Phyre^2

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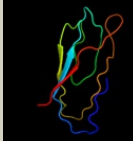
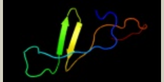
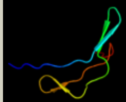
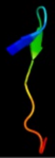
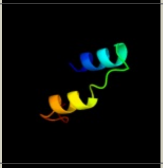
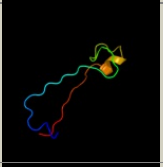
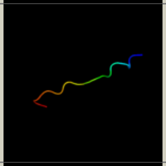
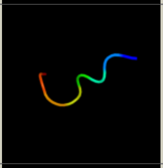
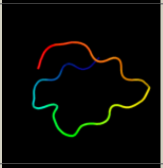
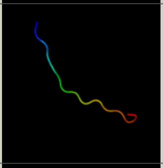
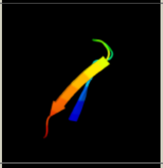
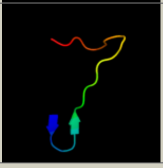
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jhja_	Alignment		58.5	17	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**APC10-like
2	c3k7cC_	Alignment		58.5	23	**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
3	d1gqpa_	Alignment		39.7	14	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**APC10-like
4	c1wwyA_	Alignment		26.1	33	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**thioredoxin-like protein 1; **PDBTitle:** solution structure of the duf1000 domain of a thioredoxin-like protein2 1
5	d2edma1	Alignment		18.9	15	**Fold:**WSSV envelope protein-like **Superfamily:**WSSV envelope protein-like **Family:**WSSV envelope protein-like
6	c3zvkG_	Alignment		15.6	27	**PDB header:**antitoxin/toxin/dna **Chain:** G: **PDB Molecule:**antitoxin of toxin-antitoxin system vapb; **PDBTitle:** crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
7	c1gqpB_	Alignment		12.9	10	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**doc1/apc10; **PDBTitle:** apc10/doc1 subunit of s. cerevisiae
8	c2auwB_	Alignment		12.1	9	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ne0471; **PDBTitle:** crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
9	d1zbpa1	Alignment		11.8	18	**Fold:**ImpE-like **Superfamily:**ImpE-like **Family:**ImpE-like
10	d2auwa2	Alignment		11.7	9	**Fold:**NE0471 N-terminal domain-like **Superfamily:**NE0471 N-terminal domain-like **Family:**NE0471 N-terminal domain-like
11	d1kh0a_	Alignment		11.0	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains

12	c2lfeA_	Alignment		10.7	28	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase hecw2; **PDBTitle:** solution nmr structure of n-terminal domain of human e3 ubiquitin-2 protein ligase hecw2, northeast structural genomics consortium (nesg)3 target ht6306a
13	d1m0da_	Alignment		10.7	19	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Endonuclease I (Holliday junction resolvase)
14	d1xoya_	Alignment		9.4	31	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Hypothetical protein AT3g04780/F7O18 27
15	c3tndF_	Alignment		8.8	20	**PDB header:**translation, toxin **Chain:** F: **PDB Molecule:**antitoxin vapb; **PDBTitle:** crystal structure of shigella flexneri vapbc toxin-antitoxin complex
16	c3i08D_	Alignment		8.7	50	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**neurogenic locus notch homolog protein 1; **PDBTitle:** crystal structure of the s1-cleaved notch1 negative2 regulatory region (nrr)
17	c3bv8A_	Alignment		8.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tetrahydrodipicolinate acetyltransferase; **PDBTitle:** crystal structure of the n-terminal domain of tetrahydrodipicolinate2 acetyltransferase from staphylococcus aureus
18	d2ux9a1	Alignment		7.7	13	**Fold:**Dodecin subunit-like **Superfamily:**Dodecin-like **Family:**Dodecin-like
19	d1jmla_	Alignment		7.6	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains
20	d1jo0a_	Alignment		7.6	19	**Fold:**IF3-like **Superfamily:**YhbY-like **Family:**YhbY-like
21	c2l02B_	Alignment	not modelled	7.4	8	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein bt2368 from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr375
22	c2vxaL_	Alignment	not modelled	7.3	13	**PDB header:**flavoprotein **Chain:** L: **PDB Molecule:**dodecin; **PDBTitle:** h.halophila dodecin in complex with riboflavin
23	d1k52a_	Alignment	not modelled	7.0	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains
24	d1jaea1	Alignment	not modelled	6.8	13	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
25	c3ulxA_	Alignment	not modelled	6.8	29	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**stress-induced transcription factor nac1; **PDBTitle:** crystal structural of the conserved domain of rice stress-responsive2 nac1
26	d1hz6a_	Alignment	not modelled	6.7	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains
27	c1jy4A_	Alignment	not modelled	6.2	22	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**b4dimer; **PDBTitle:** b4dimer: a de novo designed eight-stranded beta-sheet2 assembled using a disulfide bond
28	c2y9iB_	Alignment	not modelled	6.1	8	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**carbohydrate binding family 6; **PDBTitle:** cbm62 in complex with xyloglucan oligosaccharide
						PDB header:metal binding protein **Chain:** I: **PDB Molecule:**protein transport protein sece2;

29	c3onrl_	Alignment	not modelled	6.0	23	**PDBTitle:** crystal structure of the calcium chelating immunodominant antigen,2 calcium dodecin (rv0379),from mycobacterium tuberculosis with a novel3 calcium-binding site
30	c1dfwA_	Alignment	not modelled	5.7	43	**PDB header:**immune system **Chain:** A: **PDB Molecule:**lung surfactant protein b; **PDBTitle:** conformational mapping of the n-terminal segment of2 surfactant protein b in lipid using 13c-enhanced fourier3 transform infrared spectroscopy (ftir)
31	d1zo0a1	Alignment	not modelled	5.7	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**Ornithine decarboxylase antizyme-like
32	d1mhhe_	Alignment	not modelled	5.3	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains
33	c3oqtP_	Alignment	not modelled	5.3	12	**PDB header:**flavoprotein **Chain:** P: **PDB Molecule:**rv1498a protein; **PDBTitle:** crystal structure of rv1498a protein from mycobacterium tuberculosis
34	d1hkya_	Alignment	not modelled	5.2	80	**Fold:**Hairpin loop containing domain-like **Superfamily:**Hairpin loop containing domain-like **Family:**Pan module (APPLE domain)
35	c1xctL_	Alignment	not modelled	5.2	20	**PDB header:**immune system **Chain:** L: **PDB Molecule:**protein l; **PDBTitle:** complex hcv core-fab 19d9d6-protein l mutant (d55a, l57h, y64w) in2 space group p21212
36	d1tnsa_	Alignment	not modelled	5.0	17	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like