Phyre^{2}

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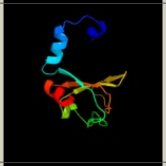
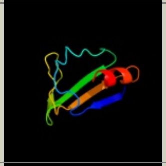
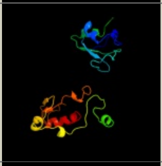
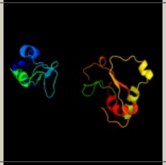
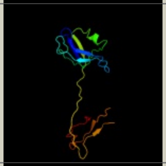
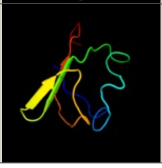
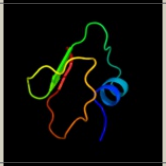
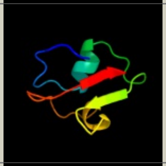
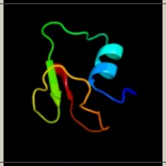
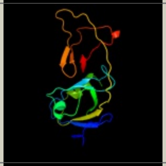
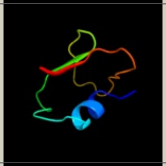
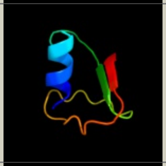
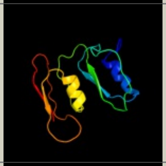
Description	P60869
Date	Thu Jan 5 12:07:13 GMT 2012
Unique Job ID	12a21bd2baa0167c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1vcta2	Alignment		99.5	23	**Fold:**TrkA C-terminal domain-like **Superfamily:**TrkA C-terminal domain-like **Family:**TrkA C-terminal domain-like
2	d2fy8a2	Alignment		99.5	13	**Fold:**TrkA C-terminal domain-like **Superfamily:**TrkA C-terminal domain-like **Family:**TrkA C-terminal domain-like
3	c2bknA_	Alignment		99.5	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**hypothetical protein ph0236; **PDBTitle:** structure analysis of unknown function protein
4	c3jxoB_	Alignment		99.3	20	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**trka-n domain protein; **PDBTitle:** crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
5	c2fy8A_	Alignment		99.1	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**calcium-gated potassium channel mthk; **PDBTitle:** crystal structure of mthk rck domain in its ligand-free gating-ring2 form
6	c1lnqC_	Alignment		99.1	23	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**potassium channel related protein; **PDBTitle:** crystal structure of mthk at 3.3 a
7	c3l4bG_	Alignment		98.5	20	**PDB header:**transport protein **Chain:** G: **PDB Molecule:**trka k+ channel protien tm1088b; **PDBTitle:** crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
8	c3mt5A_	Alignment		97.7	10	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**potassium large conductance calcium-activated channel, **PDBTitle:** crystal structure of the human bk gating apparatus
9	c3u6nC_	Alignment		97.7	9	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**high-conductance ca2+-activated k+ channel protein; **PDBTitle:** open structure of the bk channel gating ring
10	c2ka9A_	Alignment		87.5	14	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**disks large homolog 4; **PDBTitle:** solution structure of psd-95 pdz12 complexed with cypin2 peptide
11	c3nafA_	Alignment		85.1	14	**PDB header:**ion transport **Chain:** A: **PDB Molecule:**calcium-activated potassium channel subunit alpha-1; **PDBTitle:** structure of the intracellular gating ring from the human high-2 conductance ca2+ gated k+ channel (bk channel)

12	c1u3bA_	Alignment		77.7	15	**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
13	d1zud21	Alignment		76.7	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
14	d2cu3a1	Alignment		76.0	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
15	c2kl0A_	Alignment		72.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thiamin biosynthesis this; **PDBTitle:** solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
16	c3r0hA_	Alignment		70.3	18	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**inactivation-no-after-potential d protein; **PDBTitle:** structure of inad pdz45 in complex with ng2 peptide
17	c3cwiA_	Alignment		64.6	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**thiamine-biosynthesis protein this; **PDBTitle:** crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
18	d1tygb_	Alignment		62.9	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
19	c2zc3F_	Alignment		59.1	9	**PDB header:**biosynthetic protein **Chain:** F: **PDB Molecule:**penicillin-binding protein 2x; **PDBTitle:** penicillin-binding protein 2x (pbp 2x) acyl-enzyme complex2 (biapenem) from streptococcus pneumoniae
20	c1p1dA_	Alignment		56.0	15	**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
21	c1tygG_	Alignment	not modelled	53.0	20	**PDB header:**biosynthetic protein **Chain:** G: **PDB Molecule:**yjbs; **PDBTitle:** structure of the thiazole synthase/this complex
22	d1v62a_	Alignment	not modelled	50.8	15	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
23	c2jreA_	Alignment	not modelled	48.1	14	**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
24	c2d8iA_	Alignment	not modelled	44.8	17	**PDB header:**immune system, signaling protein **Chain:** A: **PDB Molecule:**t-cell lymphoma invasion and metastasis 1 **PDBTitle:** solution structure of the pdz domain of t-cell lymphoma2 invasion and metastasis 1 varian
25	c2ejyA_	Alignment	not modelled	43.1	24	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**55 kda erythrocyte membrane protein; **PDBTitle:** solution structure of the p55 pdz t85c domain complexed2 with the glycophorin c f127c peptide
26	d1qlca_	Alignment	not modelled	40.9	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
27	c3ggeA_	Alignment	not modelled	40.6	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**pdz domain-containing protein gipc2; **PDBTitle:** crystal structure of the pdz domain of pdz domain-containing protein2 gipc2
28	c2qt5A_	Alignment	not modelled	39.5	18	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**glutamate receptor-interacting protein 1; **PDBTitle:** crystal structure of grip1 pdz12 in complex with the fras12 peptide

29	d1wi2a_	Alignment	not modelled	39.2	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
30	d1uhpa_	Alignment	not modelled	38.5	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
31	d1i16a_	Alignment	not modelled	38.3	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**Interleukin 16
32	d1d5ga_	Alignment	not modelled	37.1	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
33	d1um1a_	Alignment	not modelled	35.6	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
34	c2xkxB_	Alignment	not modelled	34.9	16	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**disks large homolog 4; **PDBTitle:** single particle analysis of psd-95 in negative stain
35	c2xrfA_	Alignment	not modelled	34.9	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uridine phosphorylase 2; **PDBTitle:** crystal structure of human uridine phosphorylase 2
36	d1wf8a1	Alignment	not modelled	33.8	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
37	c2fneB_	Alignment	not modelled	31.8	15	**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
38	c4a8aI_	Alignment	not modelled	30.7	19	**PDB header:**hydrolase/hydrolase **Chain:** I: **PDB Molecule:**periplasmic ph-dependent serine endoprotease degq; **PDBTitle:** asymmetric cryo-em reconstruction of e. coli degq 12-mer in complex2 with lysozyme
39	c2dazA_	Alignment	not modelled	30.0	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the 7th pdz domain of inad-like2 protein
40	c2d92A_	Alignment	not modelled	28.9	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the fifth pdz domain of inad-like2 protein
41	d2byga1	Alignment	not modelled	28.6	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
42	c2yt7A_	Alignment	not modelled	28.6	18	**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
43	c2dluA_	Alignment	not modelled	28.1	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the second pdz domain of human inad-2 like protein
44	d2fe5a1	Alignment	not modelled	27.9	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
45	d1v6ba_	Alignment	not modelled	27.8	12	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
46	c3tl6B_	Alignment	not modelled	27.8	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of purine nucleoside phosphorylase from entamoeba2 histolytica
47	c2djtA_	Alignment	not modelled	27.7	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**unnamed protein product; **PDBTitle:** solution structures of the pdz domain of human unnamed2 protein product
48	d1rp5a2	Alignment	not modelled	27.0	9	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
49	c2dm8A_	Alignment	not modelled	26.6	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the eighth pdz domain of human inad-2 like protein
50	d1uita_	Alignment	not modelled	26.4	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
51	c3kzeA_	Alignment	not modelled	25.9	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**t-lymphoma invasion and metastasis-inducing protein 1; **PDBTitle:** crystal structure of t-cell lymphoma invasion and metastasis-1 pdz in2 complex with ssrkeyya peptide
52	d1pyya2	Alignment	not modelled	25.4	9	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
53	d1tp5a1	Alignment	not modelled	24.7	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
54	d1x6da1	Alignment	not modelled	24.6	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**Interleukin 16
						PDB header:sugar binding protein

55	c2rqeA_	Alignment	not modelled	24.4	15	**Chain:** A: **PDB Molecule:**beta-1,3-glucan-binding protein; **PDBTitle:** solution structure of the silkworm bgrp/gnbp3 n-terminal2 domain reveals the mechanism for b-1,3-glucan specific3 recognition
56	d1ufxa_	Alignment	not modelled	24.3	27	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
57	d1g9oa_	Alignment	not modelled	24.0	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
58	c2ogpA_	Alignment	not modelled	23.3	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning-defective 3 homolog; **PDBTitle:** solution structure of the second pdz domain of par-3
59	c3krmB_	Alignment	not modelled	23.1	12	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**insulin-like growth factor 2 mrna-binding protein **PDBTitle:** imp1 kh34
60	d1zoka1	Alignment	not modelled	23.0	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
61	c2opgB_	Alignment	not modelled	22.7	13	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** the crystal structure of the 10th pdz domain of mpdz
62	d1x5qa1	Alignment	not modelled	22.5	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
63	d1rzxa_	Alignment	not modelled	22.4	25	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
64	c2dmzA_	Alignment	not modelled	21.8	12	**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
65	d2i0ia1	Alignment	not modelled	21.7	27	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
66	d1va8a1	Alignment	not modelled	21.7	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
67	d1be9a_	Alignment	not modelled	21.5	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
68	d1r61a_	Alignment	not modelled	21.0	20	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Putative cyclase **Family:**Putative cyclase
69	c3npgD_	Alignment	not modelled	20.3	17	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**uncharacterized duf364 family protein; **PDBTitle:** crystal structure of a protein with unknown function from duf3642 family (ph1506) from pyrococcus horikoshii at 2.70 a resolution
70	d2fnea1	Alignment	not modelled	20.1	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
71	d1wgka_	Alignment	not modelled	19.8	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog
72	c2vwrA_	Alignment	not modelled	19.7	15	**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
73	c2hc8A_	Alignment	not modelled	19.6	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation-transporting atpase, p-type; **PDBTitle:** structure of the a. fulgidus copa a-domain
74	c2yubA_	Alignment	not modelled	19.6	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lim domain kinase 2; **PDBTitle:** solution structure of the pdz domain from mouse lim domain2 kinase
75	c2eehA_	Alignment	not modelled	19.4	22	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**pdz domain-containing protein 7; **PDBTitle:** solution structure of first pdz domain of pdz domain2 containing protein 7
76	d1n7ea_	Alignment	not modelled	19.2	15	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
77	c1mhsA_	Alignment	not modelled	18.9	18	**PDB header:**membrane protein, proton transport **Chain:** A: **PDB Molecule:**plasma membrane atpase; **PDBTitle:** model of neurospora crassa proton atpase
78	c3ixzA_	Alignment	not modelled	18.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**potassium-transporting atpase alpha; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
79	c2k1zA_	Alignment	not modelled	17.4	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning-defective 3 homolog; **PDBTitle:** solution structure of par-3 pdz3
80	c2egkC_	Alignment	not modelled	17.1	18	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**general receptor for phosphoinositides 1- **PDBTitle:** crystal structure of tamalin pdz-intrinsic ligand fusion2 protein
81	d1whaa_	Alignment	not modelled	17.1	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like

						Family:PDZ domain
82	c2jilA_	Alignment	not modelled	16.4	20	**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)
83	c2vspA_	Alignment	not modelled	16.3	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**pdz domain-containing protein 1; **PDBTitle:** crystal structure of the fourth pdz domain of pdz domain-2 containing protein 1
84	c2xlkB_	Alignment	not modelled	16.2	16	**PDB header:**hydrolase/rna **Chain:** B: **PDB Molecule:**csy4 endoribonuclease; **PDBTitle:** crystal structure of the csy4-crrna complex, orthorhombic form
85	d1ozia_	Alignment	not modelled	16.0	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
86	d1wpga1	Alignment	not modelled	15.9	19	**Fold:**Double-stranded beta-helix **Superfamily:**Calcium ATPase, transduction domain A **Family:**Calcium ATPase, transduction domain A
87	d1ueqa_	Alignment	not modelled	15.8	13	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
88	c2q3gA_	Alignment	not modelled	15.4	22	**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
89	c2k9xA_	Alignment	not modelled	15.2	26	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of urm1 from trypanosoma brucei
90	d2piaa1	Alignment	not modelled	15.2	29	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
91	d1qava_	Alignment	not modelled	14.8	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
92	d1wi4a1	Alignment	not modelled	14.8	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
93	c3kw0D_	Alignment	not modelled	14.5	38	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cysteine peptidase; **PDBTitle:** crystal structure of cysteine peptidase (np_982244.1) from bacillus2 cereus atcc 10987 at 2.50 a resolution
94	d1kwaa_	Alignment	not modelled	14.5	24	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
95	d1y7ma2	Alignment	not modelled	14.4	10	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
96	c3pr9A_	Alignment	not modelled	14.3	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase; **PDBTitle:** structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
97	d2h1qa1	Alignment	not modelled	14.1	15	**Fold:**PLP-dependent transferase-like **Superfamily:**Dhaf3308-like **Family:**Dhaf3308-like
98	c2gzvA_	Alignment	not modelled	14.1	31	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**prkca-binding protein; **PDBTitle:** the cystal structure of the pdz domain of human pick1 (casp target)
99	c3eggC_	Alignment	not modelled	13.9	17	**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