Phyre2

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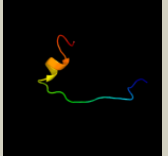
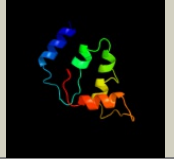
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1euva_	Alignment		97.9	19	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Adenain-like
2	d2g4da1	Alignment		97.6	19	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Adenain-like
3	d2bkra1	Alignment		97.5	18	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Adenain-like
4	c2oixA_	Alignment		97.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**xanthomonas outer protein d; **PDBTitle:** xanthomonas xopd c470a mutant
5	c3eayA_	Alignment		97.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sentrin-specific protease 7; **PDBTitle:** crystal structure of the human senp7 catalytic domain
6	d1th0a_	Alignment		97.0	18	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Adenain-like
7	d2iy1a1	Alignment		96.8	18	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Adenain-like
8	d1nlna_	Alignment		68.5	26	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Adenain-like
9	d1xd3a_	Alignment		58.4	16	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Ubiquitin carboxyl-terminal hydrolase UCH-L
10	d2cpqa1	Alignment		56.6	38	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
11	d2etla1	Alignment		55.7	18	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Ubiquitin carboxyl-terminal hydrolase UCH-L

12	c2wdtA_	Alignment		46.9	22	**PDB header:**hydrolase/protein binding **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase l3; **PDBTitle:** crystal structure of plasmodium falciparum uchl3 in complex2 with the suicide inhibitor ubvme
13	c3a7sA_	Alignment		24.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase isozyme l5; **PDBTitle:** catalytic domain of uch37
14	c3mstA_	Alignment		17.5	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative nitrate transport protein; **PDBTitle:** crystal structure of a putative nitrate transport protein (tvn0104)2 from thermoplasma volcanium at 1.35 a resolution
15	c3ihrA_	Alignment		15.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase isozyme l5; **PDBTitle:** crystal structure of uch37
16	d1cjaa_	Alignment		15.0	15	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Actin-fragmin kinase, catalytic domain
17	c3zrhA_	Alignment		13.8	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin thioesterase zranb1; **PDBTitle:** crystal structure of the lys29, lys33-linkage-specific trabid otu2 deubiquitinase domain reveals an ankyrin-repeat ubiquitin binding3 domain (ankubd)
18	c3dcyA_	Alignment		13.4	17	**PDB header:**apoptosis regulator **Chain:** A: **PDB Molecule:**regulator protein; **PDBTitle:** crystal structure a tp53-induced glycolysis and apoptosis2 regulator protein from homo sapiens.
19	c2qqpD_	Alignment		13.0	27	**PDB header:**virus **Chain:** D: **PDB Molecule:**small capsid protein; **PDBTitle:** crystal structure of authentic providence virus
20	c2of6C_	Alignment		10.7	50	**PDB header:**virus **Chain:** C: **PDB Molecule:**envelope glycoprotein e; **PDBTitle:** structure of immature west nile virus
21	d1s2xa_	Alignment	not modelled	10.7	47	**Fold:**STAT-like **Superfamily:**Cag-Z **Family:**Cag-Z
22	c1s2xA_	Alignment	not modelled	10.7	47	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cag-z; **PDBTitle:** crystal structure of cag-z from helicobacter pylori
23	d1z21a1	Alignment	not modelled	10.6	21	**Fold:**Type III secretion system domain **Superfamily:**Type III secretion system domain **Family:**YopR Core
24	c2i3eA_	Alignment	not modelled	10.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**g-rich; **PDBTitle:** solution structure of catalytic domain of goldfish rich2 protein
25	d1aina_	Alignment	not modelled	10.0	23	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
26	c1uzgA_	Alignment	not modelled	9.9	50	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**major envelope protein e; **PDBTitle:** crystal structure of the dengue type 3 virus envelope2 protein
27	d1u7za_	Alignment	not modelled	9.9	15	**Fold:**Ribokinase-like **Superfamily:**CoaB-like **Family:**CoaB-like
28	c2ka2A_	Alignment	not modelled	9.8	43	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints

29	c2ka1B_	Alignment	not modelled	9.8	43	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
30	d1zrua3	Alignment	not modelled	9.7	27	**Fold:**Pseudo beta-prism **Superfamily:**Bacteriophage trimeric proteins domain **Family:**Lactophage receptor-binding protein N-terminal domain
31	c2ka2B_	Alignment	not modelled	9.3	43	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
32	c2ka1A_	Alignment	not modelled	9.3	43	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
33	d2arha1	Alignment	not modelled	9.1	41	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**Aq 1966-like
34	d1svba2	Alignment	not modelled	9.0	50	**Fold:**Viral glycoprotein, central and dimerisation domains **Superfamily:**Viral glycoprotein, central and dimerisation domains **Family:**Viral glycoprotein, central and dimerisation domains
35	c3lcnC_	Alignment	not modelled	8.8	46	**PDB header:**nuclear protein **Chain:** C: **PDB Molecule:**mrna transport factor gfd1; **PDBTitle:** nab2:gfd1 complex
36	c3lcnD_	Alignment	not modelled	8.5	46	**PDB header:**nuclear protein **Chain:** D: **PDB Molecule:**mrna transport factor gfd1; **PDBTitle:** nab2:gfd1 complex
37	d1sjpa2	Alignment	not modelled	8.3	28	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
38	c2f9jP_	Alignment	not modelled	8.2	27	**PDB header:**rna binding protein **Chain:** P: **PDB Molecule:**splicing factor 3b subunit 1; **PDBTitle:** 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
39	d1ok8a2	Alignment	not modelled	8.2	50	**Fold:**Viral glycoprotein, central and dimerisation domains **Superfamily:**Viral glycoprotein, central and dimerisation domains **Family:**Viral glycoprotein, central and dimerisation domains
40	c2j5dA_	Alignment	not modelled	7.9	50	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** nmr structure of bnip3 transmembrane domain in lipid2 bicelles
41	c1p58C_	Alignment	not modelled	7.8	50	**PDB header:**virus **Chain:** C: **PDB Molecule:**major envelope protein e; **PDBTitle:** complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
42	c3uajA_	Alignment	not modelled	7.8	50	**PDB header:**viral protein/immune system **Chain:** A: **PDB Molecule:**envelope protein; **PDBTitle:** crystal structure of the envelope glycoprotein ectodomain from dengue2 virus serotype 4 in complex with the fab fragment of the chimpanzee3 monoclonal antibody 5h2
43	d1f74a_	Alignment	not modelled	7.7	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
44	c1urzC_	Alignment	not modelled	7.7	50	**PDB header:**virus/viral protein **Chain:** C: **PDB Molecule:**envelope protein; **PDBTitle:** low ph induced, membrane fusion conformation of the2 envelope protein of tick-borne encephalitis virus
45	d1o22a_	Alignment	not modelled	7.3	70	**Fold:**Hypothetical protein TM0875 **Superfamily:**Hypothetical protein TM0875 **Family:**Hypothetical protein TM0875
46	d1ufwa_	Alignment	not modelled	7.1	23	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
47	d1rmka_	Alignment	not modelled	6.8	83	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Conotoxin
48	c3dxeC_	Alignment	not modelled	6.7	24	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**amyloid beta a4 protein-binding family b member **PDBTitle:** crystal structure of the intracellular domain of human app2 (t668a mutant) in complex with fe65-ptb2
49	c3c6dB_	Alignment	not modelled	6.6	50	**PDB header:**virus **Chain:** B: **PDB Molecule:**polyprotein; **PDBTitle:** the pseudo-atomic structure of dengue immature virus
50	c3siiA_	Alignment	not modelled	6.5	35	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**poly(adp-ribose) glycohydrolase; **PDBTitle:** the x-ray crystal structure of poly(adp-ribose) glycohydrolase bound2 to the inhibitor adp-hpd from thermomonospora curvata
51	c3ogzA_	Alignment	not modelled	6.1	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-sugar pyrophosphorylase; **PDBTitle:** protein structure of usp from l. major in apo-form
52	d1dm5a_	Alignment	not modelled	6.1	23	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
53	d1srva_	Alignment	not modelled	5.9	31	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain

54	d2ptza1	Alignment	not modelled	5.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
55	c1bmxA_	Alignment	not modelled	5.8	32	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**human immunodeficiency virus type 1 capsid; **PDBTitle:** hiv-1 capsid protein major homology region peptide analog,2 nmr, 8 structures
56	d1vlya1	Alignment	not modelled	5.7	15	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**Aminomethyltransferase beta-barrel domain **Family:**Aminomethyltransferase beta-barrel domain
57	c2vc6A_	Alignment	not modelled	5.4	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of mosa from s. meliloti with pyruvate bound
58	d1sx5a_	Alignment	not modelled	5.3	21	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease EcoRV
59	c1gp8A_	Alignment	not modelled	5.2	13	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (scaffolding protein); **PDBTitle:** nmr solution structure of the coat protein-binding domain2 of bacteriophage p22 scaffolding protein
60	d1t6t1_	Alignment	not modelled	5.2	8	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
61	d1k8ga2	Alignment	not modelled	5.2	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
62	c1w9zB_	Alignment	not modelled	5.1	35	**PDB header:**virus coat protein **Chain:** B: **PDB Molecule:**vp9; **PDBTitle:** structure of bannavirus vp9