# University Faculty Details Proforma for DU Web-site

| Title | Dr. | First Name | Manish | Last Name | Kumar | Photograph |
|---|---|---|---|---|---|---|
| Designation | | Assistant Professor | | | |  |
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**Educational Qualifications**

| Degree | Institution | Year |
|---|---|---|
| Ph.D. | CSIR-Institute of Microbial Technology, Chandigarh | 2008 |
| Advance Post Graduate Diploma in Bioinformatics | Jawaharlal Nehru University, New Delhi | 2003 |
| PG | Guru Nanak Dev University, Amritsar | 2002 |
| UG | Gaya College, Gaya | 1998 |

**Career Profile**

Post-doctoral Fellow, Department of Biology, McGill University, Montreal, Canada (Jan 2009-May 2010)

**Administrative Assignments**

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**Areas of Interest / Specialization**

Use of Computational Biology, Bioinformatics, Next Generation Sequencing, Protein and Genome Sequence Analysis and Machine Learning Methods in:

- Evolutionary analysis and classification of proteins.
- Discerning large-scale evolutionary trends in genome evolution.
- Prediction of novel activities and biological functions of proteins, and inference of organismal biology from comparative sequence and genome analysis.
- Evolutionary Analysis of antimicrobial drug resistance.

**Subjects Taught**

- Computational methods in biology,
- Bioinformatics
- Research Methodology
- OMICS Biology

**Research Guidance**

**Publications Profile**

***Supervision of Doctoral Thesis, under progress***

*Manisha Aswal, Since 2018*
*Deeksha Pandey, Since 2016*
*Anjali Garg, Since 2015*

***Supervision of awarded Doctoral Thesis***

*Abhishikha Srivastava,* (2013)
*Bandana Kumari,* (2012)
*Ravindra Kumar,* (2010)

***Supervision of awarded M. Phil dissertations***

*Sohani Singh Jain* (2012)

***Research papers published in Refereed/Peer Reviewed Journals***

**(# Corresponding Author, * Equal Contribution)**

#46. Singhal N, Maurya AK, Mohanty S, **Kumar M,** Virdi JS. Evaluation of bile salt hydrolases, cholesterol-lowering capabilities and probiotic potential of Enterococcus faecium isolated from rhizosphere. **Frontiers in Microbiology,** section Food Microbiology

45. Singhal N, Maurya AK, Singh NS, **Kumar M,** Virdi JS. (2019) Antimicrobial resistance and its relationship with biofilm production and virulence-related factors in Yersinia enterocolitica biotype 1A. **Heliyon.** 5(5):e01777. [PMID: 31193467]

44. Sharma, D., Garg, A., **Kumar, M.,** Khan, A.U. (2019). Proteome profiling of carbapenem-resistant K. pneumoniae clinical isolate (NDM-4): Exploring the mechanism of resistance and potential drug targets. **J Proteomics.** 200:102-110. [PMID: 30953729]

#43. Singhal, N., Pandey, D., **Kumar, M.** and Virdi, J. S. (2019) Molecular analysis of ampR and ampD to understand variability in inducible expression of "BlaB-like" cephalosporinase in Yersinia enterocolitica biotype 1A. **Gene.** 704:25-30. [PMID 30980942]

#42. Singhal, N., Pandey, D., Singh, N.S., **Kumar, M.** and Virdi, J. S. (2019). ampD homologs in biotypes of Yersinia enterocolitica: Implications in regulation of chromosomal AmpC-type cephalosporinases. **Infection, Genetics and Evolution.** 69:211-215. [PMID 30710654]

#41. Singhal, N., Pandey, D., **Kumar, M.** and Virdi, J. S. (2019). Molecular Characteristics of "BlaB-like" Chromosomal Inducible Cephalosporinase of Yersinia enterocolitica Biotype 1A Strains. **Microbial Drug Resistance.** [PMID 30817214]

#40. Kumari, B., Kumar, R. and **Kumar, M.** (2019). Identifying residues that determine palmitoylation using association rule mining. **Bioinformatics.** [PMID 30649192]

#39. Kumari, B., Kumar, R. and **Kumar, M.** (2018). Comparative functional analysis of proteins containing low-complexity predicted amyloid regions. **PeerJ.** 6:e5823. [PMID 30397544]

#38. Garg A, Kumari B, Singhal N, **Kumar M.** (2018) Using molecular-mimicry-inducing pathways of pathogens as novel drug targets. **Drug Discovery Today.** 30256-3. [PMID: 30366058]

#37. Srivastava, A.*, Kumar, R.*, and **Kumar, M.** (2018) BlaPred: predicting and classifying beta-lactamase using a 3-tier prediction system via Chou's general PseAAC. **Journal of Theoretical Biology.** 457:29-36. [PMID: 30138632]

#36. Kumari, B., Kumar, R. and **Kumar, M.** (2018). Prediction of rare palmitoylation events in proteins. **Journal of Computational Biology**. Sep;25(9):997-1008. doi: 10.1089/cmb.2017.0069. [PMID 29963911]

#35. Garg, A., Kumari, B., and **Kumar, M. Emerging Role of HSP70 in Human Diseases.** Heat Shock Proteins, Vol. 14, Alexzander A. A. Asea and Punit Kaur (Eds): HSP70 in Human Diseases and Disorders.

#34. Srivastava, A. and **Kumar, M. (2018)** Prediction of Zinc Binding Sites in Proteins using Sequence Derived Information. ***Journal of Bimolecular Structure & Dynamics*** **Jan 15:1-11. doi:** 10.1080/07391102.2017.1417910. [PMID: 29241411]

#33. Garg, A., Kumari, B., Kumar, R. and **Kumar, M. (2017)** miPepBase: A database of experimentally verified peptides involved in molecular mimicry. ***Frontiers in Microbiology, section Microbial Immunology*** 8:2053. doi: 10.3389/fmicb.2017.02053. [PMID: 29109711]

#32. Kumar, R., Kumari, B. and **Kumar, M. (2017)** Proteome-wide prediction and annotation of mitochondrial and sub-mitochondrial proteins by incorporating domain information. ***Mitochondrion*** pii: S1567-7249(17)30032-6. doi: 10.1016/j.mito.**2017**.10.004. [PMID: 29032233]

#31. Kumar, R., Kumari, B. and **Kumar, M. (2017)** Prediction of endoplasmic reticulum resident proteins using fragmented amino acid composition and support vector machine. ***Peer J.*** 5:e3561. [PMID: 28890846]

30. Singhal, N., **Kumar, M.** and Virdi, J.S. MALDI-TOP MS in clinical parasitology: applications, constrains and prospects. ***Parasitology.*** 2016;143(12):1491-500. [PMID: 27387025]

#29. Kumar, R., Kumari, B. and **Kumar, M.** (**2016**). PredHSP: Sequence Based Proteome-Wide Heat Shock Protein Prediction and Classification Tool to Unlock the Stress Biology. ***PLoS One***. 11(5):e0155872. [PMID: 27195495]

28. Rani, S., Srivastava, A., **Kumar, M.** and Goel, M. (**2016**). CrAgDb – A database of annotated chaperone repertoire in archaeal genomes. ***FEMS Microbiology Letters***. 363(6). [PMID: 26862144].

27. Singhal, N., **Kumar, M.** and Virdi, J.S. (**2016**). Resistance to amoxicillin-clavulanate and its relation to virulence-related factors in Yersinia enterocolitica biovar 1A. ***Indian Journal of Medical Microbiology.*** 34(1):8 [PMID: 26776125]

26. Singhal N, **Kumar M**, Kanaujia PK and Virdi JS. MALDI-TOF mass spectrometry: An emerging technology for microbial identification and diagnosis. ***Frontiers in Microbiology.*** 2015 Aug 5;6:791. [PMID: 26300860].

25. Singhal N, Srivastava A, **Kumar M**, Virdi JS. Structural Variabilities in β-Lactamase (blaA) of Different Biovars of *Yersinia enterocolitica*: Implications for β-Lactam Antibiotic and β-Lactamase Inhibitor Susceptibilities. ***PLoS One.*** 2015 10(4):e0123564. [PMID: 25919756].

#24. Kumar, R*, Srivastava A*, Kumari B and **Kumar M**. Prediction of Beta-lactamase and its Class by Chou's Pseudo-amino Acid Composition and Support Vector Machine. ***Journal of Theoretical Biology.*** 2015 Jan 21;365:96-103. [PMID: 25454009].

#23. Kumari B, Kumar R and **Kumar M**. Low complexity and disordered regions of proteins have different structural and amino acid preferences. ***Molecular Biosystems.*** 2015 Feb;11(2):585-94. [PMID: 25468592].

#22. Srivastava A, Singhal N, Goel M, Virdi JS and **Kumar M**. CBMAR: A Comprehensive Beta-Lactamase Molecular Annotation Resource. ***Database.*** 2014 Dec 3;2014:bau111. [PMID: 25475113].

#21. Kumar R*, Kumari B*, Srivastava A and **Kumar M**. NRfamPred: A proteome-scale two level method for prediction of nuclear receptor proteins and their sub-families. ***Scientific Reports.*** 4:6810. [PMID: 25351274].

20. Singhal N, **Kumar M**, Virdi JS. Molecular Analysis of β-Lactamase Genes to Understand their Differential Expression in Strains of Yersinia enterocolitica Biotype 1A. ***Scientific Reports*** 2014 4:5270. [PMID: 24920253]

#19. Kumar R, Jain S, Kumari B, **Kumar M**. Protein Sub-Nuclear Localization Prediction Using SVM and Pfam Domain Information. ***PLoS One.*** 2014: 9(6):e98345. [PMID: 24897370]

#18. Srivastava A, Singhal N, Goel M, Virdi JS, **Kumar M**. Identification of family specific fingerprints in β-lactamase families. ***The Scientific World Journal.*** 2014;2014:980572. [PMID: 24678282]

#17. Kumari B, Kumar R, **Kumar M**. PalmPred: an SVM based palmitoylation prediction method using sequence profile information. ***PLoS One.*** 2014 ;9(2):e89246. [PMID: 24586628]

16. Singhal N, Sharma P, **Kumar M**, Joshi B, Bisht D. Analysis of intracellular expressed proteins of Mycobacterium tuberculosis clinical isolates. ***Proteome Science.*** 2012; 10(1): 14. [PMID: 22375954]

15. Harbi D, Parthiban M, Gendoo DM, Ehsani S, **Kumar M,** Schmitt-Ulms G, Sowdhamini R, Harrison PM. PrionHome: a database of prions and other sequences relevant to prion phenomena. ***PLoS One.*** 2012;7(2):e31785. [PMID: 22363733]

14. Harbi D, **Kumar M** and Harrison P. LPS-Annotate: Complete annotation of compositionally biased regions in the protein knowledge base. ***Database.*** 2011 (doi: 10.1093/database/baq031). [PMID: 21216786]

13. **Kumar M**, Gromiha MM, Raghava GPS. SVM based Prediction of RNA-binding Proteins using Binding Residues and Evolutionary Information. ***Journal of Molecular Recognition.*** 2011, 24: 303. [PMID: 20677174]

12. Harrison P, Khachane A and **Kumar M**. Genomic assessment of the evolution of the prion protein gene family in vertebrates. ***Genomics***. 2010,95:268. [PMID:20206252]

11. Rashid M, Singla D, Sharma A, **Kumar M** and Raghava GPS. HMRbase: A database of hormones and their receptors. ***BMC Genomics***. 2009,10:307. [PMID: 19589147]

10. Arora PK, **Kumar M**, Chauhan A, Raghava GPS, Jain RK. OxDBase: a database of oxygenases involved in biodegradation. ***BMC Res Notes***. 2009;2:67. [PMID: 19405962]

9. Ahmed F, **Kumar M**, and Raghava GPS. Prediction of polyadenylation signals in human DNA sequences using nucleotide frequencies. ***In Silico Biology***, 2009,9:7. [PMID: 19795571]

8. **Kumar M**, Raghava GPS. Prediction of nuclear proteins using SVM and HMM models. ***BMC Bioinformatics***. 2009;10:22. [PMID: 19152693]

7. Kalita MK, Nandal UK, Pattnaik A, Sivalingam A, Ramasamy G, **Kumar M**, Raghava GPS, Gupta D. CyclinPred: A SVM-Based Method for Predicting Cyclin Protein Sequences. ***PLoS ONE***. 2008 Jul 2;3(7):e2605. [PMID: 18596929]

6. **Kumar M**, Thakur V, Raghava GPS. COPid: Composition Based Protein Identification. ***Insilico Biology*** 2008;8(2):121-8. [PMID: 18928200]

5. **Kumar M**, Gromiha MM, Raghava GPS. Identification of DNA-binding proteins using support vector machines and evolutionary profiles. ***BMC Bioinformatics***. 2007 Nov 27;8(1):463. [PMID: 17932917]

4. **Kumar M**, Gromiha MM, Raghava GPS. Prediction of RNA binding sites in a protein using SVM and PSSM profile. ***Proteins*** 2008 Apr;71(1):189-94. [PMID: 17932917]

3. Mishra NK, **Kumar M**, Raghava GPS. Support vector machine based prediction of glutathione S-transferase proteins. ***Protein & Peptide Letters.*** 2007;14(6):575-80. [PMID: 17627599]

2. **Kumar M**, Verma R, Raghava GPS. Prediction of mitochondrial proteins using support vector machine and hidden Markov model. ***Journal of Biological Chemistry***. 2006 Mar 3;281(9):5357-63. [PMID: 16339140]

**1. Kumar M,** Bhasin M, Natt NK, Raghava GPS. BhairPred: prediction of beta-hairpins in a protein from multiple alignment information using ANN and SVM techniques. ***Nucleic Acids Research.*** 2005 Jul 1;33:W154-9. [PMID: 15988830]

## Conference Organization/ Presentations

*Organizer*

1. 3rd Summer School on Bioinformatics: 26 May - 6 June 2014. Department of Biophysics, University of Delhi South Campus, New Delhi.
2. 2nd Summer School on Bioinformatics: 27 May - 7 June 2013. Department of Biophysics, University of Delhi South Campus, New Delhi.
3. 1st Summer School on Bioinformatics: 28 May - 8 June 2012. Department of Biophysics, University of Delhi South Campus, New Delhi.

*Participation as Paper/Poster Presenter*

1. CBMAR: A holistic and multidimensional database of Beta-lactamases. 27th-29th Nov 2015. Pondicherry, India
2. Exhaustive Assessment of the Evolution of the Vertebrate Prion Protein Gene Family. PrP Canada 2010: On The Horizon. March 8-10, 2010. Ottawa, Ontario, Canada.
3. Mitpred 2.0: An Improved Method of Mitochondrial Protein Prediction. 7th Swiss Proteomics Society Congress (SPS07: Pushing the limits), 3rd-5th December, 2007. Laussane, Switzerland.
4. Kernel based machine learning (SVM) for predicting cyclins. 5th International Conference on Bioinformatics 18th-20th December 2006. New Delhi- India.

*Invited Talk*

1. 6th World Congress on NanoMedical Sciences, Vigyan Bhawan, New Delhi (7-10 Jan, 2019). Title of Talk: Combating infectious disease by computational biology (Jan 8, 2019)
2. National Workshop on Computation for Biomedicine and Healthcare, Indraprastha Institute of Information Technology, New Delhi (Dec 10-14, 2018). Title of Talk: Data Driven Approach for Health Research (Dec 12, 2018)
3. National Workshop on Data Curation and Database Development, National Institute of Plant Genome Research, New Delhi (Dec 11-12, 2018). Title of Talk: New Trends in Data Curation and Databases (Dec 11, 2018)
4. National Symposium on Database Development and Biocuration, University of Delhi South Campus (April 6-7, 2018). Title of Talk: Role of manual and automatic curation in modern biological research (April 6, 2018).
5. 2nd International Caparica Conference in Antibiotic Resistance at Cost de Caparica, Portugal (12-15 June 2017). Title of Talk: Development of knowledge base of Beta-lactamases for mining their functional characters and reaction dynamics (15 June 2017).
6. Emerging Trends in Bioinformatics & Health Informatics at Indian Institute of Information Technology, New Delhi on 16-May-2017. Title of Talk: Understanding antibiotic resistance with in-silico tools (16-May-2017).
7. Recent Trends in Bioinformatics during 07-08 March 2017. Department of Biotechnology, Guru Nanak Dev University, Amritsar (Punjab), India. Title of Talk: Use of Next Generation Sequencing in Modern Biological Research (08 March 2017)
8. Introduction to Perl programing language for biologists during 7-13 November 2016. Pt. J. N. M. Medical College, Raipur (C.G.), India.
9. Bioinformatics databases for the analysis and study of antimicrobial resistance. (In Antibiotic Resistance: A Major Global Threat. Annual Microbiology Festival "Microquest-16" of Bhaskaracharya College of applied sciences.) 16th March 2016.
10. Using Bioinformatics and Proteomics to Understand Microbial Antibiotics Resistance. (In National workshop on Bioinformatics-based Genomic & Proteomic Data Analysis in Microbial

Domain) March 04-09, 2016. National Bureau of Agriculturally Important Microorganisms. Indian Council of Agricultural Research, Govt. of India Mau (Uttar Pradesh) 275103, India

11. Computational Approach to Understand Proteomes and Antibiotics Resistance (In 5th National Science Day Symposium 27-28 Feb, 2015. University of Delhi South Campus, New Delhi)
12. Combating Infectious Disease by Bioinformatics Approach. (In International Conference IC LIFE 2014 JIIT Noida 29-30 August 2014 (Session Chair).
13. Protein Sequence-Structure-Function Relationship. Protein sequence-structure-function relationship. (In 3rd National Science Day Symposium 27-28 Feb, 2013. University of Delhi South Campus, New Delhi).
14. Next Generation Sequencing: A new challenge for both biology and computer science. (In Workshop on High Performance Computing at Inter University Accelerator Center, Aruna Asaf Ali Marg, New Delhi. 25 May 2011)
15. Discovering new members of prion gene family. (In 1st National Science Day Symposium 28 Feb, 2011. University of Delhi South Campus, New Delhi).
16. A quest to predict protein function. (Indian Institute of Chemical Biology, Kolkata. 27 Nov 2009).

**Research Projects (Major Grants/Research Collaboration)**

**As PI:**

1. In-silico analysis and functional characterization of intergenic regions of ESKAPE pathogens to develop novel drug targets. [Funding Agency: ICMR]
2. In-silico protein sequence analysis and function prediction. [Funding Agency: DST]
3. Analysis of protein sequence analysis, structure and function relationship using computational tools and developing new tools to predict protein function. [Funding Agency: UGC]

**As Co-PI:**

1. Genome mining of *Pichia pastoris* for the development of yeast cell surface display technology using its native cell wall anchoring proteins: bioprocess optimization and its biotechnological applications. [Funding Agency: DST]
2. Unfolded protein response: Achilles heels of fungal pathogenesis. [Funding Agency: DST]
3. Comparative Genomics of β-lactamase (Bla) Genes to identify target sequences for B-lactamase inhibitors. [Funding Agency: ICMR]

**Awards and Distinctions**

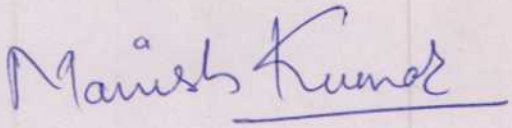
1. 2014: **Long Term HRD Fellowship in Foreign Institute** from Department of Health Research, Government of India, New Delhi (not availed).
2. 2014- till date: **Editorial Board Member 'Scientific Reports'** of Nature Publishing Group.
3. 2007: **Travel award** to attend 2007 congress of the Swiss Proteomics Society held at Lausanne, Switzerland.
4. 2005-2008: **Senior Research Fellowship**, Council of Scientific and Industrial Research, Govt. of India.
5. 2003-2005: **Junior Research Fellowship**, Council of Scientific and Industrial Research, Govt. of India.
6. 2002-2003: **Scholarship from the Department of Biotechnology**, Govt. of India, to pursue Advanced Diploma (PG) in Bioinformatics from Jawaharlal Nehru University, New Delhi (India).
7. 2000-2002: **Scholarship from the Department of Biotechnology**, Government of India, to earn Masters of Science in Biotechnology from Guru Nanak Dev University, Amritsar (INDIA).

**Association With Professional Bodies**

1. Member of Antimicrobial Resistance Databases expert group of Joint Research Centre (JRC) of the European Commission.
2. 2014 to till date: Editorial Board Member of 'Scientific Reports', Nature Publishing Group.
3. 2018 to till date: Review Editor in Bioinformatics and Computational Biology, part of the journal(s) Frontiers in Genetics, Plant Science and Bioengineering and Biotechnology.

**Other Activities**

4. 09-07-2010 – 31-03-2018: Resident Tutor, Saramati PG Men's Hostel, University of Delhi South Campus.
5. 01-06-2010 – till date: Member, Departmental Research Committee of Department of Biophysics, University of Delhi South Campus.
6. 08-10-2013 – 07-10-2015: Member, Board of Research Studies, Faculty of Interdisciplinary and Applied Sciences, University of Delhi South Campus.
7. 04-04-2014 – 03-04-2017: Member, Faculty, Faculty of Interdisciplinary and Applied Sciences, University of Delhi South Campus.



**MANISH KUMAR**

डा. मनीष कुमार **22-Jul-2019**
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