Phyre^2

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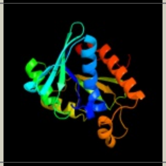
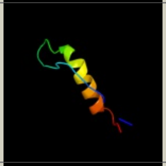
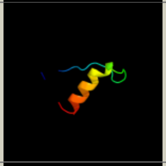
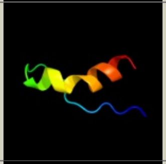
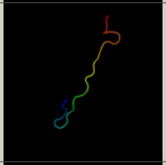
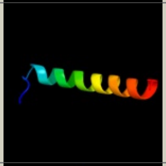
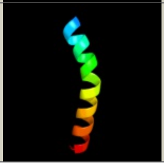
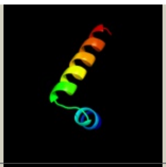
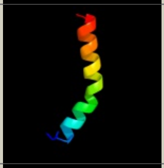
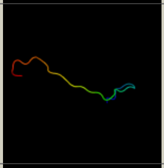
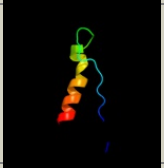
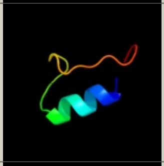
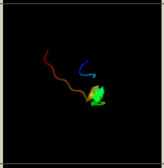
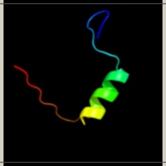
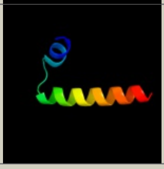
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ptha_	Alignment		100.0	100	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Peptidyl-tRNA hydrolase-like **Family:**Peptidyl-tRNA hydrolase-like
2	c3neaA_	Alignment		100.0	44	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of peptidyl-trna hydrolase from francisella2 tularensis
3	c3v2iA_	Alignment		100.0	56	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** structure of a peptidyl-trna hydrolase (pth) from burkholderia2 thailandensis
4	c2z2jA_	Alignment		100.0	39	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of peptidyl-trna hydrolase from mycobacterium2 tuberculosis
5	d1ryba_	Alignment		100.0	33	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Peptidyl-tRNA hydrolase-like **Family:**Peptidyl-tRNA hydrolase-like
6	d1cfza_	Alignment		83.8	28	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**HybD-like **Family:**Hydrogenase maturating endopeptidase HybD
7	c2e85B_	Alignment		76.7	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hydrogenase 3 maturation protease; **PDBTitle:** crystal structure of the hydrogenase 3 maturation protease
8	d1c8ba_	Alignment		50.1	43	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**HybD-like **Family:**Germination protease
9	c2jvaA_	Alignment		39.2	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase domain protein; **PDBTitle:** nmr solution structure of peptidyl-trna hydrolase domain protein from2 pseudomonas syringae pv. tomato. northeast structural genomics3 consortium target psr211
10	d2ea9a1	Alignment		36.7	24	**Fold:**Profilin-like **Superfamily:**YeeU-like **Family:**YagB/YeeU/YfjZ-like
11	d2inwa1	Alignment		34.8	21	**Fold:**Profilin-like **Superfamily:**YeeU-like **Family:**YagB/YeeU/YfjZ-like

12	c3tgnA_	Alignment		33.9	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**adc operon repressor adcr; **PDBTitle:** crystal structure of the zinc-dependent marr family transcriptional2 regulator adcr in the zn(ii)-bound state
13	d2h28a1	Alignment		33.0	21	**Fold:**Profilin-like **Superfamily:**YeeU-like **Family:**YagB/YeeU/YfjZ-like
14	c2jy9A_	Alignment		32.4	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative trna hydrolase domain; **PDBTitle:** nmr structure of putative trna hydrolase domain from2 salmonella typhimurium. northeast structural genomics3 consortium target str220
15	c3pu6A_	Alignment		31.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of an uncharacterized protein from wolinella2 succinogenes
16	c3mpoD_	Alignment		23.3	11	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted hydrolase of the had superfamily; **PDBTitle:** the crystal structure of a hydrolase from lactobacillus brevis
17	c3gygA_	Alignment		21.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ntd biosynthesis operon putative hydrolase ntdb; **PDBTitle:** crystal structure of yhjk (haloacid dehalogenase-like hydrolase2 protein) from bacillus subtilis
18	d1am7a_	Alignment		20.5	12	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Lambda lysozyme
19	c3ippA_	Alignment		20.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative thiosulfate sulfurtransferase ynje; **PDBTitle:** crystal structure of sulfur-free ynje
20	c3s2wB_	Alignment		17.0	3	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** the crystal structure of a marr transcriptional regulator from2 methanosarcina mazei go1
21	c2bb3B_	Alignment	not modelled	16.0	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cobalamin biosynthesis precorrin-6y methylase (cbie); **PDBTitle:** crystal structure of cobalamin biosynthesis precorrin-6y methylase2 (cbie) from archaeoglobus fulgidus
22	c1ynmA_	Alignment	not modelled	15.3	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**r.hinp1i restriction endonuclease; **PDBTitle:** crystal structure of restriction endonuclease hinp1i
23	d2nqra3	Alignment	not modelled	15.3	20	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
24	c3kp3B_	Alignment	not modelled	14.0	3	**PDB header:**transcription regulator/antibiotic **Chain:** B: **PDB Molecule:**transcriptional regulator tcar; **PDBTitle:** staphylococcus epidermidis in complex with ampicillin
25	c3n39D_	Alignment	not modelled	13.9	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**protein nrdi; **PDBTitle:** ribonucleotide reductase dimanganese(ii)-nrdf from escherichia coli in2 complex with nrdi
26	c1ujlA_	Alignment	not modelled	13.4	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily h **PDBTitle:** solution structure of the herg k+ channel s5-p2 extracellular linker
27	c3ndcB_	Alignment	not modelled	13.4	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**precorrin-4 c(11)-methyltransferase; **PDBTitle:** crystal structure of precorrin-4 c11-methyltransferase from2 rhodobacter capsulatus
28	d2bb3a1	Alignment	not modelled	13.3	33	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase

29	c3hzuA_	Alignment	not modelled	13.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiosulfate sulfurtransferase ssea; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase ssea2 (rhodanese) from mycobacterium tuberculosis
30	c2jcyA_	Alignment	not modelled	11.8	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** x-ray structure of mutant 1-deoxy-d-xylulose 5-phosphate2 reductoisomerase, dxr, rv2870c, from mycobacterium3 tuberculosis
31	c2ofpB_	Alignment	not modelled	10.8	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ketopantoate reductase; **PDBTitle:** crystal structure of escherichia coli ketopantoate2 reductase in a ternary complex with nadp+ and pantoate
32	d1r0ka3	Alignment	not modelled	10.7	26	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
33	d1s2oa1	Alignment	not modelled	10.6	23	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
34	c3bpqD_	Alignment	not modelled	10.4	39	**PDB header:**toxin **Chain:** D: **PDB Molecule:**toxin rele3; **PDBTitle:** crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
35	d1q0qa3	Alignment	not modelled	10.3	22	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
36	c3e8mD_	Alignment	not modelled	10.1	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acylneuraminate cytidylyltransferase; **PDBTitle:** structure-function analysis of 2-keto-3-deoxy-d-glycero-d-galacto-2 nononate-9-phosphate (kdn) phosphatase defines a new clad within the3 type c0 had subfamily
37	c3ecoB_	Alignment	not modelled	9.9	3	**PDB header:**transcription **Chain:** B: **PDB Molecule:**mepr; **PDBTitle:** crystal structure of mepr, a transcription regulator of the2 staphylococcus aureus multidrug efflux pump mepa
38	c3av6A_	Alignment	not modelled	9.8	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna (cytosine-5)-methyltransferase 1; **PDBTitle:** crystal structure of mouse dna methyltransferase 1 with adomet
39	d1lama2	Alignment	not modelled	9.8	25	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Leucine aminopeptidase (Aminopeptidase A), N-terminal domain
40	c3euwB_	Alignment	not modelled	9.7	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**myo-inositol dehydrogenase; **PDBTitle:** crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
41	c3n1uA_	Alignment	not modelled	9.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, had superfamily, subfamily iii a; **PDBTitle:** structure of putative had superfamily (subfamily iii a) hydrolase from2 legionella pneumophila
42	c3bj6B_	Alignment	not modelled	9.0	6	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of marr family transcription regulator sp03579
43	c1uarA_	Alignment	not modelled	9.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhodanese; **PDBTitle:** crystal structure of rhodanese from thermus thermophilus hb8
44	d3eeqa2	Alignment	not modelled	8.9	22	**Fold:**CbiG N-terminal domain-like **Superfamily:**CbiG N-terminal domain-like **Family:**CbiG N-terminal domain-like
45	d2bgxa2	Alignment	not modelled	8.7	15	**Fold:**N-acetylmuramoyl-L-alanine amidase-like **Superfamily:**N-acetylmuramoyl-L-alanine amidase-like **Family:**N-acetylmuramoyl-L-alanine amidase-like
46	d1fima_	Alignment	not modelled	8.3	14	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
47	d1bofa2	Alignment	not modelled	8.0	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
48	d1wvia_	Alignment	not modelled	8.0	7	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
49	c3rfqC_	Alignment	not modelled	7.4	14	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**pterin-4-alpha-carbinolamine dehydratase moab2; **PDBTitle:** crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
50	d1mv8a2	Alignment	not modelled	7.3	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
51	c3ikmD_	Alignment	not modelled	7.3	26	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna polymerase subunit gamma-1; **PDBTitle:** crystal structure of human mitochondrial dna polymerase2 holoenzyme
52	d2etha1	Alignment	not modelled	7.2	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
53	d2nu7b2	Alignment	not modelled	7.1	18	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like

						Family: Succinyl-CoA synthetase, beta-chain, N-terminal domain
54	c3fzqA_	Alignment	not modelled	7.1	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of putative haloacid dehalogenase-like hydrolase2 (yp_001086940.1) from clostridium difficile 630 at 2.10 a resolution
55	c2bh7A_	Alignment	not modelled	7.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylmuramoyl-l-alanine amidase; **PDBTitle:** crystal structure of a semet derivative of amid at 2.22 angstroms
56	c2zetD_	Alignment	not modelled	7.1	9	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**melanophilin; **PDBTitle:** crystal structure of the small gtpase rab27b complexed with2 the slp homology domain of slac2-a/melanophilin
57	d1k1ea_	Alignment	not modelled	7.0	8	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Probable phosphatase YrbI
58	c3r6mD_	Alignment	not modelled	6.9	29	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**yeaz, resuscitation promoting factor; **PDBTitle:** crystal structure of vibrio parahaemolyticus yeaz
59	c3l6dB_	Alignment	not modelled	6.9	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
60	d2f1ka2	Alignment	not modelled	6.8	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
61	c3kbqA_	Alignment	not modelled	6.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ta0487; **PDBTitle:** the crystal structure of the protein cina with unknown function from2 thermoplasma acidophilum
62	c1okgA_	Alignment	not modelled	6.7	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible 3-mercaptopyruvate sulfurtransferase; **PDBTitle:** 3-mercaptopyruvate sulfurtransferase from leishmania major
63	c3mn1B_	Alignment	not modelled	6.6	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable yrbi family phosphatase; **PDBTitle:** crystal structure of probable yrbi family phosphatase from pseudomonas2 syringae pv.phaseolica 1448a
64	d1ys9a1	Alignment	not modelled	6.6	10	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
65	c2cftA_	Alignment	not modelled	6.5	23	**PDB header:**phosphatase **Chain:** A: **PDB Molecule:**pyridoxal phosphate phosphatase; **PDBTitle:** crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
66	c3nt5B_	Alignment	not modelled	6.5	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; **PDBTitle:** crystal structure of myo-inositol dehydrogenase from bacillus subtilis2 with bound cofactor and product inosose
67	c2p9jH_	Alignment	not modelled	6.4	10	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**hypothetical protein aq2171; **PDBTitle:** crystal structure of aq2171 from aquifex aeolicus
68	c3boqB_	Alignment	not modelled	6.4	7	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of marr family transcriptional regulator from2 silicibacter pomeroyi
69	c2xtsD_	Alignment	not modelled	6.1	13	**PDB header:**oxidoreductase/electron transport **Chain:** D: **PDB Molecule:**cytochrome; **PDBTitle:** crystal structure of the sulfane dehydrogenase soxcd from paracoccus2 pantotrophus
70	c3oopA_	Alignment	not modelled	6.0	4	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2960 protein; **PDBTitle:** the structure of a protein with unknown function from listeria innocua2 clip11262
71	d1gcya1	Alignment	not modelled	5.8	67	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
72	c2hx1D_	Alignment	not modelled	5.8	24	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted sugar phosphatases of the had **PDBTitle:** crystal structure of possible sugar phosphatase, had2 superfamily (zp_00311070.1) from cytophaga hutchinsonii3 atcc 33406 at 2.10 a resolution
73	d2al3a1	Alignment	not modelled	5.8	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
74	c2r8zC_	Alignment	not modelled	5.6	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; **PDBTitle:** crystal structure of yrbi phosphatase from escherichia coli in complex2 with a phosphate and a calcium ion
75	d1yv9a1	Alignment	not modelled	5.6	3	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
76	d1k47a2	Alignment	not modelled	5.4	7	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Phosphomevalonate kinase (PMK)
77	d1kmma1	Alignment	not modelled	5.4	16	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
78	d1y5ea1	Alignment	not modelled	5.4	10	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like

79	d1s3ja_	Alignment	not modelled	5.3	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
80	c2pjkA_	Alignment	not modelled	5.3	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**178aa long hypothetical molybdenum cofactor **PDBTitle:** structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
81	d2j49a1	Alignment	not modelled	5.3	8	**Fold:**Taf5 N-terminal domain-like **Superfamily:**Taf5 N-terminal domain-like **Family:**Taf5 N-terminal domain-like
82	c3e6mD_	Alignment	not modelled	5.2	9	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**marr family transcriptional regulator; **PDBTitle:** the crystal structure of a marr family transcriptional2 regulator from silicibacter pomeroyi dss.
83	c3au9A_	Alignment	not modelled	5.2	30	**PDB header:**isomerase/isomerase inhibitor **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of the quaternary complex-1 of an isomerase
84	d1ydfa1	Alignment	not modelled	5.1	7	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like