Phyre2

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Description	P33346
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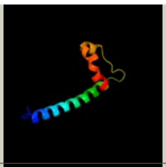
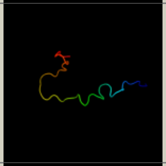
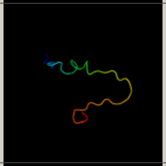
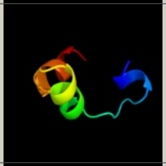
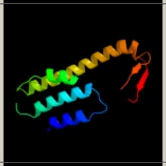
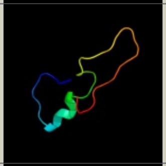
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1uuha_	Alignment		77.3	14	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**Link domain
2	d2pf5a1	Alignment		57.4	10	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**Link domain
3	c3u5gB_	Alignment		41.6	19	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**40s ribosomal protein s1-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution
4	d1oyza_	Alignment		37.7	16	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**PBS lyase HEAT-like repeat
5	d2nrac1	Alignment		36.2	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Replication initiation protein
6	d2awna1	Alignment		36.1	8	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
7	d1nosa_	Alignment		35.2	22	**Fold:**Nitric oxide (NO) synthase oxygenase domain **Superfamily:**Nitric oxide (NO) synthase oxygenase domain **Family:**Nitric oxide (NO) synthase oxygenase domain
8	c2xzm4_	Alignment		34.1	15	**PDB header:**ribosome **Chain:** 4: **PDB Molecule:**40s ribosomal protein s3a; **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
9	c1yzxB_	Alignment		30.6	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase kappa 1; **PDBTitle:** crystal structure of human kappa class glutathione2 transferase
10	d1pc6a_	Alignment		28.7	10	**Fold:**NinB **Superfamily:**NinB **Family:**NinB
11	d1jjcb1	Alignment		25.9	21	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Domains B1 and B5 of PheRS-beta, PheT

12	d1xvla1	Alignment		22.5	17	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
13	c2b0tA_	Alignment		22.4	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadp isocitrate dehydrogenase; **PDBTitle:** structure of monomeric nadp isocitrate dehydrogenase
14	d2cyya1	Alignment		22.4	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
15	d1te4a_	Alignment		21.7	12	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**PBS lyase HEAT-like repeat
16	d1itwa_	Alignment		21.2	18	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Monomeric isocitrate dehydrogenase
17	d2cg4a1	Alignment		21.2	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
18	d1vb5a_	Alignment		21.0	16	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
19	d2b59b2	Alignment		20.2	19	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Pre-dockerin domain
20	c2dbbA_	Alignment		19.8	17	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph0061; **PDBTitle:** crystal structure of ph0061
21	c3somO_	Alignment	not modelled	19.6	14	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**methylmalonic aciduria and homocystinuria type c protein; **PDBTitle:** crystal structure of human mmachc
22	d2cfxa1	Alignment	not modelled	19.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
23	d1i1ga1	Alignment	not modelled	19.0	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
24	c3f6wE_	Alignment	not modelled	18.8	23	**PDB header:**dna binding protein **Chain:** E: **PDB Molecule:**xre-family like protein; **PDBTitle:** xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
25	c3gkuB_	Alignment	not modelled	18.2	9	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**probable rna-binding protein; **PDBTitle:** crystal structure of a probable rna-binding protein from clostridium2 symbiosum atcc 14940
26	c1k98A_	Alignment	not modelled	17.5	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionine synthase; **PDBTitle:** adomet complex of meth c-terminal fragment
27	d1sbqa_	Alignment	not modelled	17.3	8	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**Methenyltetrahydrofolate synthetase
28	c1y9qA_	Alignment	not modelled	17.1	25	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, hth_3 family; **PDBTitle:** crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
						PDB header:transcription

29	c1i1gA_	Alignment	not modelled	16.6	21	**Chain:** A: **PDB Molecule:**transcriptional regulator lrpa; **PDBTitle:** crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
30	c2wknE_	Alignment	not modelled	16.5	16	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**formamidase; **PDBTitle:** gamma lactamase from delftia acidovorans
31	d1ixsa_	Alignment	not modelled	16.3	35	**Fold:**RuvA C-terminal domain-like **Superfamily:**DNA helicase RuvA subunit, C-terminal domain **Family:**DNA helicase RuvA subunit, C-terminal domain
32	c3mfqB_	Alignment	not modelled	16.0	11	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**high-affinity zinc uptake system protein znua; **PDBTitle:** a glance into the metal binding specificity of troa: where elaborate2 behaviors occur in the active center
33	c2e1cA_	Alignment	not modelled	15.9	17	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph1519; **PDBTitle:** structure of putative hth-type transcriptional regulator ph1519/dna2 complex
34	c2rliA_	Alignment	not modelled	15.8	5	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**sco2 protein homolog, mitochondrial; **PDBTitle:** solution structure of cu(i) human sco2
35	d2hf3a1	Alignment	not modelled	15.8	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
36	c2l4aA_	Alignment	not modelled	15.5	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**leucine responsive regulatory protein; **PDBTitle:** nmr structure of the dna-binding domain of e.coli lrp
37	d1z67a1	Alignment	not modelled	15.2	9	**Fold:**YidB-like **Superfamily:**YidB-like **Family:**YidB-like
38	d1f1sa2	Alignment	not modelled	15.2	31	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
39	d1dzka_	Alignment	not modelled	15.1	22	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
40	c1u3fA_	Alignment	not modelled	14.8	9	**PDB header:**ligase **Chain:** A: **PDB Molecule:**5,10-methenyltetrahydrofolate synthetase; **PDBTitle:** structural and functional characterization of a 5,10-2 methenyltetrahydrofolate synthetase from mycoplasma3 pneumoniae (gi: 13508087)
41	c3r0eC_	Alignment	not modelled	14.0	15	**PDB header:**sugar binding protein **Chain:** C: **PDB Molecule:**lectin; **PDBTitle:** structure of remusatia vivipara lectin
42	d1yt3a2	Alignment	not modelled	13.9	27	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**RNase D C-terminal domains
43	d1bj7a_	Alignment	not modelled	13.8	22	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
44	d1a0ia1	Alignment	not modelled	13.8	27	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
45	c3hpbA_	Alignment	not modelled	13.2	20	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**snx5 protein; **PDBTitle:** crystal structure of snx5-px domain in p212121 space group
46	c2rfpA_	Alignment	not modelled	13.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ntp pyrophosphohydrolase; **PDBTitle:** crystal structure of putative ntp pyrophosphohydrolase2 (yp_001813558.1) from exiguobacterium sibiricum 255-15 at 1.74 a3 resolution
47	c3fiqA_	Alignment	not modelled	12.9	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**odorant-binding protein 1f; **PDBTitle:** odorant binding protein obp1
48	d2d7va1	Alignment	not modelled	12.6	19	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
49	c2p6tH_	Alignment	not modelled	12.6	24	**PDB header:**transcription **Chain:** H: **PDB Molecule:**transcriptional regulator, lrp/asnc family; **PDBTitle:** crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
50	c3odnA_	Alignment	not modelled	12.2	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**dally-like protein; **PDBTitle:** the crystal structure of drosophila dally-like protein core domain
51	c3bjxB_	Alignment	not modelled	12.0	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**halocarboxylic acid dehalogenase dehi; **PDBTitle:** structure of a group i haloacid dehalogenase from2 pseudomonas putida strain pp3
52	d2phcb1	Alignment	not modelled	11.6	28	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**PH0987 C-terminal domain-like
53	c2vbzA_	Alignment	not modelled	11.5	28	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
54	c2r73C_	Alignment	not modelled	11.5	19	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**trichosurin; **PDBTitle:** crystal structure of the possum milk whey lipocalin2

						trichosurin at ph 8.2
55	d1xkia_	Alignment	not modelled	11.2	43	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
56	c3ongA_	Alignment	not modelled	11.2	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin-activating enzyme e1-like; **PDBTitle:** crystal structure of uba2ufd-ubc9: insights into e1-e2 interactions in2 sumo pathways
57	d2a6ca1	Alignment	not modelled	11.1	32	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
58	d2f2ea1	Alignment	not modelled	10.9	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**HxlR-like
59	d1jd0a_	Alignment	not modelled	10.8	17	**Fold:**Carbonic anhydrase **Superfamily:**Carbonic anhydrase **Family:**Carbonic anhydrase
60	c2kebA_	Alignment	not modelled	10.8	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna polymerase subunit alpha b; **PDBTitle:** nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit
61	c3op9A_	Alignment	not modelled	10.8	26	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**pli0006 protein; **PDBTitle:** crystal structure of transcriptional regulator from listeria innocua
62	c2cfxD_	Alignment	not modelled	10.8	14	**PDB header:**transcription **Chain:** D: **PDB Molecule:**hth-type transcriptional regulator lrpc; **PDBTitle:** structure of b.subtilis lrpc
63	d1ufma_	Alignment	not modelled	10.6	0	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PCI domain (PINT motif)
64	c2e4jA_	Alignment	not modelled	10.6	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**prostaglandin-h2 d-isomerase; **PDBTitle:** solution structure of mouse lipocalin-type prostaglandin d2 synthase
65	c1pbyA_	Alignment	not modelled	10.5	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**quinohemoprotein amine dehydrogenase 60 kda **PDBTitle:** structure of the phenylhydrazine adduct of the2 quinohemoprotein amine dehydrogenase from paracoccus3 denitrificans at 1.7 a resolution
66	d1mska_	Alignment	not modelled	10.5	24	**Fold:**Methionine synthase activation domain-like **Superfamily:**Methionine synthase activation domain-like **Family:**Methionine synthase SAM-binding domain
67	c2e7xA_	Alignment	not modelled	10.5	24	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**150aa long hypothetical transcriptional regulator; **PDBTitle:** structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
68	d1e5pa_	Alignment	not modelled	10.5	21	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
69	c3ooxA_	Alignment	not modelled	10.5	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative 2og-fe(ii) oxygenase family protein; **PDBTitle:** crystal structure of a putative 2og-fe(ii) oxygenase family protein2 (cc_0200) from caulobacter crescentus at 1.44 a resolution
70	d1rp3a1	Alignment	not modelled	10.5	44	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma3 domain
71	c2h43A_	Alignment	not modelled	10.5	23	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**fibrinogen alpha chain; **PDBTitle:** crystal structure of human fragment d complexed with ala-his-arg-pro-2 amide
72	d1soua_	Alignment	not modelled	10.4	17	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**Methenyltetrahydrofolate synthetase
73	c6rlxA_	Alignment	not modelled	10.2	44	**PDB header:**hormone(muscle relaxant) **Chain:** A: **PDB Molecule:**relaxin, a-chain; **PDBTitle:** x-ray structure of human relaxin at 1.5 angstroms. comparison to2 insulin and implications for receptor binding determinants
74	c6rlxC_	Alignment	not modelled	10.2	44	**PDB header:**hormone(muscle relaxant) **Chain:** C: **PDB Molecule:**relaxin, a-chain; **PDBTitle:** x-ray structure of human relaxin at 1.5 angstroms. comparison to2 insulin and implications for receptor binding determinants
75	d2o38a1	Alignment	not modelled	10.2	32	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
76	c2o38A_	Alignment	not modelled	10.2	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative xre family transcriptional regulator
77	d1r69a_	Alignment	not modelled	10.2	27	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
78	c2k9qB_	Alignment	not modelled	10.2	43	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of hth_xre family transcriptional2 regulator bt_p548217 from bacteroides thetaiotaomicron.3 northeast structural genomics consortium target btr244.
						PDB header:transferase inhibitor

79	c2zp2B_	Alignment	not modelled	10.0	44	**Chain:** B: **PDB Molecule:**kinase a inhibitor; **PDBTitle:** c-terminal domain of kipi from bacillus subtilis
80	c2gqqB_	Alignment	not modelled	10.0	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**leucine-responsive regulatory protein; **PDBTitle:** crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
81	d1sgva1	Alignment	not modelled	10.0	17	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
82	c3gk6A_	Alignment	not modelled	9.9	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**integron cassette protein vch_cass2; **PDBTitle:** crystal structure from the mobile metagenome of vibrio cholerae.2 integron cassette protein vch_cass2.
83	c2bnoA_	Alignment	not modelled	9.9	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
84	d1gm6a_	Alignment	not modelled	9.8	7	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
85	c3qb0C_	Alignment	not modelled	9.8	19	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**actin-related protein 4; **PDBTitle:** crystal structure of actin-related protein arp4 from s. cerevisiae2 complexed with atp
86	d1oh1a_	Alignment	not modelled	9.8	33	**Fold:**Streptavidin-like **Superfamily:**beta-Barrel protease inhibitors **Family:**Staphostatin
87	c1ocuA_	Alignment	not modelled	9.7	22	**PDB header:**sorting protein **Chain:** A: **PDB Molecule:**sorting nexin; **PDBTitle:** crystal structure of the yeast px-domain protein grd19p2 (sorting nexin 3) complexed to3 phosphatidylinosytol-3-phospahte.
88	d2o3ia1	Alignment	not modelled	9.7	14	**Fold:**CV3147-like **Superfamily:**CV3147-like **Family:**CV3147-like
89	d1whza_	Alignment	not modelled	9.6	19	**Fold:**dsRBD-like **Superfamily:**YcfA/nrd intein domain **Family:**YcfA-like
90	d1hcba_	Alignment	not modelled	9.5	16	**Fold:**Carbonic anhydrase **Superfamily:**Carbonic anhydrase **Family:**Carbonic anhydrase
91	c1jmxA_	Alignment	not modelled	9.5	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**amine dehydrogenase; **PDBTitle:** crystal structure of a quinohemoprotein amine dehydrogenase2 from pseudomonas putida
92	c2cseW_	Alignment	not modelled	9.4	20	**PDB header:**virus **Chain:** W: **PDB Molecule:**major core protein lambda 1; **PDBTitle:** features of reovirus outer-capsid protein mu1 revealed by2 electron and image reconstruction of the virion at 7.0-a3 resolution
93	c3gknA_	Alignment	not modelled	9.4	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bacterioferritin comigratory protein; **PDBTitle:** insights into the alkyl peroxide reduction activity of xanthomonas2 campestris bacterioferritin comigratory protein from the trapped3 intermediate/ligand complex structures
94	d2fswa1	Alignment	not modelled	9.4	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**HxlR-like
95	d2hy5a1	Alignment	not modelled	9.3	33	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
96	c3clcC_	Alignment	not modelled	9.3	22	**PDB header:**transcription regulator/dna **Chain:** C: **PDB Molecule:**regulatory protein; **PDBTitle:** crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
97	c2jz8A_	Alignment	not modelled	9.2	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bh09830; **PDBTitle:** solution nmr structure of bh09830 from bartonella henselae2 modeled with one zn+2 bound. northeast structural genomics3 consortium target bnr55
98	d1c0fa1	Alignment	not modelled	9.1	29	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
99	c3h32A_	Alignment	not modelled	9.1	23	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**fibrinogen alpha chain; **PDBTitle:** crystal structure of d-dimer from human fibrin complexed with gly-his-2 arg-pro-tyr-amide