Phyre^2

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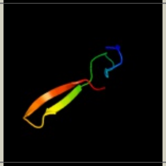
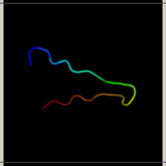
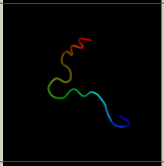
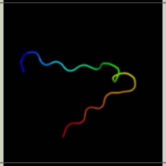
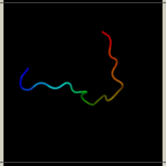
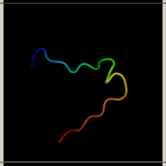
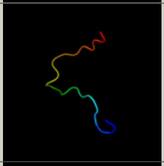
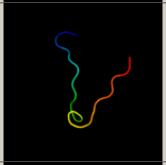
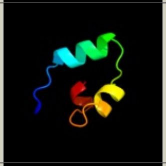
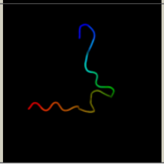
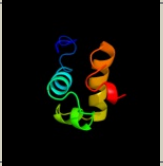
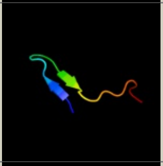
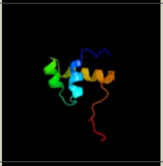
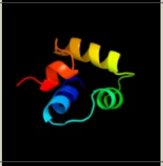
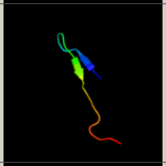
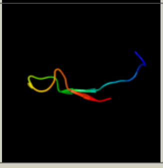
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hi2D_	Alignment		100.0	100	**PDB header:**dna binding protein/toxin **Chain:** D: **PDB Molecule:**motility quorum-sensing regulator mqsr; **PDBTitle:** structure of the n-terminal domain of the e. coli antitoxin mqsa2 (ygit/b3021) in complex with the e. coli toxin mqsr (ygiu/b3022)
2	c3gqnA_	Alignment		43.3	19	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**preneck appendage protein; **PDBTitle:** crystal structure of the pre-mature bacteriophage phi29 gene product2 12
3	c2p6cB_	Alignment		39.6	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**aq_2013 protein; **PDBTitle:** crystal structure of hypothetical protein aq_2013 from aquifex2 aeolicus vf5.
4	c1ve0A_	Alignment		37.4	19	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein (st2072); **PDBTitle:** crystal structure of uncharacterized protein st2072 from sulfolobus2 tokodaii
5	d1vmja_	Alignment		35.9	24	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
6	c2cu5C_	Alignment		34.3	20	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**conserved hypothetical protein tt1486; **PDBTitle:** crystal structure of the conserved hypothetical protein tt1486 from2 thermus thermophilus hb8
7	c2p6hB_	Alignment		31.9	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of hypothetical protein ape1520 from aeropyrum2 pernix k1
8	d1vpha_	Alignment		31.3	19	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
9	d1vmha_	Alignment		30.4	30	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
10	d2ga1a1	Alignment		29.7	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Alr1493-like
11	d1vmfa_	Alignment		25.7	24	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like

12	c3gbgA_	Alignment		23.2	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**tcp pilus virulence regulatory protein; **PDBTitle:** crystal structure of toxt from vibrio cholerae o395
13	c2l4aA_	Alignment		21.8	18	**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
14	d2ia9a1	Alignment		21.3	10	**Fold:**SpoVG-like **Superfamily:**SpoVG-like **Family:**SpoVG-like
15	d1jnpa_	Alignment		20.4	22	**Fold:**Oncogene products **Superfamily:**Oncogene products **Family:**Oncogene products
16	d2cg4a1	Alignment		20.0	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
17	d1bl0a2	Alignment		19.3	4	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
18	c2k9qB_	Alignment		18.3	26	**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.
19	d2i9xa1	Alignment		15.1	10	**Fold:**SpoVG-like **Superfamily:**SpoVG-like **Family:**SpoVG-like
20	d1a1xa_	Alignment		14.4	22	**Fold:**Oncogene products **Superfamily:**Oncogene products **Family:**Oncogene products
21	c2knaA_	Alignment	not modelled	14.4	16	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**baculoviral iap repeat-containing protein 4; **PDBTitle:** solution structure of uba domain of xiap
22	c2i9zB_	Alignment	not modelled	14.3	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative septation protein spovg; **PDBTitle:** structural genomics, the crystal structure of full-length spovg from2 staphylococcus epidermidis atcc 12228
23	d1wi9a_	Alignment	not modelled	13.1	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PCI domain (PINT motif)
24	d1d5ya2	Alignment	not modelled	12.2	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
25	d1e8ca3	Alignment	not modelled	11.8	20	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**MurCDEF
26	d1jsga_	Alignment	not modelled	10.7	25	**Fold:**Oncogene products **Superfamily:**Oncogene products **Family:**Oncogene products
27	c3beyC_	Alignment	not modelled	9.4	21	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**conserved protein o27018; **PDBTitle:** crystal structure of the protein o27018 from methanobacterium2 thermoautotrophicum. northeast structural genomics consortium target3 tt217
28	d1ixsa_	Alignment	not modelled	9.3	21	**Fold:**RuvA C-terminal domain-like **Superfamily:**DNA helicase RuvA subunit, C-terminal domain **Family:**DNA helicase RuvA subunit, C-terminal domain
						PDB header:replication

29	c2vn2B_	Alignment	not modelled	8.6	16	**Chain:** B: **PDB Molecule:**chromosome replication initiation protein; **PDBTitle:** crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426
30	d1wspa1	Alignment	not modelled	8.0	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**DIX domain
31	d1a9xa1	Alignment	not modelled	8.0	11	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
32	d1au7a2	Alignment	not modelled	8.0	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**POU-specific domain
33	c2f4qA_	Alignment	not modelled	8.0	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**type i topoisomerase, putative; **PDBTitle:** crystal structure of deinococcus radiodurans topoisomerase ib
34	c1xofB_	Alignment	not modelled	7.9	18	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**bbahett1; **PDBTitle:** heterooligomeric beta beta alpha miniprotein
35	c3gqhB_	Alignment	not modelled	7.9	19	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**preneck appendage protein; **PDBTitle:** crystal structure of the bacteriophage phi29 gene product2 12 c-terminal fragment
36	c2v79B_	Alignment	not modelled	7.7	10	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**dna replication protein dnad; **PDBTitle:** crystal structure of the n-terminal domain of dnad from2 bacillus subtilis
37	d2f5ga1	Alignment	not modelled	7.3	14	**Fold:**Ferredoxin-like **Superfamily:**Transposase IS200-like **Family:**Transposase IS200-like
38	c1ezeA_	Alignment	not modelled	6.2	30	**PDB header:**transferase inhibitor **Chain:** A: **PDB Molecule:**cholesteryl ester transferase inhibitor protein; **PDBTitle:** structural studies of a baboon (papio sp.) plasma protein2 inhibitor of cholesteryl ester transferase.
39	d1q08a_	Alignment	not modelled	6.0	18	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
40	c3r0aB_	Alignment	not modelled	6.0	15	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
41	d1e3oc2	Alignment	not modelled	5.8	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**POU-specific domain
42	c2abjG_	Alignment	not modelled	5.6	27	**PDB header:**transferase **Chain:** G: **PDB Molecule:**branched-chain-amino-acid aminotransferase, cytosolic; **PDBTitle:** crystal structure of human branched chain amino acid transaminase in a2 complex with an inhibitor, c16h10n2o4f3scl, and pyridoxal 5'3 phosphate.
43	c1nzeA_	Alignment	not modelled	5.6	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxygen-evolving enhancer protein 3; **PDBTitle:** crystal structure of psbq polypeptide of photosystem ii2 from higher plants
44	d1nzea_	Alignment	not modelled	5.6	12	**Fold:**Four-helical up-and-down bundle **Superfamily:**Oxygen-evolving enhancer protein 3, **Family:**Oxygen-evolving enhancer protein 3,
45	d2hkua2	Alignment	not modelled	5.5	20	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
46	d2h7aa1	Alignment	not modelled	5.3	19	**Fold:**YcgL-like **Superfamily:**YcgL-like **Family:**YcgL-like
47	d2hqya2	Alignment	not modelled	5.2	32	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**FemXAB nonribosomal peptidyltransferases
48	d1bhga2	Alignment	not modelled	5.2	12	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
49	c1hjpA_	Alignment	not modelled	5.2	11	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**ruva; **PDBTitle:** holliday junction binding protein ruva from e. coli
50	d2vzsa4	Alignment	not modelled	5.1	21	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain