Phyre2

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Description	P64594
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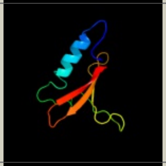
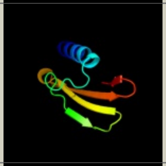
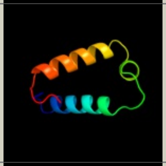
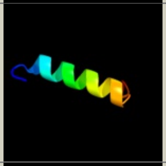
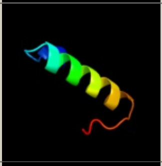
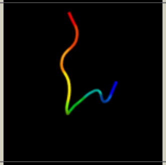
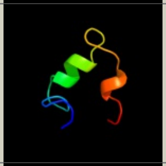
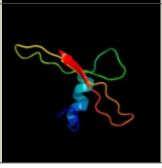
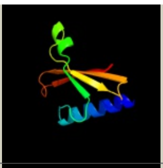
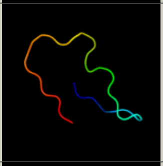
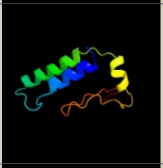
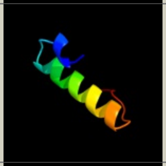
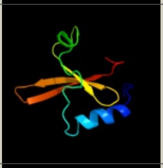
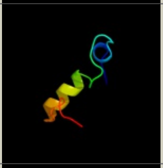
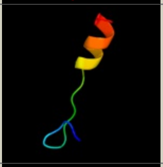
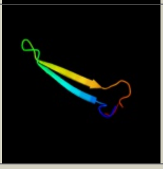
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kheA_	Alignment		82.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**toxin-like protein; **PDBTitle:** solution structure of the bacterial toxin rele from thermus2 thermophilus hb8
2	c2otrA_	Alignment		63.3	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hp0892; **PDBTitle:** solution structure of conserved hypothetical protein hp0892 from2 helicobacter pylori
3	c3g5oC_	Alignment		62.1	21	**PDB header:**toxin/antitoxin **Chain:** C: **PDB Molecule:**uncharacterized protein rv2866; **PDBTitle:** the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
4	d1wmia1	Alignment		52.9	20	**Fold:**RelE-like **Superfamily:**RelE-like **Family:**RelE-like
5	d2a6sa1	Alignment		35.3	9	**Fold:**RelE-like **Superfamily:**RelE-like **Family:**YoeB/Txe-like
6	d2jeka1	Alignment		32.2	12	**Fold:**Rv1873-like **Superfamily:**Rv1873-like **Family:**Rv1873-like
7	c2l9vA_	Alignment		24.4	25	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**pre-mrna-processing factor 40 homolog a; **PDBTitle:** nmr structure of the ff domain l24a mutant's folding transition state
8	d1b79a_	Alignment		20.1	3	**Fold:**N-terminal domain of DnaB helicase **Superfamily:**N-terminal domain of DnaB helicase **Family:**N-terminal domain of DnaB helicase
9	c2zkr3_	Alignment		17.8	44	**PDB header:**ribosomal protein/rna **Chain:** 3: **PDB Molecule:**60s ribosomal protein l39e; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
10	d1q46a1	Alignment		16.9	30	**Fold:**SAM domain-like **Superfamily:**eIF2alpha middle domain-like **Family:**eIF2alpha middle domain-like
11	c3kixy_	Alignment		16.8	16	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:** **PDBTitle:** structure of rele nuclease bound to the 70s ribosome2 (postcleavage state; part 3 of 4)

12	c3bpqD_	Alignment		16.7	10	**PDB header:**toxin **Chain:** D: **PDB Molecule:**toxin rele3; **PDBTitle:** crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
13	c3qvaB_	Alignment		16.6	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**transthyretin-like protein; **PDBTitle:** structure of klebsiella pneumoniae 5-hydroxyisourate hydrolase
14	d3elna1	Alignment		16.5	25	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Cysteine dioxygenase type I
15	d1jwea_	Alignment		16.4	3	**Fold:**N-terminal domain of DnaB helicase **Superfamily:**N-terminal domain of DnaB helicase **Family:**N-terminal domain of DnaB helicase
16	d1z8ma1	Alignment		15.7	17	**Fold:**RelE-like **Superfamily:**RelE-like **Family:**RelE-like
17	d1cmca_	Alignment		15.4	24	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Met repressor, MetJ (MetR)
18	c4a1bB_	Alignment		15.1	19	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**rpl39; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 3.
19	d1tf5a2	Alignment		14.6	24	**Fold:**Helical scaffold and wing domains of SecA **Superfamily:**Helical scaffold and wing domains of SecA **Family:**Helical scaffold and wing domains of SecA
20	c3q2bA_	Alignment		13.4	7	**PDB header:**actin-binding protein **Chain:** A: **PDB Molecule:**cofilin/actin-depolymerizing factor homolog 1; **PDBTitle:** crystal structure of an actin depolymerizing factor
21	d1rfya_	Alignment	not modelled	12.9	52	**Fold:**Long alpha-hairpin **Superfamily:**Transcriptional repressor TraM **Family:**Transcriptional repressor TraM
22	d1nkta2	Alignment	not modelled	12.8	29	**Fold:**Helical scaffold and wing domains of SecA **Superfamily:**Helical scaffold and wing domains of SecA **Family:**Helical scaffold and wing domains of SecA
23	c3pnxF_	Alignment	not modelled	12.5	13	**PDB header:**transferase **Chain:** F: **PDB Molecule:**putative sulfurtransferase dsre; **PDBTitle:** crystal structure of a putative sulfurtransferase dsre (swol_2425)2 from syntrophomonas wolfei str. goettingen at 1.92 a resolution
24	c3m9hB_	Alignment	not modelled	12.4	36	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain of the2 mycobacterium tuberculosis proteasomal atpase mpa
25	d1np3a1	Alignment	not modelled	12.1	21	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Acetohydroxy acid isomeroreductase (ketol-acid reductoisomerase, KARI)
26	c1wloA_	Alignment	not modelled	12.0	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sufe protein; **PDBTitle:** solution structure of the hypothetical protein from thermus2 thermophilus hb8
27	d1upgb_	Alignment	not modelled	11.6	52	**Fold:**Long alpha-hairpin **Superfamily:**Transcriptional repressor TraM **Family:**Transcriptional repressor TraM
28	c2vzdD_	Alignment	not modelled	11.6	29	**PDB header:**cell adhesion **Chain:** D: **PDB Molecule:**paxillin;

28	c2vzdD_	Alignment	not modelled	11.6	29	**PDBTitle:** crystal structure of the c-terminal calponin homology2 domain of alpha parvin in complex with paxillin ld1 motif
29	d1m15a2	Alignment	not modelled	11.5	32	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
30	c3pz8A_	Alignment	not modelled	11.2	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**segment polarity protein dishevelled homolog dvl-1; **PDBTitle:** crystal structure of dvl1-dix(y17d) mutant
31	d3ecfa1	Alignment	not modelled	11.1	46	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Ava4193-like
32	c3gxvA_	Alignment	not modelled	11.1	14	**PDB header:**hydrolase/replication **Chain:** A: **PDB Molecule:**replicative dna helicase; **PDBTitle:** three-dimensional structure of n-terminal domain of dnab2 helicase from helicobacter pylori and its interactions with3 primase
33	c2lhuA_	Alignment	not modelled	11.1	36	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**mybpc3 protein; **PDBTitle:** structural insight into the unique cardiac myosin binding protein-c2 motif: a partially folded domain
34	d2ahob1	Alignment	not modelled	11.0	41	**Fold:**SAM domain-like **Superfamily:**eIF2alpha middle domain-like **Family:**eIF2alpha middle domain-like
35	d1sqda2	Alignment	not modelled	11.0	8	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
36	d1u6ra2	Alignment	not modelled	10.6	25	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
37	c3oeiH_	Alignment	not modelled	10.6	16	**PDB header:**toxin, protein binding **Chain:** H: **PDB Molecule:**relk (toxin rv3358); **PDBTitle:** crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
38	d1qk1a2	Alignment	not modelled	10.4	28	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
39	c2rjbD_	Alignment	not modelled	10.3	8	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein ydcj (sf1787)2 from shigella flexneri which includes domain duf1338.3 northeast structural genomics consortium target sfr276
40	d1crka2	Alignment	not modelled	10.1	26	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
41	c3l2eB_	Alignment	not modelled	9.5	32	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycocyamine kinase beta chain; **PDBTitle:** glycocyamine kinase, alpha-beta heterodimer from marine worm2 namalycastis sp.
42	d1ni2a3	Alignment	not modelled	9.4	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
43	c3jq3A_	Alignment	not modelled	9.4	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lombricine kinase; **PDBTitle:** crystal structure of lombricine kinase, complexed with substrate adp
44	d1h4ra3	Alignment	not modelled	9.3	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
45	d1ef1a3	Alignment	not modelled	9.3	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
46	c1rl9A_	Alignment	not modelled	9.2	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arginine kinase; **PDBTitle:** crystal structure of creatine-adp arginine kinase ternary2 complex
47	c1x67A_	Alignment	not modelled	9.2	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**drebrin-like protein; **PDBTitle:** solution structure of the cofilin homology domain of hip-552 (drebrin-like protein)
48	d1g0wa2	Alignment	not modelled	9.1	25	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
49	d3cipg1	Alignment	not modelled	9.0	13	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
50	c3ju6A_	Alignment	not modelled	8.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arginine kinase; **PDBTitle:** crystal structure of dimeric arginine kinase in complex with2 amppnp and arginine
51	d1oo2a_	Alignment	not modelled	8.6	31	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
52	c2kmaA_	Alignment	not modelled	8.5	26	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**talin 1; **PDBTitle:** nmr structure of the f0f1 double domain (residues 1-202) of2 the talin ferm domain
53	c2h1xB_	Alignment	not modelled	8.4	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**5-hydroxyisourate hydrolase (formerly known as **PDBTitle:** crystal structure of 5-hydroxyisourate hydrolase (formerly2 known as trp, transthyretin related protein)
						PDB header:ribosome

54	c4a1aM_	Alignment	not modelled	8.3	18	**Chain:** M: **PDB Molecule:**60s ribosomal protein l5; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
55	c2l7qA_	Alignment	not modelled	8.0	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein found in conjugate transposon; **PDBTitle:** solution nmr structure of conjugate transposon protein bvu_1572(27-2 141) from bacteroides vulgatus, northeast structural genomics3 consortium target bvr155
56	d1qh4a2	Alignment	not modelled	7.9	25	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
57	c2r5uD_	Alignment	not modelled	7.9	10	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**replicative dna helicase; **PDBTitle:** crystal structure of the n-terminal domain of dnab helicase from2 mycobacterium tuberculosis
58	c1t0yA_	Alignment	not modelled	7.5	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**tubulin folding cofactor b; **PDBTitle:** solution structure of a ubiquitin-like domain from tubulin-2 binding cofactor b
59	d1t0ya_	Alignment	not modelled	7.5	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
60	c3csxA_	Alignment	not modelled	7.5	40	**PDB header:**metal binding protein,unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structural characterization of a protein in the duf6832 family- crystal structure of cce_0567 from the3 cyanobacterium cyanothece 51142.
61	d1o66a_	Alignment	not modelled	7.5	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
62	c2fh4C_	Alignment	not modelled	7.4	19	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**gelsolin; **PDBTitle:** c-terminal half of gelsolin soaked in egta at ph 8
63	d1kgia_	Alignment	not modelled	7.4	35	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
64	d1vrpa2	Alignment	not modelled	7.3	25	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
65	d1t3ya1	Alignment	not modelled	7.2	19	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Cofilin-like
66	d1qnaa2	Alignment	not modelled	6.9	13	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
67	d1tdha3	Alignment	not modelled	6.7	14	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
68	d2bo4a1	Alignment	not modelled	6.7	45	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**MGS-like
69	c3osqA_	Alignment	not modelled	6.6	36	**PDB header:**fluorescent protein, transport protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein, green fluorescent **PDBTitle:** maltose-bound maltose sensor engineered by insertion of circularly2 permuted green fluorescent protein into e. coli maltose binding3 protein at position 175
70	c3pz7A_	Alignment	not modelled	6.6	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**dixin; **PDBTitle:** crystal structure of ccd1-dix domain
71	d2djfa1	Alignment	not modelled	6.5	21	**Fold:**Streptavidin-like **Superfamily:**Dipeptidyl peptidase I (cathepsin C), exclusion domain **Family:**Dipeptidyl peptidase I (cathepsin C), exclusion domain
72	c2js5B_	Alignment	not modelled	6.4	27	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr structure of protein q60c73_metca. northeast structural2 genomics consortium target mcr1
73	c1t0fC_	Alignment	not modelled	6.2	57	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**transposon tn7 transposition protein tnsc; **PDBTitle:** crystal structure of the tnsa/tnsc(504-555) complex
74	d1udma_	Alignment	not modelled	6.1	18	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Cofilin-like
75	c2kj6A_	Alignment	not modelled	6.1	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**tubulin folding cofactor b; **PDBTitle:** nmr solution structure of a tubulin folding cofactor b2 obtained from arabidopsis thaliana: northeast structural3 genomics consortium target ar3436a
76	d1cjxa2	Alignment	not modelled	6.0	31	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
77	d2g3ra1	Alignment	not modelled	6.0	67	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
78	d1uzca_	Alignment	not modelled	5.9	27	**Fold:**Another 3-helical bundle **Superfamily:**FF domain **Family:**FF domain

79	d2zpya3	Alignment	not modelled	5.7	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
80	d1d0na4	Alignment	not modelled	5.7	19	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
81	d1tfpa_	Alignment	not modelled	5.6	31	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
82	d2fh1a1	Alignment	not modelled	5.6	15	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
83	d2f7fa1	Alignment	not modelled	5.6	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
84	c3k1lA_	Alignment	not modelled	5.6	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**fancl; **PDBTitle:** crystal structure of fancl
85	c2rooA_	Alignment	not modelled	5.4	20	**PDB header:**toxin **Chain:** A: **PDB Molecule:**neurotoxin magi-4; **PDBTitle:** solution structure of magi4, a spider toxin from macrothele2 gigas
86	d1f86a_	Alignment	not modelled	5.4	27	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
87	d1kl9a1	Alignment	not modelled	5.1	23	**Fold:**SAM domain-like **Superfamily:**eIF2alpha middle domain-like **Family:**eIF2alpha middle domain-like
88	c1i0eD_	Alignment	not modelled	5.1	25	**PDB header:**transferase **Chain:** D: **PDB Molecule:**creatine kinase,m chain; **PDBTitle:** crystal structure of creatine kinase from human muscle