Phyre^2

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Description	P76210
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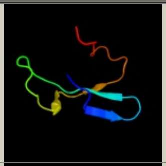
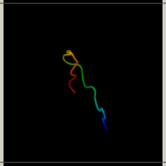
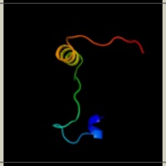
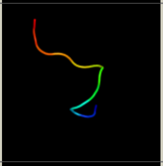
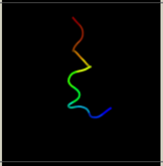
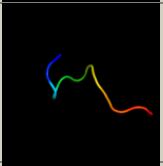
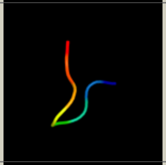
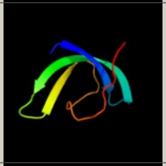
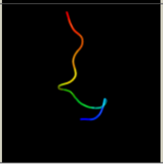
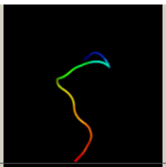
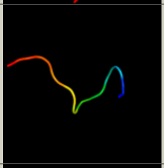
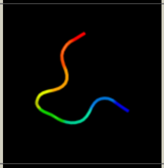
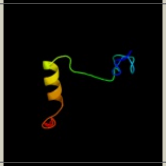
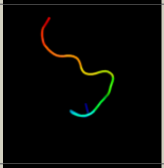
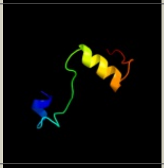
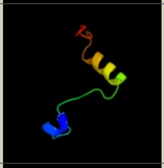
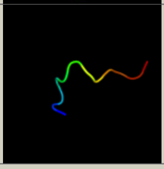
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1oz2a2	Alignment		26.3	30	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
2	c2wzoA_	Alignment		23.5	36	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**transforming growth factor beta regulator 1; **PDBTitle:** the structure of the fyr domain
3	d1pkua1	Alignment		23.4	15	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
4	c2vytA_	Alignment		16.5	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**sex comb on midleg-like protein 2; **PDBTitle:** the mbt repeats of human scml2 bind to peptides containing2 mono methylated lysine.
5	c2r58A_	Alignment		13.9	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**polycomb protein scm; **PDBTitle:** crystal structure of the two mbt repeats from sex-comb on midleg (scm)2 in complex with di-methyl lysine
6	d1j6ra_	Alignment		13.1	21	**Fold:**Methionine synthase activation domain-like **Superfamily:**Methionine synthase activation domain-like **Family:**Hypothetical protein TM0269
7	d1oi1a2	Alignment		12.9	33	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
8	d1oi1a1	Alignment		12.8	33	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
9	c2fkkA_	Alignment		12.6	50	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**baseplate structural protein gp10; **PDBTitle:** crystal structure of the c-terminal domain of the bacteriophage t42 gene product 10
10	c2eqmA_	Alignment		12.1	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 20-like 1; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 20-like 1 [homo sapiens]
11	d1wjra_	Alignment		12.0	33	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat

12	d1oz2a1	Alignment		12.0	33	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
13	d1wjsa_	Alignment		10.6	42	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
14	c2fl8N_	Alignment		9.7	50	**PDB header:**virus/viral protein **Chain:** N: **PDB Molecule:**baseplate structural protein gp10; **PDBTitle:** fitting of the gp10 trimer structure into the cryoem map of the2 bacteriophage t4 baseplate in the hexagonal conformation.
15	d3bbba1	Alignment		9.4	14	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
16	d1wjqa_	Alignment		9.3	50	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
17	c3mpdA_	Alignment		9.2	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** crystal structure of nucleoside diphosphate kinase from2 encephalitozoon cuniculi, cubic form, apo
18	d1u8wa_	Alignment		8.9	10	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
19	d1oz2a3	Alignment		8.5	20	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
20	c3feoB_	Alignment		8.3	25	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**mbt domain-containing protein 1; **PDBTitle:** the crystal structure of mbtd1
21	c3orqA_	Alignment	not modelled	7.8	15	**PDB header:**ligase,biosynthetic protein **Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide synthetase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp
22	c3ceyA_	Alignment	not modelled	7.7	42	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**lethal(3)malignant brain tumor-like 2 protein; **PDBTitle:** crystal structure of l3mbtl2
23	c2ym9C_	Alignment	not modelled	7.3	29	**PDB header:**cell invasion **Chain:** C: **PDB Molecule:**cell invasion protein sipd; **PDBTitle:** sipd from salmonella typhimurium
24	d1m9fd_	Alignment	not modelled	7.3	35	**Fold:**Retrovirus capsid protein, N-terminal core domain **Superfamily:**Retrovirus capsid protein, N-terminal core domain **Family:**Retrovirus capsid protein, N-terminal core domain
25	d1q8ha_	Alignment	not modelled	6.9	71	**Fold:**GLA-domain **Superfamily:**GLA-domain **Family:**GLA-domain
26	c1q8hA_	Alignment	not modelled	6.9	71	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**osteocalcin; **PDBTitle:** crystal structure of porcine osteocalcin
27	c3kztB_	Alignment	not modelled	6.7	29	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function (np_812423.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution
28	c3ngtJ_	Alignment	not modelled	6.5	11	**PDB header:**transferase **Chain:** J: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** structure of leishmania ndkb complexed with amp.

29	c1oz3C_	Alignment	not modelled	6.5	60	**PDB header:**transcription **Chain:** C: **PDB Molecule:**lethal(3)malignant brain tumor-like protein; **PDBTitle:** crystal structure of 3-mbt repeats of lethal (3) malignant brain tumor2 (native-i) at 1.85 angstrom
30	d2jaaa1	Alignment	not modelled	6.4	18	**Fold:**IpaD-like **Superfamily:**IpaD-like **Family:**IpaD-like
31	c3ut1A_	Alignment	not modelled	6.4	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lethal(3)malignant brain tumor-like protein 3; **PDBTitle:** crystal structure of the 3-mbt repeat domain of l3mbtl3
32	d1q3ma_	Alignment	not modelled	6.3	71	**Fold:**GLA-domain **Superfamily:**GLA-domain **Family:**GLA-domain
33	d2o8ra3	Alignment	not modelled	6.2	25	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
34	c3bp1A_	Alignment	not modelled	6.2	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph-dependent 7-cyano-7-deazaguanine reductase; **PDBTitle:** crystal structure of putative 7-cyano-7-deazaguanine2 reductase quef from vibrio cholerae o1 biovar eltor
35	d2py5a1	Alignment	not modelled	6.2	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
36	d2pxrc1	Alignment	not modelled	6.2	35	**Fold:**Retrovirus capsid protein, N-terminal core domain **Superfamily:**Retrovirus capsid protein, N-terminal core domain **Family:**Retrovirus capsid protein, N-terminal core domain
37	d1kp0a1	Alignment	not modelled	6.0	33	**Fold:**Ribonuclease H-like motif **Superfamily:**Creatinase/prolidase N-terminal domain **Family:**Creatinase/prolidase N-terminal domain
38	d1s57a_	Alignment	not modelled	5.8	13	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
39	c1j1eB_	Alignment	not modelled	5.8	14	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**troponin t; **PDBTitle:** crystal structure of the 52kda domain of human cardiac2 troponin in the ca2+ saturated form
40	c3zvmA_	Alignment	not modelled	5.6	18	**PDB header:**hydrolase/transferase/dna **Chain:** A: **PDB Molecule:**bifunctional polynucleotide phosphatase/kinase; **PDBTitle:** the structural basis for substrate recognition by mammalian2 polynucleotide kinase 3' phosphatase
41	c3nzzA_	Alignment	not modelled	5.5	29	**PDB header:**cell invasion **Chain:** A: **PDB Molecule:**cell invasion protein sipd; **PDBTitle:** crystal structure of the salmonella type iii secretion system tip2 protein sipd
42	c2kn8A_	Alignment	not modelled	5.5	43	**PDB header:**protein binding, dna binding protein **Chain:** A: **PDB Molecule:**dna cleavage and packaging protein large subunit, ul89; **PDBTitle:** nmr structure of the c-terminal domain of pul89
43	c3r9lA_	Alignment	not modelled	5.5	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** crystal structure of nucleoside diphosphate kinase from giardia2 lamblia featuring a disordered dinucleotide binding site
44	d1iowa1	Alignment	not modelled	5.5	20	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
45	c1j1eC_	Alignment	not modelled	5.2	47	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**troponin i; **PDBTitle:** crystal structure of the 52kda domain of human cardiac2 troponin in the ca2+ saturated form
46	c2izpB_	Alignment	not modelled	5.1	29	**PDB header:**toxin **Chain:** B: **PDB Molecule:**putative membrane antigen; **PDBTitle:** bipd - an invasion prtein associated with the type-iii2 secretion system of burkholderia pseudomallei.