Phyre^2

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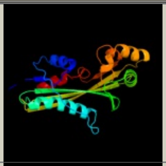
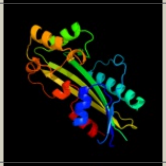
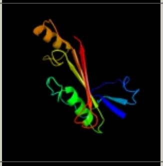
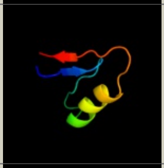
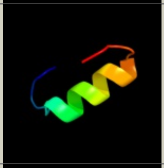
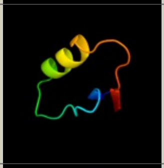
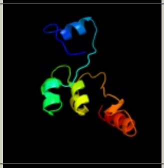
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ex2a_	Alignment		100.0	35	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**Maf-like
2	d2amha1	Alignment		100.0	19	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**Maf-like
3	c2p5xB_	Alignment		100.0	29	**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	d1k7ka_	Alignment		97.2	17	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
5	d2cara1	Alignment		96.6	13	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
6	d1v7ra_	Alignment		96.5	16	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
7	d1vp2a_	Alignment		95.7	15	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
8	c3tquD_	Alignment		93.7	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**non-canonical purine ntp pyrophosphatase; **PDBTitle:** structure of a ham1 protein from coxiella burnetii
9	d1b78a_	Alignment		92.6	17	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
10	d1pdaa1	Alignment		52.2	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
11	c2ypnA_	Alignment		50.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (hydroxymethylbilane synthase); **PDBTitle:** hydroxymethylbilane synthase

12	c3eq1A_	Alignment		47.6	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		39.2	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the first pdz domain of inad-like2 protein
14	d1pyya1	Alignment		37.1	24	**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
15	d1k25a1	Alignment		34.8	24	**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
16	c2o2tB_	Alignment		34.6	22	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** the crystal structure of the 1st pdz domain of mpdz
17	c3jr2D_	Alignment		28.0	10	**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
18	c2e7kA_	Alignment		27.8	24	**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
19	d1pyya2	Alignment		25.7	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
20	d1rp5a2	Alignment		24.2	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
21	d1gh9a_	Alignment	not modelled	24.0	30	**Fold:**Rubredoxin-like **Superfamily:**Hypothetical protein MTH1184 **Family:**Hypothetical protein MTH1184
22	c3eggC_	Alignment	not modelled	24.0	22	**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
23	d1e94a_	Alignment	not modelled	23.7	19	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
24	d1k25a2	Alignment	not modelled	23.0	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
25	d1u5wa1	Alignment	not modelled	22.9	14	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**YjjX-like
26	d1v8aa_	Alignment	not modelled	18.9	11	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
27	c1tuoA_	Alignment	not modelled	18.2	10	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative phosphomannomutase; **PDBTitle:** crystal structure of putative phosphomannomutase from2 thermus thermophilus hb8
28	d1wh1a_	Alignment	not modelled	17.7	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain

29	d1g3ka_	Alignment	not modelled	17.6	15	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
30	d1ujva_	Alignment	not modelled	15.7	12	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
31	c1t6zB_	Alignment	not modelled	15.7	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin kinase/fmn adenylyltransferase; **PDBTitle:** crystal structure of riboflavin bound tm379
32	c3op1A_	Alignment	not modelled	15.0	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**macrolide-efflux protein; **PDBTitle:** crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
33	d1v6ba_	Alignment	not modelled	14.9	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
34	c3a11D_	Alignment	not modelled	14.1	16	**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
35	d1y0ua_	Alignment	not modelled	14.1	47	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
36	c3ouvA_	Alignment	not modelled	14.0	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine protein kinase; **PDBTitle:** semet derivative of l512m mutant of pasta domain 3 of mycobacterium2 tuberculosis pknb
37	d2z3ba1	Alignment	not modelled	14.0	7	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
38	c1nl3B_	Alignment	not modelled	13.4	13	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**preprotein translocase seca 1 subunit; **PDBTitle:** crystal structure of the seca protein translocation atpase2 from mycobacterium tuberculosis in apo form
39	c2x0kB_	Alignment	not modelled	13.0	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin biosynthesis protein ribf; **PDBTitle:** crystal structure of modular fad synthetase from2 corynebacterium ammoniagenes
40	d2eyqa2	Alignment	not modelled	12.6	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
41	d1m4ya_	Alignment	not modelled	12.1	11	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
42	c3juxA_	Alignment	not modelled	12.0	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein translocase subunit seca; **PDBTitle:** structure of the translocation atpase seca from thermotoga2 maritima
43	c3pvsA_	Alignment	not modelled	11.5	18	**PDB header:**recombination **Chain:** A: **PDB Molecule:**replication-associated recombination protein a; **PDBTitle:** structure and biochemical activities of escherichia coli mgsa
44	d1sknp_	Alignment	not modelled	11.5	25	**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
45	d1vaea_	Alignment	not modelled	11.2	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
46	d1jgta2	Alignment	not modelled	10.7	32	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
47	d2b8na1	Alignment	not modelled	10.6	16	**Fold:**GckA/TtuD-like **Superfamily:**GckA/TtuD-like **Family:**GckA/TtuD-like
48	c2qjoB_	Alignment	not modelled	10.1	14	**PDB header:**transferase, hydrolase **Chain:** B: **PDB Molecule:**bifunctional nmn adenylyltransferase/nudix hydrolase; **PDBTitle:** crystal structure of a bifunctional nmn adenylyltransferase/adp ribose2 pyrophosphatase (nadm) complexed with adprp and nad from3 synechocystis sp.
49	c2du4B_	Alignment	not modelled	10.1	37	**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
50	c2pnyA_	Alignment	not modelled	9.9	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase 2; **PDBTitle:** structure of human isopentenyl-diphosphate delta-isomerase 2
51	d1gpua2	Alignment	not modelled	9.7	9	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like Pyr module
52	c2kz5A_	Alignment	not modelled	9.7	25	**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
53	c3diwB_	Alignment	not modelled	9.4	26	**PDB header:**signaling protein/cell adhesion **Chain:** B: **PDB Molecule:**tax1-binding protein 3; **PDBTitle:** c-terminal beta-catenin bound tip-1 structure

54	d1x4pa1	Alignment	not modelled	9.2	39	**Fold:**Surp module (SWAP domain) **Superfamily:**Surp module (SWAP domain) **Family:**Surp module (SWAP domain)
55	d1ujda_	Alignment	not modelled	8.9	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
56	d1t1va_	Alignment	not modelled	8.8	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**SH3BGR (SH3-binding, glutamic acid-rich protein-like)
57	c3b76A_	Alignment	not modelled	8.7	23	**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
58	d1i16a_	Alignment	not modelled	8.5	24	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**Interleukin 16
59	d1zwya1	Alignment	not modelled	8.3	16	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**YjjX-like
60	c3dzvB_	Alignment	not modelled	8.2	13	**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
61	d1kwma2	Alignment	not modelled	8.1	5	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
62	d1q7xa_	Alignment	not modelled	8.1	27	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
63	d2fi0a1	Alignment	not modelled	8.0	28	**Fold:**SP0561-like **Superfamily:**SP0561-like **Family:**SP0561-like
64	d2boaa2	Alignment	not modelled	8.0	5	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
65	c2ktaA_	Alignment	not modelled	8.0	22	**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
66	d1ayea2	Alignment	not modelled	7.8	20	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
67	d1fmfa_	Alignment	not modelled	7.8	9	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
68	c1m1zB_	Alignment	not modelled	7.8	43	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactam synthetase; **PDBTitle:** beta-lactam synthetase apo enzyme
69	c1u37A_	Alignment	not modelled	7.7	11	**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
70	c2xi1A_	Alignment	not modelled	7.7	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**nef; **PDBTitle:** crystal structure of the hiv-1 nef sequenced from a patient's sample
71	d1p5dx2	Alignment	not modelled	7.4	16	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
72	d1whda_	Alignment	not modelled	7.2	12	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
73	c3hrdC_	Alignment	not modelled	7.2	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nicotinate dehydrogenase fad-subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
74	d1pyta_	Alignment	not modelled	7.1	20	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
75	c2ehrA_	Alignment	not modelled	7.1	15	**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
76	c3e7lD_	Alignment	not modelled	7.1	16	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
77	d1mfga_	Alignment	not modelled	7.1	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
78	c3k2tA_	Alignment	not modelled	7.1	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lmo2511 protein; **PDBTitle:** crystal structure of lmo2511 protein from listeria2 monocytogenes, northeast structural genomics consortium3 target lkr84a
						Fold:PDZ domain-like

79	d1ozia_	Alignment	not modelled	7.0	27	**Superfamily:**PDZ domain-like **Family:**PDZ domain
80	d1nsaa2	Alignment	not modelled	7.0	15	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
81	d2h3la1	Alignment	not modelled	7.0	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
82	c1u38A_	Alignment	not modelled	6.9	11	**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
83	d1nfpa_	Alignment	not modelled	6.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Non-fluorescent flavoprotein (luxF, FP390)
84	c2edpA_	Alignment	not modelled	6.8	9	**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
85	d2dlda2	Alignment	not modelled	6.8	11	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
86	c3cyyA_	Alignment	not modelled	6.7	17	**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
87	d1f2ea2	Alignment	not modelled	6.6	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
88	c2eq9C_	Alignment	not modelled	6.5	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
89	d1pcaa1	Alignment	not modelled	6.4	20	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
90	c2dluA_	Alignment	not modelled	6.4	18	**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
91	c2ragB_	Alignment	not modelled	6.3	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dipeptidase; **PDBTitle:** crystal structure of aminohydrolase from caulobacter crescentus
92	d1um7a_	Alignment	not modelled	6.2	27	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
93	c2eq7C_	Alignment	not modelled	6.2	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**2-oxoglutarate dehydrogenase e2 component; **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
94	d1u3ba2	Alignment	not modelled	6.2	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
95	c3gkxB_	Alignment	not modelled	6.2	19	**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
96	d1ueqa_	Alignment	not modelled	6.2	12	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
97	c3sbxC_	Alignment	not modelled	6.1	19	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium marinum bound to adenosine 5'-monophosphate amp
98	c2klxA_	Alignment	not modelled	6.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** solution structure of glutaredoxin from bartonella henselae str.2 houston
99	d1ojra_	Alignment	not modelled	6.0	24	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase