Phyre^2

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Description	P28247
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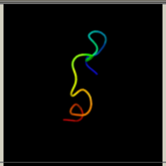
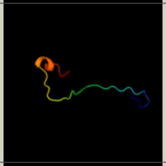
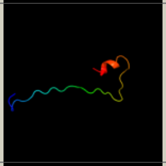
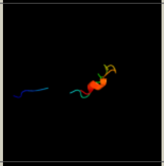
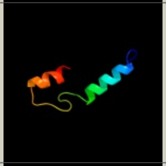
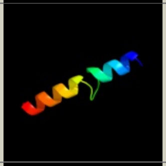
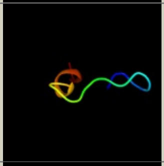
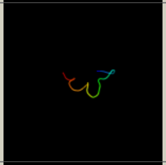
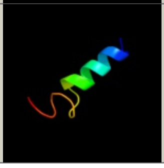
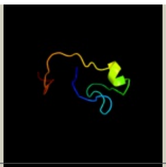
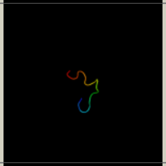
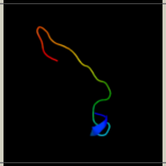
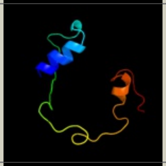
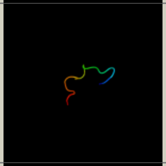
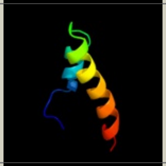
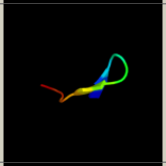
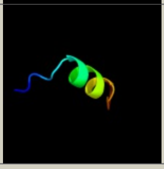
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3jruB_	Alignment		30.5	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable cytosol aminopeptidase; **PDBTitle:** crystal structure of leucyl aminopeptidase (pepa) from xoo0834,2 xanthomonas oryzae pv. oryzae kacc10331
2	c3ij3A_	Alignment		29.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** 1.8 angstrom resolution crystal structure of cytosol aminopeptidase2 from coxiella burnetii
3	c3h8gC_	Alignment		28.4	27	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida
4	c1lanA_	Alignment		28.1	29	**PDB header:**hydrolase (alpha-aminoacylpeptide) **Chain:** A: **PDB Molecule:**leucine aminopeptidase; **PDBTitle:** leucine aminopeptidase complex with l-leucinal
5	d1v9va1	Alignment		28.0	16	**Fold:**Bromodomain-like **Superfamily:**MAST3 pre-PK domain-like **Family:**MAST3 pre-PK domain-like
6	d1lama1	Alignment		25.9	35	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Leucine aminopeptidase, C-terminal domain
7	c3bj4B_	Alignment		22.1	36	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**potassium voltage-gated channel subfamily kqt **PDBTitle:** the kcnq1 (kv7.1) c-terminus, a multi-tiered scaffold for2 subunit assembly and protein interaction
8	d1gyta2	Alignment		20.0	41	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Leucine aminopeptidase, C-terminal domain
9	c2hc9A_	Alignment		18.1	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leucine aminopeptidase 1; **PDBTitle:** structure of caenorhabditis elegans leucine aminopeptidase-zinc2 complex (lap1)
10	c1gytG_	Alignment		17.7	41	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** e. coli aminopeptidase a (pepa)
11	c3hfeC_	Alignment		16.9	45	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**potassium voltage-gated channel subfamily kqt member 1; **PDBTitle:** a trimeric form of the kv7.1 a domain tail

12	c3h7hA_	Alignment		13.4	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt4; **PDBTitle:** crystal structure of the human transcription elongation factor dsif,2 hspt4/hspt5 (176-273)
13	c3kzwD_	Alignment		13.0	24	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** crystal structure of cytosol aminopeptidase from staphylococcus aureus2 col
14	c3iwcD_	Alignment		12.8	29	**PDB header:**lyase **Chain:** D: **PDB Molecule:**s-adenosylmethionine decarboxylase; **PDBTitle:** t. maritima adometdc complex with s-adenosylmethionine2 methyl ester
15	c2obvA_	Alignment		12.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**s-adenosylmethionine synthetase isoform type-1; **PDBTitle:** crystal structure of the human s-adenosylmethionine synthetase 1 in2 complex with the product
16	c3kr5E_	Alignment		12.5	24	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**m17 leucyl aminopeptidase; **PDBTitle:** structure of a protease 4
17	c2kztA_	Alignment		12.1	29	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**programmed cell death protein 4; **PDBTitle:** structure of the tandem ma-3 region of pdcd4
18	d2d8xa1	Alignment		10.4	55	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
19	c3imlB_	Alignment		9.9	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosylmethionine synthetase; **PDBTitle:** crystal structure of s-adenosylmethionine synthetase from burkholderia2 pseudomallei
20	d1sr9a1	Alignment		8.5	40	**Fold:**RuvA C-terminal domain-like **Superfamily:**post-HMGL domain-like **Family:**DmpG/LeuA communication domain-like
21	c1mtpB_	Alignment	not modelled	8.5	33	**PDB header:**structural genomics **Chain:** B: **PDB Molecule:**serine proteinase inhibitor (serpin), chain b; **PDBTitle:** the x-ray crystal structure of a serpin from a thermophilic2 prokaryote
22	d2q49a2	Alignment	not modelled	8.2	11	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
23	d1edla_	Alignment	not modelled	8.1	44	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules
24	c2wshC_	Alignment	not modelled	7.8	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**endonuclease ii; **PDBTitle:** structure of bacteriophage t4 endoii e118a mutant
25	d1uc2a_	Alignment	not modelled	7.8	16	**Fold:**Hypothetical protein PH1602 **Superfamily:**Hypothetical protein PH1602 **Family:**Hypothetical protein PH1602
26	c2eloA_	Alignment	not modelled	7.2	71	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 12th c2h2 zinc finger of human2 zinc finger protein 406
27	d1vjpa1	Alignment	not modelled	7.0	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
28	d1fc2c_	Alignment	not modelled	6.7	41	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules

29	d1ryqa_	Alignment	not modelled	6.7	28	**Fold:**Rubredoxin-like **Superfamily:**RNA polymerase subunits **Family:**RpoE2-like
30	d2db7a1	Alignment	not modelled	6.5	18	**Fold:**Orange domain-like **Superfamily:**Orange domain-like **Family:**Hairy Orange domain
31	c2zbtB_	Alignment	not modelled	6.4	33	**PDB header:**lyase **Chain:** B: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs; **PDBTitle:** crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
32	c3so4C_	Alignment	not modelled	6.3	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**methionine-adenosyltransferase; **PDBTitle:** methionine-adenosyltransferase from entamoeba histolytica
33	c3femB_	Alignment	not modelled	6.3	40	**PDB header:**biosynthetic protein, transferase **Chain:** B: **PDB Molecule:**pyridoxine biosynthesis protein snz1; **PDBTitle:** structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae
34	d2p02a2	Alignment	not modelled	6.1	47	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
35	d1prtc2	Alignment	not modelled	6.1	78	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**Aerolysin/Pertussis toxin (APT) domain
36	c2epgB_	Alignment	not modelled	6.1	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ttha1785; **PDBTitle:** crystal structure of ttha1785
37	c2nv2U_	Alignment	not modelled	5.9	33	**PDB header:**lyase/transferase **Chain:** U: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs; **PDBTitle:** structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
38	c3mtvA_	Alignment	not modelled	5.8	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**papain-like cysteine protease; **PDBTitle:** the crystal structure of the prrsv nonstructural protein nsp1
39	d1vkna2	Alignment	not modelled	5.8	24	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
40	c3rv2B_	Alignment	not modelled	5.8	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosylmethionine synthase; **PDBTitle:** crystal structure of s-adenosylmethionine synthetase from2 mycobacterium marinum