IDPbyNMR
ITC BUDAPEST 2011

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Peter Tompa's Lab

Short Note About Myself

- Origin: India.
- Education: Schooling -> Vivekananda Institution, Howrah.
  Under Graduation -> 4 years Bachelor of Technology in Biotechnology from West Bengal university of Technology ,India, 2008.
  Post Graduate Certificate-> Bioinformatics from Cardiff university , UK,2009.
  Post Graduation -> MSc in Bioinformatics with Systems Biology from Birkbeck, University of London, 2010.

Experience in Bioinformatics

- Developed Protein Database using Java Programme by SQL command.

  Supervisor : J.S. Pahwa

  Department: Computer Science & Informatics, Cardiff University.

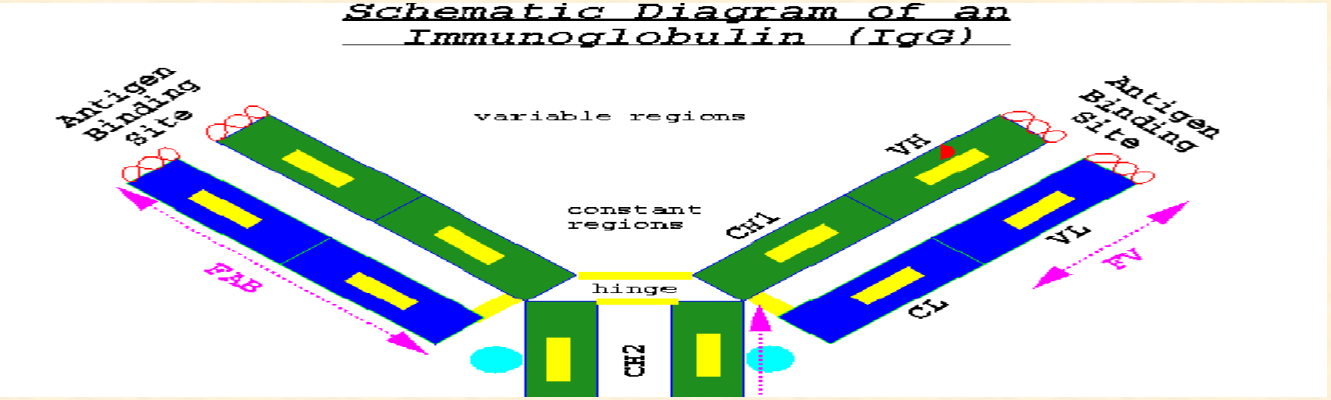
- Looking at preferred pairing of mouse antibody germline sequences using Abysis .

  Supervisor : Dr Andrew Martin

  Department: Research Department of Structural and Molecular Biology, UCL.

Preferred Germline Pairing In Antibodies of Mouse

- In present century one third of drug has been developed using antibody as a drug molecules.
- Little was known before about the preferences for how light and heavy chains pair.
- In this research, aim was to see whether pairing occurs randomly or they have any preference.



Basic Antibody Structure (Brief Introduction to Antibody Structure, Figure 1, 2000)

Preferred Germline Pairing In Antibodies of Mouse

- In order to understand the nature of pairing, first step started with extraction of light and heavy chain sequence of mouse from ‘KabatMan’ database using KabatMan Query language and V-gene sequence including their germline Id from ‘Vbase 2’database.
- After running blast and tblastn, we did statistical analysis where our p-value is significant.
- Which means pairing between V-genes are not random they follow some preference during pairing.

Outline overview Ubiquitin System

The idea is about structural disorder in ubiquitin ligases and the whole system has to be able to recognize the many unpredictable misfolded states of all the proteins in the cell.

- Collect from databases human E1, E2 and E3 sequences.
- Predict disorder for them …… Predict also potential binding sites .
- Collect binding partners of E3 ligases, try find out if they are co-factor bona fide substrates.

Thank you so much to all.