Phyre^2

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Description	Q96PG8
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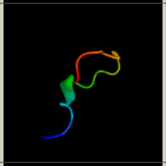
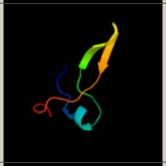
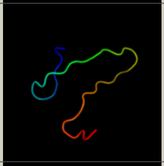
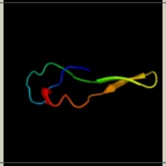
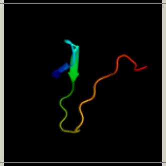
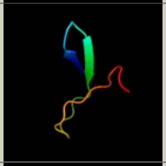
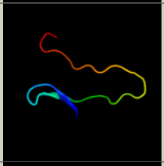
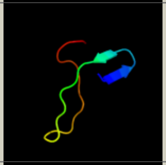
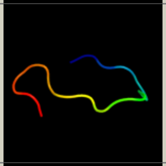
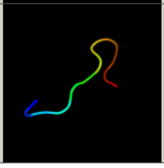
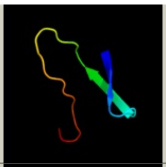
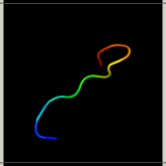
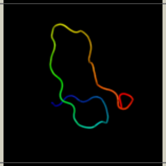
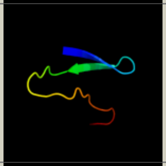
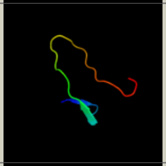
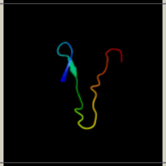
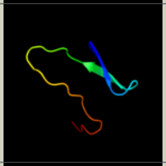
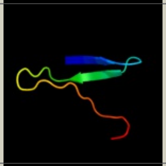
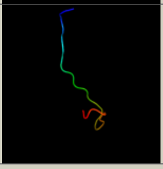
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fqmA_	Alignment		44.5	48	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**non-structural protein 5a; **PDBTitle:** crystal structure of a novel dimeric form of hcv ns5a domain i protein
2	d2i9wa2	Alignment		33.5	42	**Fold:**Sec-C motif **Superfamily:**Sec-C motif **Family:**Sec-C motif
3	c2x2zE_	Alignment		20.0	36	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**apical membrane antigen 1, putative; **PDBTitle:** crystal structure ama1 from toxoplasma gondii
4	d1miqa_	Alignment		17.4	19	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Pepsin-like
5	c2y8rD_	Alignment		16.9	36	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**apical membrane antigen, putative; **PDBTitle:** crystal structure of apo ama1 mutant (tyr230ala) from2 toxoplasma gondii
6	d1dpja_	Alignment		15.7	23	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Pepsin-like
7	d2apra_	Alignment		15.3	14	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Pepsin-like
8	d1qs8a_	Alignment		14.6	21	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Pepsin-like
9	d1wkra_	Alignment		13.6	29	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Pepsin-like
10	d1qxfa_	Alignment		12.6	39	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein S27e
11	c3iz6X_	Alignment		11.6	50	**PDB header:**ribosome **Chain:** X: **PDB Molecule:**40s ribosomal protein s27 (s27e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome

12	d4pepa_	Alignment		10.9	31	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Pepsin-like
13	c2xzm6_	Alignment		10.4	17	**PDB header:**ribosome **Chain:** 6: **PDB Molecule:**rps27e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
14	d1pfza_	Alignment		10.3	20	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Pepsin-like
15	d2asia_	Alignment		10.1	27	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Pepsin-like
16	d3cmsa_	Alignment		9.8	28	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Pepsin-like
17	c3fnuA_	Alignment		9.2	29	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**hap protein; **PDBTitle:** crystal structure of kni-10006 bound histo-aspartic protease (hap)2 from plasmodium falciparum
18	d1ls5a_	Alignment		8.8	19	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Pepsin-like
19	c1tzsA_	Alignment		8.8	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cathepsin e; **PDBTitle:** crystal structure of an activation intermediate of2 cathepsin e
20	c2l23A_	Alignment		8.8	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**mediator of rna polymerase ii transcription subunit 25; **PDBTitle:** nmr structure of the acid (activator interacting domain) of the human2 mediator med25 protein
21	c1avfJ_	Alignment	not modelled	8.8	24	**PDB header:**aspartyl protease **Chain:** J: **PDB Molecule:**gastricsin; **PDBTitle:** activation intermediate 2 of human gastricsin from human2 stomach
22	d3psga_	Alignment	not modelled	8.4	29	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Pepsin-like
23	c2bjuA_	Alignment	not modelled	8.3	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**plasmepsin ii; **PDBTitle:** plasmepsin ii complexed with a highly active achiral2 inhibitor
24	d2bjua1	Alignment	not modelled	8.3	23	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Pepsin-like
25	c1b5fC_	Alignment	not modelled	7.6	27	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein (cardosin a); **PDBTitle:** native cardosin a from cynara cardunculus l.
26	d1oewa_	Alignment	not modelled	7.3	21	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Pepsin-like
27	d1psoe_	Alignment	not modelled	6.7	32	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Pepsin-like
28	c1qdmA_	Alignment	not modelled	6.6	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prophytepsin; **PDBTitle:** crystal structure of prophytepsin, a zymogen of a barley2 vacuolar aspartic proteinase.
						PDB header:plant protein

29	c3vlaA_	Alignment	not modelled	6.3	20	**Chain:** A: **PDB Molecule:**edgp; **PDBTitle:** crystal structure of edgp
30	d1mppa_	Alignment	not modelled	6.1	27	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Pepsin-like
31	c3oadA_	Alignment	not modelled	5.9	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**renin; **PDBTitle:** design and optimization of new piperidines as renin inhibitors
32	d1qdma2	Alignment	not modelled	5.8	26	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Pepsin-like
33	c3lvwA_	Alignment	not modelled	5.2	63	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamate--cysteine ligase; **PDBTitle:** glutathione-inhibited scgcl
34	c2x0bC_	Alignment	not modelled	5.1	29	**PDB header:**hydrolase/hormone **Chain:** C: **PDB Molecule:**renin; **PDBTitle:** crystal structure of human angiotensinogen complexed with renin
35	c2nr6B_	Alignment	not modelled	5.0	30	**PDB header:**hydrolase/immune system **Chain:** B: **PDB Molecule:**aspartic protease bla g 2; **PDBTitle:** crystal structure of the complex of antibody and the allergen bla g 2