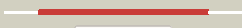























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2861c_(mapB)_3173170_3174027
Date	Wed Aug 7 12:50:53 BST 2019
Unique Job ID	5706ec8c0ac646b2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1yj3A_	 Alignment		100.0	100	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure analysis of product bound methionine aminopeptidase2 type 1c from mycobacterium tuberculosis
2	c4fukB_	 Alignment		100.0	45	PDB header: hydrolase Chain: B: PDB Molecule: methionine aminopeptidase; PDBTitle: aminopeptidase from trypanosoma brucei
3	c3s6bA_	 Alignment		100.0	46	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure of methionine aminopeptidase 1b from plasmodium2 falciparum, pf10_0150
4	c2g6pA_	 Alignment		100.0	49	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
5	c2gz5A_	 Alignment		100.0	49	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase 1; PDBTitle: human type 1 methionine aminopeptidase in complex with ovalicin at 1.12 ang
6	c3tavA_	 Alignment		100.0	37	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure of a methionine aminopeptidase from mycobacterium2 abscessus
7	d2gg2a1	 Alignment		100.0	51	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
8	c4fo7B_	 Alignment		100.0	49	PDB header: hydrolase Chain: B: PDB Molecule: methionine aminopeptidase; PDBTitle: pseudomonas aeruginosa metap, in mn form
9	d1o0xa_	 Alignment		100.0	37	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
10	c3mx6A_	 Alignment		100.0	46	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure of methionine aminopeptidase from rickettsia2 prowazekii bound to methionine
11	d1qxva_	 Alignment		100.0	36	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase

12	c1w7vD_	Alignment		100.0	25	PDB header: hydrolase Chain: D: PDB Molecule: xaa-pro aminopeptidase; PDBTitle: znmg substituted aminopeptidase p from e. coli
13	c5wzeC_	Alignment		100.0	24	PDB header: hydrolase Chain: C: PDB Molecule: aminopeptidase p; PDBTitle: the structure of pseudomonas aeruginosa aminopeptidase pepp
14	c4km3B_	Alignment		100.0	28	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
15	c3rvaA_	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: organophosphorus acid anhydrolase; PDBTitle: crystal structure of organophosphorus acid anhydrolase from2 alteromonas nacleodii
16	c5x49A_	Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: probable xaa-pro aminopeptidase 3; PDBTitle: crystal structure of human mitochondrial x-prolyl aminopeptidase2 (xpnpep3)
17	c3l24A_	Alignment		100.0	18	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
18	c4qr8B_	Alignment		100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: xaa-pro dipeptidase; PDBTitle: crystal structure of e coli pepq
19	c2oknB_	Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: xaa-pro dipeptidase; PDBTitle: crystal strcture of human prolidase
20	c3ig4E_	Alignment		100.0	20	PDB header: hydrolase Chain: E: PDB Molecule: xaa-pro aminopeptidase; PDBTitle: structure of a putative aminopeptidase p from bacillus anthracis
21	c4r60A_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: proline dipeptidase; PDBTitle: crystal structure of xaa-pro dipeptidase from xanthomonas campestris
22	c2zsgB_	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: aminopeptidase p, putative; PDBTitle: crystal structure of x-pro aminopeptidase from thermotoga maritima2 msb8
23	c1chmA_	Alignment	not modelled	100.0	22	PDB header: creatinase Chain: A: PDB Molecule: creatine amidinohydrolase; PDBTitle: enzymatic mechanism of creatine amidinohydrolase as deduced2 from crystal structures
24	c5cnxB_	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: aminopeptidase ypdf; PDBTitle: crystal structure of xaa-pro aminopeptidase from escherichia coli k12
25	c6mrfA_	Alignment	not modelled	100.0	43	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure of a methionine aminopeptidase metap from2 acinetobacter baumannii
26	c4egeA_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidase pepe; PDBTitle: crystal structure of dipeptidase pepe from mycobacterium ulcerans
27	c5cdlA_	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: proline dipeptidase; PDBTitle: proline dipeptidase from deinococcus radiodurans (selenomethionine2 derivative)
28	c1wy2B_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: xaa-pro dipeptidase; PDBTitle: crystal structure of the prolidase from pyrococcus horikoshii ot3

29	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-terminal 2 42 residues deletion)
30	c3q6dA	Alignment	not modelled	100.0	27	PDB header: viral protein Chain: A: PDB Molecule: proline dipeptidase; PDBTitle: xaa-pro dipeptidase from bacillus anthracis.
31	c4fkCA	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: xaa-pro aminopeptidase; PDBTitle: recombinant prolidase from thermococcus sibiricus
32	c3cb5A	Alignment	not modelled	100.0	10	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)
33	c2howB	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: 356aa long hypothetical dipeptidase; PDBTitle: dipeptidase (ph0974) from pyrococcus horikoshii ot3
34	c4zngA	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: prolidase; PDBTitle: x-ray crystallography of recombinant lactococcus lactis prolidase
35	d1chma2	Alignment	not modelled	100.0	21	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
36	d1b6aa2	Alignment	not modelled	100.0	24	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
37	c5xevA	Alignment	not modelled	100.0	21	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
38	c5ce6A	Alignment	not modelled	100.0	14	PDB header: transcription Chain: A: PDB Molecule: fact-spt16; PDBTitle: n-terminal domain of fact complex subunit spt16 from cicer arietinum2 (chickpea)
39	c5e5bA	Alignment	not modelled	100.0	13	PDB header: transcription Chain: A: PDB Molecule: fact complex subunit spt16; PDBTitle: crystal structure of human spt16 n-terminal domain
40	c3ctzA	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: xaa-pro aminopeptidase 1; PDBTitle: structure of human cytosolic x-prolyl aminopeptidase
41	c6a8mA	Alignment	not modelled	100.0	12	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)
42	d2v3za2	Alignment	not modelled	100.0	26	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
43	d1pv9a2	Alignment	not modelled	100.0	27	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
44	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
45	c2v6cA	Alignment	not modelled	100.0	18	PDB header: transcription regulator Chain: A: PDB Molecule: proliferation-associated protein 2g4; PDBTitle: crystal structure of erbb3 binding protein 1 (ebp1)
46	c2q8kA	Alignment	not modelled	100.0	19	PDB header: transcription Chain: A: PDB Molecule: proliferation-associated protein 2g4; PDBTitle: the crystal structure of ebp1
47	c4s2tP	Alignment	not modelled	100.0	18	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
48	c5jqkA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: peptidase, putative; PDBTitle: the xray crystal structure of p. falciparum aminopeptidase p
49	d1xgsa2	Alignment	not modelled	100.0	29	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
50	c3bitA	Alignment	not modelled	100.0	11	PDB header: transcription Chain: A: PDB Molecule: fact complex subunit spt16; PDBTitle: crystal structure of yeast spt16 n-terminal domain
51	c5jr6B	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: peptidase, putative; PDBTitle: the xray crystal structure of p. falciparum aminopeptidase p in2 complex with apstatin
52	c1xgnB	Alignment	not modelled	100.0	30	PDB header: aminopeptidase Chain: B: PDB Molecule: methionine aminopeptidase; PDBTitle: methionine aminopeptidase from hyperthermophile pyrococcus2 furiosus
53	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
54	c4ipaC	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: C: PDB Molecule: putative curved dna-binding protein; PDBTitle: structure of a thermophilic arx1
						PDB header: hydrolase

55	c1yw7A_	Alignment	not modelled	100.0	24	Chain: A: PDB Molecule: methionine aminopeptidase 2; PDBTitle: h-metap2 complexed with a444148
56	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
57	c3tb5C_	Alignment	not modelled	100.0	32	PDB header: hydrolase Chain: C: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure of the enterococcus faecalis methionine2 aminopeptidase apo form
58	c1kp0B_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: creatine amidinohydrolase; PDBTitle: the crystal structure analysis of creatine amidinohydrolase2 from actinobacillus
59	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
60	d1kp0a2	Alignment	not modelled	100.0	19	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
61	c3prdA_	Alignment	not modelled	51.2	31	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
62	d1w26a3	Alignment	not modelled	38.6	21	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
63	d1l1pa_	Alignment	not modelled	34.8	25	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
64	d1t1la3	Alignment	not modelled	33.7	25	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
65	c1w26B_	Alignment	not modelled	33.3	23	PDB header: chaperone Chain: B: PDB Molecule: trigger factor; PDBTitle: trigger factor in complex with the ribosome forms a2 molecular cradle for nascent proteins
66	c3mpbA_	Alignment	not modelled	30.8	14	PDB header: isomerase Chain: A: PDB Molecule: sugar isomerase; PDBTitle: z5688 from e. coli o157:h7 bound to fructose
67	c1i19B_	Alignment	not modelled	28.4	16	PDB header: oxidoreductase Chain: B: PDB Molecule: cholesterol oxidase; PDBTitle: crystal structure of cholesterol oxidase from b.sterolicum
68	c2y0aA_	Alignment	not modelled	27.6	26	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
69	c1t11A_	Alignment	not modelled	25.0	16	PDB header: chaperone Chain: A: PDB Molecule: trigger factor; PDBTitle: trigger factor
70	c4mspB_	Alignment	not modelled	23.0	20	PDB header: isomerase Chain: B: PDB Molecule: peptidyl-prolyl cis-trans isomerase fkbp14; PDBTitle: crystal structure of human peptidyl-prolyl cis-trans isomerase fkbp222 (aka fkbp14) containing two ef-hand motifs
71	c2bvfa_	Alignment	not modelled	20.6	20	PDB header: oxidase Chain: A: PDB Molecule: 6-hydroxy-d-nicotine oxidase; PDBTitle: crystal structure of 6-hydroxy-d-nicotine oxidase from2 arthrobacter nicotinovorans. crystal form 3 (p1)
72	d1kt0a2	Alignment	not modelled	19.6	24	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
73	c1t3mA_	Alignment	not modelled	19.1	2	PDB header: hydrolase Chain: A: PDB Molecule: putative l-asparaginase; PDBTitle: structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
74	c4qbfF_	Alignment	not modelled	18.9	13	PDB header: hydrolase Chain: F: PDB Molecule: vrr-nuc; PDBTitle: vrr_nuc domain protein
75	d1j3ba1	Alignment	not modelled	18.3	9	Fold: PEP carboxykinase-like Superfamily: PEP carboxykinase-like Family: PEP carboxykinase C-terminal domain
76	c2c5qE_	Alignment	not modelled	18.2	17	PDB header: structural genomics,unknown function Chain: E: PDB Molecule: rraa-like protein yer010c; PDBTitle: crystal structure of yeast yer010cp
77	c2gezE_	Alignment	not modelled	18.0	4	PDB header: hydrolase Chain: E: PDB Molecule: l-asparaginase alpha subunit; PDBTitle: crystal structure of potassium-independent plant asparaginase
78	c2zakB_	Alignment	not modelled	17.6	2	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
79	c3nojA_	Alignment	not modelled	16.5	20	PDB header: lyase Chain: A: PDB Molecule: 4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate PDBTitle: the structure of hmg/cha aldolase from the protocatechuate degradation2 pathway of pseudomonas putida
80	c5w8pA_	Alignment	not modelled	16.2	15	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus
						PDB header: oxidoreductase

81	c3w8wA_	Alignment	not modelled	16.1	14	Chain: A: PDB Molecule: putative fad-dependent oxygenase encm; PDBTitle: the crystal structure of encm
82	c5zr0A_	Alignment	not modelled	15.7	21	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
83	c2ktgA_	Alignment	not modelled	15.5	20	PDB header: ca-binding protein Chain: A: PDB Molecule: calmodulin, putative; PDBTitle: calmodulin like protein from entamoeba histolytica: solution structure2 and calcium binding properties of a partially folded protein
84	c6c80B_	Alignment	not modelled	14.9	19	PDB header: immune system Chain: B: PDB Molecule: cytokinin oxidase luckx1.1; PDBTitle: crystal structure of a flax cytokinin oxidase
85	c4dt4A_	Alignment	not modelled	13.9	22	PDB header: isomerase Chain: A: PDB Molecule: fkbp-type 16 kda peptidyl-prolyl cis-trans isomerase; PDBTitle: crystal structure of the ppiase-chaperone slpa with the chaperone2 binding site occupied by the linker of the purification tag
86	d1ii2a1	Alignment	not modelled	13.6	14	Fold: PEP carboxykinase-like Superfamily: PEP carboxykinase-like Family: PEP carboxykinase C-terminal domain
87	c1qs2A_	Alignment	not modelled	13.5	14	PDB header: toxin Chain: A: PDB Molecule: adp-ribosyltransferase; PDBTitle: crystal structure of vip2 with nad
88	c2a8lB_	Alignment	not modelled	13.1	9	PDB header: hydrolase Chain: B: PDB Molecule: threonine aspartase 1; PDBTitle: crystal structure of human taspase1 (t234a mutant)
89	c4pu6A_	Alignment	not modelled	13.0	2	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
90	c4gduB_	Alignment	not modelled	12.5	7	PDB header: hydrolase Chain: B: PDB Molecule: l-asparaginase; PDBTitle: crystal structure of sulfate-bound human l-asparaginase protein
91	d2olra1	Alignment	not modelled	12.1	13	Fold: PEP carboxykinase-like Superfamily: PEP carboxykinase-like Family: PEP carboxykinase C-terminal domain
92	c4dipD_	Alignment	not modelled	12.0	14	PDB header: isomerase Chain: D: PDB Molecule: peptidyl-prolyl cis-trans isomerase fkbp14; PDBTitle: crystal structure of human peptidyl-prolyl cis-trans isomerase fkbp14
93	c3ds8A_	Alignment	not modelled	11.9	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2722 protein; PDBTitle: the crysatl structure of the gene lin2722 products from listeria2 innocua
94	c2zyiB_	Alignment	not modelled	11.7	32	PDB header: hydrolase Chain: B: PDB Molecule: lipase, putative; PDBTitle: a. fulgidus lipase with fatty acid fragment and calcium
95	d1ex9a_	Alignment	not modelled	11.5	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
96	c2nyuA_	Alignment	not modelled	11.4	20	PDB header: transferase Chain: A: PDB Molecule: putative ribosomal rna methyltransferase 2; PDBTitle: crystal structure of human ftsj homolog 2 (e.coli) protein in complex2 with s-adenosylmethionine
97	c3jr1A_	Alignment	not modelled	11.3	14	PDB header: transferase Chain: A: PDB Molecule: putative fructosamine-3-kinase; PDBTitle: crystal structure of putative fructosamine-3-kinase (yp_719053.1) from2 haemophilus somnus 129pt at 2.32 a resolution
98	c2ki0A_	Alignment	not modelled	11.1	23	PDB header: de novo protein Chain: A: PDB Molecule: ds119; PDBTitle: nmr structure of a de novo designed beta alpha beta
99	c4kkpA_	Alignment	not modelled	11.1	18	PDB header: structural protein Chain: A: PDB Molecule: rbma protein; PDBTitle: crystal structure of vibrio cholerae rbma (crystal form 2)