Phyre^2

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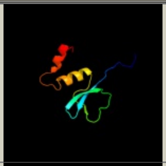
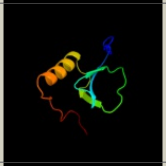
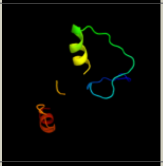
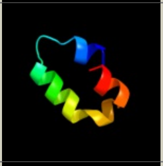
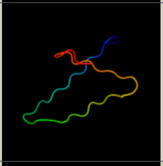
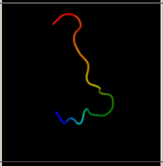
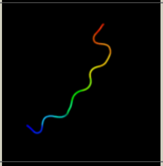
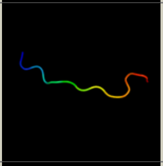
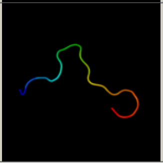
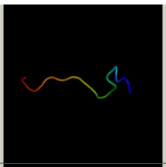
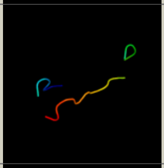
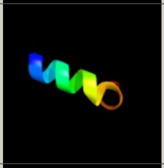
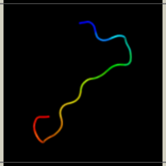
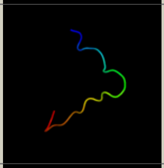
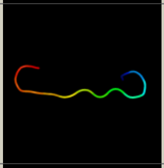
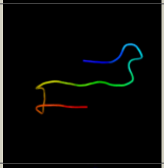
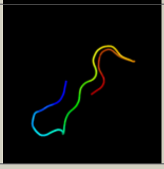
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2gpfa1	Alignment		100.0	23	**Fold:**MbtH/L9 domain-like **Superfamily:**MbtH-like **Family:**MbtH-like
2	c2khrA_	Alignment		100.0	39	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**protein mbth; **PDBTitle:** solution structure of rv2377c, a mbth-like protein from mycobacterium2 tuberculosis
3	d2pstx1	Alignment		100.0	23	**Fold:**MbtH/L9 domain-like **Superfamily:**MbtH-like **Family:**MbtH-like
4	c2jh3C_	Alignment		21.2	22	**PDB header:**ribosomal protein **Chain:** C: **PDB Molecule:**ribosomal protein s2-related protein; **PDBTitle:** the crystal structure of dr2241 from deinococcus2 radiodurans at 1.9 a resolution reveals a multi-domain3 protein with structural similarity to chelatases but also4 with two additional novel domains
5	d2b6ca1	Alignment		19.2	13	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**BC3264-like
6	d1j0ha2	Alignment		18.4	13	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
7	d1iqqa_	Alignment		16.0	20	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
8	d1f8ab1	Alignment		12.2	28	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
9	d2zjrg1	Alignment		11.3	38	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
10	c3cf5G_	Alignment		11.3	38	**PDB header:**ribosome/antibiotic **Chain:** G: **PDB Molecule:**50s ribosomal protein l13; **PDBTitle:** thiopeptide antibiotic thiostrepton bound to the large ribosomal2 subunit of deinococcus radiodurans
11	d1k9ra_	Alignment		10.9	37	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain

12	d1nmva1	Alignment		10.7	28	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
13	c2ai4A_	Alignment		10.6	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein so1698; **PDBTitle:** structure of protein of unknown function so1698 from shewanella2 oneidensis
14	c3pfyA_	Alignment		10.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**otu domain-containing protein 5; **PDBTitle:** the catalytic domain of human otud5
15	c1ymzA_	Alignment		10.4	25	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cc45; **PDBTitle:** cc45, an artificial ww domain designed using statistical2 coupling analysis
16	c2zajA_	Alignment		10.3	30	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**membrane-associated guanylate kinase, ww and pdz **PDBTitle:** solution structure of the short-isoform of the second ww2 domain from the human membrane-associated guanylate kinase,3 ww and pdz domain-containing protein 1 (magi-1)
17	d2ho2a1	Alignment		10.0	43	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
18	d1g0wa2	Alignment		9.9	10	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
19	c3mc2C_	Alignment		9.8	19	**PDB header:**lyase inhibitor **Chain:** C: **PDB Molecule:**inhibitor of carbonic anhydrase; **PDBTitle:** crystal structure of the murine inhibitor of carbonic anhydrase
20	d1u6ra2	Alignment		9.7	10	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
21	c2ftcH_	Alignment	not modelled	9.6	15	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**39s ribosomal protein l13, mitochondrial; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
22	c2ysbA_	Alignment	not modelled	9.2	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**salvador homolog 1 protein; **PDBTitle:** solution structure of the first ww domain from the mouse2 salvador homolog 1 protein (sav1)
23	c3d5bN_	Alignment	not modelled	8.9	31	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**50s ribosomal protein l13; **PDBTitle:** structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of one 70s ribosome. the entire crystal3 structure contains two 70s ribosomes as described in remark 400.
24	d1m15a2	Alignment	not modelled	8.9	15	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
25	d2ysca1	Alignment	not modelled	8.9	50	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
26	d1pina1	Alignment	not modelled	8.8	36	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
27	c2kykA_	Alignment	not modelled	8.5	27	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase itchy homolog; **PDBTitle:** the sandwich region between two lmp2a py motif regulates the2 interaction between aip4ww2domain and py motif
						PDB header:hydrolase/dna

28	c3nicA_	Alignment	not modelled	8.3	27	**Chain:** A: **PDB Molecule:**eco29kir; **PDBTitle:** dna binding and cleavage by the giy-yig endonuclease r.eco29ki2 inactive variant y49f
29	c1qk1H_	Alignment	not modelled	8.2	15	**PDB header:**transferase (creatine kinase) **Chain:** H: **PDB Molecule:**creatine kinase, ubiquitous mitochondrial; **PDBTitle:** crystal structure of human ubiquitous mitochondrial2 creatine kinase
30	d2j01n1	Alignment	not modelled	8.2	31	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
31	c2lawA_	Alignment	not modelled	8.2	27	**PDB header:**signaling protein/transcription **Chain:** A: **PDB Molecule:**yorkie homolog; **PDBTitle:** structure of the second ww domain from human yap in complex with a2 human smad1 derived peptide
32	d2ilxa1	Alignment	not modelled	8.1	23	**Fold:**LigT-like **Superfamily:**LigT-like **Family:**2',3'-cyclic nucleotide 3'-phosphodiesterase, catalytic domain
33	d1qh4a2	Alignment	not modelled	8.0	10	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
34	c3l4hA_	Alignment	not modelled	7.8	33	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase hecw1; **PDBTitle:** helical box domain and second ww domain of the human e3 ubiquitin-2 protein ligase hecw1
35	c3bboL_	Alignment	not modelled	7.8	46	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**ribosomal protein l13; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
36	d1qk1a2	Alignment	not modelled	7.7	15	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
37	c1tk7A_	Alignment	not modelled	7.6	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cg4244-pb; **PDBTitle:** nmr structure of ww domains (ww3-4) from suppressor of2 deltex
38	c2lb0A_	Alignment	not modelled	7.6	33	**PDB header:**signaling protein/transcription **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase smurf1; **PDBTitle:** structure of the first ww domain of human smurf1 in complex with a di-2 phosphorylated human smad1 derived peptide
39	c2ysgA_	Alignment	not modelled	7.5	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**syntaxin-binding protein 4; **PDBTitle:** solution structure of the ww domain from the human syntaxin-2 binding protein 4
40	c1e0mA_	Alignment	not modelled	7.4	31	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**wwprototype; **PDBTitle:** prototype ww domain
41	d2jmfa1	Alignment	not modelled	7.3	33	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
42	d1vrpa2	Alignment	not modelled	7.1	10	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
43	d2f21a1	Alignment	not modelled	7.0	29	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
44	d1crka2	Alignment	not modelled	7.0	10	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
45	c1wr4A_	Alignment	not modelled	7.0	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin-protein ligase nedd4-2; **PDBTitle:** solution structure of the second ww domain of nedd4-2
46	c1ce2A_	Alignment	not modelled	7.0	13	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**protein (lactoferrin); **PDBTitle:** structure of diferric buffalo lactoferrin at 2.5a resolution
47	c2lazA_	Alignment	not modelled	6.9	33	**PDB header:**signaling protein/transcription **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase smurf1; **PDBTitle:** structure of the first ww domain of human smurf1 in complex with a2 mono-phosphorylated human smad1 derived peptide
48	c2dx0B_	Alignment	not modelled	6.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phospholipase c, gamma 2; **PDBTitle:** crystal structure of the n-terminal sh2 domain of mouse2 phospholipase c-gamma 2
49	d2itka1	Alignment	not modelled	6.9	38	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
50	d1b1xa2	Alignment	not modelled	6.8	6	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
51	c2djyA_	Alignment	not modelled	6.8	33	**PDB header:**ligase/signaling protein **Chain:** A: **PDB Molecule:**smad ubiquitination regulatory factor 2; **PDBTitle:** solution structure of smurf2 ww3 domain-smad7 py peptide2 complex
52	d1dota2	Alignment	not modelled	6.8	6	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
53	c1yr3A_	Alignment	not modelled	6.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xanthosine phosphorylase; **PDBTitle:** escherichia coli purine nucleoside phosphorylase ii, the2 product of the xapa gene
						PDB header:transferrin **Chain:** A: **PDB Molecule:**lactoferrin;

54	c1lfgA_	Alignment	not modelled	6.6	19	**PDBTitle:** molecular replacement solution of the structure of apolactoferrin, a2 protein displaying large-scale conformational change
55	c2krxA_	Alignment	not modelled	6.6	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**asl3597 protein; **PDBTitle:** solution nmr structure of asl3597 from nostoc sp. pcc7120. northeast2 structural genomics consortium target id nsr244.
56	c1rl9A_	Alignment	not modelled	6.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arginine kinase; **PDBTitle:** crystal structure of creatine-adp arginine kinase ternary2 complex
57	c2vncB_	Alignment	not modelled	6.5	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycogen operon protein glgx; **PDBTitle:** crystal structure of glycogen debranching enzyme trex from2 sulfolobus solfataricus
58	c3l2eB_	Alignment	not modelled	6.5	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycocyamine kinase beta chain; **PDBTitle:** glycocyamine kinase, alpha-beta heterodimer from marine worm2 namalycastis sp.
59	c2kxqA_	Alignment	not modelled	6.4	26	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase smurf2; **PDBTitle:** solution structure of smurf2 ww2 and ww3 bound to smad7 py motif2 containing peptide
60	c1yiuA_	Alignment	not modelled	6.4	27	**PDB header:**ligase **Chain:** A: **PDB Molecule:**itchy e3 ubiquitin protein ligase; **PDBTitle:** itch e3 ubiquitin ligase ww3 domain
61	c2l4jA_	Alignment	not modelled	6.4	32	**PDB header:**transcription **Chain:** A: **PDB Molecule:**yes-associated protein 2 (yap2); **PDBTitle:** yap ww2
62	c3bvsA_	Alignment	not modelled	6.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkylpurine dna glycosylase alkd; **PDBTitle:** crystal structure of bacillus cereus alkylpurine dna glycosylase alkd
63	d1i8gb_	Alignment	not modelled	6.3	36	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
64	d1iama2	Alignment	not modelled	6.3	43	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
65	d2e45a1	Alignment	not modelled	6.2	67	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
66	c1ryxA_	Alignment	not modelled	6.1	6	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**ovotransferrin; **PDBTitle:** crystal structure of hen serum transferrin in apo- form
67	d1g3pa1	Alignment	not modelled	6.0	29	**Fold:**N-terminal domains of the minor coat protein g3p **Superfamily:**N-terminal domains of the minor coat protein g3p **Family:**N-terminal domains of the minor coat protein g3p
68	c3ju6A_	Alignment	not modelled	5.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arginine kinase; **PDBTitle:** crystal structure of dimeric arginine kinase in complex with2 amppnp and arginine
69	c2yscA_	Alignment	not modelled	5.6	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**amyloid beta a4 precursor protein-binding family **PDBTitle:** solution structure of the ww domain from the human amyloid2 beta a4 precursor protein-binding family b member 3, apbb3
70	c2jmfA_	Alignment	not modelled	5.6	28	**PDB header:**ligase/signaling protein **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase suppressor of deltex; **PDBTitle:** solution structure of the su(dx) ww4- notch py peptide2 complex
71	d1dota1	Alignment	not modelled	5.5	6	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
72	c2yshA_	Alignment	not modelled	5.5	32	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**growth-arrest-specific protein 7; **PDBTitle:** solution structure of the ww domain from the human growth-2 arrest-specific protein 7, gas-7
73	c2hauA_	Alignment	not modelled	5.4	19	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**serotransferrin; **PDBTitle:** apo-human serum transferrin (non-glycosylated)
74	c1i0eD_	Alignment	not modelled	5.3	10	**PDB header:**transferase **Chain:** D: **PDB Molecule:**creatine kinase,m chain; **PDBTitle:** crystal structure of creatine kinase from human muscle
75	c2ysfA_	Alignment	not modelled	5.2	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase itchy homolog; **PDBTitle:** solution structure of the fourth ww domain from the human2 e3 ubiquitin-protein ligase itchy homolog, itch
76	c2kieA_	Alignment	not modelled	5.2	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inositol polyphosphate 5-phosphatase ocrl-1; **PDBTitle:** a ph domain within ocrl bridges clathrin mediated membrane2 trafficking to phosphoinositide metabolis
77	d2c5ra1	Alignment	not modelled	5.2	23	**Fold:**Phage replication organizer domain **Superfamily:**Phage replication organizer domain **Family:**Phage replication organizer domain
78	c2kq0A_	Alignment	not modelled	5.2	36	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase nedd4; **PDBTitle:** human nedd4 3rd ww domain complex with ebola zaire virus matrix2 protein vp40 derived peptide ilptappeymea
						Fold:beta-clip

79	d1ejxb_	Alignment	not modelled	5.1	27	**Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit