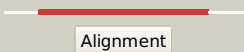

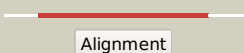

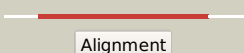

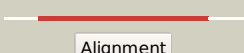





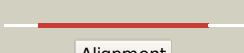

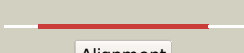


















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3305c_(amiA1)_3691810_3692979
Date	Thu Aug 8 16:20:51 BST 2019
Unique Job ID	df0a4c0f1d3cb66a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ewtC_	 Alignment		100.0	29	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
2	c3ramC_	 Alignment		100.0	20	PDB header: hydrolase Chain: C: PDB Molecule: hmra protein; PDBTitle: crystal structure of hmra
3	c2q43A_	 Alignment		100.0	28	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
4	c1lysjB_	 Alignment		100.0	30	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	c3pfoB_	 Alignment		100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: putative acetylnithine deacetylase; PDBTitle: crystal structure of a putative acetylnithine deacetylase (rpa2325)2 from rhodopseudomonas palustris cga009 at 1.90 a resolution
6	c3io1B_	 Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: aminobenzoyl-glutamate utilization protein; PDBTitle: crystal structure of aminobenzoyl-glutamate utilization2 protein from klebsiella pneumoniae
7	c2z0gA_	 Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: cytosolic non-specific dipeptidase; PDBTitle: crystal structure of mouse carnosinase cn2 complexed with zn and2 bestatin
8	c3dljB_	 Alignment		100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: beta-ala-his dipeptidase; PDBTitle: crystal structure of human carnosine dipeptidase 1
9	c1cg2D_	 Alignment		100.0	15	PDB header: metallocarboxypeptidase Chain: D: PDB Molecule: carboxypeptidase g2; PDBTitle: carboxypeptidase g2
10	c4g1pA_	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: cys-gly metallo-dipeptidase dug1; PDBTitle: structural and mechanistic basis of substrate recognition by novel di-2 peptidase dug1p from saccharomyces cerevisiae
11	c5k8nE_	 Alignment		100.0	13	PDB header: hydrolase Chain: E: PDB Molecule: 5-nitroanthranilic acid aminohydrolase; PDBTitle: 5naa-bound 5-nitroanthranilate aminohydrolase

12	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
13	c2rb7A	Alignment		100.0	15	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
14	c1lfwA	Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: pepv; PDBTitle: crystal structure of pepv
15	c3gb0A	Alignment		100.0	16	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
16	c1vgvB	Alignment		100.0	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: succinyl-diaminopimelate desuccinylase; PDBTitle: crystal structure of succinyl diaminopimelate desuccinylase
17	c3pfeA	Alignment		100.0	12	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
18	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
19	c3ic1A	Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: succinyl-diaminopimelate desuccinylase; PDBTitle: crystal structure of zinc-bound succinyl-diaminopimelate desuccinylase2 from haemophilus influenzae
20	c2f7vA	Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: acetyl-citrulline deacetylase; PDBTitle: structure of acetyl-citrulline deacetylase complexed with2 one co
21	c6c0dA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: amidase, hydantoinase/carbamoylase family; PDBTitle: crystal structure of an amidase (hydantoinase/carbamoylase family)2 from burkholderia phymatum
22	c3mruB	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: aminoacyl-histidine dipeptidase; PDBTitle: crystal structure of aminoacylhistidine dipeptidase from vibrio2 alginolyticus
23	c5i4mB	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: amidase, hydantoinase/carbamoylase family; PDBTitle: crystal structure of amidase, hydantoinase/carbamoylase family from2 burkholderia vietnamiensis
24	c3n5fB	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: n-carbamoyl-l-amino acid hydrolase; PDBTitle: crystal structure of l-n-carbamoylase from geobacillus2 stearothermophilus cect43
25	c3ifeA	Alignment	not modelled	100.0	13	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'.
26	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
27	c3tx8A	Alignment	not modelled	100.0	16	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
						PDB header: hydrolase

28	c2v8gD	Alignment	not modelled	100.0	18	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
29	c4wjbB	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: putative amidohydrolase/peptidase; PDBTitle: x-ray crystal structure of a putative amidohydrolase/peptidase from2 burkholderia cenocepacia
30	c2qyvB	Alignment	not modelled	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
31	c3khzA	Alignment	not modelled	100.0	13	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
32	c5tp4B	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: amidase, hydantoinase/carbamoylase family; PDBTitle: crystal structure of a hydantoinase/carbamoylase family amidase from2 burkholderia ambifaria
33	c4pxeB	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: ureidoglycolate hydrolase; PDBTitle: the crystal structure of atuah in complex with glyoxylate
34	c3ct9B	Alignment	not modelled	100.0	13	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
35	c1vixA	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: peptidase t; PDBTitle: crystal structure of a putative peptidase t
36	c4q7aD	Alignment	not modelled	100.0	13	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 sphaerobacter thermophilus
37	d1xmba1	Alignment	not modelled	100.0	37	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
38	c3x3eA	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: n-acetyl-lysine deacetylase; PDBTitle: crystal structure of lysk from thermus thermophilus complex with2 lysine
39	d1ysja1	Alignment	not modelled	100.0	39	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
40	c4mmoB	Alignment	not modelled	100.0	9	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
41	c5ds0F	Alignment	not modelled	100.0	11	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
42	c1yloA	Alignment	not modelled	100.0	11	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
43	c3isxA	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase; PDBTitle: crystal structure of endoglucanase (tm1050) from thermotoga maritima2 at 1.40 a resolution
44	c1vheA	Alignment	not modelled	100.0	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: aminopeptidase/glucanase homolog; PDBTitle: crystal structure of a aminopeptidase/glucanase homolog
45	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
46	c2cf4A	Alignment	not modelled	100.0	10	PDB header: hydrolase Chain: A: PDB Molecule: protein ph0519; PDBTitle: pyrococcus horikoshii tet1 peptidase can assemble into a2 tetrahedron or a large octahedral shell
47	c1y0yA	Alignment	not modelled	100.0	15	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
48	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
49	d1lfwa1	Alignment	not modelled	100.0	17	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
50	c3ki9F	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: F: PDB Molecule: glutamyl aminopeptidase; PDBTitle: crystal structure of pepa from streptococcus pneumoniae
51	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
52	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
53	d1cq2a1	Alignment	not modelled	100.0	19	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases

						Family: Bacterial dinuclear zinc exopeptidases
54	d1z2la1	Alignment	not modelled	100.0	17	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
55	d1vixa1	Alignment	not modelled	100.0	22	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
56	c4h2kA	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: succinyl-diaminopimelate desuccinylase; PDBTitle: crystal structure of the catalytic domain of succinyl-diaminopimelate2 desuccinylase from haemophilus influenzae
57	c3t6mA	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: succinyl-diaminopimelate desuccinylase; PDBTitle: crystal structure of the catalytic domain of dape protein from 2 v.cholerea in the zn bound form
58	d1vgya1	Alignment	not modelled	99.9	12	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
59	c3cpxC	Alignment	not modelled	99.9	12	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
60	d1vhea2	Alignment	not modelled	99.9	19	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
61	d1fnoa4	Alignment	not modelled	99.9	19	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
62	d1yloa2	Alignment	not modelled	99.9	18	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
63	d1xf0a2	Alignment	not modelled	99.9	16	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
64	d1vh0a2	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	21	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
66	c1q7IA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: aminoacylase-1; PDBTitle: zn-binding domain of the t347g mutant of human aminoacylase-2 i
67	d2greA2	Alignment	not modelled	99.7	16	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
68	d2fvga2	Alignment	not modelled	99.7	11	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
69	c2greC	Alignment	not modelled	99.7	11	PDB header: hydrolase Chain: C: PDB Molecule: deblocking aminopeptidase; PDBTitle: crystal structure of deblocking aminopeptidase from bacillus cereus
70	d1cg2a2	Alignment	not modelled	99.6	18	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
71	d1z2la2	Alignment	not modelled	99.6	13	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
72	d1vgya2	Alignment	not modelled	99.6	18	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
73	c6qqIB	Alignment	not modelled	99.5	17	PDB header: transferase Chain: B: PDB Molecule: glutamine cyclotransferase; PDBTitle: crystal structure of porphyromonas gingivalis glutaminy cyclase
74	d1r3na2	Alignment	not modelled	99.5	15	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
75	d1ysja2	Alignment	not modelled	99.4	23	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
76	c4fu0A	Alignment	not modelled	99.4	16	PDB header: hydrolase Chain: A: PDB Molecule: leucine aminopeptidase; PDBTitle: crystal structure of a leucine aminopeptidase precursor (bt_2548) from 2 bacteroides thetaiotaomicron vpi-5482 at 1.30 a resolution
77	d1rtqa	Alignment	not modelled	99.4	14	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
78	d1tkja1	Alignment	not modelled	99.3	20	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
79	c4f9vB	Alignment	not modelled	99.2	19	PDB header: transferase, hydrolase Chain: B: PDB Molecule: c932412; PDBTitle: structure of c113a/c136a mutant variant of glycosylated glutaminy2 cyclase from drosophila melanogaster PDB header: hydrolase

80	c5gneA_	Alignment	not modelled	99.2	19	Chain: A: PDB Molecule: leucine aminopeptidase; PDBTitle: crystal structure of lapb from legionella pneumophila
81	c3pb6X_	Alignment	not modelled	99.1	17	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
82	d1xmba2	Alignment	not modelled	99.1	23	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
83	c3tc8A_	Alignment	not modelled	99.1	16	PDB header: hydrolase Chain: A: PDB Molecule: leucine aminopeptidase; PDBTitle: crystal structure of a zn-dependent exopeptidase (bdi_3547) from2 parabacteroides distasonis atcc 8503 at 1.06 a resolution
84	d1lfwa2	Alignment	not modelled	99.1	16	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
85	c6eslB_	Alignment	not modelled	99.1	19	PDB header: hydrolase Chain: B: PDB Molecule: bacterial leucyl aminopeptidase; PDBTitle: crystal structure of the legionella pneumoppila lapa
86	c3guxA_	Alignment	not modelled	99.0	19	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
87	c4mhza_	Alignment	not modelled	98.9	16	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
88	c4fbeA_	Alignment	not modelled	98.9	15	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 drosophila melanogaster
89	c1q7lB_	Alignment	not modelled	98.9	17	PDB header: hydrolase Chain: B: PDB Molecule: aminoacylase-1; PDBTitle: zn-binding domain of the t347g mutant of human aminoacylase-2 i
90	d1y0ya2	Alignment	not modelled	98.9	19	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
91	d2afwa1	Alignment	not modelled	98.8	13	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Glutaminy-peptide cyclotransferase-like
92	d3bi1a3	Alignment	not modelled	98.4	13	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: FoH catalytic domain-like
93	c2ek8A_	Alignment	not modelled	98.3	22	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: aminopeptidase from aneurinibacillus sp. strain am-1
94	d1y7ea2	Alignment	not modelled	98.2	11	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
95	c1y7eA_	Alignment	not modelled	98.1	12	PDB header: hydrolase Chain: A: PDB Molecule: probable m18-family aminopeptidase 1; PDBTitle: the crystal structure of aminopeptidase i from borrelia burgdorferi2 b31
96	c3iibA_	Alignment	not modelled	98.1	24	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
97	d1fnoa3	Alignment	not modelled	98.0	8	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
98	d1de4c3	Alignment	not modelled	97.6	14	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: FoH catalytic domain-like
99	c3varA_	Alignment	not modelled	97.4	14	PDB header: hydrolase Chain: A: PDB Molecule: aspartyl aminopeptidase; PDBTitle: crystal structure of dnpep, znzn form
100	c2glfB_	Alignment	not modelled	97.0	15	PDB header: hydrolase Chain: B: PDB Molecule: probable m18-family aminopeptidase 1; PDBTitle: crystal structure of aminipeptidase (m18 family) from thermotoga2 maritima
101	c4r12A_	Alignment	not modelled	96.6	23	PDB header: protein binding Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the gamma-secretase component nicastrin
102	c3l6sA_	Alignment	not modelled	96.5	8	PDB header: hydrolase Chain: A: PDB Molecule: aspartyl aminopeptidase; PDBTitle: crystal structure of human aspartyl aminopeptidase (dnpep), in complex2 with aspartic acid hydroxamate
103	c2ijzF_	Alignment	not modelled	95.9	13	PDB header: hydrolase Chain: F: PDB Molecule: probable m18-family aminopeptidase 2; PDBTitle: crystal structure of aminopeptidase
104	c4tweA_	Alignment	not modelled	95.6	18	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 (naaladasel)
105	c5a63A_	Alignment	not modelled	95.4	17	PDB header: hydrolase Chain: A: PDB Molecule: nicastrin;

105	c3b03A	Alignment	not modelled	93.4	17	PDBTitle: cryo-em structure of the human gamma-secretase complex at 3.4 angstrom2 resolution. PDB header: hydrolase
106	c2ootA	Alignment	not modelled	95.3	13	Chain: A: PDB Molecule: glutamate carboxypeptidase 2; PDBTitle: a high resolution structure of ligand-free human glutamate2 carboxypeptidase ii
107	c3rbuA	Alignment	not modelled	95.2	13	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
108	c4uisA	Alignment	not modelled	95.1	15	PDB header: hydrolase Chain: A: PDB Molecule: gamma-secretase; PDBTitle: the cryoem structure of human gamma-secretase complex
109	c4emeB	Alignment	not modelled	95.1	8	PDB header: hydrolase Chain: B: PDB Molecule: m18 aspartyl aminopeptidase; PDBTitle: x-ray crystal structure and specificity of the plasmodium falciparum2 malaria aminopeptidase
110	c2qljR	Alignment	not modelled	94.6	10	PDB header: hydrolase Chain: R: PDB Molecule: PDBTitle: crystal structure of aminopeptidase i from clostridium2 acetobutylicum
111	c4r8fB	Alignment	not modelled	94.4	11	PDB header: hydrolase Chain: B: PDB Molecule: vacuolar aminopeptidase 1; PDBTitle: crystal structure of yeast aminopeptidase 1 (ape1)
112	c1cx8F	Alignment	not modelled	94.1	11	PDB header: metal transport Chain: F: PDB Molecule: transferrin receptor protein; PDBTitle: crystal structure of the ectodomain of human transferrin receptor
113	c3peiA	Alignment	not modelled	93.2	9	PDB header: hydrolase Chain: A: PDB Molecule: cytosol aminopeptidase; PDBTitle: crystal structure of cytosol aminopeptidase from francisella2 tularensis
114	c5jm6D	Alignment	not modelled	91.8	20	PDB header: hydrolase Chain: D: PDB Molecule: aminopeptidase-like protein; PDBTitle: structure of chaetomium thermophilum mape1
115	c3kzwD	Alignment	not modelled	91.4	11	PDB header: hydrolase Chain: D: PDB Molecule: cytosol aminopeptidase; PDBTitle: crystal structure of cytosol aminopeptidase from staphylococcus aureus2 col
116	c5ntgA	Alignment	not modelled	90.8	12	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: structure of leucyl aminopeptidase from trypanosoma cruzi in complex2 with citrate
117	c3h8gC	Alignment	not modelled	89.3	20	PDB header: hydrolase Chain: C: PDB Molecule: cytosol aminopeptidase; PDBTitle: bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida
118	d1lama1	Alignment	not modelled	88.4	17	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Leucine aminopeptidase, C-terminal domain
119	c4upcA	Alignment	not modelled	88.0	16	PDB header: protein binding Chain: A: PDB Molecule: nicastrin; PDBTitle: structure of a extracellular domain
120	c4ksiA	Alignment	not modelled	87.3	15	PDB header: hydrolase Chain: A: PDB Molecule: leucine aminopeptidase 1, chloroplastic; PDBTitle: crystal structure analysis of the acidic leucine aminopeptidase of2 tomato