Phyre^2

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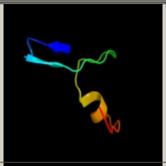
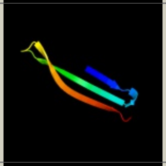
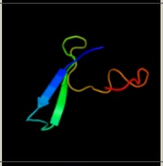
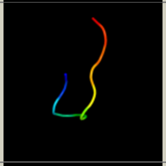
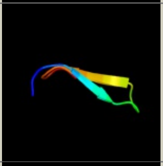
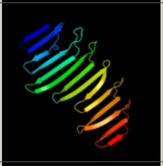
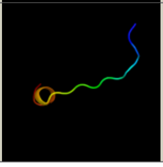
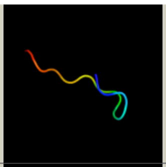
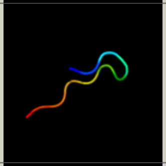
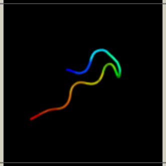
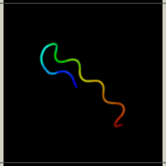
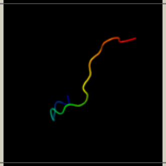
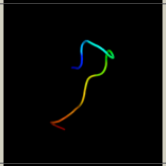
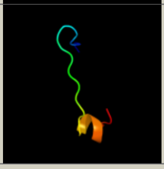
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1x3za1	Alignment		47.4	9	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
2	c3mswA_	Alignment		37.2	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein with unknown function (bf3112) from2 bacteroides fragilis nctc 9343 at 1.90 a resolution
3	d2f4ma1	Alignment		36.0	18	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
4	c3eswA_	Alignment		29.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine **PDBTitle:** complex of yeast pngase with glcnac2-iac.
5	c1j5qB_	Alignment		21.8	24	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**major capsid protein; **PDBTitle:** the structure and evolution of the major capsid protein of a large,2 lipid-containing, dna virus.
6	c2x12A_	Alignment		21.2	27	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**fimbriae-associated protein fap1; **PDBTitle:** ph-induced modulation of streptococcus parasanguinis2 adhesion by fap1 fimbriae
7	d1pk6c_	Alignment		21.1	27	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
8	d1ei5a1	Alignment		19.4	32	**Fold:**Streptavidin-like **Superfamily:**D-aminopeptidase, middle and C-terminal domains **Family:**D-aminopeptidase, middle and C-terminal domains
9	d1pk6b_	Alignment		18.3	27	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
10	c2oy7A_	Alignment		17.6	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer surface protein a; **PDBTitle:** the crystal structure of ospa mutant
11	d1bcoa1	Alignment		17.5	11	**Fold:**mu transposase, C-terminal domain **Superfamily:**mu transposase, C-terminal domain **Family:**mu transposase, C-terminal domain

12	d1c3ha_	Alignment		17.2	31	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
13	c1gr3A_	Alignment		14.6	36	**PDB header:**collagen **Chain:** A: **PDB Molecule:**collagen x; **PDBTitle:** structure of the human collagen x nc1 trimer
14	d1gr3a_	Alignment		14.6	36	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
15	c3kifD_	Alignment		14.0	32	**PDB header:**sugar binding protein **Chain:** D: **PDB Molecule:**5-bladed -propeller lectin; **PDBTitle:** the crystal structures of two fragments truncated from 5-bladed -2 propeller lectin, tachylectin-2 (lib1-b7-18 and lib2-d2-15)
16	c2ka3C_	Alignment		12.2	38	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**emilin-1; **PDBTitle:** structure of emilin-1 c1q-like domain
17	c7apiB_	Alignment		11.8	6	**PDB header:**proteinase inhibitor **Chain:** B: **PDB Molecule:**alpha 1-antitrypsin; **PDBTitle:** the s variant of human alpha1-antitrypsin, structure and implications2 for function and metabolism
18	d2jdqd1	Alignment		11.1	17	**Fold:**PB2 C-terminal domain-like **Superfamily:**PB2 C-terminal domain-like **Family:**PB2 C-terminal domain-like
19	d1pk6a_	Alignment		11.1	31	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
20	c2vtwF_	Alignment		11.0	27	**PDB header:**viral protein **Chain:** F: **PDB Molecule:**fiber protein 2; **PDBTitle:** structure of the c-terminal head domain of the fowl2 adenovirus type 1 short fibre
21	d1f1sa3	Alignment	not modelled	10.8	23	**Fold:**Hyaluronate lyase-like, C-terminal domain **Superfamily:**Hyaluronate lyase-like, C-terminal domain **Family:**Hyaluronate lyase-like, C-terminal domain
22	c1jjoE_	Alignment	not modelled	10.5	22	**PDB header:**signaling protein **Chain:** E: **PDB Molecule:**neuroserpin; **PDBTitle:** crystal structure of mouse neuroserpin (cleaved form)
23	d1m3ya2	Alignment	not modelled	10.4	33	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Group II dsDNA viruses VP **Family:**Major capsid protein vp54
24	d1o91a_	Alignment	not modelled	10.4	31	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
25	c1o91B_	Alignment	not modelled	10.4	31	**PDB header:**collagen **Chain:** B: **PDB Molecule:**collagen alpha 1(viii) chain; **PDBTitle:** crystal structure of a collagen viii nc1 domain trimer
26	c1m4xC_	Alignment	not modelled	9.7	33	**PDB header:**virus **Chain:** C: **PDB Molecule:**pbcv-1 virus capsid; **PDBTitle:** pbcv-1 virus capsid, quasi-atomic model
27	d1w9pa2	Alignment	not modelled	9.6	18	**Fold:**FKBP-like **Superfamily:**Chitinase insertion domain **Family:**Chitinase insertion domain
28	c1hleB_	Alignment	not modelled	9.5	18	**PDB header:**hydrolase inhibitor(serine proteinase) **Chain:** B: **PDB Molecule:**horse leukocyte elastase inhibitor; **PDBTitle:** crystal structure of cleaved equine leucocyte elastase2 inhibitor determined at 1.95 angstroms resolution
29	d1brwa3	Alignment	not modelled	9.4	23	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal

29	d1brwa3	Alignment	not modelled	9.4	23	domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
30	d2tpta3	Alignment	not modelled	9.0	19	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
31	d1ll7a2	Alignment	not modelled	8.9	23	**Fold:**FKBP-like **Superfamily:**Chitinase insertion domain **Family:**Chitinase insertion domain
32	c3f02C_	Alignment	not modelled	8.8	16	**PDB header:**hydrolase inhibitor **Chain:** C: **PDB Molecule:**neuroserpin; **PDBTitle:** cleaved human neuroserpin
33	d1ulva3	Alignment	not modelled	8.8	42	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**CBD9-like **Family:**Glucodextranase, domain C
34	c2qshA_	Alignment	not modelled	8.7	25	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**dna repair protein rad4; **PDBTitle:** crystal structure of rad4-rad23 bound to a mismatch dna
35	d1zaka2	Alignment	not modelled	8.6	33	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
36	c2iqcA_	Alignment	not modelled	8.2	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**fanconi anemia group f protein; **PDBTitle:** crystal structure of human fancf protein that functions in2 the assembly of a dna damage signaling complex
37	c3mmlD_	Alignment	not modelled	8.1	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**allophanate hydrolase subunit 1; **PDBTitle:** allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
38	c3rduA_	Alignment	not modelled	8.1	18	**PDB header:**biotin binding protein **Chain:** A: **PDB Molecule:**streptavidin; **PDBTitle:** crystal structure of r7-2 streptavidin complexed with peg
39	c2h4qB_	Alignment	not modelled	8.0	18	**PDB header:**hydrolase inhibitor **Chain:** B: **PDB Molecule:**heterochromatin-associated protein ment; **PDBTitle:** crystal structure of a m-loop deletion variant of ment in2 the cleaved conformation
40	d1zunb2	Alignment	not modelled	7.8	25	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain **Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
41	c1dfcB_	Alignment	not modelled	7.7	16	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**fascin; **PDBTitle:** crystal structure of human fascin, an actin-crosslinking protein
42	c9paiB_	Alignment	not modelled	7.6	12	**PDB header:**hydrolase inhibitor **Chain:** B: **PDB Molecule:**protein (plasminogen activator inhibitor-1) residues 365- **PDBTitle:** cleaved substrate variant of plasminogen activator inhibitor-1
43	c1wwtA_	Alignment	not modelled	7.5	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase, cytoplasmic; **PDBTitle:** solution structure of the tgs domain from human threonyl-2 trna synthetase
44	d2ax3a2	Alignment	not modelled	7.3	18	**Fold:**YjeF N-terminal domain-like **Superfamily:**YjeF N-terminal domain-like **Family:**YjeF N-terminal domain-like
45	d1n7oa2	Alignment	not modelled	7.3	16	**Fold:**Hyaluronate lyase-like, C-terminal domain **Superfamily:**Hyaluronate lyase-like, C-terminal domain **Family:**Hyaluronate lyase-like, C-terminal domain
46	c3kzsD_	Alignment	not modelled	7.1	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**glycosyl hydrolase family 5; **PDBTitle:** crystal structure of glycosyl hydrolase family 5 (np_809925.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution
47	c2rivB_	Alignment	not modelled	7.0	6	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**thyroxine-binding globulin; **PDBTitle:** crystal structure of the reactive loop cleaved human thyroxine binding2 globulin
48	d1azpa_	Alignment	not modelled	6.9	25	**Fold:**SH3-like barrel **Superfamily:**Chromo domain-like **Family:**"Histone-like" proteins from archaea
49	d1k8wa3	Alignment	not modelled	6.8	27	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
50	d1gxma_	Alignment	not modelled	6.8	33	**Fold:**alpha/alpha toroid **Superfamily:**Family 10 polysaccharide lyase **Family:**Family 10 polysaccharide lyase
51	d1vpra1	Alignment	not modelled	6.8	60	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Dinoflagellate luciferase repeat
52	c2l92A_	Alignment	not modelled	6.7	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**histone family protein nucleoid-structuring protein h-ns; **PDBTitle:** solution structure of the c-terminal domain of h-ns like protein bv3f
53	d1gkpa1	Alignment	not modelled	6.5	15	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
54	c2nqoB_	Alignment	not modelled	6.4	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**gamma-glutamyltranspeptidase; **PDBTitle:** crystal structure of helicobacter pylori gamma-glutamyltranspeptidase

55	c2ksnA_	Alignment	not modelled	6.3	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin domain-containing protein 2; **PDBTitle:** solution structure of the n-terminal domain of dc-ubp/ubtd2
56	c1pgsA_	Alignment	not modelled	6.3	63	**PDB header:**endoglycosidase **Chain:** A: **PDB Molecule:**peptide-n(4)-(n-acetyl-beta-d-glucosaminyl) **PDBTitle:** the three-dimensional structure of pngase f, a2 glycosylasparaginase from flavobacterium meningosepticum
57	d1w07a2	Alignment	not modelled	5.9	13	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**acyl-CoA oxidase C-terminal domains
58	c2uywA_	Alignment	not modelled	5.8	18	**PDB header:**glycoprotein **Chain:** A: **PDB Molecule:**xenavidin; **PDBTitle:** crystal structure of xenavidin
59	c3iyoA_	Alignment	not modelled	5.7	15	**PDB header:**virus **Chain:** A: **PDB Molecule:**capsid protein; **PDBTitle:** cryo-em model of virion-sized hev virion-sized capsid
60	c2dafA_	Alignment	not modelled	5.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**flj35834 protein; **PDBTitle:** solution structure of the novel identified ubiquitin-like2 domain in the human hypothetical protein flj35834
61	c2yh5A_	Alignment	not modelled	5.7	3	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**dapx protein; **PDBTitle:** structure of the c-terminal domain of bamc
62	c2elpA_	Alignment	not modelled	5.6	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 13th c2h2 zinc finger of human2 zinc finger protein 406
63	c3nqhA_	Alignment	not modelled	5.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyl hydrolase; **PDBTitle:** crystal structure of a glycosyl hydrolase (bt_2959) from bacteroides2 thetaiotaomicron vpi-5482 at 2.11 a resolution
64	c3cw4A_	Alignment	not modelled	5.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polymerase basic protein 2; **PDBTitle:** large c-terminal domain of influenza a virus rna-dependent polymerase2 pb2
65	d2rh3a1	Alignment	not modelled	5.5	40	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**VirC2-like
66	d1s6la1	Alignment	not modelled	5.4	44	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MerB N-terminal domain-like
67	d1stma_	Alignment	not modelled	5.4	38	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Satellite viruses **Family:**Satellite viruses
68	d1z84a1	Alignment	not modelled	5.3	33	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**Hexose-1-phosphate uridylyltransferase
69	d1goia3	Alignment	not modelled	5.2	27	**Fold:**FKBP-like **Superfamily:**Chitinase insertion domain **Family:**Chitinase insertion domain
70	c1e0aB_	Alignment	not modelled	5.2	15	**PDB header:**signalling protein **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak-alpha; **PDBTitle:** cdc42 complexed with the gtpase binding domain of p212 activated kinase
71	c3fm2A_	Alignment	not modelled	5.1	9	**PDB header:**heme-binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein, distantly related to a heme **PDBTitle:** crystal structure of a putative heme-binding protein (ava_4353) from2 anabaena variabilis atcc 29413 at 1.80 a resolution
72	d2ddha2	Alignment	not modelled	5.1	17	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**acyl-CoA oxidase C-terminal domains
73	c3ew2A_	Alignment	not modelled	5.1	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**rhizavidin; **PDBTitle:** crystal structure of rhizavidin-biotin complex
74	c2c1sA_	Alignment	not modelled	5.1	9	**PDB header:**biotin binding protein **Chain:** A: **PDB Molecule:**biotin binding protein a; **PDBTitle:** x-ray structure of biotin binding protein from chicken
75	d1es0a2	Alignment	not modelled	5.0	29	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain