

# Identification of possible functionality of an unknown protein sequence

Abhishek Dasgupta (06MS07)  
Sambit Bikas Pal (06MS03)

Indian Institute of Science Education and Research, Kolkata

April 18, 2008

What we've done: in a nutshell.

- ▶ Picked a protein from SWISSPROT (ideally this would be an unknown protein sequence; however without access to an unknown sequence, we took a known one.)

What we've done: in a nutshell.

- ▶ Picked a protein from SWISSPROT (ideally this would be an unknown protein sequence; however without access to an unknown sequence, we took a known one.)
- ▶ Did a sequence search on PFAM.

What we've done: in a nutshell.

- ▶ Picked a protein from SWISSPROT (ideally this would be an unknown protein sequence; however without access to an unknown sequence, we took a known one.)
- ▶ Did a sequence search on PFAM.
- ▶ Found a match! Topoisomerase IV (PF00521)  
(what are topoisomerases?)

What we've done: in a nutshell.

- ▶ Picked a protein from SWISSPROT (ideally this would be an unknown protein sequence; however without access to an unknown sequence, we took a known one.)
- ▶ Did a sequence search on PFAM.
- ▶ Found a match! Topoisomerase IV (PF00521) (what are topoisomerases?)
- ▶ Did CLUSTALW alignment with the PFAM **seed**. Identified conserved residues.

What we've done: in a nutshell.

- ▶ Picked a protein from SWISSPROT (ideally this would be an unknown protein sequence; however without access to an unknown sequence, we took a known one.)
- ▶ Did a sequence search on PFAM.
- ▶ Found a match! Topoisomerase IV (PF00521) (what are topoisomerases?)
- ▶ Did CLUSTALW alignment with the PFAM **seed**. Identified conserved residues.
- ▶ Read the structure paper → important residues → are they there?

1.png

2.png



3.png

4.png

5.png

6.png

From the structure paper for 1ZVT ([doi:10.1016/j.jmb.2005.06.029](https://doi.org/10.1016/j.jmb.2005.06.029)) we see that topo IV is mainly encoded by **parC**, **parE**  
**parC** comprises two domains:

- ▶ (28-158) helix turn helix motif similar to CAP; contains active sites needed for DNA cleavage: Arg119 and Tyr120. Arg119 and Tyr120 was found **exactly** conserved across the test sequences (taken from Pfam seed PF00521) and our unknown protein.
- ▶ (159-340) **tower** packs against CAP domain; structural support.
- ▶ also there's a compact  $\alpha$ -helical bundle connected by long  $\alpha$ -helices to the tower domain and the C-terminal domain.

ParC27-dimer.png

# Knowing the unknown

So what is the unknown protein?

- ▶ It is most probably a **topoisomerase IV**. It contains the Arg119 and Trp120 residues as mentioned earlier.
- ▶ The topoisomerase portion starts only from sequence 42, as is evidenced by the lack of alignments before that residue.

# Thanks!

We are especially grateful to Dr. Rana Bhadra without whose help this project would not have been realised.