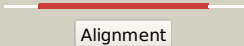

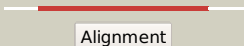

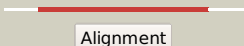







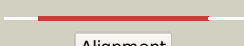

















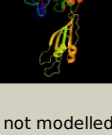


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2141c (-) _2400384_2401730
Date	Mon Aug 5 13:25:26 BST 2019
Unique Job ID	aed27ee9f287ac1a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2pokB_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peptidase, m20/m25/m40 family; <b>PDBTitle:</b> crystal structure of a m20 family metallo peptidase from streptococcus2 pneumoniae
2	<a href="#">c2zogA_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cytosolic non-specific dipeptidase; <b>PDBTitle:</b> crystal structure of mouse carnosinase cn2 complexed with zn and2 bestatin
3	<a href="#">c4g1pA_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cys-gly metallo dipeptidase dug1; <b>PDBTitle:</b> structural and mechanistic basis of substrate recognition by novel di-2 peptidase dug1p from saccharomyces cerevisiae
4	<a href="#">c3dljB_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-ala-his dipeptidase; <b>PDBTitle:</b> crystal structure of human carnosine dipeptidase 1
5	<a href="#">c3pfeA_</a>	 Alignment		100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-diaminopimelate desuccinylase; <b>PDBTitle:</b> crystal structure of a m20a metallo peptidase (dape, lpg0809) from2 legionella pneumophila subsp. pneumophila str. philadelphia 1 at 1.503 a resolution
6	<a href="#">c3pfoB_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative acetylornithine deacetylase; <b>PDBTitle:</b> crystal structure of a putative acetylornithine deacetylase (rpa2325)2 from rhodopseudomonas palustris cga009 at 1.90 a resolution
7	<a href="#">c5k8nE_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> 5-nitroanthranilic acid aminohydrolase; <b>PDBTitle:</b> 5naa-bound 5-nitroanthranilate aminohydrolase
8	<a href="#">c1vgvB_</a>	 Alignment		100.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> succinyl-diaminopimelate desuccinylase; <b>PDBTitle:</b> crystal structure of succinyl diaminopimelate desuccinylase
9	<a href="#">c1lfwA_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pepv; <b>PDBTitle:</b> crystal structure of pepv
10	<a href="#">c3mruB_</a>	 Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoacyl-histidine dipeptidase; <b>PDBTitle:</b> crystal structure of aminoacylhistidine dipeptidase from vibrio2 alginolyticus
11	<a href="#">c2rb7A_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidase, m20/m25/m40 family; <b>PDBTitle:</b> crystal structure of co-catalytic metallo peptidase (yp_387682.1) from2 desulfovibrio desulfuricans g20 at 1.60 a resolution

12	<a href="#">c1cg2D_</a>	Alignment		100.0	22	<b>PDB header:</b> metallocarboxypeptidase <b>Chain:</b> D: <b>PDB Molecule:</b> carboxypeptidase g2; <b>PDBTitle:</b> carboxypeptidase g2
13	<a href="#">c2f7vA_</a>	Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acetylcitrulline deacetylase; <b>PDBTitle:</b> structure of acetylcitrulline deacetylase complexed with2 one co
14	<a href="#">c3khzA_</a>	Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dipeptidase sac11801; <b>PDBTitle:</b> crystal structure of r350a mutant of staphylococcus aureus2 metallopeptidase (sapep/dape) in the apo-form
15	<a href="#">c4ewtC_</a>	Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> peptidase, m20/m25/m40 family; <b>PDBTitle:</b> the crystal structure of a putative aminohydrolase from methicillin2 resistant staphylococcus aureus
16	<a href="#">c3ic1A_</a>	Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-diaminopimelate desuccinylase; <b>PDBTitle:</b> crystal structure of zinc-bound succinyl-diaminopimelate desuccinylase2 from haemophilus influenzae
17	<a href="#">c3ct9B_</a>	Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acetylornithine deacetylase; <b>PDBTitle:</b> crystal structure of a putative zinc peptidase (np_812461.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.31 a resolution
18	<a href="#">c3gb0A_</a>	Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidase t; <b>PDBTitle:</b> crystal structure of aminopeptidase pept (np_980509.1) from bacillus2 cereus atcc 10987 at 2.04 a resolution
19	<a href="#">c2qyvB_</a>	Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> xaa-his dipeptidase; <b>PDBTitle:</b> crystal structure of putative xaa-his dipeptidase (yp_718209.1) from2 haemophilus somnus 129pt at 2.11 a resolution
20	<a href="#">c3rzaA_</a>	Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tripeptidase; <b>PDBTitle:</b> crystal structure of a tripeptidase (sav1512) from staphylococcus2 aureus subsp. aureus mu50 at 2.10 a resolution
21	<a href="#">c3ifeA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidase t; <b>PDBTitle:</b> 1.55 angstrom resolution crystal structure of peptidase t (pept-1)2 from bacillus anthracis str. 'ames ancestor'.
22	<a href="#">c3tx8A_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-diaminopimelate desuccinylase; <b>PDBTitle:</b> crystal structure of a succinyl-diaminopimelate desuccinylase (arge)2 from corynebacterium glutamicum atcc 13032 at 2.97 a resolution
23	<a href="#">c5i4mB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> amidase, hydantoinase/carbamoylase family; <b>PDBTitle:</b> crystal structure of amidase, hydantoinase/carbamoylase family from2 burkholderia vietnamiensis
24	<a href="#">c3n5fB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> n-carbamoyl-l-amino acid hydrolase; <b>PDBTitle:</b> crystal structure of l-n-carbamoylase from geobacillus2 stearothermophilus cect43
25	<a href="#">c2v8gD_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-alanine synthase; <b>PDBTitle:</b> crystal structure of beta-alanine synthase from2 saccharomyces kluuyveri in complex with the product beta-3 alanine
26	<a href="#">c4q7aD_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> n-acetyl-ornithine/n-acetyl-lysine deacetylase; <b>PDBTitle:</b> crystal structure of n-acetyl-ornithine/n-acetyl-lysine deacetylase2 from sphaerobacter thermophilus
27	<a href="#">c1vixA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidase t; <b>PDBTitle:</b> crystal structure of a putative peptidase t
						<b>PDB header:</b> hydrolase

28	<a href="#">c4pxeB_</a>	Alignment	not modelled	100.0	19	<b>Chain:</b> B: <b>PDB Molecule:</b> ureidoglycolate hydrolase; <b>PDBTitle:</b> the crystal structure of atuah in complex with glyoxylate
29	<a href="#">c2imoA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> allantoate amidohydrolase; <b>PDBTitle:</b> crystal structure of allantoate amidohydrolase from escherichia coli2 at ph 4.6
30	<a href="#">c4wjbb_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative amidohydrolase/peptidase; <b>PDBTitle:</b> x-ray crystal structure of a putative amidohydrolase/peptidase from2 burkholderia cenocepacia
31	<a href="#">c1ysjB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein yxep; <b>PDBTitle:</b> crystal structure of bacillus subtilis yxep protein (apc1829), a2 dinuclear metal binding peptidase from m20 family
32	<a href="#">c3x3eA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetyl-lysine deacetylase; <b>PDBTitle:</b> crystal structure of lysk from thermus thermophilus complex with2 lysine
33	<a href="#">c3ramC_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> hmra protein; <b>PDBTitle:</b> crystal structure of hmra
34	<a href="#">c6c0dA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amidase, hydantoinase/carbamoylase family; <b>PDBTitle:</b> crystal structure of an amidase (hydantoinase/carbamoylase family)2 from burkholderia phymatum
35	<a href="#">c4mmoB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> sso-cp2 metallo-carboxypeptidase; <b>PDBTitle:</b> the crystal structure of a m20 family metallo-carboxypeptidase sso-cp22 from sulfolobus solfataricus
36	<a href="#">c2q43A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> iaa-amino acid hydrolase ilr1-like 2; <b>PDBTitle:</b> ensemble refinement of the protein crystal structure of iaa-aminoacid2 hydrolase from arabidopsis thaliana gene at5g56660
37	<a href="#">c5tp4B_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> amidase, hydantoinase/carbamoylase family; <b>PDBTitle:</b> crystal structure of a hydantoinase/carbamoylase family amidase from2 burkholderia ambifaria
38	<a href="#">c5ds0F_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> peptidase m42; <b>PDBTitle:</b> crystal structure of tet aminopeptidase from marine sediment archaeon2 thaumarchaeota archaeon scgc ab-539-e09
39	<a href="#">c3isxA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase; <b>PDBTitle:</b> crystal structure of endoglucanase (tm1050) from thermotoga maritima2 at 1.40 a resolution
40	<a href="#">d1lfwal</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
41	<a href="#">c1vheA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase/glucanase homolog; <b>PDBTitle:</b> crystal structure of a aminopeptidase/glucanase homolog
42	<a href="#">c4wwwvA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase from family m42; <b>PDBTitle:</b> aminopeptidase apdkam598 from the archaeon desulfurococcus2 kamchatkensis
43	<a href="#">c3io1B_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> aminobenzoyl-glutamate utilization protein; <b>PDBTitle:</b> crystal structure of aminobenzoyl-glutamate utilization2 protein from klebsiella pneumoniae
44	<a href="#">c1yloA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein sf2450; <b>PDBTitle:</b> crystal structure of protein of unknown function (possible2 aminopeptidase) s2589 from shigella flexneri 2a str. 2457t
45	<a href="#">c1vhoA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase; <b>PDBTitle:</b> crystal structure of a putative peptidase/endoglucanase
46	<a href="#">c2cf4A_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein ph0519; <b>PDBTitle:</b> pyrococcus horikoshii tet1 peptidase can assemble into a2 tetrahedron or a large octahedral shell
47	<a href="#">c1y0yA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> frv operon protein frvx; <b>PDBTitle:</b> crystal structure of tetrahedral aminopeptidase from p. horikoshii in2 complex with amastatin
48	<a href="#">d1z2la1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
49	<a href="#">d1cg2a1</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
50	<a href="#">c2pe3A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 354aa long hypothetical operon protein frv; <b>PDBTitle:</b> crystal structure of frv operon protein frvx (ph1821)from pyrococcus2 horikoshii ot3
51	<a href="#">d1vixa1</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
52	<a href="#">c1q7lA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aminoacylase-1; <b>PDBTitle:</b> zn-binding domain of the t347g mutant of human aminoacylase-2 i
53	<a href="#">c3ki9F_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> glutamyl aminopeptidase;

						<b>PDBTitle:</b> crystal structure of pepa from streptococcus pneumoniae
54	<a href="#">c3t6mA</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-diaminopimelate desuccinylase; <b>PDBTitle:</b> crystal structure of the catalytic domain of dape protein from 2 v.cholerea in the zn bound form
55	<a href="#">c4h2kA</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-diaminopimelate desuccinylase; <b>PDBTitle:</b> crystal structure of the catalytic domain of succinyl-diaminopimelate2 desuccinylase from haemophilus influenzae
56	<a href="#">c2fvga</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase; <b>PDBTitle:</b> crystal structure of endoglucanase (tm1049) from thermotoga maritima2 at 2.01 a resolution
57	<a href="#">d1fnoa4</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
58	<a href="#">d1vgya1</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
59	<a href="#">d1r3na1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
60	<a href="#">d1vhea2</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
61	<a href="#">c3cpxC</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> aminopeptidase, m42 family; <b>PDBTitle:</b> crystal structure of putative m42 glutamyl aminopeptidase2 (yp_676701.1) from cytophaga hutchinsonii atcc 33406 at 2.39 a3 resolution
62	<a href="#">d1yloa2</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
63	<a href="#">d1xmba1</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
64	<a href="#">d1vhooa2</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
65	<a href="#">d1xfoa2</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
66	<a href="#">c2greC</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> deblocking aminopeptidase; <b>PDBTitle:</b> crystal structure of deblocking aminopeptidase from bacillus cereus
67	<a href="#">d1ysja1</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
68	<a href="#">d2grea2</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
69	<a href="#">d2fvga2</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
70	<a href="#">c6qqLB</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamine cyclotransferase; <b>PDBTitle:</b> crystal structure of porphyromonas gingivalis glutaminy cyclase
71	<a href="#">d1tkja1</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
72	<a href="#">d1rtqa</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
73	<a href="#">c4fuua</a>	Alignment	not modelled	99.8	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> leucine aminopeptidase; <b>PDBTitle:</b> crystal structure of a leucine aminopeptidase precursor (bt_2548) from 2 bacteroides thetaiotaomicron vpi-5482 at 1.30 a resolution
74	<a href="#">c5gneA</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> leucine aminopeptidase; <b>PDBTitle:</b> crystal structure of labp from legionella pneumophila
75	<a href="#">c3tc8A</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> leucine aminopeptidase; <b>PDBTitle:</b> crystal structure of a zn-dependent exopeptidase (bdi_3547) from 2 parabacteroides distasonis atcc 8503 at 1.06 a resolution
76	<a href="#">c6esiB</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bacterial leucyl aminopeptidase; <b>PDBTitle:</b> crystal structure of the legionella pneumoppila lapa
77	<a href="#">c4fbeA</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cg5976, isoform b; <b>PDBTitle:</b> crystal structure of the c136a/c164a variant of mitochondrial isoform2 of glutaminy cyclase from drosophila melanogaster
78	<a href="#">c3pb6X</a>	Alignment	not modelled	99.6	27	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> glutaminy-peptide cyclotransferase-like protein; <b>PDBTitle:</b> crystal structure of the catalytic domain of human golgi-resident2 glutaminy cyclase at ph 6.5 <b>PDB header:</b> transferase, hydrolase

79	<a href="#">c4f9vB_</a>	Alignment	not modelled	99.6	20	<b>Chain:</b> B: <b>PDB Molecule:</b> cg32412; <b>PDBTitle:</b> structure of c113a/c136a mutant variant of glycosylated glutaminyl2 cyclase from drosophila melanogaster
80	<a href="#">c4mhzA_</a>	Alignment	not modelled	99.6	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaminyl cyclase, putative; <b>PDBTitle:</b> crystal structure of apo-form glutaminyl cyclase from ixodes2 scapularis in complex with pbd150
81	<a href="#">c3guxA_</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative zn-dependent exopeptidase; <b>PDBTitle:</b> crystal structure of a putative zn-dependent exopeptidase (bvu_1317)2 from bacteroides vulgatus atcc 8482 at 1.80 a resolution
82	<a href="#">d2afwa1</a>	Alignment	not modelled	99.4	21	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Glutaminyl-peptide cyclotransferase-like
83	<a href="#">c2ek8A_</a>	Alignment	not modelled	99.4	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase; <b>PDBTitle:</b> aminopeptidase from aneurinibacillus sp. strain am-1
84	<a href="#">c1q7lB_</a>	Alignment	not modelled	99.4	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoacylase-1; <b>PDBTitle:</b> zn-binding domain of the t347g mutant of human aminoacylase-2 i
85	<a href="#">d1vgya2</a>	Alignment	not modelled	99.4	21	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Bacterial exopeptidase dimerisation domain <b>Family:</b> Bacterial exopeptidase dimerisation domain
86	<a href="#">d3bi1a3</a>	Alignment	not modelled	99.3	20	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> FolH catalytic domain-like
87	<a href="#">d1cq2a2</a>	Alignment	not modelled	99.3	27	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Bacterial exopeptidase dimerisation domain <b>Family:</b> Bacterial exopeptidase dimerisation domain
88	<a href="#">c3iibA_</a>	Alignment	not modelled	99.3	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidase m28; <b>PDBTitle:</b> crystal structure of peptidase m28 precursor (yp_926796.1) from2 shewanella amazonensis sb2b at 1.70 a resolution
89	<a href="#">d1de4c3</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> FolH catalytic domain-like
90	<a href="#">c2qlfB_</a>	Alignment	not modelled	99.1	28	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable m18-family aminopeptidase 1; <b>PDBTitle:</b> crystal structure of aminopeptidase (m18 family) from thermotoga2 maritima
91	<a href="#">d1z2la2</a>	Alignment	not modelled	99.1	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Bacterial exopeptidase dimerisation domain <b>Family:</b> Bacterial exopeptidase dimerisation domain
92	<a href="#">d1lfa2</a>	Alignment	not modelled	99.1	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Bacterial exopeptidase dimerisation domain <b>Family:</b> Bacterial exopeptidase dimerisation domain
93	<a href="#">d1y0ya2</a>	Alignment	not modelled	99.1	26	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
94	<a href="#">c2ijzF_</a>	Alignment	not modelled	99.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> probable m18-family aminopeptidase 2; <b>PDBTitle:</b> crystal structure of aminopeptidase
95	<a href="#">c3varA_</a>	Alignment	not modelled	98.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartyl aminopeptidase; <b>PDBTitle:</b> crystal structure of dnpep, znzn form
96	<a href="#">d1ysja2</a>	Alignment	not modelled	98.9	27	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Bacterial exopeptidase dimerisation domain <b>Family:</b> Bacterial exopeptidase dimerisation domain
97	<a href="#">d1y7ea2</a>	Alignment	not modelled	98.9	22	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
98	<a href="#">d1r3na2</a>	Alignment	not modelled	98.9	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Bacterial exopeptidase dimerisation domain <b>Family:</b> Bacterial exopeptidase dimerisation domain
99	<a href="#">c2ootA_</a>	Alignment	not modelled	98.9	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate carboxypeptidase 2; <b>PDBTitle:</b> a high resolution structure of ligand-free human glutamate carboxypeptidase ii
100	<a href="#">c1y7eA_</a>	Alignment	not modelled	98.9	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable m18-family aminopeptidase 1; <b>PDBTitle:</b> the crystal structure of aminopeptidase i from borrelia burgdorferi2 b31
101	<a href="#">c3l6sA_</a>	Alignment	not modelled	98.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartyl aminopeptidase; <b>PDBTitle:</b> crystal structure of human aspartyl aminopeptidase (dnpep), in complex2 with aspartic acid hydroxamate
102	<a href="#">c3rbuA_</a>	Alignment	not modelled	98.9	27	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate carboxypeptidase 2; <b>PDBTitle:</b> n-terminally avitev-tagged human glutamate carboxypeptidase ii in2 complex with 2-pmpa
103	<a href="#">c4tweA_</a>	Alignment	not modelled	98.9	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylated-alpha-linked acidic dipeptidase-like protein; <b>PDBTitle:</b> structure of ligand-free n-acetylated-alpha-linked-acidic-dipeptidase2 like protein (naaladasel)
104	<a href="#">c4r8fB_</a>	Alignment	not modelled	98.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> vacuolar aminopeptidase 1; <b>PDBTitle:</b> crystal structure of yeast aminopeptidase 1 (ape1)
						<b>PDB header:</b> metal transport

105	<a href="#">c1cx8F_</a>	Alignment	not modelled	98.8	20	<b>Chain:</b> F; <b>PDB Molecule:</b> transferrin receptor protein; <b>PDBTitle:</b> crystal structure of the ectodomain of human transferrin receptor
106	<a href="#">c4emeB_</a>	Alignment	not modelled	98.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> m18 aspartyl aminopeptidase; <b>PDBTitle:</b> x-ray crystal structure and specificity of the plasmodium falciparum2 malaria aminopeptidase
107	<a href="#">c4r12A_</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the gamma-secretase component nicastrin
108	<a href="#">c5a63A_</a>	Alignment	not modelled	98.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> nicastrin; <b>PDBTitle:</b> cryo-em structure of the human gamma-secretase complex at 3.4 angstrom2 resolution.
109	<a href="#">d1xmba2</a>	Alignment	not modelled	97.8	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Bacterial exopeptidase dimerisation domain <b>Family:</b> Bacterial exopeptidase dimerisation domain
110	<a href="#">c4uisA_</a>	Alignment	not modelled	97.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> gamma-secretase; <b>PDBTitle:</b> the cryoem structure of human gamma-secretase complex
111	<a href="#">c4upcA_</a>	Alignment	not modelled	97.6	23	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> nicastrin; <b>PDBTitle:</b> structure of a extracellular domain
112	<a href="#">c2gliR_</a>	Alignment	not modelled	97.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> R; <b>PDB Molecule:</b> <b>PDBTitle:</b> crystal structure of aminopeptidase i from clostridium2 acetobutylicum
113	<a href="#">c3k9tA_</a>	Alignment	not modelled	96.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative peptidase; <b>PDBTitle:</b> crystal structure of putative peptidase (np_348812.1) from clostridium2 acetobutylicum at 2.37 a resolution
114	<a href="#">c5jm6D_</a>	Alignment	not modelled	95.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> aminopeptidase-like protein; <b>PDBTitle:</b> structure of chaetomium thermophilum mape1
115	<a href="#">d1fnoa3</a>	Alignment	not modelled	93.3	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Bacterial exopeptidase dimerisation domain <b>Family:</b> Bacterial exopeptidase dimerisation domain
116	<a href="#">c5nthA_</a>	Alignment	not modelled	89.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative aminopeptidase; <b>PDBTitle:</b> structure of leucyl aminopeptidase from leishmania major in complex2 with actinonin
117	<a href="#">c3kzwD_</a>	Alignment	not modelled	89.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> cytosol aminopeptidase; <b>PDBTitle:</b> crystal structure of cytosol aminopeptidase from staphylococcus aureus2 col
118	<a href="#">c5ntgA_</a>	Alignment	not modelled	86.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> aminopeptidase; <b>PDBTitle:</b> structure of leucyl aminopeptidase from trypanosoma cruzi in complex2 with citrate
119	<a href="#">c1lanA_</a>	Alignment	not modelled	85.2	13	<b>PDB header:</b> hydrolase (alpha-aminoacylpeptide) <b>Chain:</b> A; <b>PDB Molecule:</b> leucine aminopeptidase; <b>PDBTitle:</b> leucine aminopeptidase complex with l-leucinal
120	<a href="#">c2hc9A_</a>	Alignment	not modelled	81.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> leucine aminopeptidase 1; <b>PDBTitle:</b> structure of caenorhabditis elegans leucine aminopeptidase-zinc2 complex (lap1)