Phyre^2

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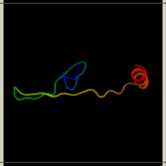
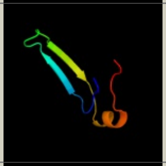
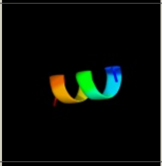
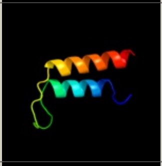
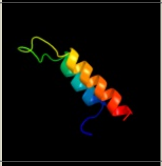
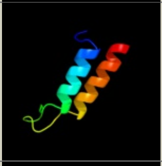
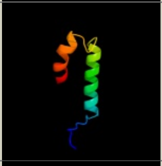
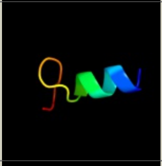
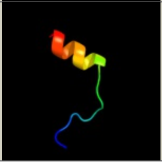
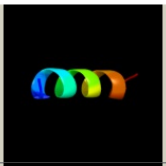
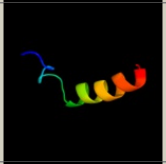
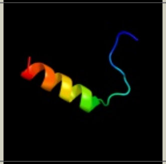
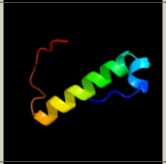
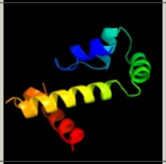
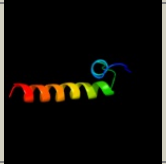
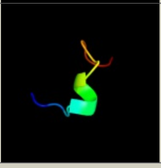
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2yukA_	Alignment		38.4	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**myeloid/lymphoid or mixed-lineage leukemia **PDBTitle:** solution structure of the hmg box of human myeloid/lymphoid2 or mixed-lineage leukemia protein 3 homolog
2	c2ph5A_	Alignment		28.3	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homospermidine synthase; **PDBTitle:** crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
3	d1lnla2	Alignment		21.0	21	**Fold:**C-terminal domain of mollusc hemocyanin **Superfamily:**C-terminal domain of mollusc hemocyanin **Family:**C-terminal domain of mollusc hemocyanin
4	d1qnta2	Alignment		19.6	36	**Fold:**Ribonuclease H-like motif **Superfamily:**Methylated DNA-protein cysteine methyltransferase domain **Family:**Methylated DNA-protein cysteine methyltransferase domain
5	d1iwpg_	Alignment		15.6	18	**Fold:**Open three-helical up-and-down bundle **Superfamily:**Diol dehydratase, gamma subunit **Family:**Diol dehydratase, gamma subunit
6	d1eexg_	Alignment		15.6	21	**Fold:**Open three-helical up-and-down bundle **Superfamily:**Diol dehydratase, gamma subunit **Family:**Diol dehydratase, gamma subunit
7	c1uc5M_	Alignment		15.6	21	**PDB header:**lyase **Chain:** M: **PDB Molecule:**diol dehydrase gamma subunit; **PDBTitle:** structure of diol dehydratase complexed with (r)-1,2-2 propanediol
8	c2wbqA_	Alignment		15.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-arginine beta-hydroxylase; **PDBTitle:** crystal structure of vioc in complex with (2s,3s)-2 hydroxyarginine
9	d2al1a1	Alignment		14.9	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
10	d1k1fa_	Alignment		14.8	43	**Fold:**Bcr-Abl oncoprotein oligomerization domain **Superfamily:**Bcr-Abl oncoprotein oligomerization domain **Family:**Bcr-Abl oncoprotein oligomerization domain
11	c2blcA_	Alignment		14.3	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrofolate reductase-thymidylate synthase; **PDBTitle:** sp21 double mutant p. vivax dihydrofolate reductase in2 complex with des-chloropyrimethamine

12	c2y94C_	Alignment		14.3	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**5'-amp-activated protein kinase catalytic subunit alpha-1; **PDBTitle:** structure of an active form of mammalian ampk
13	d1bg3a1	Alignment		13.9	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
14	d1j3ka_	Alignment		13.5	26	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
15	c3dg8B_	Alignment		13.4	26	**PDB header:**oxidoreductase, transferase **Chain:** B: **PDB Molecule:**bifunctional dihydrofolate reductase-thymidylate **PDBTitle:** quadruple mutant (n51i+c59r+s108n+i164l) plasmodium2 falciparum dihydrofolate reductase-thymidylate synthase3 (pfdhfr-ts) complexed with rjf670, nadph, and dump
16	d1bdga1	Alignment		12.9	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
17	d1js8a2	Alignment		12.7	15	**Fold:**C-terminal domain of mollusc hemocyanin **Superfamily:**C-terminal domain of mollusc hemocyanin **Family:**C-terminal domain of mollusc hemocyanin
18	c3lsgD_	Alignment		12.5	14	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**two-component response regulator yesn; **PDBTitle:** the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
19	c2r6fA_	Alignment		12.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**excinuclease abc subunit a; **PDBTitle:** crystal structure of bacillus stearothermophilus uvra
20	c2l1nA_	Alignment		11.4	44	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of the protein yp_399305.1
21	c2vbeA_	Alignment	not modelled	10.8	16	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**tailspike-protein; **PDBTitle:** tailspike protein of bacteriophage sf6
22	c3pmmA_	Alignment	not modelled	10.3	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative cytoplasmic protein; **PDBTitle:** the crystal structure of a possible member of gh105 family from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578
23	d1pdza1	Alignment	not modelled	9.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
24	c2j4tB_	Alignment	not modelled	9.7	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**angiogenin-4; **PDBTitle:** biological and structural features of murine angiogenin-4,2 an angiogenic protein
25	c2kjgA_	Alignment	not modelled	9.6	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**archaeal protein sso6904; **PDBTitle:** solution structure of an archaeal protein sso6904 from2 hyperthermophilic sulfolobus solfataricus
26	d1t44g_	Alignment	not modelled	9.5	15	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
27	c3cuoB_	Alignment	not modelled	9.4	27	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**uncharacterized hth-type transcriptional regulator ygav; **PDBTitle:** crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
28	c1skhA_	Alignment	not modelled	9.1	50	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**major prion protein 2; **PDBTitle:** n-terminal (1-30) of bovine prion protein

29	d1czan1	Alignment	not modelled	9.1	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
30	c2vq8A_	Alignment	not modelled	9.0	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rnase zf-1a; **PDBTitle:** rnase zf-1a
31	c2lbbA_	Alignment	not modelled	9.0	38	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**acyl coa binding protein; **PDBTitle:** solution structure of acyl coa binding protein from babesia bovis t2bo
32	c3cw1A_	Alignment	not modelled	8.8	24	**PDB header:**splicing **Chain:** A: **PDB Molecule:**small nuclear ribonucleoprotein-associated proteins b and **PDBTitle:** crystal structure of human spliceosomal u1 snrnp
33	d1l6sa_	Alignment	not modelled	8.8	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
34	c3ixzB_	Alignment	not modelled	8.8	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**potassium-transporting atpase subunit beta; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
35	c2w7nA_	Alignment	not modelled	8.4	20	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**trfb transcriptional repressor protein; **PDBTitle:** crystal structure of kora bound to operator dna: insight2 into repressor cooperation in rp4 gene regulation
36	d1bg3a3	Alignment	not modelled	8.3	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
37	d1j72a1	Alignment	not modelled	8.2	19	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
38	d1dkua1	Alignment	not modelled	8.1	26	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
39	c3ljeA_	Alignment	not modelled	8.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zebrafish rnase5; **PDBTitle:** the x-ray structure of zebrafish rnase5
40	d1gv7a_	Alignment	not modelled	7.9	45	**Fold:**RNase A-like **Superfamily:**RNase A-like **Family:**Ribonuclease A-like
41	c3l6wB_	Alignment	not modelled	7.9	15	**PDB header:**oxygen binding **Chain:** B: **PDB Molecule:**hemocyanin 1; **PDBTitle:** structure of the collar functional unit (klh1-h) of keyhole2 limpet hemocyanin
42	d1m58a_	Alignment	not modelled	7.9	20	**Fold:**RNase A-like **Superfamily:**RNase A-like **Family:**Ribonuclease A-like
43	c2vq9A_	Alignment	not modelled	7.8	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rnase 1; **PDBTitle:** rnase zf-3e
44	d1oj8a_	Alignment	not modelled	7.7	20	**Fold:**RNase A-like **Superfamily:**RNase A-like **Family:**Ribonuclease A-like
45	c2p6zA_	Alignment	not modelled	7.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**recombinant amphinase-2; **PDBTitle:** enzymatic and structural characterisation of amphinase, a2 novel cytotoxic ribonuclease from rana pipiens oocytes
46	d1m07a_	Alignment	not modelled	7.6	13	**Fold:**RNase A-like **Superfamily:**RNase A-like **Family:**Ribonuclease A-like
47	d1m5ha1	Alignment	not modelled	7.5	35	**Fold:**Ferredoxin-like **Superfamily:**Formylmethanofuran:tetrahydromethanopterin formyltransferase **Family:**Formylmethanofuran:tetrahydromethanopterin formyltransferase
48	d1e0na_	Alignment	not modelled	7.5	83	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
49	d1onca_	Alignment	not modelled	7.5	13	**Fold:**RNase A-like **Superfamily:**RNase A-like **Family:**Ribonuclease A-like
50	d1czan3	Alignment	not modelled	7.4	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
51	d1d0na4	Alignment	not modelled	7.2	14	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
52	c2jpiA_	Alignment	not modelled	7.2	17	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** chemical shift assignments of pa4090 from pseudomonas2 aeruginosa
53	d1k59a_	Alignment	not modelled	7.1	45	**Fold:**RNase A-like **Superfamily:**RNase A-like **Family:**Ribonuclease A-like
54	c3pgwB_	Alignment	not modelled	7.1	24	**PDB header:**splicing/dna/rna **Chain:** B: **PDB Molecule:**sm b; **PDBTitle:** crystal structure of human u1 snrnp
55	d3buxb1	Alignment	not modelled	7.0	12	**Fold:**EF Hand-like **Superfamily:**EF-hand

						Family:EF-hand modules in multidomain proteins
56	d1un3a_	Alignment	not modelled	6.9	45	**Fold:**RNase A-like **Superfamily:**RNase A-like **Family:**Ribonuclease A-like
57	d1v4sa1	Alignment	not modelled	6.9	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
58	d1agia_	Alignment	not modelled	6.9	36	**Fold:**RNase A-like **Superfamily:**RNase A-like **Family:**Ribonuclease A-like
59	d2akza1	Alignment	not modelled	6.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
60	c3obkH_	Alignment	not modelled	6.7	30	**PDB header:**lyase **Chain:** H: **PDB Molecule:**delta-aminolevulinic acid dehydratase; **PDBTitle:** crystal structure of delta-aminolevulinic acid dehydratase2 (porphobilinogen synthase) from toxoplasma gondii me49 in complex3 with the reaction product porphobilinogen
61	d1kvza_	Alignment	not modelled	6.7	20	**Fold:**RNase A-like **Superfamily:**RNase A-like **Family:**Ribonuclease A-like
62	d2fug71	Alignment	not modelled	6.5	24	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Nqo15-like
63	c2zpoA_	Alignment	not modelled	6.3	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease; **PDBTitle:** crystal structure of green turtle egg white ribonuclease
64	c3oioA_	Alignment	not modelled	6.1	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (arac-type dna-binding domain- **PDBTitle:** crystal structure of transcriptional regulator (arac-type dna-binding2 domain-containing proteins) from chromobacterium violaceum
65	c2vefB_	Alignment	not modelled	5.9	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** dihydropteroate synthase from streptococcus pneumoniae
66	d1nrja_	Alignment	not modelled	5.9	25	**Fold:**Profilin-like **Superfamily:**SNARE-like **Family:**SRP alpha N-terminal domain-like
67	c2k9sA_	Alignment	not modelled	5.8	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arabinose operon regulatory protein; **PDBTitle:** solution structure of dna binding domain of e. coli arac
68	c3mklB_	Alignment	not modelled	5.7	17	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator gadx; **PDBTitle:** crystal structure of dna-binding transcriptional dual regulator from2 escherichia coli k-12
69	d1iyxa1	Alignment	not modelled	5.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
70	d2hkja2	Alignment	not modelled	5.6	21	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
71	d2ebfx3	Alignment	not modelled	5.6	36	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**PMT C-terminal domain like
72	d1rkea1	Alignment	not modelled	5.6	25	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
73	d5ruba1	Alignment	not modelled	5.6	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
74	d1w6ta1	Alignment	not modelled	5.5	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
75	c3n9tA_	Alignment	not modelled	5.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pnpc; **PDBTitle:** cryatal structure of hydroxyquinol 1,2-dioxygenase from pseudomonas2 putida dll-e4
76	d1qo7a_	Alignment	not modelled	5.3	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Epoxide hydrolase
77	d1hbka_	Alignment	not modelled	5.2	23	**Fold:**Acyl-CoA binding protein-like **Superfamily:**Acyl-CoA binding protein **Family:**Acyl-CoA binding protein
78	c2copA_	Alignment	not modelled	5.1	25	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**acyl-coenzyme a binding domain containing 6; **PDBTitle:** solution structure of rsgi ruh-040, an acbp domain from2 human cdna
79	c2k29A_	Alignment	not modelled	5.1	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
80	d2qn6b1	Alignment	not modelled	5.1	16	**Fold:**Ferredoxin-like **Superfamily:**eIF-2-alpha, C-terminal domain **Family:**eIF-2-alpha, C-terminal domain
81	c2mltA_	Alignment	not modelled	5.0	32	**PDB header:**toxin (hemolytic polypeptide) **Chain:** A: **PDB Molecule:**melittin; **PDBTitle:** melittin