







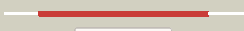










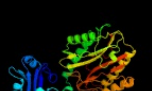




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2535c_(pepQ)_2859310_2860428
Date	Wed Aug 7 12:50:17 BST 2019
Unique Job ID	6028ea6979667b56

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4zngA_	 Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: prolidase; PDBTitle: x-ray crystallography of recombinant lactococcus lactis prolidase
2	c5cnxB_	 Alignment		100.0	35	PDB header: hydrolase Chain: B: PDB Molecule: aminopeptidase ypdf; PDBTitle: crystal structure of xaa-pro aminopeptidase from escherichia coli k12
3	c3q6dA_	 Alignment		100.0	42	PDB header: viral protein Chain: A: PDB Molecule: proline dipeptidase; PDBTitle: xaa-pro dipeptidase from bacillus anthracis.
4	c4egeA_	 Alignment		100.0	34	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidase pepe; PDBTitle: crystal structure of dipeptidase pepe from mycobacterium ulcerans
5	c4r60A_	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: proline dipeptidase; PDBTitle: crystal structure of xaa-pro dipeptidase from xanthomonas campestris
6	c4fkcA_	 Alignment		100.0	32	PDB header: hydrolase Chain: A: PDB Molecule: xaa-pro aminopeptidase; PDBTitle: recombinant prolidase from thermococcus sibiricus
7	c1wy2B_	 Alignment		100.0	35	PDB header: hydrolase Chain: B: PDB Molecule: xaa-pro dipeptidase; PDBTitle: crystal structure of the prolidase from pyrococcus horikoshii ot3
8	c5cdlA_	 Alignment		100.0	39	PDB header: hydrolase Chain: A: PDB Molecule: proline dipeptidase; PDBTitle: proline dipeptidase from deinococcus radiodurans (selenomethionine2 derivative)
9	c2howB_	 Alignment		100.0	34	PDB header: hydrolase Chain: B: PDB Molecule: 356aa long hypothetical dipeptidase; PDBTitle: dipeptidase (ph0974) from pyrococcus horikoshii ot3
10	c2zsgB_	 Alignment		100.0	33	PDB header: hydrolase Chain: B: PDB Molecule: aminopeptidase p, putative; PDBTitle: crystal structure of x-pro aminopeptidase from thermotoga maritima2 msb8
11	c1chmA_	 Alignment		100.0	22	PDB header: creatinase Chain: A: PDB Molecule: creatine amidinohydrolase; PDBTitle: enzymatic mechanism of creatine amidinohydrolase as deduced2 from crystal structures

12	c5wzeC_	Alignment		100.0	29	PDB header: hydrolase Chain: C; PDB Molecule: aminopeptidase p; PDBTitle: the structure of pseudomonas aeruginosa aminopeptidase pepp
13	c3ctzA_	Alignment		100.0	25	PDB header: hydrolase Chain: A; PDB Molecule: xaa-pro aminopeptidase 1; PDBTitle: structure of human cytosolic x-prolyl aminopeptidase
14	c5x49A_	Alignment		100.0	26	PDB header: hydrolase Chain: A; PDB Molecule: probable xaa-pro aminopeptidase 3; PDBTitle: crystal structure of human mitochondrial x-prolyl aminopeptidase2 (xpnpep3)
15	c4s2tP_	Alignment		100.0	24	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
16	c1w7vD_	Alignment		100.0	27	PDB header: hydrolase Chain: D; PDB Molecule: xaa-pro aminopeptidase; PDBTitle: znmg substituted aminopeptidase p from e. coli
17	c2oknB_	Alignment		100.0	24	PDB header: hydrolase Chain: B; PDB Molecule: xaa-pro dipeptidase; PDBTitle: crystal strcture of human prolidase
18	c3ig4E_	Alignment		100.0	22	PDB header: hydrolase Chain: E; PDB Molecule: xaa-pro aminopeptidase; PDBTitle: structure of a putative aminopeptidase p from bacillus anthracis
19	c5jqkA_	Alignment		100.0	23	PDB header: hydrolase Chain: A; PDB Molecule: peptidase, putative; PDBTitle: the xray crystal structure of p. falciparum aminopeptidase p
20	c6a9vA_	Alignment		100.0	22	PDB header: hydrolase Chain: A; PDB Molecule: intermediate cleaving peptidase 55; PDBTitle: crystal structure of icp55 from saccharomyces cerevisiae (n-terminal2 42 residues deletion)
21	c3rvaA_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A; PDB Molecule: organophosphorus acid anhydrolase; PDBTitle: crystal structure of organophosphorus acid anhydrolase from2 alteromonas macleodii
22	c5jr6B_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B; PDB Molecule: peptidase, putative; PDBTitle: the xray crystal structure of p. falciparum aminopeptidase p in2 complex with apstatin
23	c4b28A_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: A; PDB Molecule: metallopeptidase, family m24, putative; PDBTitle: crystal structure of dmsp lyase rddddp from roseobacter denitrificans
24	c4qr8B_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: B; PDB Molecule: xaa-pro dipeptidase; PDBTitle: crystal structure of e coli pepq
25	c3l24A_	Alignment	not modelled	100.0	23	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
26	c5ce6A_	Alignment	not modelled	100.0	17	PDB header: transcription Chain: A; PDB Molecule: fact-spt16; PDBTitle: n-terminal domain of fact complex subunit spt16 from cicer arietinum2 (chickpea)
27	c5xevA_	Alignment	not modelled	100.0	28	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
28	c5e5bA_	Alignment	not modelled	100.0	16	PDB header: transcription Chain: A; PDB Molecule: fact complex subunit spt16; PDBTitle: crystal structure of human spt16 n-terminal domain

29	c3cb5A	Alignment	not modelled	100.0	17	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)
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	23	PDB header: hydrolase Chain: B: PDB Molecule: methionine aminopeptidase; PDBTitle: aminopeptidase from trypanosoma brucei
33	c1kp0B	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: creatine amidinohydrolase; PDBTitle: the crystal structure analysis of creatine amidinohydrolase2 from actinobacillus
34	c2g6pA	Alignment	not modelled	100.0	23	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	c2gz5A	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase 1; PDBTitle: human type 1 methionine aminopeptidase in complex with ovalicin at 1.12 ang
36	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
37	d1pv9a2	Alignment	not modelled	100.0	43	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
38	c1yj3A	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure analysis of product bound methionine aminopeptidase2 type 1c from mycobacterium tuberculosis
39	d1chma2	Alignment	not modelled	100.0	26	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
40	c3mx6A	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure of methionine aminopeptidase from rickettsia2 prowazekii bound to methionine
41	c4fo7B	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: methionine aminopeptidase; PDBTitle: pseudomonas aeruginosa metap, in mn form
42	d2gg2a1	Alignment	not modelled	100.0	24	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
43	c3tavA	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure of a methionine aminopeptidase from mycobacterium2 abscessus
44	d2v3za2	Alignment	not modelled	100.0	34	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
45	d1o0xa	Alignment	not modelled	100.0	22	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
46	c6mrfA	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure of a methionine aminopeptidase metap from2 acinetobacter baumannii
47	d1qxya	Alignment	not modelled	100.0	25	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
48	c4km3B	Alignment	not modelled	100.0	22	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
49	d1b6aa2	Alignment	not modelled	100.0	19	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
50	d1xgsa2	Alignment	not modelled	100.0	24	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	26	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	25	PDB header: aminopeptidase Chain: B: PDB Molecule: methionine aminopeptidase; PDBTitle: methionine aminopeptidase from hyperthermophile pyrococcus2 furiosus
						Fold: Creatinase/aminopeptidase

55	d1kp0a2	Alignment	not modelled	100.0	24	Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
56	c1b6aA_	Alignment	not modelled	100.0	23	PDB header: angiogenesis inhibitor Chain: A: PDB Molecule: methionine aminopeptidase; PDBTitle: human methionine aminopeptidase 2 complexed with tnp-470
57	c3fm3B_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: methionine aminopeptidase 2; PDBTitle: crystal structure of an encephalitozoon cuniculi methionine2 aminopeptidase type 2
58	c4ipaC_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: C: PDB Molecule: putative curved dna-binding protein; PDBTitle: structure of a thermophilic arx1
59	c1yw7A_	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase 2; PDBTitle: h-metap2 complexed with a444148
60	c4b6at_	Alignment	not modelled	100.0	21	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	c5e2cA_	Alignment	not modelled	99.8	98	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
62	c3ovkD_	Alignment	not modelled	99.7	34	PDB header: hydrolase Chain: D: PDB Molecule: aminopeptidase p, xaa-pro dipeptidase; PDBTitle: crystal structure of an xxa-pro aminopeptidase from streptococcus2 pyogenes
63	c3il0B_	Alignment	not modelled	99.7	23	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
64	c3pn9C_	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: C: PDB Molecule: proline dipeptidase; PDBTitle: crystal structure of a proline dipeptidase from streptococcus2 pneumoniae tigr4
65	d1chma1	Alignment	not modelled	99.6	20	Fold: Ribonuclease H-like motif Superfamily: Creatinase/prolidase N-terminal domain Family: Creatinase/prolidase N-terminal domain
66	c3qc0D_	Alignment	not modelled	99.6	40	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
67	c3i7mA_	Alignment	not modelled	99.6	15	PDB header: hydrolase Chain: A: PDB Molecule: xaa-pro dipeptidase; PDBTitle: n-terminal domain of xaa-pro dipeptidase from lactobacillus brevis.
68	c30ooA_	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: A: PDB Molecule: proline dipeptidase; PDBTitle: the structure of a proline dipeptidase from streptococcus agalactiae2 2603v
69	c3o5vA_	Alignment	not modelled	99.6	13	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
70	d1pv9a1	Alignment	not modelled	99.4	18	Fold: Ribonuclease H-like motif Superfamily: Creatinase/prolidase N-terminal domain Family: Creatinase/prolidase N-terminal domain
71	d2v3za1	Alignment	not modelled	98.7	17	Fold: Ribonuclease H-like motif Superfamily: Creatinase/prolidase N-terminal domain Family: Creatinase/prolidase N-terminal domain
72	d1kp0a1	Alignment	not modelled	98.0	19	Fold: Ribonuclease H-like motif Superfamily: Creatinase/prolidase N-terminal domain Family: Creatinase/prolidase N-terminal domain
73	c2c5qE_	Alignment	not modelled	44.2	11	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: rraa-like protein yer010c; PDBTitle: crystal structure of yeast yer010cp
74	c1t3mA_	Alignment	not modelled	33.4	20	PDB header: hydrolase Chain: A: PDB Molecule: putative l-asparaginase; PDBTitle: structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
75	d1l1pa_	Alignment	not modelled	32.0	33	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
76	c2y0oA_	Alignment	not modelled	30.4	13	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
77	c2gezE_	Alignment	not modelled	29.1	18	PDB header: hydrolase Chain: E: PDB Molecule: l-asparaginase alpha subunit; PDBTitle: crystal structure of potassium-independent plant asparaginase
78	c3fhkF_	Alignment	not modelled	28.7	13	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: upf0403 protein yphp; PDBTitle: crystal structure of apc1446, b.subtilis yphp disulfide isomerase
79	d1t11a3	Alignment	not modelled	26.8	29	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
80	c2zakB_	Alignment	not modelled	25.5	20	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
81	c4pu6A_	Alignment	not modelled	23.4	22	PDB header: hydrolase Chain: A: PDB Molecule: l-asparaginase alpha subunit; PDBTitle: crystal structure of potassium-dependent plant-type l-asparaginase2 from phaseolus vulgaris in complex with k+ cations
82	d1w26a3	Alignment	not modelled	21.7	42	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
83	c4qnnC_	Alignment	not modelled	20.7	13	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
84	c2a8lB_	Alignment	not modelled	19.8	22	PDB header: hydrolase Chain: B: PDB Molecule: threonine aspartase 1; PDBTitle: crystal structure of human taspase1 (t234a mutant)
85	c4gduB_	Alignment	not modelled	17.8	24	PDB header: hydrolase Chain: B: PDB Molecule: l-asparaginase; PDBTitle: crystal structure of sulfate-bound human l-asparaginase protein
86	d1lpbb2	Alignment	not modelled	16.5	27	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
87	c1w26B_	Alignment	not modelled	16.1	42	PDB header: chaperone Chain: B: PDB Molecule: trigger factor; PDBTitle: trigger factor in complex with the ribosome forms a2 molecular cradle for nascent proteins
88	d1rp1a2	Alignment	not modelled	16.0	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
89	c3prdA_	Alignment	not modelled	15.8	25	PDB header: chaperone, isomerase Chain: A: PDB Molecule: fkbp-type peptidyl-prolyl cis-trans isomerase; PDBTitle: structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
90	c4rwrB_	Alignment	not modelled	15.7	67	PDB header: viral protein Chain: B: PDB Molecule: stage ii sporulation protein d; PDBTitle: 2.1 angstrom crystal structure of stage ii sporulation protein d from2 bacillus anthracis
91	c5iltA_	Alignment	not modelled	15.7	67	PDB header: hydrolase Chain: A: PDB Molecule: stage ii sporulation protein d; PDBTitle: 2.6 angstrom resolution crystal structure of stage ii sporulation2 protein d (spoid) from clostridium difficile in complex with3 triacetylchitotriose
92	d1letha2	Alignment	not modelled	15.6	27	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
93	d1hpla2	Alignment	not modelled	15.5	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
94	c2pplA_	Alignment	not modelled	15.3	23	PDB header: hydrolase Chain: A: PDB Molecule: pancreatic lipase-related protein 1; PDBTitle: human pancreatic lipase-related protein 1
95	c5zr0A_	Alignment	not modelled	15.3	33	PDB header: chaperone Chain: A: PDB Molecule: maltose-binding periplasmic protein,trigger factor; PDBTitle: solution structure of peptidyl-prolyl cis/trans isomerase domain of2 trigger factor in complex with mbp
96	c1utyA_	Alignment	not modelled	15.1	24	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 2; PDBTitle: crystal structure of the rna binding domain of bluetongue virus non-2 structural protein 2(ns2)
97	d1utyA_	Alignment	not modelled	15.1	24	Fold: BTV NS2-like ssRNA-binding domain Superfamily: BTV NS2-like ssRNA-binding domain Family: BTV NS2-like ssRNA-binding domain
98	c6e7kB_	Alignment	not modelled	14.6	20	PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein lipase; PDBTitle: structure of the lipoprotein lipase gpibp1 complex that mediates2 plasma triglyceride hydrolysis
99	d1bu8a2	Alignment	not modelled	14.1	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain