NARENDRA KUMAR (PhD) | Assistant Professor

Department of Biotechnology and Bioinformatics
Jaypee University of Information Technology, Solan, HP, INDIA
Mobile: +91 9891287635
Emails: narekum@gmail.com
Website: https://narekum.github.io

Professional Profile

- 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.

Career Summary

Assistant Professor, Jaypee University of Information Technology, Solan   **Dec 2017 to present**

Teaching: Undergraduate courses in Bioinformatics
- Teaching theory courses, namely Programming Languages, Computational Genomics, Biological computation and Structural Bioinformatics
- Teaching laboratory courses, namely Programming Languages for Bioinformatics, R

Research: Computational Genomics, Data Mining, Computational Software development

Freelancing in NGS data analysis   **Jan 2017 to Nov 2017**

- Setup and maintained Google Cloud based NGS Data analysis pipelines and tools upto date with various genomic resources for ChIP-seq, RNA-seq and differential gene expression analysis.

Postdoctoral Computational Biologist, University of Glasgow, UK   **Apr 2013 to Dec 2016**

Highlights
- 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.

Project: Investigating the role of erythroid transcription factors in K562 cells.
- ChIP-seq analysis of in-house and publicly available NGS data.
- Genome-wide identification of regulatory elements such as enhancers using clustering methods.
- Investigating possible role of TF binding motifs arrangement in gene regulation.
- RNA-seq data analysis for differential gene expression in knock-out cells.

Project: Identifying chromatin boundaries.
- Profiling various histones modifications in chromatin.
- DNaseDGF and nucleosome data analysis for open chromatin.

Postdoctoral Fellow, Georgia Institute of Technology, Atlanta, US   Sep 2010 to Jan 2013

Project: Development of high precision enzyme function prediction algorithms.
- EFICAz2.5, an enzyme function prediction server was developed and applied to 373 proteomes.
- A computational metabolomics approach was developed to identify differentially expressed metabolites.

Research Associate, National Institute of Immunology, INDIA   Jan 2010 to Aug 2010

Project: Understanding the role of malarial calcium-dependent protein kinase (pfCDPK1).
- Homology based modeling of pfCDPK1 in active and inactive conformations that led to better understanding of calcium signaling in Plasmodium falciparum malarial parasite.

Project: Structure Based Sequence Analysis of Polyketide Synthases
- Contributed to the structural modeling and visualization module of SBSPKS, a popular webserver for sequence and structure-based analysis of polyketide synthases.

Research Scholar, National Institute of Immunology, INDIA   2003 to Jan 2009

Thesis title: Modeling protein-peptide complexes using rotamer library approach: application to prediction of substrates for MHC and kinases (*Supervisor:* Dr. Debasisa Mohanty)
Project highlights:
- Developed a structure based program for identification of substrates for protein kinases and MHC proteins.
- The program models protein-peptide complexes by rotamer library approach and scores substrates using residue based statistical pair-potential and MM/PBSA approach.
- The program has been benchmarked on known substrates of protein kinase and MHC proteins.

Education and Qualifications

Year	Degree	Institution	Field of Study
2003-2009	Ph.D	National Institute of Immunology, New Delhi, INDIA	Computational Structural Biology
2001-2003	M.Sc. (Biomedical Sciences)	Dr. B R Ambedkar Center for Biomedical Research, University of Delhi, INDIA	Molecular Biology, Genetics, Immunology, Physiology, Pharmacology etc.
1998-2001	B.Sc. (General)	SGTB Khalsa College, University of Delhi, INDIA	Zoology, Botany, Chemistry

RESEARCH 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.

Manuscripts submitted
1. **Characterization of Nucleocapsid (N) Protein from Novel Coronavirus SARS-CoV-2**
Kumar, A.; Parveen, A.; Kumar, N.; Bairy, S.; Kaushik, V.; Chandola, C.; Sharma, J.; Sharma, P.; Agarwal, A.; Pandey, A.; Goyal, P.; Neerathilingam, M. Characterization of Nucleocapsid (N) Protein from Novel Coronavirus SARS-CoV-2. Preprints 2020, 2020050413 (doi: 10.20944/preprints202005.0413.v1).

Technical Expertise

- **Next Generation Sequencing Data Analysis**
  - ChIP-seq analysis, Peak finding, Motif search
  - RNA-seq analysis, transcriptome assembly and differential expression analysis
  - DNase-DGF, CAGE, nucleosome data analysis
  - Experimental/High Throughput Genomic Data Handling & Analysis
- **Computational Structural Biology**
  - Protein Modeling, Molecular Dynamics Simulations
  - Protein-Protein / Protein-Peptide/drug Interaction
  - High Throughput Virtual Screening, Scoring Functions.
  - Comparative Sequence Analysis
  - Interactive Database / Web Interface Generation
  - Statistical Analysis using R and Other Tools
- **Operating System**
  - UNIX (Linux/Irix/Solaris), Mac OS, Windows
- **Programming Skills**
  - Perl, Python, R, Unix Shell Scripts, HTML
  - Web Interface, CGI Scripts

Bioinformatics Software Developed (https://github.com/narekum)

- **VSVina**: Virtual screening of ligands
- **locStack**: A program for meta-analysis of genomic features using NGS.
- **vChIP:** SVM based identification of transcription factor binding sites.
- **MODPROPEP**, a structure based program for analysis and prediction of substrates for protein kinases and MHC proteins).

- EFICAz2.5: A High Precision enzyme function prediction program.
- A Genome-Wide Enzyme Function Annotation Database
- SUNPRO: A Database of Structure & FUNction Predictions of Proteins from Representative Organisms
  SBSPKS: structure based sequence analysis of polyketide synthases
- PDF Library, a local resource for archiving and retrieval of peer-reviewed research articles that facilitates fast and easy access of articles to user's convenience and preference.

Awards / Honours

1. Senior Research Fellowship (SRF), awarded by Council of Scientific and Industrial Research (CSIR), Government of India, from July 2005 – June 2008.
2. CSIR Junior Research Fellowship (JRF) in July 2003 – June 2005.
3. Qualified National Eligibility Test (NET) for Lectureship, conducted by CSIR and University Grant Commission (UGC), as top 20% of qualified students.

Conferences & Workshops

1. Attended National Conference on "Emerging Areas in Biomedical Sciences", 28th-30th December, 2002, Bundelkhand University, Jhansi, Utter Pradesh, INDIA.
2. Attended II Annual Conference of the Society of Pharmacovigilance (INDIA), 1st-2nd March, 2003, V. P. Chest Institute, University of Delhi, Delhi, INDIA.
3. Presented poster titled "Structure based approach for predicting MHC binding peptides" at the second Indian symposium of protein society – protein structure and function, Indian Institute of Technology Bombay, Mumbai (2004)
4. Presented poster titled "Structure based approach for predicting substrates for protein kinases" at International conference on bioinformatics (IncoB), Hotel Ashoka, New Delhi (2006)
5. Participated in "Accelrys Discovery Studio 1.5 workshop" conducted by Accelrys and University of Pune, INDIA, during March 15 to 17, 2006.
6. Presented poster titled "MODPROPEP: a program for structure based prediction of substrates for protein kinases and MHC proteins" at Bangalore Bio, BIEC, Bangalore (2008)
7. Attended 20th Annual Suddath Symposium - Prions & Protein Misfolding at Georgia Tech, Atlanta, US, 2012
8. Attended Wellcome Trust Waddington Symposium: Epigenetics in dialogue with the GENOME, 1st -5th June, 2015, Edinburgh, UK.
9. Chaired a session at 1st International Conference on Recent Trends in Biotechnology and Bioinformatics (ICBAB), 1-3 Aug, 2019 at Jaypee University of Information Technology, Waknaghat, HP, INDIA.