Phyre^2

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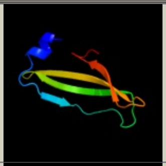
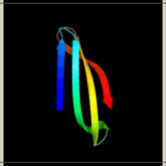
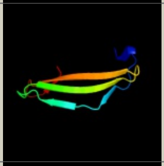
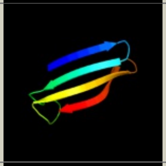
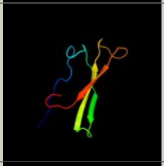
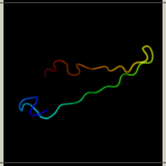
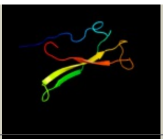
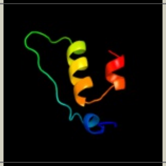
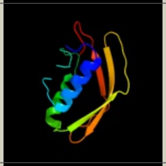
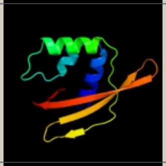
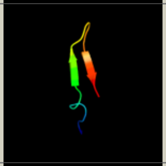
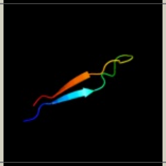
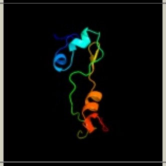
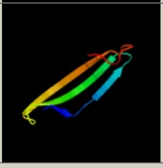
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qguA_	Alignment		84.4	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable signal peptide protein; **PDBTitle:** three-dimensional structure of the phospholipid-binding protein from2 ralstonia solanacearum q8xv73_ralsq in complex with a phospholipid at3 the resolution 1.53 a. northeast structural genomics consortium4 target rsr89
2	c3dukD_	Alignment		78.3	9	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**ntf2-like protein of unknown function; **PDBTitle:** crystal structure of a ntf2-like protein of unknown function2 (mfla_0564) from methylobacillus flagellatus kt at 2.200 a resolution
3	d2cw9a1	Alignment		77.9	16	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**TIM44-like
4	d1vqqa1	Alignment		76.0	11	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Penicillin binding protein 2a (PBP2A), N-terminal domain
5	c3qk9B_	Alignment		75.0	11	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**mitochondrial import inner membrane translocase subunit **PDBTitle:** yeast tim44 c-terminal domain complexed with cymal-3
6	c3fkaD_	Alignment		71.4	17	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**uncharacterized ntf-2 like protein; **PDBTitle:** crystal structure of a ntf-2 like protein of unknown function2 (spo1084) from silicibacter pomeroyi dss-3 at 1.69 a resolution
7	d3blza1	Alignment		64.6	11	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Sbal0622-like
8	d1w8oa3	Alignment		50.6	10	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
9	d2fxta1	Alignment		35.3	9	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**TIM44-like
10	d1dmua_	Alignment		32.1	10	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease BglI
11	c3f7sA_	Alignment		31.5	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized ntf2-like protein; **PDBTitle:** crystal structure of a ntf2-like protein of unknown function (pp_4556)2 from pseudomonas putida kt2440 at 2.11 a resolution

12	c2berA_	Alignment		22.7	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**bacterial sialidase; **PDBTitle:** y370g active site mutant of the sialidase from2 micromonospora viridifaciens in complex with beta-neu5ac3 (sialic acid).
13	d1m98a2	Alignment		21.6	20	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Orange carotenoid protein, C-terminal domain
14	c3gwrA_	Alignment		20.3	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**putative calcium/calmodulin-dependent protein kinase type **PDBTitle:** crystal structure of putative calcium/calmodulin-dependent protein2 kinase type ii association domain (yp_315894.1) from thiobacillus3 denitrificans atcc 25259 at 2.00 a resolution
15	c3k7cC_	Alignment		16.1	11	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**putative ntf2-like transpeptidase; **PDBTitle:** crystal structure of putative ntf2-like transpeptidase (np_281412.1)2 from campylobacter jejuni at 2.00 a resolution
16	d1kkea2	Alignment		14.9	35	**Fold:**Virus attachment protein globular domain **Superfamily:**Virus attachment protein globular domain **Family:**Reovirus attachment protein sigma 1 head domain
17	d2j2za2	Alignment		13.2	19	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
18	d1ub1a_	Alignment		12.7	19	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**Methyl-CpG-binding domain, MBD
19	c1kkeA_	Alignment		12.5	35	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**sigma 1 protein; **PDBTitle:** crystal structure of reovirus attachment protein sigma12 trimer
20	d3cnxa1	Alignment		10.7	9	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SAV4671-like
21	c1mwuA_	Alignment	not modelled	10.1	11	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**penicillin-binding protein 2a; **PDBTitle:** structure of methicillin acyl-penicillin binding protein 2a2 from methicillin resistant staphylococcus aureus strain3 27r at 2.60 a resolution.
22	d2duya1	Alignment	not modelled	9.9	27	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**ComEA-like
23	d2r4ia1	Alignment	not modelled	9.7	9	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**CHU142-like
24	d1g2qa_	Alignment	not modelled	9.6	15	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
25	c2zxkB_	Alignment	not modelled	9.4	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**red chlorophyll catabolite reductase, **PDBTitle:** crystal structure of semet-red chlorophyll catabolite2 reductase
26	c3lo2A_	Alignment	not modelled	9.2	35	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (y21a mutant)
27	c3lo2B_	Alignment	not modelled	9.2	35	**PDB header:**antimicrobial protein **Chain:** B: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (y21a mutant)
28	c3gzrA_	Alignment	not modelled	9.2	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein with a ntf2-like fold; **PDBTitle:** crystal structure of an uncharacterized protein with a cystatin-like2 fold (cc_2572) from caulobacter vibrioides at 1.40 a resolution

29	c2veeC_	Alignment	not modelled	9.1	12	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**protoglobin; **PDBTitle:** structure of protoglobin from methanosarcina acetivorans2 c2a
30	d1ea9c2	Alignment	not modelled	8.5	23	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
31	c2e26A_	Alignment	not modelled	7.8	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**reelin; **PDBTitle:** crystal structure of two repeat fragment of reelin
32	c3s6xA_	Alignment	not modelled	7.8	35	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**outer capsid protein sigma-1; **PDBTitle:** structure of reovirus attachment protein sigma1 in complex with alpha-2 2,3-sialyllactose
33	d1sf9a_	Alignment	not modelled	7.2	11	**Fold:**SH3-like barrel **Superfamily:**Hypothetical protein YfhH **Family:**Hypothetical protein YfhH
34	c2v6yA_	Alignment	not modelled	7.1	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aaa family atpase, p60 katanin; **PDBTitle:** structure of the mit domain from a s. solfataricus vps4-2 like atpase
35	d1kt0a2	Alignment	not modelled	6.8	19	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
36	c3ke7A_	Alignment	not modelled	6.7	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative ketosteroid isomerase; **PDBTitle:** crystal structure of putative ketosteroid isomerase (yp_001303366.1)2 from parabacteroides distasonis atcc 8503 at 1.45 a resolution
37	d2gxfa1	Alignment	not modelled	6.7	8	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**YybH-like
38	c3lo1A_	Alignment	not modelled	6.6	35	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (y16a mutant)
39	d3bb9a1	Alignment	not modelled	6.6	14	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SO0125-like
40	c3ie4A_	Alignment	not modelled	6.3	15	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gram-negative binding protein 3; **PDBTitle:** b-glucan binding domain of drosophila gnbp3 defines a novel2 family of pattern recognition receptor
41	c2ky8A_	Alignment	not modelled	5.6	27	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**methyl-cpg-binding domain protein 2; **PDBTitle:** solution structure and dynamic analysis of chicken mbd2 methyl binding2 domain bound to a target methylated dna sequence
42	d2dloa2	Alignment	not modelled	5.5	43	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
43	d3b7ca1	Alignment	not modelled	5.5	16	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SO0125-like
44	c2vtwF_	Alignment	not modelled	5.3	19	**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