Phyre^2

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Description	P0AEM4
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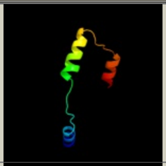
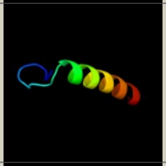
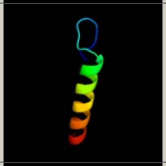
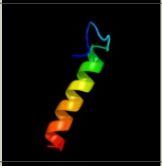
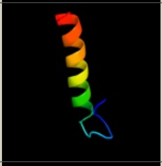
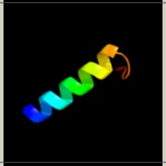
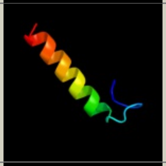
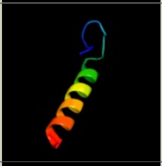
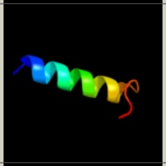
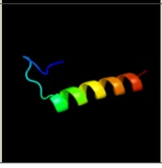
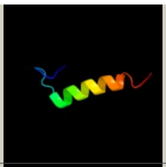
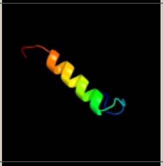
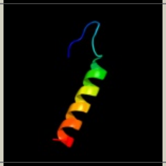
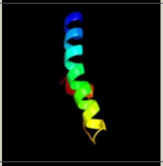
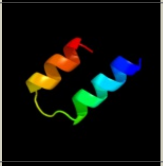
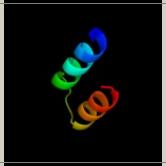
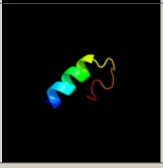
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1rp3b_	Alignment		98.0	31	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Anti-sigma factor FlgM **Family:**Anti-sigma factor FlgM
2	c3q71A_	Alignment		40.3	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 14; **PDBTitle:** human parp14 (artd8) - macro domain 2 in complex with adenosine-5-2 diphosphoribose
3	c2x47A_	Alignment		40.3	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**macro domain-containing protein 1; **PDBTitle:** crystal structure of human macrod1
4	d1zr5a1	Alignment		29.3	14	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
5	c1zr5B_	Alignment		26.3	14	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**h2afy protein; **PDBTitle:** crystal structure of the macro-domain of human core histone variant2 macroh2a1.2
6	c2fqxA_	Alignment		25.8	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**membrane lipoprotein tmpc; **PDBTitle:** pnra from treponema pallidum complexed with guanosine
7	d1yd9a1	Alignment		25.8	14	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
8	d1spva_	Alignment		25.6	11	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
9	c3kxeD_	Alignment		24.6	14	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**antitoxin protein pard-1; **PDBTitle:** a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
10	c3s99A_	Alignment		24.0	27	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**basic membrane lipoprotein; **PDBTitle:** crystal structure of a basic membrane lipoprotein from brucella2 melitensis, iodide soak
11	c3kh6A_	Alignment		22.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 15; **PDBTitle:** human poly(adp-ribose) polymerase 15, macro domain 2 in2 complex with adenosine-5-diphosphoribose

12	c3q6zA_	Alignment		19.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 14; **PDBTitle:** human parp14 (artd8)-macro domain 1 in complex with adenosine-5-2 diphosphoribose
13	d1vhua_	Alignment		18.3	14	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
14	d1y0na_	Alignment		16.0	39	**Fold:**YehU-like **Superfamily:**YehU-like **Family:**YehU-like
15	c2xd7B_	Alignment		15.3	7	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**core histone macro-h2a.2; **PDBTitle:** crystal structure of the macro domain of human core histone2 h2a
16	d2g3ba2	Alignment		15.1	17	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
17	d1sjpa2	Alignment		14.7	26	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
18	c3tqnC_	Alignment		14.2	20	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional regulator, gntr family; **PDBTitle:** structure of the transcriptional regulator of the gntr family, from2 coxiella burnetii.
19	d1kida_	Alignment		13.8	19	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
20	d1ioka2	Alignment		12.7	22	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
21	c1d8lA_	Alignment	not modelled	12.1	21	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**protein (holliday junction dna helicase ruva); **PDBTitle:** e. coli holliday junction binding protein ruva nh2 region2 lacking domain iii
22	d1we3a2	Alignment	not modelled	11.8	15	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
23	d1chda_	Alignment	not modelled	9.8	21	**Fold:**Methylesterase CheB, C-terminal domain **Superfamily:**Methylesterase CheB, C-terminal domain **Family:**Methylesterase CheB, C-terminal domain
24	d1oela2	Alignment	not modelled	9.7	22	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
25	c3eetA_	Alignment	not modelled	9.1	25	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative gntr-family transcriptional regulator; **PDBTitle:** crystal structure of putative gntr-family transcriptional2 regulator
26	c2lciA_	Alignment	not modelled	9.0	13	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**protein or36; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or36 (casd3 target)
27	c2wv0H_	Alignment	not modelled	9.0	36	**PDB header:**transcription **Chain:** H: **PDB Molecule:**hth-type transcriptional repressor yvoa; **PDBTitle:** crystal structure of the gntr-hutc family member yvoa from2 bacillus subtilis
28	c2dx6B	Alignment	not modelled	8.9	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ttha0132;

28	c2dx6B_	Alignment	not modelled	8.9	11	**PDBTitle:** crystal structure of conserved hypothetical protein, ttha0132 from2 thermus thermophilus hb8
29	d1n7ka_	Alignment	not modelled	8.3	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
30	d1v4ra1	Alignment	not modelled	8.1	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
31	d1iq8a1	Alignment	not modelled	8.1	46	**Fold:**TIM beta/alpha-barrel **Superfamily:**tRNA-guanine transglycosylase **Family:**tRNA-guanine transglycosylase
32	c3ic7A_	Alignment	not modelled	8.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator of gntr family2 from bacteroides thetaiotaomicron
33	d2pgga1	Alignment	not modelled	7.7	24	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
34	d1bvsa2	Alignment	not modelled	7.3	20	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
35	d1t95a1	Alignment	not modelled	6.6	15	**Fold:**RuvA C-terminal domain-like **Superfamily:**Hypothetical protein AF0491, middle domain **Family:**Hypothetical protein AF0491, middle domain
36	c3gqeA_	Alignment	not modelled	6.6	11	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** crystal structure of macro domain of venezuelan equine encephalitis2 virus
37	d1rkta2	Alignment	not modelled	6.4	14	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
38	c3m6cA_	Alignment	not modelled	6.2	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**60 kda chaperonin 1; **PDBTitle:** crystal structure of mycobacterium tuberculosis groel1 apical domain
39	c1iq8B_	Alignment	not modelled	6.2	46	**PDB header:**transferase **Chain:** B: **PDB Molecule:**archaeosine trna-guanine transglycosylase; **PDBTitle:** crystal structure of archaeosine trna-guanine2 transglycosylase from pyrococcus horikoshii
40	c1jrjA_	Alignment	not modelled	5.9	13	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**exendin-4; **PDBTitle:** solution structure of exendin-4 in 30-vol% trifluoroethanol
41	c3dtkA_	Alignment	not modelled	5.9	23	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**irre protein; **PDBTitle:** crystal structure of the irre protein, a central regulator2 of dna damage repair in deinococcaceae
42	c3bwgA_	Alignment	not modelled	5.7	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**uncharacterized hth-type transcriptional regulator yydk; **PDBTitle:** the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168
43	c3l9vE_	Alignment	not modelled	5.6	9	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**putative thiol-disulfide isomerase or thioredoxin; **PDBTitle:** crystal structure of salmonella enterica serovar typhimurium srga
44	d1r5ya_	Alignment	not modelled	5.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**tRNA-guanine transglycosylase **Family:**tRNA-guanine transglycosylase
45	d1w7ca3	Alignment	not modelled	5.5	21	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
46	c3ng3A_	Alignment	not modelled	5.5	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**deoxyribose-phosphate aldolase; **PDBTitle:** crystal structure of deoxyribose phosphate aldolase from mycobacterium2 avium 104 in a schiff base with an unknown aldehyde
47	d1ub3a_	Alignment	not modelled	5.5	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
48	d1mzha_	Alignment	not modelled	5.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
49	d1xw3a1	Alignment	not modelled	5.2	19	**Fold:**ParB/Sulfiredoxin **Superfamily:**ParB/Sulfiredoxin **Family:**Sulfiredoxin-like
50	d1wuea1	Alignment	not modelled	5.1	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like