lysine deacetylase; PDBTitle: crystal structure of n-acetyl-ornithine/n-acetyl-lysine deacetylase2 from spbaerobacter thermophilus
19	c4g1pA_	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: cys-gly metallodipeptidase dug1; PDBTitle: structural and mechanistic basis of substrate recognition by novel di-2 peptidase dug1p from saccharomyces cerevisiae
20	c3x3eA_	Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: n-acetyl-lysine deacetylase; PDBTitle: crystal structure of lysk from thermus thermophilus complex with2 lysine
21	c3pfeA_	Alignment	not modelled	100.0	19	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
22	c3ramC_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: C: PDB Molecule: hmra protein; PDBTitle: crystal structure of hmra
23	c1ysjB_	Alignment	not modelled	100.0	18	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
24	c3ifeA_	Alignment	not modelled	100.0	18	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'.
25	c5i4mB_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: amidase, hydantoinase/carbamoylase family; PDBTitle: crystal structure of amidase, hydantoinase/carbamoylase family from2 burkholderia vietnamiensis
26	c2v8gD_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: D: PDB Molecule: beta-alanine synthase; PDBTitle: crystal structure of beta-alanine synthase from2 saccharomyces kluveri in complex with the product beta-3 alanine
27	c1fwA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: pepv; PDBTitle: crystal structure of pepv
28	c1vixA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: peptidase t; PDBTitle: crystal structure of a putative peptidase t

29	c3n5fB_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: n-carbamoyl-l-amino acid hydrolase; PDBTitle: crystal structure of l-n-carbamoylase from geobacillus2 stearothermophilus cect43
30	c2imoA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: allantoate amidohydrolase; PDBTitle: crystal structure of allantoate amidohydrolase from escherichia coli2 at ph 4.6
31	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
32	c4wjbb_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: putative amidohydrolase/peptidase; PDBTitle: x-ray crystal structure of a putative amidohydrolase/peptidase from2 burkholderia cenocepacia
33	c3khzA_	Alignment	not modelled	100.0	18	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
34	c4pxeB_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: ureidoglycolate hydrolase; PDBTitle: the crystal structure of atuah in complex with glyoxylate
35	c6c0dA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: amidase, hydantoinase/carbamoylase family; PDBTitle: crystal structure of an amidase (hydantoinase/carbamoylase family)2 from burkholderia phymatum
36	c5ds0F_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: F: PDB Molecule: peptidase m42; PDBTitle: crystal structure of tet aminopeptidase from marine sediment archaeon2 thaumarchaeota archaeon scgc ab-539-e09
37	c5tp4B_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: amidase, hydantoinase/carbamoylase family; PDBTitle: crystal structure of a hydantoinase/carbamoylase family amidase from2 burkholderia ambifaria
38	c1vheA_	Alignment	not modelled	100.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: aminopeptidase/glucanase homolog; PDBTitle: crystal structure of a aminopeptidase/glucanase homolog
39	c4wwwvA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase from family m42; PDBTitle: aminopeptidase apdkam598 from the archaeon desulfurococcus2 kamchatkensis
40	c3isxA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase; PDBTitle: crystal structure of endoglucanase (tm1050) from thermotoga maritima2 at 1.40 a resolution
41	c2cf4A_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: protein ph0519; PDBTitle: pyrococcus horikoshii tet1 peptidase can assemble into a2 tetrahedron or a large octahedral shell
42	c4mmoB_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: sso-cp2 metallo-carboxypeptidase; PDBTitle: the crystal structure of a m20 family metallo-carboxypeptidase sso-cp22 from sulfolobus solfataricus
43	c1yloA_	Alignment	not modelled	100.0	14	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
44	c2pe3A_	Alignment	not modelled	100.0	13	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
45	c3io1B_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: aminobenzoyl-glutamate utilization protein; PDBTitle: crystal structure of aminobenzoyl-glutamate utilization2 protein from klebsiella pneumoniae
46	c1y0yA_	Alignment	not modelled	100.0	17	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: frv operon protein frvx; PDBTitle: crystal structure of tetrahedral aminopeptidase from p. horikoshii in2 complex with amastatin
47	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
48	c3ki9F_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: F: PDB Molecule: glutamyl aminopeptidase; PDBTitle: crystal structure of pepa from streptococcus pneumoniae
49	c2fvgA_	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase; PDBTitle: crystal structure of endoglucanase (tm1049) from thermotoga maritima2 at 2.01 a resolution
50	c3cpxC_	Alignment	not modelled	100.0	14	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
51	c4h2kA_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: succinyl-diaminopimelate desuccinylase; PDBTitle: crystal structure of the catalytic domain of succinyl-diaminopimelate2 desuccinylase from haemophilus influenzae
52	d1z2la1	Alignment	not modelled	100.0	17	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
53	d1vixa1	Alignment	not modelled	100.0	24	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases

54	c3t6mA	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: succinyl-diaminopimelate desuccinylase; PDBTitle: crystal structure of the catalytic domain of dape protein from <i>2 v.cholerea</i> in the zn bound form
55	d1lfwA1	Alignment	not modelled	100.0	19	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
56	c2greC	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: C: PDB Molecule: deblocking aminopeptidase; PDBTitle: crystal structure of deblocking aminopeptidase from <i>bacillus cereus</i>
57	d1cg2a1	Alignment	not modelled	100.0	33	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
58	d1fnoa4	Alignment	not modelled	100.0	20	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
59	d1vhea2	Alignment	not modelled	100.0	24	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
60	d1yloa2	Alignment	not modelled	100.0	23	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
61	d1xfoa2	Alignment	not modelled	100.0	19	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
62	d1vgya1	Alignment	not modelled	100.0	21	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
63	d1vhoa2	Alignment	not modelled	99.9	21	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
64	d1xmba1	Alignment	not modelled	99.9	17	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
65	d1r3na1	Alignment	not modelled	99.9	18	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
66	d2fvga2	Alignment	not modelled	99.9	16	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
67	c1q7IA	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: aminoacylase-1; PDBTitle: zn-binding domain of the t347g mutant of human aminoacylase-2 i
68	d1ysja1	Alignment	not modelled	99.9	17	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
69	d2grea2	Alignment	not modelled	99.9	26	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
70	c2glfB	Alignment	not modelled	99.6	12	PDB header: hydrolase Chain: B: PDB Molecule: probable m18-family aminopeptidase 1; PDBTitle: crystal structure of aminopeptidase (m18 family) from <i>thermotoga2 maritima</i>
71	c6qqB	Alignment	not modelled	99.6	20	PDB header: transferase Chain: B: PDB Molecule: glutamine cyclotransferase; PDBTitle: crystal structure of porphyromonas gingivalis glutaminy cyclase
72	c4fuuA	Alignment	not modelled	99.5	17	PDB header: hydrolase Chain: A: PDB Molecule: leucine aminopeptidase; PDBTitle: crystal structure of a leucine aminopeptidase precursor (bt_2548) from <i>2 bacteroides thetaiotaomicron vpi-5482</i> at 1.30 a resolution
73	c3l6sA	Alignment	not modelled	99.5	12	PDB header: hydrolase Chain: A: PDB Molecule: aspartyl aminopeptidase; PDBTitle: crystal structure of human aspartyl aminopeptidase (dnpep), in complex2 with aspartic acid hydroxamate
74	d1vgya2	Alignment	not modelled	99.4	28	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
75	d1y0ya2	Alignment	not modelled	99.4	22	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
76	c4r8fB	Alignment	not modelled	99.4	13	PDB header: hydrolase Chain: B: PDB Molecule: vacuolar aminopeptidase 1; PDBTitle: crystal structure of yeast aminopeptidase 1 (ape1)
77	c3tc8A	Alignment	not modelled	99.4	22	PDB header: hydrolase Chain: A: PDB Molecule: leucine aminopeptidase; PDBTitle: crystal structure of a zn-dependent exopeptidase (bdi_3547) from <i>2 parabacteroides distasonis atcc 8503</i> at 1.06 a resolution
78	c4fbeA	Alignment	not modelled	99.4	21	PDB header: transferase, hydrolase Chain: A: PDB Molecule: cg5976, isoform b; PDBTitle: crystal structure of the c136a/c164a variant of mitochondrial isoform2 of glutaminy cyclase from <i>drosophila melanogaster</i>
79	d1cg2a2	Alignment	not modelled	99.4	22	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
						PDB header: hydrolase

80	c4emeB_	Alignment	not modelled	99.4	11	Chain: B: PDB Molecule: m18 aspartyl aminopeptidase; PDBTitle: x-ray crystal structure and specificity of the plasmodium falciparum2 malaria aminopeptidase
81	c3varA_	Alignment	not modelled	99.4	11	PDB header: hydrolase Chain: A: PDB Molecule: aspartyl aminopeptidase; PDBTitle: crystal structure of dnpep, znzn form
82	c4mhzA_	Alignment	not modelled	99.4	21	PDB header: transferase Chain: A: PDB Molecule: glutaminy cyclase, putative; PDBTitle: crystal structure of apo-form glutaminy cyclase from ixodes2 scapularis in complex with pbd150
83	c2ijzF_	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: F: PDB Molecule: probable m18-family aminopeptidase 2; PDBTitle: crystal structure of aminopeptidase
84	c4f9vB_	Alignment	not modelled	99.4	19	PDB header: transferase, hydrolase Chain: B: PDB Molecule: cg32412; PDBTitle: structure of c113a/c136a mutant variant of glycosylated glutaminy2 cyclase from drosophila melanogaster
85	d1tkja1	Alignment	not modelled	99.3	24	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
86	c1y7eA_	Alignment	not modelled	99.3	13	PDB header: hydrolase Chain: A: PDB Molecule: probable m18-family aminopeptidase 1; PDBTitle: the crystal structure of aminopeptidase i from borrelia burgdorferi2 b31
87	c3pb6X_	Alignment	not modelled	99.2	25	PDB header: transferase Chain: X: PDB Molecule: glutaminy-peptide cyclotransferase-like protein; PDBTitle: crystal structure of the catalytic domain of human golgi-resident2 glutaminy cyclase at ph 6.5
88	d1z2la2	Alignment	not modelled	99.2	14	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
89	c1q7lB_	Alignment	not modelled	99.2	26	PDB header: hydrolase Chain: B: PDB Molecule: aminoacylase-1; PDBTitle: zn-binding domain of the t347g mutant of human aminoacylase-2 i
90	d1y7ea2	Alignment	not modelled	99.2	14	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
91	d2afwa1	Alignment	not modelled	99.2	21	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Glutaminy-peptide cyclotransferase-like
92	c5gneA_	Alignment	not modelled	99.1	19	PDB header: hydrolase Chain: A: PDB Molecule: leucine aminopeptidase; PDBTitle: crystal structure of lapb from legionella pneumophila
93	d1r3na2	Alignment	not modelled	99.1	20	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
94	c6eslB_	Alignment	not modelled	99.1	17	PDB header: hydrolase Chain: B: PDB Molecule: bacterial leucyl aminopeptidase; PDBTitle: crystal structure of the legionella pneumoppila lapa
95	d1rtqa_	Alignment	not modelled	99.0	16	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
96	c5jm6D_	Alignment	not modelled	99.0	10	PDB header: hydrolase Chain: D: PDB Molecule: aminopeptidase-like protein; PDBTitle: structure of chaetomium thermophilum mape1
97	d1ysja2	Alignment	not modelled	98.9	22	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
98	c3guxA_	Alignment	not modelled	98.9	17	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
99	c2qljR_	Alignment	not modelled	98.9	10	PDB header: hydrolase Chain: R: PDB Molecule: PDBTitle: crystal structure of aminopeptidase i from clostridium2 acetobutylicum
100	d1lfwa2	Alignment	not modelled	98.9	15	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
101	c2ek8A_	Alignment	not modelled	98.8	26	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: aminopeptidase from aneurinibacillus sp. strain am-1
102	c3iibA_	Alignment	not modelled	98.5	20	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
103	d3bi1a3	Alignment	not modelled	98.1	16	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: FolH catalytic domain-like
104	d1de4c3	Alignment	not modelled	97.9	20	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: FolH catalytic domain-like
105	d1xmba2	Alignment	not modelled	97.7	13	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
106	c3rhuA_	Alignment	not modelled	95.5	21	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: glutamate carboxypeptidase 2;

106	c1b0A_	Alignment	not modelled	95.3	21	PDBTitle: n-terminally avitev-tagged human glutamate carboxypeptidase ii in2 complex with 2-pmpa PDB header: hydrolase
107	c2ootA_	Alignment	not modelled	95.4	21	Chain: A; PDB Molecule: glutamate carboxypeptidase 2; PDBTitle: a high resolution structure of ligand-free human glutamate2 carboxypeptidase ii
108	c4r12A_	Alignment	not modelled	95.2	18	PDB header: protein binding Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the gamma-secretase component nicastrin
109	c4tweA_	Alignment	not modelled	95.2	24	PDB header: hydrolase Chain: A; PDB Molecule: n-acetylated-alpha-linked acidic dipeptidase-like protein; PDBTitle: structure of ligand-free n-acetylated-alpha-linked-acidic-dipeptidase2 like protein (naaladase1)
110	d1fnoa3	Alignment	not modelled	95.1	14	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
111	c5a63A_	Alignment	not modelled	94.5	19	PDB header: hydrolase Chain: A; PDB Molecule: nicastrin; PDBTitle: cryo-em structure of the human gamma-secretase complex at 3.4 angstrom2 resolution.
112	c1cx8F_	Alignment	not modelled	94.0	19	PDB header: metal transport Chain: F; PDB Molecule: transferrin receptor protein; PDBTitle: crystal structure of the ectodomain of human transferrin receptor
113	c4uisA_	Alignment	not modelled	93.8	25	PDB header: hydrolase Chain: A; PDB Molecule: gamma-secretase; PDBTitle: the cryoem structure of human gamma-secretase complex
114	c4efdF_	Alignment	not modelled	91.4	18	PDB header: hydrolase Chain: F; PDB Molecule: aminopeptidase; PDBTitle: crystal structure of an m17 aminopeptidase from trypanosoma brucei,2 tb427tmp.02.4440
115	c5ntgA_	Alignment	not modelled	91.2	15	PDB header: hydrolase Chain: A; PDB Molecule: aminopeptidase; PDBTitle: structure of leucyl aminopeptidase from trypanosoma cruzi in complex2 with citrate
116	c3peiA_	Alignment	not modelled	90.7	11	PDB header: hydrolase Chain: A; PDB Molecule: cytosol aminopeptidase; PDBTitle: crystal structure of cytosol aminopeptidase from francisella2 tularensis
117	c3kzwD_	Alignment	not modelled	90.6	13	PDB header: hydrolase Chain: D; PDB Molecule: cytosol aminopeptidase; PDBTitle: crystal structure of cytosol aminopeptidase from staphylococcus aureus2 col
118	c3ij3A_	Alignment	not modelled	89.2	21	PDB header: hydrolase Chain: A; PDB Molecule: cytosol aminopeptidase; PDBTitle: 1.8 angstrom resolution crystal structure of cytosol aminopeptidase2 from coxiella burnetii
119	c2hc9A_	Alignment	not modelled	88.7	23	PDB header: hydrolase Chain: A; PDB Molecule: leucine aminopeptidase 1; PDBTitle: structure of caenorhabditis elegans leucine aminopeptidase-zinc2 complex (lap1)
120	c3h8gC_	Alignment	not modelled	87.3	17	PDB header: hydrolase Chain: C; PDB Molecule: cytosol aminopeptidase; PDBTitle: bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida