Phyre^2

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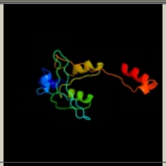
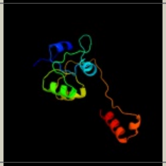
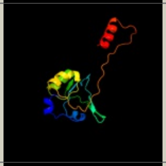
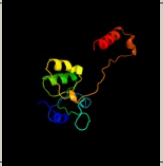
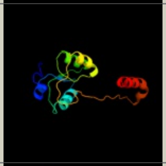
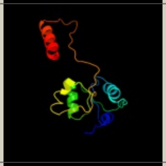
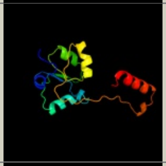
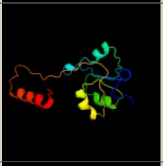
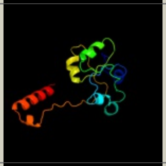
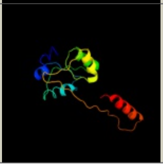
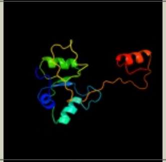
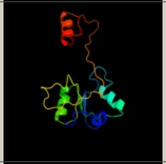
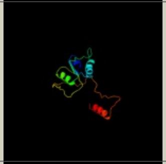
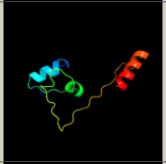
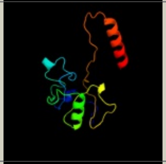
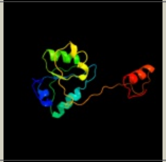
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mz1D_	Alignment		99.7	18	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** the crystal structure of a possible transcription regulator protein2 from sinorhizobium meliloti 1021
2	c3hhfB_	Alignment		99.7	20	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, lysr family; **PDBTitle:** structure of crga regulatory domain, a lysr-type transcriptional2 regulator from neisseria meningitidis.
3	c3t1bB_	Alignment		99.5	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, lysr family; **PDBTitle:** crystal structure of the full-length aphb n100e variant
4	c3hhgF_	Alignment		99.5	21	**PDB header:**transcription regulator **Chain:** F: **PDB Molecule:**transcriptional regulator, lysr family; **PDBTitle:** structure of crga, a lysr-type transcriptional regulator from2 neisseria meningitidis.
5	c3fd3A_	Alignment		99.5	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**chromosome replication initiation inhibitor protein; **PDBTitle:** structure of the c-terminal domains of a lysr family protein from2 agrobacterium tumefaciens str. c58.
6	c3kosA_	Alignment		99.5	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional activator ampr; **PDBTitle:** structure of the ampr effector binding domain from citrobacter2 freundii
7	c2uyeA_	Alignment		99.3	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein; **PDBTitle:** double mutant y110s,f111v dntr from burkholderia sp. strain2 dnt in complex with thiocyanate
8	d1utha_	Alignment		99.3	7	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
9	c3oxnD_	Alignment		99.3	13	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**putative transcriptional regulator, lysr family; **PDBTitle:** the crystal structure of a putative transcriptional regulator from2 vibrio parahaemolyticus
10	c2qsxB_	Alignment		99.3	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**putative transcriptional regulator, lysr family; **PDBTitle:** crystal structure of putative transcriptional regulator lysr from2 vibrio parahaemolyticus
11	c3ispA_	Alignment		99.2	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator **PDBTitle:** crystal structure of argp from mycobacterium tuberculosis

12	c2hxrA_	Alignment		99.2	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator cynr; **PDBTitle:** structure of the ligand binding domain of e. coli cynr, a2 transcriptional regulator controlling cyanate metabolism
13	c1al3A_	Alignment		99.2	9	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**cys regulon transcriptional activator cysb; **PDBTitle:** cofactor binding fragment of cysb from klebsiella aerogenes
14	d1al3a_	Alignment		99.2	9	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
15	c3fzvC_	Alignment		99.2	16	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** crystal structure of pa01 protein, putative lysr family2 transcriptional regulator from pseudomonas aeruginosa
16	c2ql3G_	Alignment		99.1	17	**PDB header:**transcription **Chain:** G: **PDB Molecule:**probable transcriptional regulator, lysr family protein; **PDBTitle:** crystal structure of the c-terminal domain of a probable lysr family2 transcriptional regulator from rhodococcus sp. rha1
17	c3fzjC_	Alignment		99.1	10	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**lysr type regulator of tsambcd; **PDBTitle:** tsar low resolution crystal structure, tetragonal form
18	d1i6aa_	Alignment		99.1	12	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
19	d2fyia1	Alignment		99.1	10	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
20	c2h9qC_	Alignment		99.1	14	**PDB header:**transcription **Chain:** C: **PDB Molecule:**hth-type transcriptional regulator catm; **PDBTitle:** crystal structure of the effector binding domain of a catm2 variant (r156h)
21	c1iz1B_	Alignment	not modelled	99.0	10	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**lysr-type regulatory protein; **PDBTitle:** crystal structure of cbnr, a lysr family transcriptional2 regulator
22	d2esna2	Alignment	not modelled	99.0	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
23	c2esnC_	Alignment	not modelled	99.0	12	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** the crystal structure of probable transcriptional regulator pa04772 from pseudomonas aeruginosa
24	c3n6uA_	Alignment	not modelled	99.0	9	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**lysr type regulator of tsambcd; **PDBTitle:** effector binding domain of tsar in complex with its inducer p-2 toluenesulfonate
25	c3jv9B_	Alignment	not modelled	99.0	7	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, lysr family; **PDBTitle:** the structure of a reduced form of oxyr from n. meningitidis
26	d1ixca2	Alignment	not modelled	98.9	9	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
27	c3ho7A_	Alignment	not modelled	98.9	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**oxyr; **PDBTitle:** crystal structure of oxyr from porphyromonas gingivalis
28	c2f7cA_	Alignment	not modelled	98.8	13	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator catm; **PDBTitle:** catm effector binding domain with its effector cis,cis-muconate
						PDB header:transcription

29	c2h9bB_	Alignment	not modelled	98.8	15	**Chain:** B: **PDB Molecule:**hth-type transcriptional regulator benm; **PDBTitle:** crystal structure of the effector binding domain of a benm variant2 (benm r156h/t157s)
30	c2f78A_	Alignment	not modelled	98.6	15	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator benm; **PDBTitle:** benm effector binding domain with its effector benzoate
31	c3onmB_	Alignment	not modelled	97.8	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator lrha; **PDBTitle:** effector binding domain of lysr-type transcription factor rovm from y.2 pseudotuberculosis
32	d1twya_	Alignment	not modelled	59.1	6	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
33	c1twyG_	Alignment	not modelled	49.8	8	**PDB header:**structural genomics, unknown function **Chain:** G: **PDB Molecule:**abc transporter, periplasmic substrate-binding protein; **PDBTitle:** crystal structure of an abc-type phosphate transport receptor from2 vibrio cholerae
34	c3c5tB_	Alignment	not modelled	36.4	27	**PDB header:**signaling protein/signaling protein **Chain:** B: **PDB Molecule:**exendin-4; **PDBTitle:** crystal structure of the ligand-bound glucagon-like peptide-1 receptor2 extracellular domain
35	c3lr1A_	Alignment	not modelled	34.1	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tungstate abc transporter, periplasmic tungstate- **PDBTitle:** the crystal structure of the tungstate abc transporter from2 geobacter sulfurreducens
36	c1vi7A_	Alignment	not modelled	33.4	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yigz; **PDBTitle:** crystal structure of an hypothetical protein
37	d1vi7a1	Alignment	not modelled	33.3	19	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**YigZ N-terminal domain-like
38	c3muqB_	Alignment	not modelled	31.6	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the crystal structure of a conserved functionally unknown protein from2 vibrio parahaemolyticus rimd 2210633
39	d1wj9a2	Alignment	not modelled	30.7	16	**Fold:**Ferredoxin-like **Superfamily:**CRISPR-associated protein **Family:**CRISPR-associated protein
40	d1amfa_	Alignment	not modelled	28.8	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
41	c1wj9A_	Alignment	not modelled	25.6	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**crispr-associated protein; **PDBTitle:** crystal structure of a crispr-associated protein from2 thermus thermophilus
42	c3qrqA_	Alignment	not modelled	25.6	18	**PDB header:**rna binding protein/rna **Chain:** A: **PDB Molecule:**putative uncharacterized protein tthb192; **PDBTitle:** structure of thermus thermophilus cse3 bound to an rna representing a2 pre-cleavage complex
43	d1atga_	Alignment	not modelled	19.4	4	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
44	c2h5yC_	Alignment	not modelled	17.0	11	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**molybdate-binding periplasmic protein; **PDBTitle:** crystallographic structure of the molybdate-binding protein of2 xanthomonas citri at 1.7 ang resolution bound to molybdate
45	d2gk3a1	Alignment	not modelled	14.9	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**STM3548-like
46	c3rhtB_	Alignment	not modelled	14.2	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**(gatase1)-like protein; **PDBTitle:** crystal structure of type 1 glutamine amidotransferase (gatase1)-like2 protein from planctomyces limnophilus
47	d2ezwa1	Alignment	not modelled	12.3	18	**Fold:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Superfamily:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Family:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
48	c2pksC_	Alignment	not modelled	11.6	13	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** C: **PDB Molecule:**thrombin heavy chain fragment; **PDBTitle:** thrombin in complex with inhibitor
49	d1sbpa_	Alignment	not modelled	10.1	7	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
50	d1ezxc_	Alignment	not modelled	9.8	13	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Eukaryotic proteases
51	d1ixha_	Alignment	not modelled	8.4	10	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
52	c1jrjA_	Alignment	not modelled	7.3	27	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**exendin-4; **PDBTitle:** solution structure of exendin-4 in 30-vol% trifluoroethanol
53	c3fj7A_	Alignment	not modelled	6.7	8	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**major antigenic peptide peb3; **PDBTitle:** crystal structure of l-phospholactate bound peb3
54	c1nauA_	Alignment	not modelled	6.6	0	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**glucagon; **PDBTitle:** nmr solution structure of the glucagon antagonist

						[deshis1,2 desphe6, glu9]glucagon amide in the presence of3 perdeuterated dodecylphosphocholine micelles
55	d1rgig3	Alignment	not modelled	6.4	10	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
56	d1iaua_	Alignment	not modelled	6.2	13	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Eukaryotic proteases
57	c1d0rA_	Alignment	not modelled	6.1	9	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**glucagon-like peptide-1-(7-36)-amide; **PDBTitle:** solution structure of glucagon-like peptide-1-(7-36)-amide2 in trifluoroethanol/water
58	d1j72a3	Alignment	not modelled	6.1	14	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
59	c1aksB_	Alignment	not modelled	6.0	7	**PDB header:**serine protease **Chain:** B: **PDB Molecule:**alpha trypsin; **PDBTitle:** crystal structure of the first active autolysate form of2 the porcine alpha trypsin
60	d1os8a_	Alignment	not modelled	5.9	6	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
61	c1ca0C_	Alignment	not modelled	5.8	21	**PDB header:**complex (serine protease/inhibitor) **Chain:** C: **PDB Molecule:**bovine chymotrypsin; **PDBTitle:** bovine chymotrypsin complexed to appi
62	c2cveA_	Alignment	not modelled	5.7	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha1053; **PDBTitle:** crystal structure of a conserved hypothetical protein tt1547 from2 thermus thermophilus hb8
63	d2qqra1	Alignment	not modelled	5.5	10	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
64	c1lypA_	Alignment	not modelled	5.2	24	**PDB header:**lipopolysaccharide-binding protein **Chain:** A: **PDB Molecule:**cap18; **PDBTitle:** the solution structure of the active domain of cap18: a2 lipopolysaccharide binding protein from rabbit leukocytes
65	c2mltB_	Alignment	not modelled	5.0	58	**PDB header:**toxin (hemolytic polypeptide) **Chain:** B: **PDB Molecule:**melittin; **PDBTitle:** melittin
66	c1bh1A_	Alignment	not modelled	5.0	58	**PDB header:**toxin **Chain:** A: **PDB Molecule:**melittin; **PDBTitle:** structural studies of d-pro melittin, nmr, 20 structures