Phyre2

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Description	P75711
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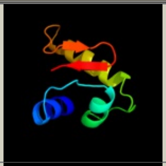
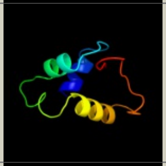
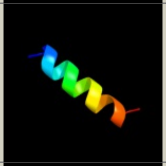
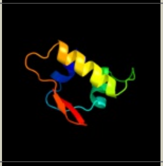
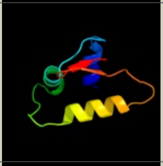
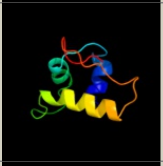
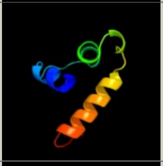
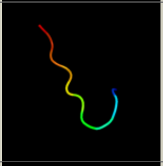
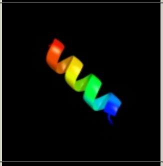
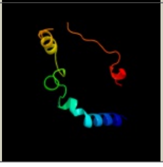
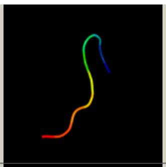
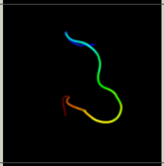
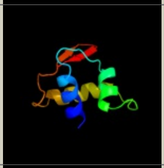
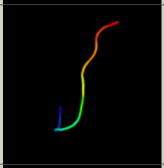
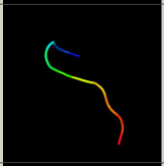
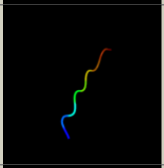
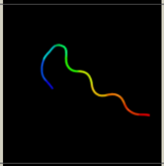
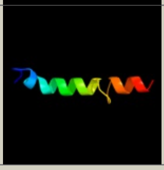
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k4jA_	Alignment		48.2	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** arsr dna binding domain
2	d1opca_	Alignment		35.8	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
3	c2v1yA_	Alignment		33.6	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic **PDBTitle:** structure of a phosphoinositide 3-kinase alpha adaptor-2 binding domain (abd) in a complex with the ish2 domain3 from p85 alpha
4	d1gxqa_	Alignment		31.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
5	c3q9vB_	Alignment		31.1	25	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna-binding response regulator; **PDBTitle:** crystal structure of rra c-terminal domain(123-221) from deinococcus2 radiodurans
6	c2hqnA_	Alignment		29.5	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
7	c2hwvA_	Alignment		27.1	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-binding response regulator vicr; **PDBTitle:** crystal structure of an essential response regulator dna binding2 domain, vicrc in enterococcus faecalis, a member of the yycf3 subfamily.
8	c2kq0A_	Alignment		25.2	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
9	c2vxzA_	Alignment		14.9	7	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**pyrsv_gp04; **PDBTitle:** crystal structure of hypothetical protein pyrsv_gp04 from2 pyrobaculum spherical virus
10	c3q9sA_	Alignment		13.2	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding response regulator; **PDBTitle:** crystal structure of rra(1-215) from deinococcus radiodurans
11	c2j7uA_	Alignment		12.7	28	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**rna dependent rna polymerase; **PDBTitle:** dengue virus ns5 rna dependent rna polymerase domain

12	d2f21a1	Alignment		12.7	40	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
13	c2kykA_	Alignment		11.4	38	**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
14	c2zxjB_	Alignment		10.4	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein walr; **PDBTitle:** crystal structure of yycf dna-binding domain from staphylococcus2 aureus
15	c2lazA_	Alignment		10.1	40	**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
16	c1wmvA_	Alignment		9.9	50	**PDB header:**oxidoreductase, apoptosis **Chain:** A: **PDB Molecule:**ww domain containing oxidoreductase; **PDBTitle:** solution structure of the second ww domain of wwox
17	c3ml6D_	Alignment		9.8	44	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**chimeric complex between protein dishevlled2 homolog dvl-2 **PDBTitle:** a complex between dishevlled2 and clathrin adaptor ap-2
18	c2jzyA_	Alignment		9.7	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein pcor; **PDBTitle:** solution structure of c-terminal effector domain of2 putative two-component-system response regulator involved3 in copper resistance from klebsiella pneumoniae
19	c2zajA_	Alignment		9.7	40	**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)
20	c1k6nH_	Alignment		9.6	37	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**photosynthetic reaction center h subunit; **PDBTitle:** e(l212)a,d(l213)a double mutant structure of photosynthetic reaction2 center from rhodobacter sphaeroides
21	c2lb0A_	Alignment	not modelled	9.0	40	**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
22	c2pmuD_	Alignment	not modelled	8.9	18	**PDB header:**transcription regulation **Chain:** D: **PDB Molecule:**response regulator phop; **PDBTitle:** crystal structure of the dna-binding domain of phop
23	d1tk7a2	Alignment	not modelled	8.8	50	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
24	c2dmvA_	Alignment	not modelled	8.8	40	**PDB header:**ligase **Chain:** A: **PDB Molecule:**itchy homolog e3 ubiquitin protein ligase; **PDBTitle:** solution structure of the second ww domain of itchy homolog2 e3 ubiquitin protein ligase (itch)
25	c3l81A_	Alignment	not modelled	8.7	44	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ap-4 complex subunit mu-1; **PDBTitle:** crystal structure of adaptor protein complex 4 (ap-4) mu4 subunit c-2 terminal domain, in complex with a sorting peptide from the amyloid3 precursor protein (app)
26	d1wfxa_	Alignment	not modelled	8.4	18	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**Tpt1/KptA
27	c2ysbA_	Alignment	not modelled	8.3	50	**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)
28	c1bw8A_	Alignment	not modelled	8.3	44	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**protein (mu2 adaptin subunit); **PDBTitle:** mu2 adaptin subunit (ap50) of ap2 adaptor (second

						domain),2 complexed with egfr internalization peptide fyralm
29	c2lawA_	Alignment	not modelled	8.0	50	**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
30	c1eysH_	Alignment	not modelled	7.9	41	**PDB header:**electron transport **Chain:** H: **PDB Molecule:**photosynthetic reaction center; **PDBTitle:** crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
31	d1i8gb_	Alignment	not modelled	7.8	40	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
32	c2jmfA_	Alignment	not modelled	7.7	50	**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
33	d2pr9a1	Alignment	not modelled	7.6	44	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Second domain of Mu2 adaptin subunit (ap50) of ap2 adaptor **Family:**Second domain of Mu2 adaptin subunit (ap50) of ap2 adaptor
34	c1ymzA_	Alignment	not modelled	7.5	50	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cc45; **PDBTitle:** cc45, an artificial ww domain designed using statistical2 coupling analysis
35	c1wr7A_	Alignment	not modelled	7.3	50	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nedd4-2; **PDBTitle:** solution structure of the third ww domain of nedd4-2
36	c2l4jA_	Alignment	not modelled	7.2	60	**PDB header:**transcription **Chain:** A: **PDB Molecule:**yes-associated protein 2 (yap2); **PDBTitle:** yap ww2
37	c2yshA_	Alignment	not modelled	7.2	40	**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
38	d1ys7a1	Alignment	not modelled	7.2	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
39	c2gwwB_	Alignment	not modelled	7.1	50	**PDB header:**cell adhesion, structural protein **Chain:** B: **PDB Molecule:**ipaa; **PDBTitle:** human vinculin (head domain, vh1, residues 1-258) in2 complex with shigella's ipaa vinculin binding site3 (residues 602-633)
40	c3ll6B_	Alignment	not modelled	7.1	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cyclin g-associated kinase; **PDBTitle:** crystal structure of the human cyclin g associated kinase (gak)
41	d1nmva1	Alignment	not modelled	7.0	40	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
42	d2jmfa1	Alignment	not modelled	6.8	50	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
43	d1f8ab1	Alignment	not modelled	6.7	40	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
44	c1wr4A_	Alignment	not modelled	6.7	40	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin-protein ligase nedd4-2; **PDBTitle:** solution structure of the second ww domain of nedd4-2
45	c3ogfA_	Alignment	not modelled	6.6	43	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo designed dimeric trefoil-fold sub-domain which **PDBTitle:** crystal structure of difoil-4p homo-trimer: de novo designed dimeric2 trefoil-fold sub-domain which forms homo-trimer assembly
46	c1e0mA_	Alignment	not modelled	6.5	50	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**wwprototype; **PDBTitle:** prototype ww domain
47	c2ez5W_	Alignment	not modelled	6.5	30	**PDB header:**signalling protein,ligase **Chain:** W: **PDB Molecule:**e3 ubiquitin-protein ligase nedd4; **PDBTitle:** solution structure of the dnedd4 ww3* domain- comm lpsy2 peptide complex
48	c1w63P_	Alignment	not modelled	6.3	56	**PDB header:**endocytosis **Chain:** P: **PDB Molecule:**adaptor-related protein complex 1, mu 1 subunit; **PDBTitle:** ap1 clathrin adaptor core
49	d1tk7a1	Alignment	not modelled	6.2	50	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
50	c1yiuA_	Alignment	not modelled	6.2	40	**PDB header:**ligase **Chain:** A: **PDB Molecule:**itchy e3 ubiquitin protein ligase; **PDBTitle:** itch e3 ubiquitin ligase ww3 domain
51	c2oqrA_	Alignment	not modelled	6.2	8	**PDB header:**transcription,signaling protein **Chain:** A: **PDB Molecule:**sensory transduction protein regx3; **PDBTitle:** the structure of the response regulator regx3 from mycobacterium2 tuberculosis
52	d1iqoa_	Alignment	not modelled	6.0	21	**Fold:**Hypothetical protein MTH1880 **Superfamily:**Hypothetical protein MTH1880 **Family:**Hypothetical protein MTH1880
53	c2dwvB_	Alignment	not modelled	5.9	50	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**salvador homolog 1 protein; **PDBTitle:** solution structure of the second ww domain from mouse2

						salvador homolog 1 protein (mww45)
54	d1k9ra_	Alignment	not modelled	5.9	50	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
55	c2ysgA_	Alignment	not modelled	5.7	60	**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
56	d1flca2	Alignment	not modelled	5.7	57	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Esterase domain of haemagglutinin-esterase-fusion glycoprotein HEF1
57	c2ysdA_	Alignment	not modelled	5.7	33	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**membrane-associated guanylate kinase, ww and pdz **PDBTitle:** solution structure of the first ww domain from the human2 membrane-associated guanylate kinase, ww and pdz domain-3 containing protein 1. magi-1
58	c2ysfA_	Alignment	not modelled	5.4	50	**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
59	c3ol0C_	Alignment	not modelled	5.3	46	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**de novo designed monomer trefoil-fold sub-domain which **PDBTitle:** crystal structure of monofoil-4p homo-trimer: de novo designed monomer2 trefoil-fold sub-domain which forms homo-trimer assembly
60	d2csba2	Alignment	not modelled	5.3	36	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
61	c2jkrM_	Alignment	not modelled	5.2	44	**PDB header:**endocytosis **Chain:** M: **PDB Molecule:**ap-2 complex subunit mu-1; **PDBTitle:** ap2 clathrin adaptor core with dileucine peptide rm(2 phosphos)qikrllse
62	c2ftcK_	Alignment	not modelled	5.2	0	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**39s ribosomal protein l19, mitochondrial; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome