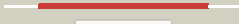



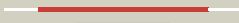



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0734_(mapA)_826673_827473
Date	Fri Jul 26 01:50:31 BST 2019
Unique Job ID	001ab5b7b1916f33

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4fukB_</a>	 Alignment		100.0	35	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> methionine aminopeptidase; <b>PDBTitle:</b> aminopeptidase from trypanosoma brucei
2	<a href="#">c3tavA_</a>	 Alignment		100.0	74	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine aminopeptidase; <b>PDBTitle:</b> crystal structure of a methionine aminopeptidase from mycobacterium2 abscessus
3	<a href="#">c3s6bA_</a>	 Alignment		100.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine aminopeptidase; <b>PDBTitle:</b> crystal structure of methionine aminopeptidase 1b from plasmodium2 falciparum, pf10_0150
4	<a href="#">c2g6pA_</a>	 Alignment		100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine aminopeptidase 1; <b>PDBTitle:</b> crystal structure of truncated (delta 1-89) human methionine2 aminopeptidase type 1 in complex with pyridyl pyrimidine derivative
5	<a href="#">c2gz5A_</a>	 Alignment		100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine aminopeptidase 1; <b>PDBTitle:</b> human type 1 methionine aminopeptidase in complex with ovalicin at 1.12 ang
6	<a href="#">c1vj3A_</a>	 Alignment		100.0	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine aminopeptidase; <b>PDBTitle:</b> crystal structure analysis of product bound methionine aminopeptidase2 type 1c from mycobacterium tuberculosis
7	<a href="#">d2gg2a1</a>	 Alignment		100.0	38	<b>Fold:</b> Creatinase/aminopeptidase <b>Superfamily:</b> Creatinase/aminopeptidase <b>Family:</b> Creatinase/aminopeptidase
8	<a href="#">d1o0xa_</a>	 Alignment		100.0	40	<b>Fold:</b> Creatinase/aminopeptidase <b>Superfamily:</b> Creatinase/aminopeptidase <b>Family:</b> Creatinase/aminopeptidase
9	<a href="#">c4fo7B_</a>	 Alignment		100.0	37	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> methionine aminopeptidase; <b>PDBTitle:</b> pseudomonas aeruginosa metap, in mn form
10	<a href="#">c3mx6A_</a>	 Alignment		100.0	37	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine aminopeptidase; <b>PDBTitle:</b> crystal structure of methionine aminopeptidase from rickettsia2 prowazekii bound to methionine
11	<a href="#">c4km3B_</a>	 Alignment		100.0	36	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> methionine aminopeptidase; <b>PDBTitle:</b> discovery of a novel structural motif in methionine aminopeptidase2 from streptococci with possible post-translational modification

12	<a href="#">c1w7vD_</a>	Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> xaa-pro aminopeptidase; <b>PDBTitle:</b> znmg substituted aminopeptidase p from e. coli
13	<a href="#">c4qr8B_</a>	Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> xaa-pro dipeptidase; <b>PDBTitle:</b> crystal structure of e coli pepq
14	<a href="#">c5wzeC_</a>	Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> aminopeptidase p; <b>PDBTitle:</b> the structure of pseudomonas aeruginosa aminopeptidase pepp
15	<a href="#">c3l24A_</a>	Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> xaa-pro dipeptidase; <b>PDBTitle:</b> crystal structure of the nerve agent degrading2 organophosphate anhydrolase/prolidase in complex with3 inhibitors
16	<a href="#">d1qxya_</a>	Alignment		100.0	32	<b>Fold:</b> Creatinase/aminopeptidase <b>Superfamily:</b> Creatinase/aminopeptidase <b>Family:</b> Creatinase/aminopeptidase
17	<a href="#">c3rvaA_</a>	Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> organophosphorus acid anhydrolase; <b>PDBTitle:</b> crystal structure of organophosphorus acid anhydrolase from2 alteromonas macleodii
18	<a href="#">c5x49A_</a>	Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable xaa-pro aminopeptidase 3; <b>PDBTitle:</b> crystal structure of human mitochondrial x-prolyl aminopeptidase2 (xpnpep3)
19	<a href="#">c2oknB_</a>	Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> xaa-pro dipeptidase; <b>PDBTitle:</b> crystal strcture of human prolidase
20	<a href="#">c4r60A_</a>	Alignment		100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> proline dipeptidase; <b>PDBTitle:</b> crystal structure of xaa-pro dipeptidase from xanthomonas campestris
21	<a href="#">c6mrfA_</a>	Alignment	not modelled	100.0	37	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine aminopeptidase; <b>PDBTitle:</b> crystal structure of a methionine aminopeptidase metap from2 acinetobacter baumannii
22	<a href="#">c3ig4E_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> xaa-pro aminopeptidase; <b>PDBTitle:</b> structure of a putative aminopeptidase p from bacillus anthracis
23	<a href="#">c1chmA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> creatinase <b>Chain:</b> A: <b>PDB Molecule:</b> creatine amidinohydrolase; <b>PDBTitle:</b> enzymatic mechanism of creatine amidinohydrolase as deduced2 from crystal structures
24	<a href="#">c2zsqB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> aminopeptidase p, putative; <b>PDBTitle:</b> crystal structure of x-pro aminopeptidase from thermotoga maritima2 msb8
25	<a href="#">c6a9vA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> intermediate cleaving peptidase 55; <b>PDBTitle:</b> crystal structure of icp55 from saccharomyces cerevisiae (n-terminal2 42 residues deletion)
26	<a href="#">c5cnxB_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> aminopeptidase ypdf; <b>PDBTitle:</b> crystal structure of xaa-pro aminopeptidase from escherichia coli k12
27	<a href="#">c4egeA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptidase pepe; <b>PDBTitle:</b> crystal structure of dipeptidase pepe from mycobacterium ulcerans
28	<a href="#">c5ce6A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fact-spt16; <b>PDBTitle:</b> n-terminal domain of fact complex subunit spt16 from cicer arietinum2 (chickpea)

29	<a href="#">d1b6aa2</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Creatinase/aminopeptidase <b>Superfamily:</b> Creatinase/aminopeptidase <b>Family:</b> Creatinase/aminopeptidase
30	<a href="#">c5cdA_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> proline dipeptidase; <b>PDBTitle:</b> proline dipeptidase from deinococcus radiodurans (selenomethionine2 derivative)
31	<a href="#">c1wy2B_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> xaa-pro dipeptidase; <b>PDBTitle:</b> crystal structure of the prolidase from pyrococcus horikoshii ot3
32	<a href="#">c3q6dA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> proline dipeptidase; <b>PDBTitle:</b> xaa-pro dipeptidase from bacillus anthracis.
33	<a href="#">c4fkcA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> xaa-pro aminopeptidase; <b>PDBTitle:</b> recombinant prolidase from thermococcus sibiricus
34	<a href="#">c2howB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 356aa long hypothetical dipeptidase; <b>PDBTitle:</b> dipeptidase (ph0974) from pyrococcus horikoshii ot3
35	<a href="#">c4zngA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> prolidase; <b>PDBTitle:</b> x-ray crystallography of recombinant lactococcus lactis prolidase
36	<a href="#">c3cb5A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fact complex subunit spt16; <b>PDBTitle:</b> crystal structure of the s. pombe peptidase homology domain of fact2 complex subunit spt16 (form a)
37	<a href="#">d1chma2</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Creatinase/aminopeptidase <b>Superfamily:</b> Creatinase/aminopeptidase <b>Family:</b> Creatinase/aminopeptidase
38	<a href="#">d2v3za2</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Creatinase/aminopeptidase <b>Superfamily:</b> Creatinase/aminopeptidase <b>Family:</b> Creatinase/aminopeptidase
39	<a href="#">c5e5bA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fact complex subunit spt16; <b>PDBTitle:</b> crystal structure of human spt16 n-terminal domain
40	<a href="#">c5xevA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> xaa-pro dipeptidase,peptidase-related protein; <b>PDBTitle:</b> crystal structure of a novel xaa-pro dipeptidase from deinococcus2 radiodurans
41	<a href="#">d1pv9a2</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Creatinase/aminopeptidase <b>Superfamily:</b> Creatinase/aminopeptidase <b>Family:</b> Creatinase/aminopeptidase
42	<a href="#">c6a8mA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> fact complex subunit spt16; <b>PDBTitle:</b> n-terminal domain of fact complex subunit spt16 from eremothecium2 gossypii (ashbya gossypii)
43	<a href="#">c3ctzA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> xaa-pro aminopeptidase 1; <b>PDBTitle:</b> structure of human cytosolic x-prolyl aminopeptidase
44	<a href="#">c4s2tP_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> P: <b>PDB Molecule:</b> protein app-1; <b>PDBTitle:</b> crystal structure of x-prolyl aminopeptidase from caenorhabditis2 elegans: a cytosolic enzyme with a di-nuclear active site
45	<a href="#">c2v6cA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> proliferation-associated protein 2g4; <b>PDBTitle:</b> crystal structure of erbb3 binding protein 1 (ebp1)
46	<a href="#">c4b28A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> metallopeptidase, family m24, putative; <b>PDBTitle:</b> crystal structure of dmsp lyase rdddp from roseobacter denitrificans
47	<a href="#">c2q8kA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> proliferation-associated protein 2g4; <b>PDBTitle:</b> the crystal structure of ebp1
48	<a href="#">c5jqkA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidase, putative; <b>PDBTitle:</b> the xray crystal structure of p. falciiparum aminopeptidase p
49	<a href="#">d1xgsa2</a>	Alignment	not modelled	100.0	31	<b>Fold:</b> Creatinase/aminopeptidase <b>Superfamily:</b> Creatinase/aminopeptidase <b>Family:</b> Creatinase/aminopeptidase
50	<a href="#">c3bitA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fact complex subunit spt16; <b>PDBTitle:</b> crystal structure of yeast spt16 n-terminal domain
51	<a href="#">c5jr6B_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peptidase, putative; <b>PDBTitle:</b> the xray crystal structure of p. falciiparum aminopeptidase p in2 complex with apstatin
52	<a href="#">c1xgnB_</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> aminopeptidase <b>Chain:</b> B: <b>PDB Molecule:</b> methionine aminopeptidase; <b>PDBTitle:</b> methionine aminopeptidase from hyperthermophile pyrococcus2 furiosus
53	<a href="#">c1b6aA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> angiogenesis inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> methionine aminopeptidase; <b>PDBTitle:</b> human methionine aminopeptidase 2 complexed with tnp-470
54	<a href="#">c3fm3B_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> methionine aminopeptidase 2; <b>PDBTitle:</b> crystal structure of an encephalitozoon cuniculi methionine2 aminopeptidase type 2
						<b>PDB header:</b> hydrolase

55	<a href="#">c4ipaC_</a>	Alignment	not modelled	100.0	20	<b>Chain:</b> C: <b>PDB Molecule:</b> putative curved dna-binding protein; <b>PDBTitle:</b> structure of a thermophilic arx1
56	<a href="#">c1yw7A_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine aminopeptidase 2; <b>PDBTitle:</b> h-metap2 complexed with a444148
57	<a href="#">c3tb5C_</a>	Alignment	not modelled	100.0	35	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> methionine aminopeptidase; <b>PDBTitle:</b> crystal structure of the enterococcus faecalis methionine2 aminopeptidase apo form
58	<a href="#">c1kp0B_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> creatine amidinohydrolase; <b>PDBTitle:</b> the crystal structure analysis of creatine amidinohydrolase2 from actinobacillus
59	<a href="#">d1kp0a2</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Creatinase/aminopeptidase <b>Superfamily:</b> Creatinase/aminopeptidase <b>Family:</b> Creatinase/aminopeptidase
60	<a href="#">c4b6at_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> 60s ribosomal protein l21-a; <b>PDBTitle:</b> cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
61	<a href="#">c2y0oA_</a>	Alignment	not modelled	28.6	27	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> probable d-lyxose ketol-isomerase; <b>PDBTitle:</b> the structure of a d-lyxose isomerase from the sigmab2 regulon of bacillus subtilis
62	<a href="#">c3mpbA_</a>	Alignment	not modelled	27.2	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> sugar isomerase; <b>PDBTitle:</b> z5688 from e. coli o157:h7 bound to fructose
63	<a href="#">c4mozC_</a>	Alignment	not modelled	24.8	24	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> fructose-bisphosphate aldolase; <b>PDBTitle:</b> fructose-bisphosphate aldolase from slackia heliotrinireducens dsm2 20476
64	<a href="#">c3jr1A_</a>	Alignment	not modelled	21.2	7	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative fructosamine-3-kinase; <b>PDBTitle:</b> crystal structure of putative fructosamine-3-kinase (yp_719053.1) from2 haemophilus somnus 129pt at 2.32 a resolution
65	<a href="#">d1kt0a2</a>	Alignment	not modelled	20.0	24	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> FKBP immunophilin/proline isomerase
66	<a href="#">d1j3ba1</a>	Alignment	not modelled	19.9	14	<b>Fold:</b> PEP carboxykinase-like <b>Superfamily:</b> PEP carboxykinase-like <b>Family:</b> PEP carboxykinase C-terminal domain
67	<a href="#">c2hl7A_</a>	Alignment	not modelled	19.1	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c-type biogenesis protein ccmh; <b>PDBTitle:</b> crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
68	<a href="#">d1l1pa_</a>	Alignment	not modelled	18.1	30	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> FKBP immunophilin/proline isomerase
69	<a href="#">c2kw0A_</a>	Alignment	not modelled	18.0	6	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ccmh protein; <b>PDBTitle:</b> solution structure of n-terminal domain of ccmh from escherichia.coli
70	<a href="#">d1w26a3</a>	Alignment	not modelled	16.7	16	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> FKBP immunophilin/proline isomerase
71	<a href="#">c2c5qE_</a>	Alignment	not modelled	16.6	14	<b>PDB header:</b> structural genomics,unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> rraa-like protein yer010c; <b>PDBTitle:</b> crystal structure of yeast yer010cp
72	<a href="#">c3prdA_</a>	Alignment	not modelled	16.1	24	<b>PDB header:</b> chaperone, isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> fkbp-type peptidyl-prolyl cis-trans isomerase; <b>PDBTitle:</b> structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
73	<a href="#">c2ki0A_</a>	Alignment	not modelled	14.4	23	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> ds119; <b>PDBTitle:</b> nmr structure of a de novo designed beta alpha beta
74	<a href="#">c2yqkA_</a>	Alignment	not modelled	13.9	13	<b>PDB header:</b> transcription/apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> arginine-glutamic acid dipeptide repeats protein; <b>PDBTitle:</b> solution structure of the sant domain in arginine-glutamic2 acid dipeptide (re) repeats
75	<a href="#">d1t11a3</a>	Alignment	not modelled	11.5	40	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> FKBP immunophilin/proline isomerase
76	<a href="#">c2k3uA_</a>	Alignment	not modelled	10.5	31	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> chemotaxis inhibitory protein; <b>PDBTitle:</b> structure of the tyrosine-sulfated c5a receptor n-terminus2 in complex with the immune evasion protein chips.
77	<a href="#">d1xc5a1</a>	Alignment	not modelled	10.5	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Myb/SANT domain
78	<a href="#">d1iwpq_</a>	Alignment	not modelled	10.2	26	<b>Fold:</b> Open three-helical up-and-down bundle <b>Superfamily:</b> Diol dehydratase, gamma subunit <b>Family:</b> Diol dehydratase, gamma subunit
79	<a href="#">c1uc5M_</a>	Alignment	not modelled	10.0	23	<b>PDB header:</b> lyase <b>Chain:</b> M: <b>PDB Molecule:</b> diol dehydrase gamma subunit; <b>PDBTitle:</b> structure of diol dehydratase complexed with (r)-1,2-2 propanediol
80	<a href="#">d1eexq_</a>	Alignment	not modelled	10.0	23	<b>Fold:</b> Open three-helical up-and-down bundle <b>Superfamily:</b> Diol dehydratase, gamma subunit <b>Family:</b> Diol dehydratase, gamma subunit
						<b>PDB header:</b> lyase

81	<a href="#">c2pc9B_</a>	Alignment	not modelled	9.8	14	<b>Chain:</b> B; <b>PDB Molecule:</b> phosphoenolpyruvate carboxykinase [atp]; <b>PDBTitle:</b> crystal structure of atp-dependent phosphoenolpyruvate carboxykinase2 from thermus thermophilus hb8
82	<a href="#">c5i1tA_</a>	Alignment	not modelled	9.1	44	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> stage ii sporulation protein d; <b>PDBTitle:</b> 2.6 angstrom resolution crystal structure of stage ii sporulation2 protein d (spoidd) from clostridium difficile in complex with3 triacetylchitotriose
83	<a href="#">c4qb1F_</a>	Alignment	not modelled	8.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> vrr-nuc; <b>PDBTitle:</b> vrr_nuc domain protein
84	<a href="#">c4rwrB_</a>	Alignment	not modelled	8.9	28	<b>PDB header:</b> viral protein <b>Chain:</b> B; <b>PDB Molecule:</b> stage ii sporulation protein d; <b>PDBTitle:</b> 2.1 angstrom crystal structure of stage ii sporulation protein d from2 bacillus anthracis
85	<a href="#">d2crga1</a>	Alignment	not modelled	8.9	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Myb/SANT domain
86	<a href="#">c6fx6A_</a>	Alignment	not modelled	8.0	38	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> satie-ted; <b>PDBTitle:</b> thioester domain of the staphylococcus aureus tie protein
87	<a href="#">c5zr0A_</a>	Alignment	not modelled	7.7	27	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> maltose-binding periplasmic protein,trigger factor; <b>PDBTitle:</b> solution structure of peptidyl-prolyl cis/trans isomerase domain of2 trigger factor in complex with mbp
88	<a href="#">c1w26B_</a>	Alignment	not modelled	7.6	16	<b>PDB header:</b> chaperone <b>Chain:</b> B; <b>PDB Molecule:</b> trigger factor; <b>PDBTitle:</b> trigger factor in complex with the ribosome forms a2 molecular cradle for nascent proteins
89	<a href="#">c3zieC_</a>	Alignment	not modelled	7.5	31	<b>PDB header:</b> cell cycle <b>Chain:</b> C; <b>PDB Molecule:</b> sepf-like protein; <b>PDBTitle:</b> sepf-like protein from archaeoglobus fulgidus
90	<a href="#">c2kxxA_</a>	Alignment	not modelled	7.3	5	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> small protein a; <b>PDBTitle:</b> nmr structure of escherichia coli bame, a lipoprotein component of the2 beta-barrel assembly machinery complex
91	<a href="#">d2k57a1</a>	Alignment	not modelled	7.2	28	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> Ygd1/YgdR-like
92	<a href="#">d1m1fa_</a>	Alignment	not modelled	7.1	6	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cell growth inhibitor/plasmid maintenance toxic component <b>Family:</b> Kid/PemK
93	<a href="#">c2ls01_</a>	Alignment	not modelled	7.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> 1; <b>PDB Molecule:</b> zocin a endopeptidase; <b>PDB Fragment:</b> unp residues 170-285; <b>PDBTitle:</b> solution structure of the target recognition domain of zocin a
94	<a href="#">c3nojA_</a>	Alignment	not modelled	7.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> 4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate <b>PDBTitle:</b> the structure of hmg/cha aldolase from the protocatechuate degradation2 pathway of pseudomonas putida
95	<a href="#">c4mspB_</a>	Alignment	not modelled	6.9	29	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> peptidyl-prolyl cis-trans isomerase fkbp14; <b>PDBTitle:</b> crystal structure of human peptidyl-prolyl cis-trans isomerase fkbp222 (aka fkbp14) containing two ef-hand motifs
96	<a href="#">c4d4pG_</a>	Alignment	not modelled	6.6	24	<b>PDB header:</b> translation <b>Chain:</b> G; <b>PDB Molecule:</b> protein ats1, diphthamide biosynthesis protein 3; <b>PDBTitle:</b> crystal structure of the kti11 kti13 heterodimer spacegroup p65
97	<a href="#">c1kt0A_</a>	Alignment	not modelled	6.5	24	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> 51 kda fk506-binding protein; <b>PDBTitle:</b> structure of the large fkbp-like protein, fkbp51, involved in steroid2 receptor complexes
98	<a href="#">c1hxvA_</a>	Alignment	not modelled	6.5	41	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> trigger factor; <b>PDBTitle:</b> ppiase domain of the mycoplasma genitalium trigger factor
99	<a href="#">d1hxva_</a>	Alignment	not modelled	6.5	41	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> FKBP immunophilin/proline isomerase