Phyre^2

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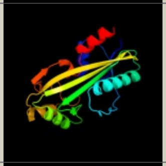
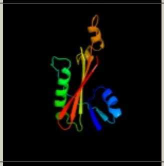
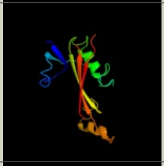
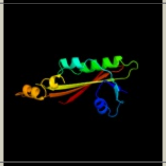
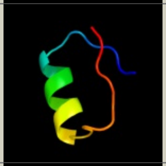
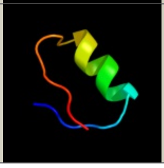
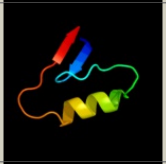
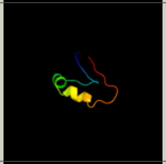
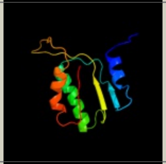
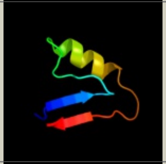
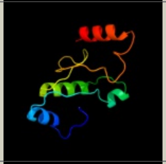
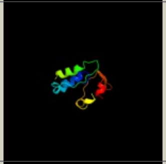
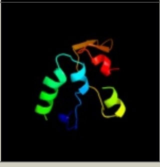
Description	P25536
Date	Thu Jan 5 11:42:03 GMT 2012
Unique Job ID	7fcec1b22acdc689

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ex2a_	Alignment		100.0	48	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**Maf-like
2	d2amha1	Alignment		100.0	20	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**Maf-like
3	c2p5xB_	Alignment		100.0	38	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**n-acetylserotonin o-methyltransferase-like protein; **PDBTitle:** crystal structure of maf domain of human n-acetylserotonin o-2 methyltransferase-like protein
4	d1v7ra_	Alignment		96.7	11	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
5	d2cara1	Alignment		95.5	23	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
6	d1k7ka_	Alignment		95.1	17	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
7	d1b78a_	Alignment		92.5	19	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
8	c3tquD_	Alignment		90.0	22	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**non-canonical purine ntp pyrophosphatase; **PDBTitle:** structure of a ham1 protein from coxiella burnetii
9	d1vp2a_	Alignment		89.6	15	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
10	d1pdaa1	Alignment		63.7	25	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
11	c2ypnA_	Alignment		62.4	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (hydroxymethylbilane synthase); **PDBTitle:** hydroxymethylbilane synthase

12	c3eq1A_	Alignment		61.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**porphobilinogen deaminase; **PDBTitle:** the crystal structure of human porphobilinogen deaminase at2 2.8a resolution
13	c2db5A_	Alignment		40.3	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the first pdz domain of inad-like2 protein
14	c2o2tB_	Alignment		38.4	24	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** the crystal structure of the 1st pdz domain of mpdz
15	c2e7kA_	Alignment		32.4	26	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**maguk p55 subfamily member 2; **PDBTitle:** solution structure of the pdz domain from human maguk p552 subfamily member 2
16	c1x3lA_	Alignment		31.2	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ph0495; **PDBTitle:** crystal structure of the ph0495 protein from pyrococccus horikoshii2 ot3
17	c3eggC_	Alignment		29.8	25	**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
18	c3jr2D_	Alignment		29.2	11	**PDB header:**biosynthetic protein **Chain:** D: **PDB Molecule:**hexulose-6-phosphate synthase sgbh; **PDBTitle:** x-ray crystal structure of the mg-bound 3-keto-l-gulonate-6-phosphate2 decarboxylase from vibrio cholerae o1 biovar el tor str. n16961
19	c3a11D_	Alignment		28.8	25	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b, delta **PDBTitle:** crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
20	d1t5oa_	Alignment		23.0	19	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
21	d1ydua1	Alignment	not modelled	21.8	20	**Fold:**At5g01610-like **Superfamily:**At5g01610-like **Family:**At5g01610-like
22	d1gh9a_	Alignment	not modelled	19.3	23	**Fold:**Rubredoxin-like **Superfamily:**Hypothetical protein MTH1184 **Family:**Hypothetical protein MTH1184
23	d1wh1a_	Alignment	not modelled	18.8	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
24	d1y0ua_	Alignment	not modelled	18.4	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
25	d1v6ba_	Alignment	not modelled	17.9	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
26	d1a9xa4	Alignment	not modelled	17.4	13	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
27	d1ujva_	Alignment	not modelled	17.2	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
28	c1tuoA_	Alignment	not modelled	17.2	11	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative phosphomannomutase; **PDBTitle:** crystal structure of putative phosphomannomutase from2 thermus thermophilus hb8
29	d2evqa2	Alignment	not modelled	15.8	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate

29	d2eyqa2	Alignment	not modelled	13.8	29	hydrolases **Family:**Tandem AAA-ATPase domain
30	c2x0kB_	Alignment	not modelled	14.7	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin biosynthesis protein ribf; **PDBTitle:** crystal structure of modular fad synthetase from2 corynebacterium ammoniagenes
31	d1i16a_	Alignment	not modelled	14.5	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**Interleukin 16
32	c3hrdC_	Alignment	not modelled	13.1	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nicotinate dehydrogenase fad-subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
33	d1gpua2	Alignment	not modelled	12.1	16	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like Pyr module
34	d1vaea_	Alignment	not modelled	12.1	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
35	d1e94a_	Alignment	not modelled	12.0	15	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
36	d1sknp_	Alignment	not modelled	11.9	23	**Fold:**A DNA-binding domain in eukaryotic transcription factors **Superfamily:**A DNA-binding domain in eukaryotic transcription factors **Family:**A DNA-binding domain in eukaryotic transcription factors
37	d1jgta2	Alignment	not modelled	11.7	32	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
38	d1ujda_	Alignment	not modelled	11.7	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
39	c2o7pA_	Alignment	not modelled	11.6	14	**PDB header:**hydrolase, oxidoreductase **Chain:** A: **PDB Molecule:**riboflavin biosynthesis protein ribd; **PDBTitle:** the crystal structure of ribd from escherichia coli in complex with2 the oxidised nadp+ cofactor in the active site of the reductase3 domain
40	d1nd9a_	Alignment	not modelled	11.4	7	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**N-terminal subdomain of bacterial translation initiation factor IF2
41	d1t1va_	Alignment	not modelled	10.6	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**SH3BGR (SH3-binding, glutamic acid-rich protein-like)
42	d1vb5a_	Alignment	not modelled	10.4	20	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
43	c3diwB_	Alignment	not modelled	10.2	23	**PDB header:**signaling protein/cell adhesion **Chain:** B: **PDB Molecule:**tax1-binding protein 3; **PDBTitle:** c-terminal beta-catenin bound tip-1 structure
44	c1u37A_	Alignment	not modelled	9.8	19	**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
45	c1u38A_	Alignment	not modelled	9.8	19	**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
46	d1rp5a2	Alignment	not modelled	9.8	11	**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
47	c2edpA_	Alignment	not modelled	9.7	18	**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
48	d1kwma2	Alignment	not modelled	9.7	10	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
49	d1x4pa1	Alignment	not modelled	9.6	28	**Fold:**Surp module (SWAP domain) **Superfamily:**Surp module (SWAP domain) **Family:**Surp module (SWAP domain)
50	d1u5wa1	Alignment	not modelled	9.6	10	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**YjjX-like
51	d1id3b_	Alignment	not modelled	9.6	12	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
52	c2ehrA_	Alignment	not modelled	9.5	14	**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
53	c1m1zB_	Alignment	not modelled	9.5	43	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactam synthetase; **PDBTitle:** beta-lactam synthetase apo enzyme
54	d1f2ea2	Alignment	not modelled	9.3	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain

55	c3b76A_	Alignment	not modelled	9.3	17	**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
56	c3cyyA_	Alignment	not modelled	9.3	22	**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
57	c2ktaA_	Alignment	not modelled	9.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative helicase; **PDBTitle:** solution nmr structure of a domain of protein a6ky75 from bacteroides2 vulgatus, northeast structural genomics target bvr106a
58	d1ayea2	Alignment	not modelled	9.1	10	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
59	d2boaa2	Alignment	not modelled	9.1	10	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
60	d1p5dx2	Alignment	not modelled	9.1	15	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
61	c1q5rD_	Alignment	not modelled	8.8	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**proteasome alpha-type subunit 1; **PDBTitle:** the rhodococcus 20s proteasome with unprocessed pro-peptides
62	d1v8aa_	Alignment	not modelled	8.8	13	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
63	d2cupa1	Alignment	not modelled	8.7	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
64	c2kz5A_	Alignment	not modelled	8.7	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor nf-e2 45 kda subunit; **PDBTitle:** solution nmr structure of transcription factor nf-e2 subunit's dna2 binding domain from homo sapiens, northeast structural genomics3 consortium target hr4653b
65	c2yt7A_	Alignment	not modelled	8.7	19	**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
66	d2h3la1	Alignment	not modelled	8.7	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
67	c2dluA_	Alignment	not modelled	8.7	23	**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
68	c2cveA_	Alignment	not modelled	8.6	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha1053; **PDBTitle:** crystal structure of a conserved hypothetical protein tt1547 from2 thermus thermophilus hb8
69	d2z3ba1	Alignment	not modelled	8.5	23	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
70	d1x63a1	Alignment	not modelled	8.5	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
71	c3qglD_	Alignment	not modelled	8.4	18	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**sorting nexin-27; **PDBTitle:** crystal structure of pdz domain of sorting nexin 27 (snx27) in complex2 with the eseskv peptide corresponding to the c-terminal tail of girk3
72	c2krgA_	Alignment	not modelled	8.3	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**na(+)/h(+) exchange regulatory cofactor nhe-rf1; **PDBTitle:** solution structure of human sodium/ hydrogen exchange2 regulatory factor 1(150-358)
73	d1v5qa_	Alignment	not modelled	8.3	29	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
74	c1v5qA_	Alignment	not modelled	8.3	29	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**glutamate receptor interacting protein 1a-l **PDBTitle:** solution structure of the pdz domain from mouse glutamate2 receptor interacting protein 1a-l (grip1) homolog
75	d1x5ra1	Alignment	not modelled	8.2	28	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
76	d1pyta_	Alignment	not modelled	8.2	10	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
77	d1k25a2	Alignment	not modelled	8.1	5	**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
78	d1g3ka_	Alignment	not modelled	8.1	23	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
79	d1b65a_	Alignment	not modelled	8.1	14	**Fold:**DmpA/ArgJ-like **Superfamily:**DmpA/ArgJ-like **Family:**DmpA-like

80	c3dzvB_	Alignment	not modelled	8.1	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**4-methyl-5-(beta-hydroxyethyl)thiazole kinase; **PDBTitle:** crystal structure of 4-methyl-5-(beta-hydroxyethyl)thiazole2 kinase (np_816404.1) from enterococcus faecalis v583 at3 2.57 a resolution
81	d1q7xa_	Alignment	not modelled	8.1	29	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
82	d1pyya2	Alignment	not modelled	8.0	16	**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
83	d1itza2	Alignment	not modelled	8.0	16	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like Pyr module
84	c2du4B_	Alignment	not modelled	8.0	21	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**o-phosphoseryl-trna synthetase; **PDBTitle:** crystal structure of archaeoglobus fulgidus o-phosphoseryl-2 trna synthetase complexed with trnacys
85	d1obxa_	Alignment	not modelled	7.9	14	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
86	c1obxA_	Alignment	not modelled	7.9	14	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**syntenin 1; **PDBTitle:** crystal structure of the complex of pdz2 of syntenin with2 an interleukin 5 receptor alpha peptide.
87	c1obyB_	Alignment	not modelled	7.9	14	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**syntenin 1; **PDBTitle:** crystal structure of the complex of pdz2 of syntenin with2 a syndecan-4 peptide.
88	d1nsaa2	Alignment	not modelled	7.9	15	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
89	c3lyvF_	Alignment	not modelled	7.8	40	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**ribosome-associated factor y; **PDBTitle:** crystal structure of a domain of ribosome-associated factor y from2 streptococcus pyogenes serotype m6. northeast structural genomics3 consortium target id dr64a
90	c2ejyA_	Alignment	not modelled	7.7	14	**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
91	d1m5za_	Alignment	not modelled	7.7	11	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
92	d1pcaa1	Alignment	not modelled	7.7	10	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
93	c3gkxB_	Alignment	not modelled	7.7	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative arsc family related protein; **PDBTitle:** crystal structure of putative arsc family related protein from2 bacteroides fragilis
94	c2iwqA_	Alignment	not modelled	7.7	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** 7th pdz domain of multiple pdz domain protein mpdz
95	d1um7a_	Alignment	not modelled	7.7	32	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
96	d1ueqa_	Alignment	not modelled	7.6	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
97	d1mfga_	Alignment	not modelled	7.6	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
98	d2a0ua1	Alignment	not modelled	7.6	27	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
99	d2dlda2	Alignment	not modelled	7.5	8	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain