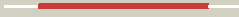























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2089c_(pepE)_2346205_2347332
Date	Mon Aug 5 13:25:20 BST 2019
Unique Job ID	aa324ccb626c3cdf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4egeA_	 Alignment		100.0	85	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidase pepe; PDBTitle: crystal structure of dipeptidase pepe from mycobacterium ulcerans
2	c4r60A_	 Alignment		100.0	35	PDB header: hydrolase Chain: A: PDB Molecule: proline dipeptidase; PDBTitle: crystal structure of xaa-pro dipeptidase from xanthomonas campestris
3	c1chmA_	 Alignment		100.0	23	PDB header: creatinase Chain: A: PDB Molecule: creatine amidinohydrolase; PDBTitle: enzymatic mechanism of creatine amidinohydrolase as deduced2 from crystal structures
4	c4fkcA_	 Alignment		100.0	35	PDB header: hydrolase Chain: A: PDB Molecule: xaa-pro aminopeptidase; PDBTitle: recombinant prolidase from thermococcus sibiricus
5	c4zngA_	 Alignment		100.0	35	PDB header: hydrolase Chain: A: PDB Molecule: prolidase; PDBTitle: x-ray crystallography of recombinant lactococcus lactis prolidase
6	c2howB_	 Alignment		100.0	34	PDB header: hydrolase Chain: B: PDB Molecule: 356aa long hypothetical dipeptidase; PDBTitle: dipeptidase (ph0974) from pyrococcus horikoshii ot3
7	c1wy2B_	 Alignment		100.0	31	PDB header: hydrolase Chain: B: PDB Molecule: xaa-pro dipeptidase; PDBTitle: crystal structure of the prolidase from pyrococcus horikoshii ot3
8	c5cxB_	 Alignment		100.0	30	PDB header: hydrolase Chain: B: PDB Molecule: aminopeptidase ypdf; PDBTitle: crystal structure of xaa-pro aminopeptidase from escherichia coli k12
9	c3q6dA_	 Alignment		100.0	30	PDB header: viral protein Chain: A: PDB Molecule: proline dipeptidase; PDBTitle: xaa-pro dipeptidase from bacillus anthracis.
10	c5cdIA_	 Alignment		100.0	32	PDB header: hydrolase Chain: A: PDB Molecule: proline dipeptidase; PDBTitle: proline dipeptidase from deinococcus radiodurans (selenomethionine2 derivative)
11	c5wzeC_	 Alignment		100.0	28	PDB header: hydrolase Chain: C: PDB Molecule: aminopeptidase p; PDBTitle: the structure of pseudomonas aeruginosa aminopeptidase pepp

12	c2zsgB_	Alignment		100.0	30	PDB header: hydrolase Chain: B: PDB Molecule: aminopeptidase p, putative; PDBTitle: crystal structure of x-pro aminopeptidase from thermotoga maritima2 msb8
13	c1w7vD_	Alignment		100.0	23	PDB header: hydrolase Chain: D: PDB Molecule: xaa-pro aminopeptidase; PDBTitle: znmg substituted aminopeptidase p from e. coli
14	c5x49A_	Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: probable xaa-pro aminopeptidase 3; PDBTitle: crystal structure of human mitochondrial x-prolyl aminopeptidase2 (xpnpep3)
15	c2oknB_	Alignment		100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: xaa-pro dipeptidase; PDBTitle: crystal strcture of human prolidase
16	c4b28A_	Alignment		100.0	22	PDB header: lyase Chain: A: PDB Molecule: metallopeptidase, family m24, putative; PDBTitle: crystal structure of dmsp lyase rddddp from roseobacter denitrificans
17	c4s2tP_	Alignment		100.0	20	PDB header: hydrolase/hydrolase inhibitor Chain: P: PDB Molecule: protein app-1; PDBTitle: crystal structure of x-prolyl aminopeptidase from caenorhabditis2 elegans: a cytosolic enzyme with a di-nuclear active site
18	c3ctzA_	Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: xaa-pro aminopeptidase 1; PDBTitle: structure of human cytosolic x-prolyl aminopeptidase
19	c5xevA_	Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: xaa-pro dipeptidase,peptidase-related protein; PDBTitle: crystal structure of a novel xaa-pro dipeptidase from deinococcus2 radiodurans
20	c3cb5A_	Alignment		100.0	20	PDB header: transcription Chain: A: PDB Molecule: fact complex subunit spt16; PDBTitle: crystal structure of the s. pombe peptidase homology domain of fact2 complex subunit spt16 (form a)
21	c3ig4E_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: E: PDB Molecule: xaa-pro aminopeptidase; PDBTitle: structure of a putative aminopeptidase p from bacillus anthracis
22	c3rvaA_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: organophosphorus acid anhydrolase; PDBTitle: crystal structure of organophosphorus acid anhydrolase from2 alteromonas macleodii
23	c5jqkA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: peptidase, putative; PDBTitle: the xray crystal structure of p. falciparum aminopeptidase p
24	c3l24A_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: xaa-pro dipeptidase; PDBTitle: crystal structure of the nerve agent degrading2 organophosphate anhydrolase/prolidase in complex with3 inhibitors
25	c4qr8B_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: xaa-pro dipeptidase; PDBTitle: crystal structure of e coli pepq
26	c5ce6A_	Alignment	not modelled	100.0	18	PDB header: transcription Chain: A: PDB Molecule: fact-spt16; PDBTitle: n-terminal domain of fact complex subunit spt16 from cicer arietinum2 (chickpea)
27	c5e5bA_	Alignment	not modelled	100.0	22	PDB header: transcription Chain: A: PDB Molecule: fact complex subunit spt16; PDBTitle: crystal structure of human spt16 n-terminal domain
28	c6a9vA_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: intermediate cleaving peptidase 55; PDBTitle: crystal structure of icp55 from saccharomyces cerevisiae (n-terminal2 42 residues deletion)
						PDB header: hydrolase

29	c5jr6B_	Alignment	not modelled	100.0	20	Chain: B: PDB Molecule: peptidase, putative; PDBTitle: the xray crystal structure of p. falciparum aminopeptidase p in2 complex with apstatin
30	c6a8mA_	Alignment	not modelled	100.0	19	PDB header: dna binding protein Chain: A: PDB Molecule: fact complex subunit spt16; PDBTitle: n-terminal domain of fact complex subunit spt16 from eremothecium2 gossypii (ashbya gossypii)
31	c3bitA_	Alignment	not modelled	100.0	15	PDB header: transcription Chain: A: PDB Molecule: fact complex subunit spt16; PDBTitle: crystal structure of yeast spt16 n-terminal domain
32	c4fukB_	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: methionine aminopeptidase; PDBTitle: aminopeptidase from trypanosoma brucei
33	c1kp0B_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: creatinase amidinohydrolase; PDBTitle: the crystal structure analysis of creatine amidinohydrolase2 from actinobacillus
34	c2g6pA_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase 1; PDBTitle: crystal structure of truncated (delta 1-89) human methionine2 aminopeptidase type 1 in complex with pyridyl pyrimidine derivative
35	c3mx6A_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure of methionine aminopeptidase from rickettsia2 prowazekii bound to methionine
36	c2gz5A_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase 1; PDBTitle: human type 1 methionine aminopeptidase in complex with ovalicin at 1.12 ang
37	d1pv9a2	Alignment	not modelled	100.0	39	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
38	c3s6bA_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure of methionine aminopeptidase 1b from plasmodium2 falciparum, pf10_0150
39	d2gg2a1	Alignment	not modelled	100.0	25	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
40	c4fo7B_	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: methionine aminopeptidase; PDBTitle: pseudomonas aeruginosa metap, in mn form
41	c1yj3A_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure analysis of product bound methionine aminopeptidase2 type 1c from mycobacterium tuberculosis
42	d1chma2	Alignment	not modelled	100.0	25	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
43	c3tavA_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure of a methionine aminopeptidase from mycobacterium2 abscessus
44	d1o0xa_	Alignment	not modelled	100.0	28	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
45	c6mrfA_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure of a methionine aminopeptidase metap from2 acinetobacter baumannii
46	d2v3za2	Alignment	not modelled	100.0	29	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
47	c4km3B_	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: methionine aminopeptidase; PDBTitle: discovery of a novel structural motif in methionine aminopeptidase2 from streptococci with possible post-translational modification
48	d1qxya_	Alignment	not modelled	100.0	28	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
49	d1b6aa2	Alignment	not modelled	100.0	16	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
50	d1xgsa2	Alignment	not modelled	100.0	25	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
51	c2v6cA_	Alignment	not modelled	100.0	19	PDB header: transcription regulator Chain: A: PDB Molecule: proliferation-associated protein 2g4; PDBTitle: crystal structure of erbb3 binding protein 1 (ebp1)
52	c2q8kA_	Alignment	not modelled	100.0	18	PDB header: transcription Chain: A: PDB Molecule: proliferation-associated protein 2g4; PDBTitle: the crystal structure of ebp1
53	c3tb5C_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: C: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure of the enterococcus faecalis methionine2 aminopeptidase apo form
54	c1xgnB_	Alignment	not modelled	100.0	27	PDB header: aminopeptidase Chain: B: PDB Molecule: methionine aminopeptidase; PDBTitle: methionine aminopeptidase from hyperthermophile pyrococcus2 furiosus
55	c1b6aA_	Alignment	not modelled	100.0	20	PDB header: angiogenesis inhibitor Chain: A: PDB Molecule: methionine aminopeptidase;

55	c1b0aA	Alignment	not modelled	100.0	20	PDBTitle: human methionine aminopeptidase 2 complexed with tnp-470
56	d1kp0a2	Alignment	not modelled	100.0	21	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
57	c4ipaC	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: C: PDB Molecule: putative curved dna-binding protein; PDBTitle: structure of a thermophilic arx1
58	c3fm3B	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: methionine aminopeptidase 2; PDBTitle: crystal structure of an encephalitozoon cuniculi methionine2 aminopeptidase type 2
59	c1yw7A	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase 2; PDBTitle: h-metap2 complexed with a444148
60	c4b6at	Alignment	not modelled	100.0	16	PDB header: ribosome Chain: T: PDB Molecule: 60s ribosomal protein l21-a; PDBTitle: cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
61	d1lchma1	Alignment	not modelled	99.9	19	Fold: Ribonuclease H-like motif Superfamily: Creatinase/prolidase N-terminal domain Family: Creatinase/prolidase N-terminal domain
62	c3pn9C	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: C: PDB Molecule: proline dipeptidase; PDBTitle: crystal structure of a proline dipeptidase from streptococcus2 pneumoniae tigr4
63	c3i7mA	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: xaa-pro dipeptidase; PDBTitle: n-terminal domain of xaa-pro dipeptidase from lactobacillus brevis.
64	c3o0oA	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: proline dipeptidase; PDBTitle: the structure of a proline dipeptidase from streptococcus agalactiae2 2603v
65	c3o5vA	Alignment	not modelled	99.7	22	PDB header: hydrolase Chain: A: PDB Molecule: x-pro dipeptidase; PDBTitle: the crystal structure of the creatinase/prolidase n-terminal domain of2 an x-pro dipeptidase from streptococcus pyogenes to 1.85a
66	c3il0B	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: B: PDB Molecule: aminopeptidase p; xaa-pro aminopeptidase; PDBTitle: the crystal structure of the aminopeptidase p, xaa-pro aminopeptidase2 from streptococcus thermophilus
67	c3ovkD	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: D: PDB Molecule: aminopeptidase p, xaa-pro dipeptidase; PDBTitle: crystal structure of an xxa-pro aminopeptidase from streptococcus2 pyogenes
68	c3qocD	Alignment	not modelled	99.6	12	PDB header: hydrolase Chain: D: PDB Molecule: putative metallopeptidase; PDBTitle: crystal structure of n-terminal domain (creatinase/prolidase like2 domain) of putative metallopeptidase from corynebacterium diphtheriae
69	c5e2cA	Alignment	not modelled	99.5	18	PDB header: hydrolase Chain: A: PDB Molecule: xaa-pro dipeptidase; PDBTitle: crystal structure of n-terminal domain of cytoplasmic peptidase pepq2 from mycobacterium tuberculosis h37rv
70	d1pv9a1	Alignment	not modelled	99.5	13	Fold: Ribonuclease H-like motif Superfamily: Creatinase/prolidase N-terminal domain Family: Creatinase/prolidase N-terminal domain
71	d1kp0a1	Alignment	not modelled	98.7	20	Fold: Ribonuclease H-like motif Superfamily: Creatinase/prolidase N-terminal domain Family: Creatinase/prolidase N-terminal domain
72	d2v3za1	Alignment	not modelled	98.7	15	Fold: Ribonuclease H-like motif Superfamily: Creatinase/prolidase N-terminal domain Family: Creatinase/prolidase N-terminal domain
73	c1t3tA	Alignment	not modelled	44.5	14	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide synthase; PDBTitle: structure of formylglycinamide synthetase
74	d1e4cp	Alignment	not modelled	33.1	15	Fold: AraD/HMP-PK domain-like Superfamily: AraD/HMP-PK domain-like Family: AraD-like aldolase/epimerase
75	c4m6rA	Alignment	not modelled	30.0	15	PDB header: lyase Chain: A: PDB Molecule: methylthioribulose-1-phosphate dehydratase; PDBTitle: structural and biochemical basis for the inhibition of cell death by2 apip, a methionine salvage enzyme
76	c4qnnC	Alignment	not modelled	27.6	10	PDB header: hydrolase Chain: C: PDB Molecule: phospholipase a 1 from hornet(vespa basalis) venom; PDBTitle: crystal structure of phospholipase a 1 from hornet(vespa basalis)2 venom
77	c2y0oA	Alignment	not modelled	27.4	20	PDB header: isomerase Chain: A: PDB Molecule: probable d-lyxose ketol-isomerase; PDBTitle: the structure of a d-lyxose isomerase from the sigmab2 regulon of bacillus subtilis
78	d1rp1a2	Alignment	not modelled	25.9	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
79	c2pplA	Alignment	not modelled	24.8	30	PDB header: hydrolase Chain: A: PDB Molecule: pancreatic lipase-related protein 1; PDBTitle: human pancreatic lipase-related protein 1
80	d1hplA2	Alignment	not modelled	23.9	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain

81	d1etha2	Alignment	not modelled	23.0	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
82	c2opiB_	Alignment	not modelled	23.0	12	PDB header: lyase Chain: B: PDB Molecule: l-fucose-1-phosphate aldolase; PDBTitle: crystal structure of l-fucose-1-phosphate aldolase from bacteroides2 thetaiotaomicron
83	d1lpbb2	Alignment	not modelled	22.9	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
84	c6e7kB_	Alignment	not modelled	22.3	20	PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein lipase; PDBTitle: structure of the lipoprotein lipase gpibp1 complex that mediates2 plasma triglyceride hydrolysis
85	d1b74a1	Alignment	not modelled	21.8	17	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
86	c1rp1A_	Alignment	not modelled	20.9	23	PDB header: hydrolase Chain: A: PDB Molecule: pancreatic lipase related protein 1; PDBTitle: dog pancreatic lipase related protein 1
87	c1hplB_	Alignment	not modelled	20.7	20	PDB header: hydrolase(carboxylic esterase) Chain: B: PDB Molecule: lipase; PDBTitle: horse pancreatic lipase. the crystal structure at 2.3 angstroms2 resolution
88	c2pvsB_	Alignment	not modelled	20.6	20	PDB header: hydrolase Chain: B: PDB Molecule: pancreatic lipase-related protein 2; PDBTitle: structure of human pancreatic lipase related protein 22 mutant n336q
89	c1b74A_	Alignment	not modelled	20.4	17	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: glutamate racemase from aquifex pyrophilus
90	d1gpla2	Alignment	not modelled	19.8	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
91	d1bu8a2	Alignment	not modelled	19.6	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
92	c2ohoA_	Alignment	not modelled	18.8	3	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: structural basis for glutamate racemase inhibitor
93	c3uhfB_	Alignment	not modelled	18.5	13	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from campylobacter jejuni2 subsp. jejuni
94	c5w16D_	Alignment	not modelled	18.3	13	PDB header: isomerase Chain: D: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from thermus thermophilus in2 complex with d-glutamate
95	c2gzmB_	Alignment	not modelled	18.0	17	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of the glutamate racemase from bacillus anthracis
96	c3outC_	Alignment	not modelled	17.8	13	PDB header: isomerase Chain: C: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from francisella tularensis2 subsp. tularensis schu s4 in complex with d-glutamate.
97	c1gplA_	Alignment	not modelled	17.1	23	PDB header: serine esterase Chain: A: PDB Molecule: rp2 lipase; PDBTitle: rp2 lipase
98	c2zakB_	Alignment	not modelled	17.1	18	PDB header: hydrolase Chain: B: PDB Molecule: l-asparaginase precursor; PDBTitle: orthorhombic crystal structure of precursor e. coli isoaspartyl2 peptidase/l-asparaginase (ecaiii) with active-site t179a mutation
99	c6btdA_	Alignment	not modelled	16.8	12	PDB header: lyase Chain: A: PDB Molecule: fucose phosphate aldolase; PDBTitle: crystal structure of deoxyribose-phosphate aldolase from bacillus2 thuringiensis involved in dispatching the ubiquitous radical sam3 enzyme byproduct 5-deoxyribose