Phyre^2

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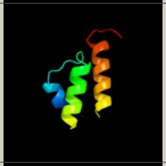
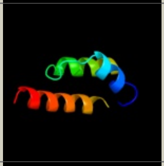
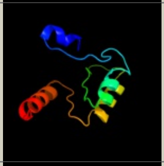
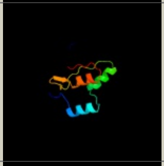
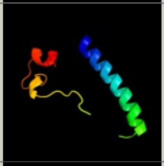
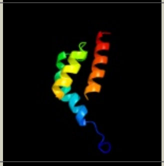
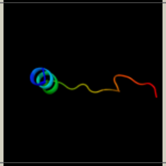
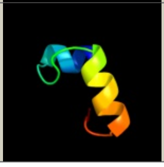
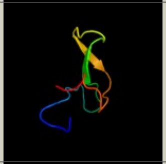
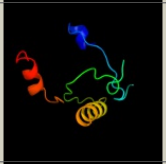
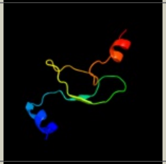
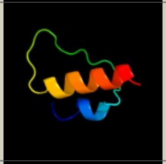
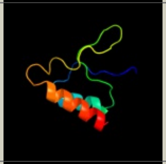
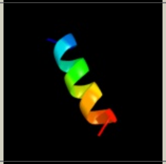
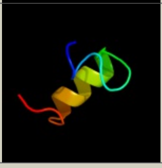
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3clqC_	Alignment		100.0	65	**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	d1pdza2	Alignment		74.3	35	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
3	d2akza2	Alignment		68.4	24	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
4	d2al1a2	Alignment		65.9	22	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
5	d1wo8a1	Alignment		60.8	19	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
6	c1vjtA_	Alignment		51.7	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** crystal structure of alpha-glucosidase (tm0752) from thermotoga2 maritima at 2.50 a resolution
7	c2cqjA_	Alignment		50.2	17	**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
8	d1alua_	Alignment		41.0	15	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Long-chain cytokines
9	d2fyma2	Alignment		40.7	15	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
10	c2re2A_	Alignment		31.9	32	**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
11	d1h3fa2	Alignment		21.9	21	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain

12	d1c06a_	Alignment		21.5	36	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
13	c2y9xG_	Alignment		20.4	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
14	c2yvqA_	Alignment		20.2	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoyl-phosphate synthase; **PDBTitle:** crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
15	d2pw4a1	Alignment		19.7	18	**Fold:**Jann2411-like **Superfamily:**Jann2411-like **Family:**Jann2411-like
16	d1b93a_	Alignment		19.4	23	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
17	c3hp7A_	Alignment		19.2	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hemolysin, putative; **PDBTitle:** putative hemolysin from streptococcus thermophilus.
18	c2htmB_	Alignment		17.0	19	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**thiazole biosynthesis protein thig; **PDBTitle:** crystal structure of ttha0676 from thermus thermophilus hb8
19	c2l58A_	Alignment		16.6	40	**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
20	d2gy9d1	Alignment		16.4	24	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
21	d1twda_	Alignment	not modelled	12.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**CutC-like **Family:**CutC-like
22	d1nuba2	Alignment	not modelled	11.7	50	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**EGF/Laminin **Family:**Follistatin (FS) module N-terminal domain, FS-N
23	c2xzmD_	Alignment	not modelled	11.6	18	**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
24	c2ldkA_	Alignment	not modelled	11.5	14	**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
25	d1jh3a_	Alignment	not modelled	10.5	25	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
26	d3cuma1	Alignment	not modelled	10.2	19	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
27	c3msuA_	Alignment	not modelled	10.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citrate synthase; **PDBTitle:** crystal structure of citrate synthase from francisella tularensis
28	c3d0iA	Alignment	not modelled	9.9	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ca_c3497;

28	c3d0jA_	Alignment	not modelled	9.9	12	**PDBTitle:** crystal structure of conserved protein of unknown function ca_c34972 from clostridium acetobutylicum atcc 824
29	c2d5nB_	Alignment	not modelled	9.8	17	**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
30	d2hsja1	Alignment	not modelled	9.8	18	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Acetylhydrolase
31	c2bibA_	Alignment	not modelled	9.8	17	**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
32	c3iefA_	Alignment	not modelled	9.8	33	**PDB header:**transferase, rna binding protein **Chain:** A: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of trna guanine-n1-methyltransferase from2 bartonella henselae using mpcs.
33	d2o34a1	Alignment	not modelled	9.7	57	**Fold:**T-fold **Superfamily:**ApbE-like **Family:**DVU1097-like
34	c2bs5A_	Alignment	not modelled	9.4	25	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**fucose-binding lectin protein; **PDBTitle:** lectin from ralstonia solanacearum complexed with 2-2 fucosyllactose
35	d1p9ka_	Alignment	not modelled	8.6	24	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**YbcJ-like
36	c1u8xX_	Alignment	not modelled	8.4	21	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**maltose-6'-phosphate glucosidase; **PDBTitle:** crystal structure of glva from bacillus subtilis, a metal-requiring,2 nad-dependent 6-phospho-alpha-glucosidase
37	c3fefB_	Alignment	not modelled	8.3	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative glucosidase lpld; **PDBTitle:** crystal structure of putative glucosidase lpld from2 bacillus subtilis
38	d1vmda_	Alignment	not modelled	8.3	19	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
39	d2isba1	Alignment	not modelled	7.8	17	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**FumA C-terminal domain-like **Family:**FumA C-terminal domain-like
40	d1vjta1	Alignment	not modelled	7.7	7	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
41	c3n5mD_	Alignment	not modelled	7.4	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**adenosylmethionine-8-amino-7-oxononanoate aminotransferase; **PDBTitle:** crystals structure of a bacillus anthracis aminotransferase
42	d2uubd1	Alignment	not modelled	7.3	35	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
43	c2i7uA_	Alignment	not modelled	7.2	43	**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
44	d1vk4a_	Alignment	not modelled	7.0	15	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
45	c1s1hD_	Alignment	not modelled	6.8	32	**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.
46	d2jeka1	Alignment	not modelled	6.5	32	**Fold:**Rv1873-like **Superfamily:**Rv1873-like **Family:**Rv1873-like
47	c2iunD_	Alignment	not modelled	6.4	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)
48	c3bbnD_	Alignment	not modelled	6.3	25	**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.
49	c1oy5B_	Alignment	not modelled	6.3	32	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of trna (m1g37) methyltransferase from aquifex2 aeolicus
50	d1oy5a_	Alignment	not modelled	6.3	32	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
51	c1s6yA_	Alignment	not modelled	6.3	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phospho-beta-glucosidase; **PDBTitle:** 2.3a crystal structure of phospho-beta-glucosidase
52	d1s4da_	Alignment	not modelled	6.1	19	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
53	c2k4mA_	Alignment	not modelled	6.1	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0146 protein mth_1000; **PDBTitle:** solution nmr structure of m. thermoautotrophicum protein2 mth_1000, northeast structural genomics consortium

						target3 tr8
54	c3btpA_	Alignment	not modelled	6.0	43	**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	c3brtC_	Alignment	not modelled	5.9	33	**PDB header:**transferase/transcription **Chain:** C: **PDB Molecule:**inhibitor of nuclear factor kappa-b kinase **PDBTitle:** nemo/ikk association domain structure
56	c2akmA_	Alignment	not modelled	5.9	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**gamma enolase; **PDBTitle:** fluoride inhibition of enolase: crystal structure of the2 inhibitory complex
57	d1t6la2	Alignment	not modelled	5.8	56	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
58	c3p04A_	Alignment	not modelled	5.8	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized bcr; **PDBTitle:** crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
59	c3bboG_	Alignment	not modelled	5.7	46	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**ribosomal protein l4; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
60	c2q7aA_	Alignment	not modelled	5.5	43	**PDB header:**heme binding protein **Chain:** A: **PDB Molecule:**cell surface heme-binding protein; **PDBTitle:** crystal structure of the cell surface heme transfer protein shp
61	c2w40C_	Alignment	not modelled	5.4	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glycerol kinase, putative; **PDBTitle:** crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
62	d1a7ha_	Alignment	not modelled	5.3	23	**Fold:**gamma-Crystallin-like **Superfamily:**gamma-Crystallin-like **Family:**Crystallins/Ca-binding development proteins
63	d1s0aa_	Alignment	not modelled	5.3	32	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
64	c3fd0B_	Alignment	not modelled	5.1	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative cystathionine beta-lyase involved in aluminum **PDBTitle:** crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_470671.1) from listeria innocua at 2.12 a3 resolution
65	d2cr9a1	Alignment	not modelled	5.1	21	**Fold:**WGR domain-like **Superfamily:**WGR domain-like **Family:**WGR domain
66	c2lf2A_	Alignment	not modelled	5.1	26	**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