Phyre2

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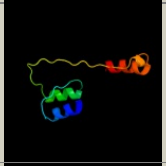
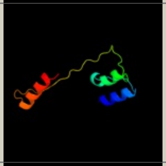
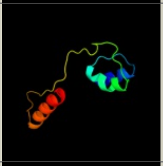
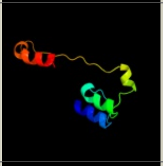
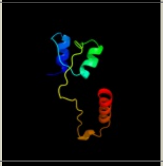
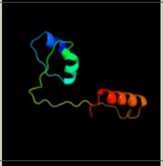
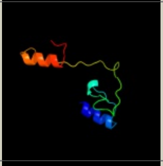
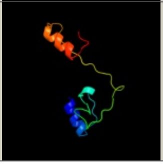
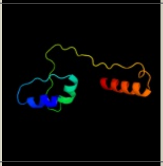
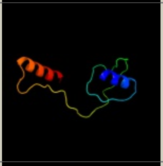
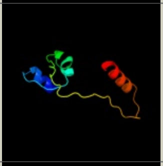
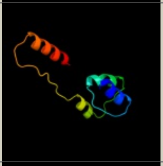
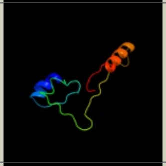
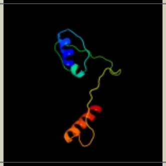
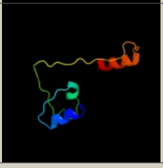
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hhfB_	Alignment		99.3	22	**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.
2	c3mz1D_	Alignment		99.3	23	**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
3	c3t1bB_	Alignment		99.2	25	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, lysr family; **PDBTitle:** crystal structure of the full-length aphb n100e variant
4	c3kosA_	Alignment		99.2	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional activator ampr; **PDBTitle:** structure of the ampr effector binding domain from citrobacter2 freundii
5	c3fd3A_	Alignment		99.2	18	**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	c3hhgF_	Alignment		99.2	24	**PDB header:**transcription regulator **Chain:** F: **PDB Molecule:**transcriptional regulator, lysr family; **PDBTitle:** structure of crga, a lysr-type transcriptional regulator from2 neisseria meningitidis.
7	c2qsxB_	Alignment		99.2	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**putative transcriptional regulator, lysr family; **PDBTitle:** crystal structure of putative transcriptional regulator lysr from2 vibrio parahaemolyticus
8	c3fzjC_	Alignment		99.1	9	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**lysr type regulator of tsambcd; **PDBTitle:** tsar low resolution crystal structure, tetragonal form
9	d1utha_	Alignment		99.1	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
10	c1al3A_	Alignment		99.0	14	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**cys regulon transcriptional activator cysb; **PDBTitle:** cofactor binding fragment of cysb from klebsiella aerogenes
11	d1al3a_	Alignment		99.0	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like

12	c2uyeA_	Alignment		99.0	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein; **PDBTitle:** double mutant y110s,f111v dntr from burkholderia sp. strain2 dnt in complex with thiocyanate
13	c3oxnD_	Alignment		99.0	11	**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
14	c3fzvC_	Alignment		99.0	18	**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
15	d1i6aa_	Alignment		98.9	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
16	c2hxrA_	Alignment		98.9	16	**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
17	c3ispA_	Alignment		98.9	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator **PDBTitle:** crystal structure of argp from mycobacterium tuberculosis
18	c3jv9B_	Alignment		98.9	9	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, lysr family; **PDBTitle:** the structure of a reduced form of oxyr from n. meningitidis
19	c1iz1B_	Alignment		98.8	11	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**lysr-type regulatory protein; **PDBTitle:** crystal structure of cbnr, a lysr family transcriptional2 regulator
20	c3n6uA_	Alignment		98.8	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
21	c2ql3G_	Alignment	not modelled	98.8	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
22	d2fyia1	Alignment	not modelled	98.7	10	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
23	c3ho7A_	Alignment	not modelled	98.7	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**oxyr; **PDBTitle:** crystal structure of oxyr from porphyromonas gingivalis
24	c2h9qC_	Alignment	not modelled	98.7	11	**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)
25	d1ixca2	Alignment	not modelled	98.6	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
26	c2f7cA_	Alignment	not modelled	98.5	11	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator catm; **PDBTitle:** catm effector binding domain with its effector cis,cis-muconate
27	d2esna2	Alignment	not modelled	98.5	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
28	c2h9bB_	Alignment	not modelled	98.4	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator benm; **PDBTitle:** crystal structure of the effector binding domain of a benm variant2 (benm r156h/t157s)

29	c2f78A_	Alignment	not modelled	98.3	16	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator benm; **PDBTitle:** benm effector binding domain with its effector benzoate
30	c2esnC_	Alignment	not modelled	98.2	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
31	c3onmB_	Alignment	not modelled	97.3	10	**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	50.5	7	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
33	c1twyG_	Alignment	not modelled	45.9	7	**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	41.9	30	**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	32.2	8	**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	d1amfa_	Alignment	not modelled	16.0	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
37	c3muqB_	Alignment	not modelled	14.9	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
38	d2i7xa1	Alignment	not modelled	11.3	14	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
39	c2i7xA_	Alignment	not modelled	11.3	14	**PDB header:**rna binding protein, protein binding **Chain:** A: **PDB Molecule:**protein cft2; **PDBTitle:** structure of yeast cpsf-100 (ydh1p)
40	c1jrjA_	Alignment	not modelled	11.1	18	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**exendin-4; **PDBTitle:** solution structure of exendin-4 in 30-vol% trifluoroethanol
41	d1atga_	Alignment	not modelled	10.6	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
42	c3cvgC_	Alignment	not modelled	10.5	14	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**putative metal binding protein; **PDBTitle:** crystal structure of a periplasmic putative metal binding protein
43	c1d0rA_	Alignment	not modelled	6.9	27	**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
44	c2h5yC_	Alignment	not modelled	6.4	12	**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