Phyre2

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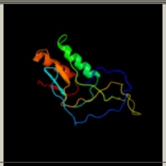
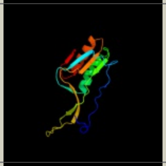
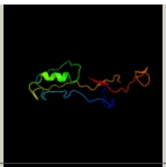
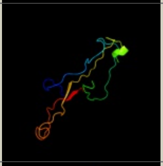
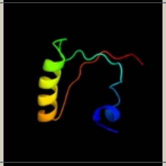
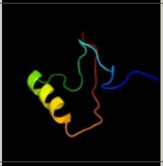
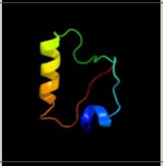
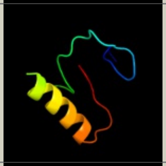
Description	P0ADY7
Date	Thu Jan 5 11:22:06 GMT 2012
Unique Job ID	b5f17fa10606483e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bboO_	Alignment		100.0	54	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**ribosomal protein l16; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
2	d2gyck1	Alignment		100.0	100	**Fold:**alpha/beta-Hammerhead **Superfamily:**Ribosomal protein L16p/L10e **Family:**Ribosomal protein L16p
3	d2j01q1	Alignment		100.0	55	**Fold:**alpha/beta-Hammerhead **Superfamily:**Ribosomal protein L16p/L10e **Family:**Ribosomal protein L16p
4	d2zjrj1	Alignment		100.0	54	**Fold:**alpha/beta-Hammerhead **Superfamily:**Ribosomal protein L16p/L10e **Family:**Ribosomal protein L16p
5	c2ftcI_	Alignment		100.0	32	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**mitochondrial ribosomal protein l16; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
6	c2zkrh_	Alignment		100.0	23	**PDB header:**ribosomal protein/rna **Chain:** H: **PDB Molecule:**rna expansion segment es12; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
7	d1jj2h_	Alignment		100.0	20	**Fold:**alpha/beta-Hammerhead **Superfamily:**Ribosomal protein L16p/L10e **Family:**Ribosomal protein L10e
8	d1ffkf_	Alignment		100.0	18	**Fold:**alpha/beta-Hammerhead **Superfamily:**Ribosomal protein L16p/L10e **Family:**Ribosomal protein L10e
9	d1vqoh1	Alignment		100.0	20	**Fold:**alpha/beta-Hammerhead **Superfamily:**Ribosomal protein L16p/L10e **Family:**Ribosomal protein L10e
10	c1s1iI_	Alignment		100.0	19	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**60s ribosomal protein l10; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
11	c4a1aH_	Alignment		100.0	24	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**60s ribosomal protein l10; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.

12	c3iz5l_	Alignment		100.0	23	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**60s ribosomal protein l10 (l10e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
13	c3izcl_	Alignment		99.9	20	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**60s ribosomal protein rpl10 (l10e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
14	d2pa2a1	Alignment		99.7	25	**Fold:**alpha/beta-Hammerhead **Superfamily:**Ribosomal protein L16p/L10e **Family:**Ribosomal protein L10e
15	c2q9vA_	Alignment		63.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**membrane-associated guanylate kinase, ww and pdz domain- **PDBTitle:** crystal structure of the c890s mutant of the 4th pdz domain of human2 membrane associated guanylate kinase
16	c1x45A_	Alignment		50.3	17	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**amyloid beta (a4) precursor protein-binding, **PDBTitle:** solution structure of the first pdz domain of amyloid beta2 a4 precursor protein-binding family a, member 1
17	d1x45a1	Alignment		48.3	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
18	c2yt7A_	Alignment		45.1	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**amyloid beta a4 precursor protein-binding family **PDBTitle:** solution structure of the pdz domain of amyloid beta a42 precursor protein-binding family a member 3
19	d1v6ba_	Alignment		40.8	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
20	d2cssa1	Alignment		40.5	15	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
21	c2i04B_	Alignment	not modelled	35.5	9	**PDB header:**peptide binding protein **Chain:** B: **PDB Molecule:**membrane-associated guanylate kinase, ww and pdz **PDBTitle:** x-ray crystal structure of magi-1 pdz1 bound to the c-2 terminal peptide of hpv18 e6
22	d1uepa_	Alignment	not modelled	35.3	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
23	d2f0aa1	Alignment	not modelled	33.4	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
24	d1rzxa_	Alignment	not modelled	33.1	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
25	c1z87A_	Alignment	not modelled	31.3	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**alpha-1-syntrophin; **PDBTitle:** solution structure of the split ph-pdz supramodule of alpha-2 syntrophin
26	c1u38A_	Alignment	not modelled	30.3	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**amyloid beta a4 precursor protein-binding, **PDBTitle:** auto-inhibition mechanism of x11s/mints family scaffold2 proteins revealed by the closed conformation of the tandem3 pdz domains
27	c2ehrA_	Alignment	not modelled	28.8	21	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the sixth pdz domain of human inad-2 like protein
28	d1wi4a1	Alignment	not modelled	28.7	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like

						Family:PDZ domain
29	d2byga1	Alignment	not modelled	28.7	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
30	c2ogpA_	Alignment	not modelled	28.1	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning-defective 3 homolog; **PDBTitle:** solution structure of the second pdz domain of par-3
31	c3cyyA_	Alignment	not modelled	27.8	18	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**tight junction protein zo-1; **PDBTitle:** the crystal structure of zo-1 pdz2 in complex with the cx43 peptide
32	d1ry4a_	Alignment	not modelled	27.3	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
33	d1nf3c_	Alignment	not modelled	26.7	15	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
34	c1p1eA_	Alignment	not modelled	26.6	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**glutamate receptor interacting protein; **PDBTitle:** structural insights into the inter-domain chaperoning of2 tandem pdz domains in glutamate receptor interacting3 proteins
35	d1vb7a_	Alignment	not modelled	25.9	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
36	d1ihja_	Alignment	not modelled	25.7	14	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
37	c2dmzA_	Alignment	not modelled	25.5	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the third pdz domain of human inad-2 like protein
38	d1ozia_	Alignment	not modelled	25.0	14	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
39	c2dc2A_	Alignment	not modelled	24.9	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**golgi associated pdz and coiled-coil motif **PDBTitle:** solution structure of pdz domain
40	d1wf8a1	Alignment	not modelled	24.7	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
41	c2gzvA_	Alignment	not modelled	24.0	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**prkca-binding protein; **PDBTitle:** the cystal structure of the pdz domain of human pick1 (casp target)
42	d1i16a_	Alignment	not modelled	24.0	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**Interleukin 16
43	d1uewa_	Alignment	not modelled	23.8	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
44	c2jreA_	Alignment	not modelled	23.8	16	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**c60-1 pdz domain peptide; **PDBTitle:** c60-1, a pdz domain designed using statistical coupling2 analysis
45	c2komA_	Alignment	not modelled	23.7	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning defective 3 homolog; **PDBTitle:** solution structure of humar par-3b pdz2 (residues 451-549)
46	d1p1da2	Alignment	not modelled	23.1	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
47	d1vq3a_	Alignment	not modelled	23.0	31	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
48	d1whaa_	Alignment	not modelled	22.7	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
49	c1u37A_	Alignment	not modelled	22.7	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**amyloid beta a4 precursor protein-binding, **PDBTitle:** auto-inhibition mechanism of x11s/mints family scaffold2 proteins revealed by the closed conformation of the tandem3 pdz domains
50	d1p1da1	Alignment	not modelled	22.6	11	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
51	d1wjla_	Alignment	not modelled	22.6	24	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
52	d1qava_	Alignment	not modelled	22.4	14	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
53	d2fcfa1	Alignment	not modelled	22.2	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
54	d1gtda_	Alignment	not modelled	22.1	14	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
						Fold:PDZ domain-like

55	d1rgwa_	Alignment	not modelled	22.0	21	**Superfamily:**PDZ domain-like **Family:**PDZ domain
56	c3l4fD_	Alignment	not modelled	21.7	29	**PDB header:**signaling protein/protein binding **Chain:** D: **PDB Molecule:**sh3 and multiple ankyrin repeat domains protein **PDBTitle:** crystal structure of betapix coiled-coil domain and shank2 pdz complex
57	c2osgB_	Alignment	not modelled	21.3	16	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**tight junction protein zo-2; **PDBTitle:** solution structure and binding property of the domain-2 swapped dimer of zo2pdz2
58	c3b76A_	Alignment	not modelled	21.2	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase lnx; **PDBTitle:** crystal structure of the third pdz domain of human ligand-of-numb2 protein-x (lnx1) in complex with the c-terminal peptide from the3 coxsackievirus and adenovirus receptor
59	d1qlca_	Alignment	not modelled	21.0	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
60	c2k1zA_	Alignment	not modelled	21.0	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning-defective 3 homolog; **PDBTitle:** solution structure of par-3 pdz3
61	c2zw2B_	Alignment	not modelled	20.4	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein sts178; **PDBTitle:** crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)
62	c2iwqA_	Alignment	not modelled	20.4	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** 7th pdz domain of multiple pdz domain protein mpdz
63	c2edvA_	Alignment	not modelled	20.0	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ferm and pdz domain-containing protein 1; **PDBTitle:** solution structure of the pdz domain from human ferm and2 pdz domain containing 1
64	c2xkxB_	Alignment	not modelled	19.7	18	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**disks large homolog 4; **PDBTitle:** single particle analysis of psd-95 in negative stain
65	d1wg6a_	Alignment	not modelled	19.6	15	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
66	c3eggC_	Alignment	not modelled	19.3	27	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**spinophilin; **PDBTitle:** crystal structure of a complex between protein phosphatase 1 alpha2 (pp1) and the pp1 binding and pdz domains of spinophilin
67	c2iwnA_	Alignment	not modelled	19.3	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** 3rd pdz domain of multiple pdz domain protein mpdz (casp2 target)
68	d2fnea1	Alignment	not modelled	18.9	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
69	d1um7a_	Alignment	not modelled	18.8	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
70	c2dkrA_	Alignment	not modelled	18.7	25	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**lin-7 homolog b; **PDBTitle:** solution structure of the pdz domain from human lin-72 homolog b
71	c2jikB_	Alignment	not modelled	18.5	14	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**synaptojanin-2 binding protein; **PDBTitle:** crystal structure of pdz domain of synaptojanin-2 binding2 protein
72	d1uhpa_	Alignment	not modelled	18.5	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
73	c2vwrA_	Alignment	not modelled	18.1	12	**PDB header:**protein-binding **Chain:** A: **PDB Molecule:**ligand of numb protein x 2; **PDBTitle:** crystal structure of the second pdz domain of numb-binding2 protein 2
74	c2edpA_	Alignment	not modelled	18.0	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**shroom family member 4; **PDBTitle:** solution structure of the pdz domain from human shroom2 family member 4
75	d1wfva_	Alignment	not modelled	17.5	14	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
76	c3hpmA_	Alignment	not modelled	17.0	7	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein interacting with prkca 1; **PDBTitle:** oxidized dimeric pick1 pdz c46g mutant in complex with the carboxyl2 tail peptide of glur2
77	c2q3gA_	Alignment	not modelled	16.8	18	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**pdz and lim domain protein 7; **PDBTitle:** structure of the pdz domain of human pdlim7 bound to a c-2 terminal extension from human beta-tropomyosin
78	c2fneB_	Alignment	not modelled	16.8	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** the crystal structure of the 13th pdz domain of mpdz
79	c3o46A_	Alignment	not modelled	16.0	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**maguk p55 subfamily member 7; **PDBTitle:** crystal structure of the pdz domain of mpp7
80	c2jilA_	Alignment	not modelled	15.6	22	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**glutamate receptor interacting protein-1; **PDBTitle:** crystal structure of 2nd pdz domain of glutamate receptor2 interacting protein-1 (grip1)

81	d1d5ga_	Alignment	not modelled	15.5	14	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
82	c2opgB_	Alignment	not modelled	15.5	9	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** the crystal structure of the 10th pdz domain of mpdz
83	d1q3oa_	Alignment	not modelled	15.4	24	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
84	d1um1a_	Alignment	not modelled	15.4	14	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
85	c2pkuA_	Alignment	not modelled	15.3	7	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**prkca-binding protein; **PDBTitle:** solution structure of pick1 pdz in complex with the2 carboxyl tail peptide of glur2
86	d1wfga_	Alignment	not modelled	15.3	24	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
87	d1zoka1	Alignment	not modelled	15.1	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
88	d1ky9b2	Alignment	not modelled	14.9	12	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
89	d1x5ra1	Alignment	not modelled	14.8	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
90	c2ka9A_	Alignment	not modelled	14.8	23	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**disks large homolog 4; **PDBTitle:** solution structure of psd-95 pdz12 complexed with cypin2 peptide
91	d1qpoa2	Alignment	not modelled	14.8	15	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
92	c2dazA_	Alignment	not modelled	14.8	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the 7th pdz domain of inad-like2 protein
93	d2i0xa1	Alignment	not modelled	14.6	15	**Fold:**Ferredoxin-like **Superfamily:**TTP0101/SSO1404-like **Family:**TTP0101/SSO1404-like
94	c2qv6D_	Alignment	not modelled	13.9	11	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**gtp cyclohydrolase iii; **PDBTitle:** gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions
95	d1v62a_	Alignment	not modelled	13.8	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
96	d1t2ma1	Alignment	not modelled	13.7	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
97	d1rgra_	Alignment	not modelled	13.5	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
98	d2fe5a1	Alignment	not modelled	13.3	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
99	c2wdtA_	Alignment	not modelled	13.2	24	**PDB header:**hydrolase/protein binding **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase l3; **PDBTitle:** crystal structure of plasmodium falciparum uchl3 in complex2 with the suicide inhibitor ubvme