Narendra Kumar, PhD

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Summary

- Interdisciplinary research background in Computational Biology, Molecular Structural Biology, Bioinformatics and Biochemistry.

- Six years of postdoctoral experience in Biological Data Analysis (Protein sequence, small molecules, and NGS), Computational data modeling, Genome Arithmetic, Data mining and Large Scale Data Modeling with Python, Perl, R and Linux shell scripting.

- Track record of bioinformatics software tool development, data analysis, and workflow design in computational screening for Genome Mining and Structure Biology.

Work Experience

Assistant Professor   Dec 2017 to present

Jaypee University of Information Technology, Solan, HP, INDIA
- Teaching: Programming Languages, Structural Biology, Computational Genomics

- Research: Genome Biology, Chromatin Structure

Postdoctoral Computational Biologist   Apr 2013 to Dec 2016

University of Glasgow, Glasgow, UK
- Established computational biology setup in an experimental lab, including purchasing, installing and managing the computational infrastructure.

- Developed Next Generation Sequencing analysis pipelines and tools for detecting DNA-binding sites, and RNA-seq based differential analysis in human genome.

Postdoctoral Fellow   Sep 2010 to Jan 2013

Georgia Institute of Technology, Atlanta, US
- Developed EFICAz2.5, a sequence based enzyme function prediction server, and applied to 373 proteomes.

- Structure modelling of whole enzyme complement of human proteome

- Developed a computational metabolomics approach to identify differentially expressed metabolites.

Research Associate   Jan 2010 to Aug 2010

National Institute of Immunology, New Delhi, INDIA

- Modelling of pfCDPK1 in active and inactive conformations in *Plasmodium falciparum* malarial parasite.

- Developed the structural visualization module of SBSPKS, a popular webserver for analysis of antibiotic synthesis.

Education

PhD, Bioinformatics, National Institute of Immunology, New Delhi, INDIA   July 2013 to Dec 2009

> Thesis title: Modelling protein-peptide complexes using rotamer library approach: application to prediction of substrates for MHC and kinases

 M.Sc. Biomedical Sciences, University of Delhi, New Delhi, INDIA   July 2001 to June 2003

> Molecular Biology, Biochemistry, Genetics, Immunology, Pharmacology, Toxicology, Human Physiology, Instrumentation, Medicinal Chemistry, Organic chemistry etc.

B.Sc. General, University of Delhi, New Delhi, INDIA   July 1998 to June 2013

> Zoology, Chemistry, Botany

Techniques Skills and Software

Next Generation Sequencing	Computational Structure Biology	Machine Learning (Scikit-learn)
Chip-seq data analysis	Protein Structure Modelling	Deep learning
RNA-seq data analysis	Protein-Peptide interaction	Algorithm Development
Transcriptome assembly	MD simulations	Perl (expert)
Differential Expression Analysis	Protein-Drug Interaction	Python
Gene regulation analysis	Metabolite Screening	R
Gene Regulatory elements	Enzyme Function Prediction	Shell Scripting
Peak Finding, Motif Search	Comparative Sequence Analysis	Web Server, CGI-Scripts
Network Biology	Interactive Database	Statistical Analysis

Software developed are available at https://github.com/narekum (NGS pipelines and tools)

Publications

1. Ashok Kumar, Gaobing Wu, Zuo Wu, Narendra Kumar, Ziduo Liu (2018) Improved catalytic properties of a serine hydroxymethyl transferase from Idiomarina loihiensis by site directed mutagenesis. *International journal of biological macromolecules,* 117, 1216-1223.
2. Shradha Khater, Money Gupta, Priyesh Agrawal, Neetu Sain, Jyoti Prava, Priya Gupta, Mansi Grover, Narendra Kumar and Debasisa Mohanty (2017) SBSPKSv2: Structure based sequence analysis of polyketide syntheses and non-ribosomal peptide synthetases. *Nucleic Acids Research* , 45, W72-W79.
3. Narendra Kumar, Nikhil Damle and Debasisa Mohanty (2015) Getting phosphorylated: Is it necessary to be accessible? *Proc Indian Natn Sci Acad*, Part A 81,493-507.
4. Narendra Kumar and Jeffrey Skolnick (2012) EFICAz2.5: application of a high-precision enzyme function predictor to 396 proteomes. *Bioinformatics*, 28:2687-2688.
5. Anwar Ahmed, Kavita Gaadhe, Guru Prasad Sharma, Narendra Kumar, Mirela Neculai, Raymond Hui, Debasisa Mohanty, Pushkar Sharma (2012) Novel insights into the regulation of malarial calcium-dependent protein kinase 1. *The FASEB Journal*, 26:3212-3221.
6. Swadha Anand, Prasad Manglam, Gitanjali Yadav, Narendra Kumar, Jyoti Shehara, Zeeshan Ansari and Debasisa Mohanty (2010) SBSPKS: Structure Based Sequence Analysis of Polyketide Synthases. *Nucleic Acids Research*,38:W487-96.
7. Narendra Kumar and Debasisa Mohanty (2010) Structure-based identification of MHC binding peptides: Benchmarking of prediction accuracy. *Molecular Biosystems*, 12:2508-20.
8. Narendra Kumar and Debasisa Mohanty (2010) Identification of substrates for Ser/Thr protein kinases using residue based statistical pair potentials. *Bioinformatics*, 26:189-197.
9. Narendra Kumar and Debasisa Mohanty (2007) MODPROPEP: a program for knowledge-based modeling of protein-peptide complexes. *Nucleic Acids Research*, 35:W549-555.

2 manuscripts under preparation