Phyre2

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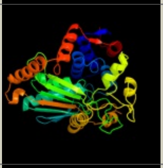
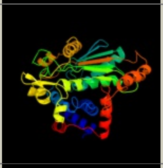
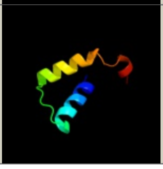
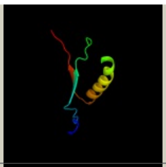
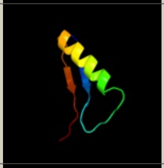
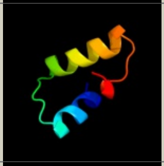
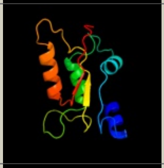
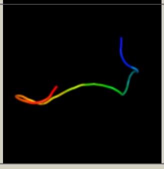
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2g8yB_	Alignment		100.0	97	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**malate/l-lactate dehydrogenases; **PDBTitle:** the structure of a putative malate/lactate dehydrogenase from e. coli.
2	c3i0pA_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of malate dehydrogenase from entamoeba histolytica
3	c1z2iA_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of agrobacterium tumefaciens malate2 dehydrogenase, new york structural genomics consortium
4	c1vbiA_	Alignment		100.0	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**type 2 malate/lactate dehydrogenase; **PDBTitle:** crystal structure of type 2 malate/lactate dehydrogenase from thermus2 thermophilus hb8
5	d1rfma_	Alignment		100.0	32	**Fold:**L-sulfolactate dehydrogenase-like **Superfamily:**L-sulfolactate dehydrogenase-like **Family:**L-sulfolactate dehydrogenase-like
6	d1xrha_	Alignment		100.0	28	**Fold:**L-sulfolactate dehydrogenase-like **Superfamily:**L-sulfolactate dehydrogenase-like **Family:**L-sulfolactate dehydrogenase-like
7	c1wtjB_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ureidoglycolate dehydrogenase; **PDBTitle:** crystal structure of delta1-piperideine-2-carboxylate2 reductase from pseudomonas syringae pvar.tomato
8	d1nxua_	Alignment		100.0	24	**Fold:**L-sulfolactate dehydrogenase-like **Superfamily:**L-sulfolactate dehydrogenase-like **Family:**L-sulfolactate dehydrogenase-like
9	c1v9nA_	Alignment		100.0	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structure of malate dehydrogenase from pyrococcus horikoshii ot3
10	c3uoeB_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dehydrogenase; **PDBTitle:** the crystal structure of dehydrogenase from sinorhizobium meliloti
11	d1jmxa1	Alignment		40.9	14	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2

12	c3irvA_	Alignment		38.1	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cysteine hydrolase; **PDBTitle:** crystal structure of cysteine hydrolase pspph_2384 from pseudomonas2 syringae pv. phaseolicola 1448a
13	c3eefA_	Alignment		34.6	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-carbamoylsarcosine amidase related protein; **PDBTitle:** crystal structure of n-carbamoylsarcosine amidase from thermoplasma2 acidophilum
14	c3kl2K_	Alignment		34.5	13	**PDB header:**structural genomics, unknown function **Chain:** K: **PDB Molecule:**putative isochorismatase; **PDBTitle:** crystal structure of a putative isochorismatase from streptomyces2 avermitilis
15	c2qiwA_	Alignment		34.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pep phosphonomutase; **PDBTitle:** crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
16	c2kebA_	Alignment		31.3	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna polymerase subunit alpha b; **PDBTitle:** nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit
17	c2ze3A_	Alignment		30.4	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dfa0005; **PDBTitle:** crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
18	d3bzra1	Alignment		28.4	20	**Fold:**EscU C-terminal domain-like **Superfamily:**EscU C-terminal domain-like **Family:**EscU C-terminal domain-like
19	c3bzrA_	Alignment		28.4	20	**PDB header:**membrane protein, protein transport **Chain:** A: **PDB Molecule:**escu; **PDBTitle:** crystal structure of escu c-terminal domain with n262d mutation, space2 group p 41 21 2
20	c1e0mA_	Alignment		28.2	36	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**wwprototype; **PDBTitle:** prototype ww domain
21	c2k29A_	Alignment	not modelled	27.8	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
22	c1yiuA_	Alignment	not modelled	27.3	50	**PDB header:**ligase **Chain:** A: **PDB Molecule:**itchy e3 ubiquitin protein ligase; **PDBTitle:** itch e3 ubiquitin ligase ww3 domain
23	c3b8iF_	Alignment	not modelled	26.9	14	**PDB header:**lyase **Chain:** F: **PDB Molecule:**pa4872 oxaloacetate decarboxylase; **PDBTitle:** crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.
24	c3ih1A_	Alignment	not modelled	26.4	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
25	c3ot4F_	Alignment	not modelled	26.2	20	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**putative isochorismatase; **PDBTitle:** structure and catalytic mechanism of bordetella bronchiseptica nicf
26	c2b34C_	Alignment	not modelled	25.9	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**mar1 ribonuclease; **PDBTitle:** structure of mar1 ribonuclease from caenorhabditis elegans
27	c2ysbA_	Alignment	not modelled	25.9	29	**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	c2jlhA_	Alignment	not modelled	25.7	23	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**yop proteins translocation protein u; **PDBTitle:** crystal structure of the cytoplasmic domain of yersinia2 pestis yscu n263a mutant

29	c3l4hA_	Alignment	not modelled	25.5	17	**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
30	d1nf9a_	Alignment	not modelled	25.5	11	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
31	d2ebfx2	Alignment	not modelled	25.5	16	**Fold:**EreA/ChaN-like **Superfamily:**EreA/ChaN-like **Family:**PMT domain-like
32	c3t7yB_	Alignment	not modelled	24.9	23	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**yop proteins translocation protein u; **PDBTitle:** structure of an autocleavage-inactive mutant of the cytoplasmic domain2 of ct091, the yscu homologue of chlamydia trachomatis
33	d1nbaa_	Alignment	not modelled	24.8	20	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
34	d1vp8a_	Alignment	not modelled	24.3	24	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
35	c1ymzA_	Alignment	not modelled	24.1	50	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cc45; **PDBTitle:** cc45, an artificial ww domain designed using statistical2 coupling analysis
36	d1qusa_	Alignment	not modelled	23.6	17	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
37	d1t57a_	Alignment	not modelled	23.2	23	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
38	c3mcwA_	Alignment	not modelled	23.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of an a putative hydrolase of the isochorismatase2 family (cv_1320) from chromobacterium violaceum atcc 12472 at 1.06 a3 resolution
39	c2ysdA_	Alignment	not modelled	22.7	27	**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
40	c3i44A_	Alignment	not modelled	22.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from bartonella2 henselae at 2.0a resolution
41	d1yaca_	Alignment	not modelled	21.5	8	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
42	d1j2ra_	Alignment	not modelled	21.4	18	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
43	d1f8ab1	Alignment	not modelled	21.3	27	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
44	c2djyA_	Alignment	not modelled	21.0	36	**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
45	c2hjpA_	Alignment	not modelled	20.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonopyruvate hydrolase; **PDBTitle:** crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
46	d1wh7a_	Alignment	not modelled	20.4	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
47	d1k9ra_	Alignment	not modelled	20.0	29	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
48	c1wr7A_	Alignment	not modelled	20.0	47	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nedd4-2; **PDBTitle:** solution structure of the third ww domain of nedd4-2
49	c3hb7G_	Alignment	not modelled	19.9	13	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**isochorismatase hydrolase; **PDBTitle:** the crystal structure of an isochorismatase-like hydrolase from2 alkaliphilus metalliredigens to 2.3a
50	d1pbya1	Alignment	not modelled	19.8	17	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
51	c2lawA_	Alignment	not modelled	19.5	29	**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
52	d1lqaa_	Alignment	not modelled	19.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
53	c2gbbA_	Alignment	not modelled	19.2	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative chorismate mutase; **PDBTitle:** crystal structure of secreted chorismate mutase from2 yersinia pestis
54	c1wr4A_	Alignment	not modelled	19.0	29	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin-protein ligase nedd4-2; **PDBTitle:** solution structure of the second ww domain of nedd4-2

55	c2kykA_	Alignment	not modelled	18.9	43	**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
56	d3ci0k2	Alignment	not modelled	18.5	19	**Fold:**SAM domain-like **Superfamily:**GspK insert domain-like **Family:**GspK insert domain-like
57	c3iwfA_	Alignment	not modelled	18.2	9	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcription regulator rpir family; **PDBTitle:** the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
58	c2jmfA_	Alignment	not modelled	18.2	33	**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
59	c1wmvA_	Alignment	not modelled	18.2	28	**PDB header:**oxidoreductase, apoptosis **Chain:** A: **PDB Molecule:**ww domain containing oxidoreductase; **PDBTitle:** solution structure of the second ww domain of wwox
60	c2p7vA_	Alignment	not modelled	17.9	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulator of sigma d; **PDBTitle:** crystal structure of the escherichia coli regulator of sigma 70, rsd,2 in complex with sigma 70 domain 4
61	d1tk7a1	Alignment	not modelled	17.8	29	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
62	c2pmzF_	Alignment	not modelled	17.6	20	**PDB header:**translation, transferase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase subunit f; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
63	d1i5hw_	Alignment	not modelled	17.0	36	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
64	d2jmfa1	Alignment	not modelled	16.8	36	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
65	d1bdga1	Alignment	not modelled	16.6	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
66	c2uygF_	Alignment	not modelled	16.0	24	**PDB header:**lyase **Chain:** F: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystallographic structure of the typeii 3-dehydroquinase2 from thermus thermophilus
67	c1zlpA_	Alignment	not modelled	15.9	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**petal death protein; **PDBTitle:** petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
68	c3e0kA_	Alignment	not modelled	15.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**amino-acid acetyltransferase; **PDBTitle:** crystal structure of c-termianl domain of n-acetylglutamate synthase2 from vibrio parahaemolyticus
69	d2cfua2	Alignment	not modelled	15.5	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Alkylsulfatase-like
70	c3eooL_	Alignment	not modelled	15.1	19	**PDB header:**lyase **Chain:** L: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
71	c2ez5W_	Alignment	not modelled	14.9	33	**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
72	c2js5B_	Alignment	not modelled	14.8	26	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr structure of protein q60c73_metca. northeast structural2 genomics consortium target mcr1
73	c3hn2A_	Alignment	not modelled	14.2	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase; **PDBTitle:** crystal structure of 2-dehydropantoate 2-reductase from geobacter2 metallireducens gs-15
74	c2yshA_	Alignment	not modelled	14.1	27	**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
75	c2yy9A_	Alignment	not modelled	14.0	31	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger and btb domain-containing protein 48; **PDBTitle:** crystal structure of btb domain from mouse hkr3
76	d2csua3	Alignment	not modelled	14.0	17	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
77	c2q81C_	Alignment	not modelled	13.6	19	**PDB header:**transcription **Chain:** C: **PDB Molecule:**miz-1 protein; **PDBTitle:** crystal structure of the miz-1 btb/poz domain
78	c3fa4D_	Alignment	not modelled	13.6	20	**PDB header:**lyase **Chain:** D: **PDB Molecule:**2,3-dimethylmalate lyase; **PDBTitle:** crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
79	d3djba1	Alignment	not modelled	13.5	17	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
80	d1xn7a_	Alignment	not modelled	13.1	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Hypothetical protein YhgG

81	d1dq3a2	Alignment	not modelled	13.1	32	**Fold:**dsRBD-like **Superfamily:**YcfA/nrd intein domain **Family:**PI-Pfui intein middle domain
82	c3le4A_	Alignment	not modelled	12.9	33	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**microprocessor complex subunit dgcr8; **PDBTitle:** crystal structure of the dgcr8 dimerization domain
83	c1ks9A_	Alignment	not modelled	12.8	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase; **PDBTitle:** ketopantoate reductase from escherichia coli
84	d1j9ia_	Alignment	not modelled	12.8	25	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Terminase gpNU1 subunit domain
85	c2r73C_	Alignment	not modelled	12.7	13	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**trichosurin; **PDBTitle:** crystal structure of the possum milk whey lipocalin2 trichosurin at ph 8.2
86	c2l4jA_	Alignment	not modelled	12.5	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**yes-associated protein 2 (yap2); **PDBTitle:** yap ww2
87	d2ieca1	Alignment	not modelled	12.5	17	**Fold:**MK0786-like **Superfamily:**MK0786-like **Family:**MK0786-like
88	d1dzka_	Alignment	not modelled	12.3	23	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
89	c2jt1A_	Alignment	not modelled	12.2	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**pefi protein; **PDBTitle:** solution nmr structure of pefi (plasmid-encoded fimbriae regulatory)2 protein from salmonella typhimurium. northeast structural genomics3 target str82
90	c2h0rD_	Alignment	not modelled	12.2	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nicotinamidase; **PDBTitle:** structure of the yeast nicotinamidase pnc1p
91	c3fiqA_	Alignment	not modelled	12.1	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**odorant-binding protein 1f; **PDBTitle:** odorant binding protein obp1
92	c2px0D_	Alignment	not modelled	12.1	11	**PDB header:**biosynthetic protein **Chain:** D: **PDB Molecule:**flagellar biosynthesis protein flhf; **PDBTitle:** crystal structure of flhf complexed with gmppnp/mg(2+)
93	c2lfcA_	Alignment	not modelled	11.9	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fumarate reductase, flavoprotein subunit; **PDBTitle:** solution nmr structure of fumarate reductase flavoprotein subunit from2 lactobacillus plantarum, northeast structural genomics consortium3 target lpr145j
94	c3drzE_	Alignment	not modelled	11.9	13	**PDB header:**unknown function **Chain:** E: **PDB Molecule:**btb/poz domain-containing protein kctd5; **PDBTitle:** x-ray crystal structure of the n-terminal btb domain of human kctd52 protein
95	c3fpvC_	Alignment	not modelled	11.9	21	**PDB header:**heme binding protein **Chain:** C: **PDB Molecule:**extracellular haem-binding protein; **PDBTitle:** crystal structure of hbps
96	d2i52a1	Alignment	not modelled	11.6	17	**Fold:**MK0786-like **Superfamily:**MK0786-like **Family:**MK0786-like
97	d1bj7a_	Alignment	not modelled	11.4	13	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
98	c2fq1A_	Alignment	not modelled	11.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isochorismatase; **PDBTitle:** crystal structure of the two-domain non-ribosomal peptide synthetase2 entb containing isochorismate lyase and aryl-carrier protein domains
99	c2lazA_	Alignment	not modelled	11.4	29	**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