Phyre2

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Description	P77779
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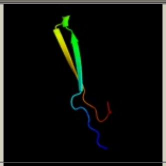
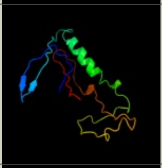
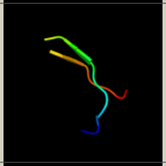
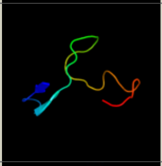
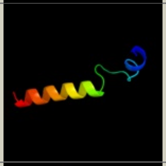
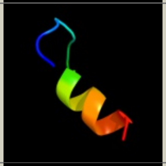
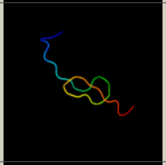
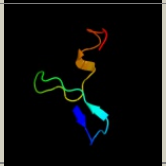
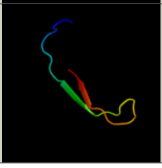
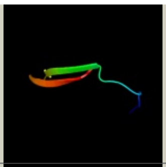
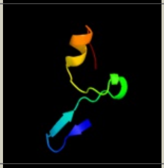
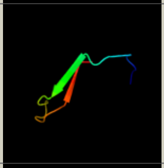
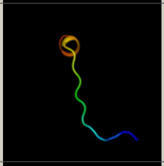
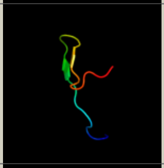
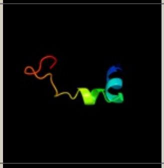
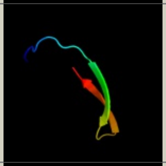
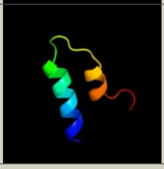
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mswA_	Alignment		70.3	26	**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
2	c2zxeB_	Alignment		53.9	16	**PDB header:**hydrolase/transport protein **Chain:** B: **PDB Molecule:**na+,k+-atpase beta subunit; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
3	d1bdsa_	Alignment		40.2	56	**Fold:**Defensin-like **Superfamily:**Defensin-like **Family:**Defensin
4	d1x3za1	Alignment		36.1	22	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
5	c2yy0D_	Alignment		19.9	30	**PDB header:**transcription **Chain:** D: **PDB Molecule:**c-myc-binding protein; **PDBTitle:** crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
6	d2b5id2	Alignment		19.4	38	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
7	c3ga2A_	Alignment		17.2	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease v; **PDBTitle:** crystal structure of the endonuclease_v (bsu36170) from2 bacillus subtilis, northeast structural genomics3 consortium target sr624
8	d2p0sa1	Alignment		16.2	44	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**PG0945 N-terminal domain-like
9	d1f00i2	Alignment		14.1	30	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
10	c3eswA_	Alignment		13.6	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine **PDBTitle:** complex of yeast pngase with glcnac2-iac.
11	d3bi7a1	Alignment		10.8	25	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**SRA domain-like

12	c2pb7A_	Alignment		10.5	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase uhrf1; **PDBTitle:** crystal structure of the sra domain of the human uhrf12 protein
13	c3swyB_	Alignment		10.3	67	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**cyclic nucleotide-gated cation channel alpha-3; **PDBTitle:** cnga3 626-672 containing clz domain
14	d2f4ma1	Alignment		9.9	24	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
15	d2zkda1	Alignment		9.7	25	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**SRA domain-like
16	d1bcoa1	Alignment		9.7	17	**Fold:**mu transposase, C-terminal domain **Superfamily:**mu transposase, C-terminal domain **Family:**mu transposase, C-terminal domain
17	d1nlna_	Alignment		9.5	21	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Adenain-like
18	c3nfvA_	Alignment		9.3	40	**PDB header:**lyase **Chain:** A: **PDB Molecule:**alginate lyase; **PDBTitle:** crystal structure of an alginate lyase (bacova_01668) from bacteroides2 ovatus at 1.95 a resolution
19	c3q0bX_	Alignment		9.2	14	**PDB header:**transferase/dna **Chain:** X: **PDB Molecule:**histone-lysine n-methyltransferase, h3 lysine-9 specific **PDBTitle:** crystal structure of suvh5 sra- fully methylated cg dna complex in2 space group p42212
20	c3lhrA_	Alignment		9.1	32	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**zinc finger protein 24; **PDBTitle:** crystal structure of the scan domain from human znf24
21	c3e21A_	Alignment	not modelled	8.7	29	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fas-associated factor 1; **PDBTitle:** crystal structure of faf-1 uba domain
22	d1brwa3	Alignment	not modelled	8.3	26	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
23	d2zo1b1	Alignment	not modelled	8.2	26	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**SRA domain-like
24	d2fi2a1	Alignment	not modelled	8.1	40	**Fold:**Acyl carrier protein-like **Superfamily:**Retrovirus capsid dimerization domain-like **Family:**SCAN domain
25	d2tpta3	Alignment	not modelled	7.5	19	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
26	c3osvC_	Alignment	not modelled	7.4	17	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**flagellar basal-body rod modification protein flgd; **PDBTitle:** the crytsal structure of flgd from p. aeruginosa
27	d1y7qa1	Alignment	not modelled	6.9	56	**Fold:**Acyl carrier protein-like **Superfamily:**Retrovirus capsid dimerization domain-like **Family:**SCAN domain
28	c3i08D_	Alignment	not modelled	6.8	28	**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)

29	d1pk6c_	Alignment	not modelled	6.8	27	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
30	c2wbmA_	Alignment	not modelled	6.7	26	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**ribosome maturation protein sdo1 homolog; **PDBTitle:** crystal structure of mthsbds, the homologue of the2 shwachman-bodian-diamond syndrome protein in the3 euriarchaeon methanothermobacter thermautotrophicus
31	c2ka3C_	Alignment	not modelled	6.5	36	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**emilin-1; **PDBTitle:** structure of emilin-1 c1q-like domain
32	c1t95A_	Alignment	not modelled	6.5	22	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein af0491; **PDBTitle:** crystal structure of the shwachman-bodian-diamond syndrome2 protein orthologue from archaeoglobus fulgidus
33	c1v7fA_	Alignment	not modelled	6.4	67	**PDB header:**toxin **Chain:** A: **PDB Molecule:**phrixotoxin 1; **PDBTitle:** solution structure of phrixotoxin 1
34	d1v7fa_	Alignment	not modelled	6.4	67	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins
35	c2ketA_	Alignment	not modelled	6.4	60	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**cathelicidin-6; **PDBTitle:** solution structure of bmap-27
36	d2doaa1	Alignment	not modelled	6.3	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ELL N2 domain-like
37	c1hcwA_	Alignment	not modelled	6.3	42	**PDB header:**growth response protein **Chain:** A: **PDB Molecule:**bba1; **PDBTitle:** 23-residue designed metal-free peptide based on the zinc2 finger domains, nmr, 35 structures
38	d1pk6b_	Alignment	not modelled	6.2	27	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
39	d1zud21	Alignment	not modelled	6.0	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
40	d1pk6a_	Alignment	not modelled	6.0	27	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
41	c2kdoA_	Alignment	not modelled	5.9	27	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**ribosome maturation protein sbds; **PDBTitle:** structure of the human shwachman-bodian-diamond syndrome protein, sbds
42	d1f1sa3	Alignment	not modelled	5.8	27	**Fold:**Hyaluronate lyase-like, C-terminal domain **Superfamily:**Hyaluronate lyase-like, C-terminal domain **Family:**Hyaluronate lyase-like, C-terminal domain
43	c2l16A_	Alignment	not modelled	5.8	55	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**sec-independent protein translocase protein tatad; **PDBTitle:** solution structure of bacillus subtilits tatad protein in dpc micelles
44	c2x12A_	Alignment	not modelled	5.6	27	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**fimbriae-associated protein fap1; **PDBTitle:** ph-induced modulation of streptococcus parasanguinis2 adhesion by fap1 fimbriae
45	d1w9pa2	Alignment	not modelled	5.6	18	**Fold:**FKBP-like **Superfamily:**Chitinase insertion domain **Family:**Chitinase insertion domain
46	d1ei5a1	Alignment	not modelled	5.6	38	**Fold:**Streptavidin-like **Superfamily:**D-aminopeptidase, middle and C-terminal domains **Family:**D-aminopeptidase, middle and C-terminal domains
47	d1s6la1	Alignment	not modelled	5.6	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MerB N-terminal domain-like
48	c3vg8F_	Alignment	not modelled	5.5	38	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**hypothetical protein tthb210; **PDBTitle:** crystal structure of hypothetical protein tthb210 from thermus2 thermophilus hb8
49	d1zaka2	Alignment	not modelled	5.4	33	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
50	d1wiba_	Alignment	not modelled	5.4	24	**Fold:**Ribosomal L11/L12e N-terminal domain **Superfamily:**Ribosomal L11/L12e N-terminal domain **Family:**Ribosomal L11/L12e N-terminal domain
51	c1gr3A_	Alignment	not modelled	5.3	45	**PDB header:**collagen **Chain:** A: **PDB Molecule:**collagen x; **PDBTitle:** structure of the human collagen x nc1 trimer
52	d1gr3a_	Alignment	not modelled	5.3	45	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
53	c1o91B_	Alignment	not modelled	5.3	27	**PDB header:**collagen **Chain:** B: **PDB Molecule:**collagen alpha 1(viii) chain; **PDBTitle:** crystal structure of a collagen viii nc1 domain trimer
54	d1o91a_	Alignment	not modelled	5.3	27	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like

55	d1c3ha_	Alignment	not modelled	5.2	31	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
56	d2vl8a1	Alignment	not modelled	5.2	74	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Glycosylating toxin catalytic domain-like
57	d2pfxa1	Alignment	not modelled	5.1	19	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
58	c1jjoE_	Alignment	not modelled	5.1	22	**PDB header:**signaling protein **Chain:** E: **PDB Molecule:**neuroserpin; **PDBTitle:** crystal structure of mouse neuroserpin (cleaved form)
59	c7apiB_	Alignment	not modelled	5.0	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
60	d2cr5a1	Alignment	not modelled	5.0	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain