Phyre^2

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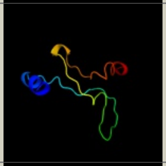
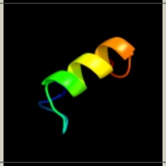
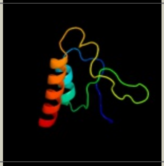
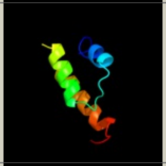
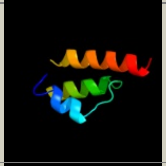
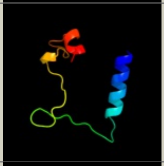
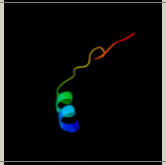
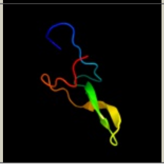
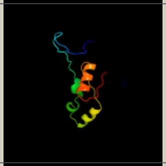
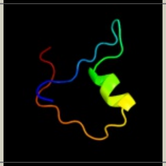
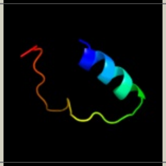
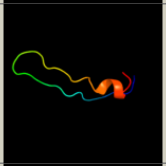
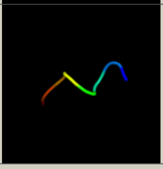
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3clqC_	Alignment		100.0	43	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a conserved protein of unknown function from2 enterococcus faecalis v583
2	d2pw4a1	Alignment		62.1	18	**Fold:**Jann2411-like **Superfamily:**Jann2411-like **Family:**Jann2411-like
3	c2cqjA_	Alignment		49.5	33	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**u3 small nucleolar ribonucleoprotein protein **PDBTitle:** solution structure of the s4 domain of u3 small nucleolar2 ribonucleoprotein protein imp3 homolog
4	c2htmB_	Alignment		45.8	22	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**thiazole biosynthesis protein thig; **PDBTitle:** crystal structure of ttha0676 from thermus thermophilus hb8
5	d1pdza2	Alignment		45.3	24	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
6	d2akza2	Alignment		38.2	18	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
7	d2al1a2	Alignment		33.9	24	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
8	d1alua_	Alignment		33.0	15	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Long-chain cytokines
9	c2re2A_	Alignment		32.2	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uncharacterized protein ta1041; **PDBTitle:** crystal structure of a putative iron-molybdenum cofactor (femo-co)2 dinitrogenase (ta1041m) from thermoplasma acidophilum dsm 1728 at3 1.30 a resolution
10	d1h3fa2	Alignment		21.6	11	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
11	c2y9xG_	Alignment		21.2	30	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**lectin-like fold protein; **PDBTitle:** crystal structure of ppo3, a tyrosinase from agaricus bisporus, in2 deoxy-form that contains additional unknown lectin-like subunit,3 with inhibitor tropolone

12	d1c06a_	Alignment		21.1	20	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
13	c3hp7A_	Alignment		19.4	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hemolysin, putative; **PDBTitle:** putative hemolysin from streptococcus thermophilus.
14	c1vjtA_	Alignment		18.3	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** crystal structure of alpha-glucosidase (tm0752) from thermotoga2 maritima at 2.50 a resolution
15	c2d5nB_	Alignment		17.7	26	**PDB header:**hydrolase, oxidoreductase **Chain:** B: **PDB Molecule:**riboflavin biosynthesis protein ribd; **PDBTitle:** crystal structure of a bifunctional deaminase and reductase2 involved in riboflavin biosynthesis
16	c2l58A_	Alignment		16.7	47	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**activator of apoptosis harakiri; **PDBTitle:** solution structure of the cytosolic fragment 22-53 of bcl-2 member2 harakiri
17	d2gy9d1	Alignment		16.4	12	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
18	d2isba1	Alignment		15.3	16	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**FumA C-terminal domain-like **Family:**FumA C-terminal domain-like
19	c3msuA_	Alignment		13.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citrate synthase; **PDBTitle:** crystal structure of citrate synthase from francisella tularensis
20	d1nuba2	Alignment		12.4	25	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**EGF/Laminin **Family:**Follistatin (FS) module N-terminal domain, FS-N
21	d2fyma2	Alignment	not modelled	12.2	18	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
22	c2ldkA_	Alignment	not modelled	12.2	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein aaur_3427 from arthrobacter2 aurescens, northeast structural genomics consortium target aar96
23	c2qnfB_	Alignment	not modelled	11.7	28	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**recombination endonuclease vii; **PDBTitle:** crystal structure of t4 endonuclease vii h43n mutant in2 complex with heteroduplex dna containing base mismatches
24	c2xzmD_	Alignment	not modelled	11.5	9	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**ribosomal protein s4 containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
25	c3d0jA_	Alignment	not modelled	11.4	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ca_c3497; **PDBTitle:** crystal structure of conserved protein of unknown function ca_c34972 from clostridium acetobutylicum atcc 824
26	c2bibA_	Alignment	not modelled	11.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**teichoic acid phosphorylcholine esterase/ choline binding **PDBTitle:** crystal structure of the complete modular teichioic acid2 phosphorylcholine esterase pce (cbpe) from streptococcus3 pneumoniae
27	d1jh3a_	Alignment	not modelled	10.4	18	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
						Fold:TBP-like

28	d1kfia4	Alignment	not modelled	9.9	29	**Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
29	d1duvg1	Alignment	not modelled	9.7	19	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
30	d1t6la2	Alignment	not modelled	9.5	67	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
31	d2o34a1	Alignment	not modelled	9.4	43	**Fold:**T-fold **Superfamily:**ApbE-like **Family:**DVU1097-like
32	d2jeka1	Alignment	not modelled	9.4	17	**Fold:**Rv1873-like **Superfamily:**Rv1873-like **Family:**Rv1873-like
33	c2bs5A_	Alignment	not modelled	9.2	20	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**fucose-binding lectin protein; **PDBTitle:** lectin from ralstonia solanacearum complexed with 2-2 fucosyllactose
34	c2hxvA_	Alignment	not modelled	8.9	29	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**diaminohydroxyphosphoribosylaminopyrimidine deaminase/ 5- **PDBTitle:** crystal structure of a diaminohydroxyphosphoribosylaminopyrimidine2 deaminase/ 5-amino-6-(5-phosphoribosylamino)uracil reductase (tm1828)3 from thermotoga maritima at 1.80 a resolution
35	d1s4da_	Alignment	not modelled	8.7	19	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
36	d1p9ka_	Alignment	not modelled	8.3	38	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**YbcJ-like
37	d3pmga4	Alignment	not modelled	8.0	19	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
38	c2i7uA_	Alignment	not modelled	7.6	48	**PDB header:**de novo protein/ligand binding protein **Chain:** A: **PDB Molecule:**four-alpha-helix bundle; **PDBTitle:** structural and dynamical analysis of a four-alpha-helix2 bundle with designed anesthetic binding pockets
39	c1zc1A_	Alignment	not modelled	7.4	20	**PDB header:**protein turnover **Chain:** A: **PDB Molecule:**ubiquitin fusion degradation protein 1; **PDBTitle:** ufd1 exhibits the aaa-atpase fold with two distinct2 ubiquitin interaction sites
40	d2uubd1	Alignment	not modelled	7.3	25	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
41	d2hsja1	Alignment	not modelled	7.1	19	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Acetylhydrolase
42	c1s1hD_	Alignment	not modelled	7.0	23	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**40s ribosomal protein s9-a; **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, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
43	c2yujA_	Alignment	not modelled	6.9	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin fusion degradation 1-like; **PDBTitle:** solution structure of human ubiquitin fusion degradation2 protein 1 homolog ufd1
44	d1twda_	Alignment	not modelled	6.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**CutC-like **Family:**CutC-like
45	c3bbnD_	Alignment	not modelled	6.3	15	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**ribosomal protein s4; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
46	c2iunD_	Alignment	not modelled	6.3	25	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**avian adenovirus celo long fibre; **PDBTitle:** structure of the c-terminal head domain of the avian2 adenovirus celo long fibre (p21 crystal form)
47	d1dxha1	Alignment	not modelled	6.1	19	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
48	c2zt9F_	Alignment	not modelled	6.0	37	**PDB header:**photosynthesis **Chain:** F: **PDB Molecule:**cytochrome b6-f complex subunit 7; **PDBTitle:** crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120
49	c2e0wA_	Alignment	not modelled	6.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gamma-glutamyltranspeptidase; **PDBTitle:** t391a precursor mutant protein of gamma-glutamyltranspeptidase from2 escherichia coli
50	c3l2eB_	Alignment	not modelled	5.9	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycocyamine kinase beta chain; **PDBTitle:** glycocyamine kinase, alpha-beta heterodimer from marine worm2 namalycastis sp.
51	c2lf2A_	Alignment	not modelled	5.7	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of the ahsa1-like protein chu_1110 from2 cytophaga hutchinsonii, northeast structural genomics consortium3 target chr152
52	c2w40C_	Alignment	not modelled	5.7	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glycerol kinase, putative; **PDBTitle:** crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
						PDB header:structural genomics, unknown function

53	c2f6sA_	Alignment	not modelled	5.6	14	**Chain:** A: **PDB Molecule:**cell filamentation protein, putative; **PDBTitle:** structure of cell filamentation protein (fic) from helicobacter pylori
54	c3btpA_	Alignment	not modelled	5.5	36	**PDB header:**dna binding protein, chaperone **Chain:** A: **PDB Molecule:**single-strand dna-binding protein; **PDBTitle:** crystal structure of agrobacterium tumefaciens vire2 in complex with2 its chaperone vire1: a novel fold and implications for dna binding
55	d2c42a2	Alignment	not modelled	5.3	44	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**PFOR PP module
56	c1yzxB_	Alignment	not modelled	5.2	45	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase kappa 1; **PDBTitle:** crystal structure of human kappa class glutathione2 transferase