Manish Kumar

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RESEARCH INTEREST

The main research focus of my laboratory is analysis of microbial genomes and proteomes using bioinformatics, chemi-informatics and phylogenomics tools to understand the mechanisms behind evolution and spread of virulence and antibiotic resistance among microbial pathogens. We use molecular modeling and computer-based simulation techniques for structure-based drug designing, translational medicine and protein family based approaches to design and identify drug-like compounds. We predict functional interactions between proteins in metabolic and signaling pathways or protein complexes and use this information to develop new drug targets. We also use Next Generation Sequencing based metagenomic data to analyze the load of antibiotic resistance genes in different biotic reservoirs.

The information content of genome databases has increased rapidly due to significant reduction in cost of high-throughput gene/genome sequencing. But the annotation pipelines for the same are comparatively less resulting in a large number of incomplete/improperly-annotated genomes. My research group is using and developing our own, 'in house' bioinformatics tools for functional annotation of genes, functional and structural prediction of encoded proteins, and reconstruction of metabolic, regulatory and transport networks for complete annotation of the sequenced genomes.

The research work from my laboratory has been generously funded from following agencies: -

Sr. No.	Funding Agency	Title of Project	Duration	Amount (Lakhs)
Ongoing				
1.	**NESTA (UK)/ BIRAC**	Resistance-genes-array based rapid detection of AMR and algorithm-driven therapy	**18 months (May 2017-Nov 2018)**	11.76
2.	**ICMR**	Structural and functional ambiguity in low complexity regions of protein sequences and their association in amyloid disorders **(PhD student SRF)**	**3 Years (2015-18)**	--
3.	**ICMR**	*In-silico* characterization of beta-lactamase for identification of unique features for novel drug target discovery **(PhD student SRF)**	**3 Years (2015-18)**	--
Submitted for funding				
4.	**Indo-Norwagian Grant for Anti-Microbial Resistance (co-ordinator ICMR)**	Investigating magnesium metallo-proteome and magnesium transporters to identify novel drug targets for combating biofilm mediated antimicrobial resistance	**NA**	**NA**
5.	**DBT**	Using computational biology to prioritize clinically approved drugs towards repurposing for tuberculosis	**NA**	**NA**
6.	**SERB/DST**	Unfolded protein response: Achilles heels of fungal pathogenesis	**NA**	**NA**

7.	**SERB/DST**	Combining computational and experimental approaches for the large scale production of humanized single chain antibody fragment (scFv) against hTNF in *E. coli and Pichia pastoris*	**NA**	**NA**
		Completed		
8.	**ICMR**	Comparative genomics of β-lactamase genes including *in-silico* analysis to identify target sequences for β- lactamase inhibitors	**3 Years (2012-15)**	**46.36**
9.	**DST**	*In-silico* protein sequence analysis and function prediction	**3 Years (2012-15)**	**16.90**
10.	**DBT**	Crystallographic structure determination of Archaeal CRISPR-Cas Proteins	**3 Years (2012-15)**	**29.22**

EDUCATION

Ph.D. from Institute of Microbial Technology, Chandigarh, India **Supervisor:** Dr. GPS Raghava	2003-8
Advance Post Graduate Diploma in Bioinformatics from Jawaharlal Nehru University, New Delhi, India	2002-3
M.Sc. Biotechnology from Guru Nanak Dev University, Amritsar, India	2000-2

RESEARCH/TEACHING EXPERIENCE

June 2010 – Present	**Assistant Professor at** Dept. of Biophysics, University of Delhi South Campus
Jan 2009 – May 2010	**Post Doctoral Scholar** at McGill University, Montreal, Canada (Advisor: Prof. Paul M. Harrison)

COURSES TAUGHT

SR. NO.	COURSE	FROM	LEVEL
1.	Bioinformatics (Theory)	June 2012	M. Sc.
2.	Bioinformatics (Practical)	Jan 2012	M. Sc.
3.	Computer Applications in Biology	Jan 2013	MPhil & Pre-PhD
4.	OMICS Biology	Jan 2016	MPhil & Pre-PhD
5.	Research Methodology	Jan 2016	MPhil & Pre-PhD

RESEARCH SUPERVISION

Level ⬇	Total	Completed	Ongoing
PhD	5	1	4
MPhil	1	1	0
MSc	1	1	0
UG (under DU CSEC)	2	2	0

LIST OF PUBLICATIONS (# Corresponding Author; *Equal contribution)

SUBMITTED / UNDER REVISION

[#]42. Kumari, B., Kumar, R. and **Kumar, M**. Prediction of rare palmitoylation events in proteins. *Journal of Computational Biology (Addressing Reviewer's Questions)*

[#]41. Srivastava, A. and **Kumar, M.** Prediction of Zinc Binding Sites in Proteins using Sequence Derived Information. ***Journal of Biomolecular Structure & Dynamics (Revision Submitted)***

[#]40. Srivastava, A., Kumar, R. and **Kumar, M.** Prediction and Classification of β-lactamases using a Three-tier Prediction System. ***Protein and Peptide Letters (Revision Submitted)***

ACCEPTED

[#]39. Garg, A., Kumari, B., Kumar, R. and **Kumar, M**. 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

[#]38. Kumar, R., Kumari, B. and **Kumar, M**. 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.

PUBLISHED

[#]37. Kumar, R., Kumari, B. and **Kumar, M.** Prediction of endoplasmic reticulum resident proteins using fragmented amino acid composition and support vector machine. ***Peer J.***

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

[#]35. 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]

34. 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].

33. 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]

32. Singhal, N., **Kumar, M.**, Sharma, P. and Bisht, D. (**2016**). Comparative protein profiling of intraphagosomal expressed proteins of *Mycobacterium bovis* BCG. ***Protein & Peptide Letters.*** 23(1):51-4. [PMID: 26548863]

31. Singhal, N., Srivastava, A., **Kumar, M.** and Virdi, J.S. (**2015**). Structural variabilities in β-Lactamase (blaA) of different biovars of *Yersinia enterocolitica*: Implications for β-Lactam Antibiotic and β-Lactamase Inhibitor Susceptibilities. ***PLoS One.*** 10(4):e0123564. [PMID: 25919756].

30. Singhal, N., **Kumar, M.**, Kanaujia, P. K. and Virdi, J.S. (**2015**). MALDI-TOF mass spectrometry: An emerging technology for microbial identification and diagnosis. ***Frontiers in Microbiology.*** 2015 Aug 5;6:791. [PMID: 26300860].

[#]29. Kumar, R.*, Srivastava, A.*, Kumari, B. and **Kumar, M.** (**2015**). Prediction of β-lactamase and its class by Chou's pseudo-amino acid composition and support vector machine. ***Journal of Theoretical Biology.*** 365:96-103. [PMID: 25454009].

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

[#]27. Srivastava, A., Singhal, N., Goel, M., Virdi, J. S. and **Kumar, M.** (**2014**). CBMAR: A comprehensive β-lactamase molecular annotation resource. ***Database.*** 2014:bau111. [PMID: 25475113].

[#]26. Kumar, R.*, Kumari, B.*, Srivastava, A. and **Kumar, M.** (**2014**). NRfamPred: A proteome-scale two level method for prediction of nuclear receptor proteins and their sub-families. ***Nature Scientific Reports.*** 4:6810. [PMID: 25351274].

25. Singhal, N., **Kumar, M.** and Virdi, J.S. (**2014**). Molecular analysis of β-lactamase genes to understand their differential expression in strains of Yersinia enterocolitica biotype 1A. 4:5270. ***Nature Scientific Reports***. 4:5270. PMID: 24920253].

#24. Kumar, R., Jain, S., Kumari, B., **Kumar, M**. (**2014**). Protein sub-Nuclear localization prediction using SVM and Pfam domain information. ***PLoS One***. 9(6):e98345. [PMID: 24897370].

#23. Srivastava, A., Singhal, N., Goel, M., Virdi, J. S. and **Kumar, M**. (**2014**). Identification of family specific fingerprints in β-lactamase families. ***ScentificWorldJournal*** 2014:980572. [PMID: 24678282]

#22. Kumari, B., Kumar, R. and **Kumar, M**. (**2014**). PalmPred: An SVM based palmitoylation prediction method using sequence profile information. ***PLoS ONE*** 9(2):e89246. [PMID: 24586628].

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

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

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

18. **Kumar, M.**, Gromiha, M.M. and Raghava, G.P.S. (**2011**). SVM based prediction of RNA-binding proteins using binding residues and evolutionary information. ***Journal of Molecular Recognition.*** 24(2):303-13. [PMID: 20677174].

17. Harrison, P.M., Khachane, A. and **Kumar, M.** (**2010**). Genomic assessment of the evolution of the prion protein gene family in vertebrates. ***Genomics***. 95(5):268-77. [PMID:20206252].

16. Rashid, M., Singla, D., Sharma, A., **Kumar, M.** and Raghava, G.P.S. (**2009**). HMRbase: A database of hormones and their receptors. ***BMC Genomics***. 10:307. [PMID: 19589147]

15. Arora, P.K., **Kumar, M.**, Chauhan, A., Raghava, G.P.S. and Jain, R.K. (**2009**). OxDBase: a database of oxygenases involved in biodegradation. ***BMC Research Notes***. 2:67. [PMID: 19405962]

14. Ahmed F, **Kumar, M.**, and Raghava, G.P.S. (**2009**). Prediction of polyadenylation signals in human DNA sequences using nucleotide frequencies. ***InSilico Biology***. 2:67. [PMID: 19795571]

13. **Kumar, M.** and Raghava, G.P.S. (**2009**). Prediction of nuclear proteins using SVM and HMM models. ***BMC Bioinformatics***. 10:22. [PMID: 19152693]

12. Kalita, M.K., Nandal, U.K., Pattnaik, A., Sivalingam, A., Ramasamy, G., **Kumar, M.**, Raghava, G.P.S. and Gupta, D. (**2008**). CyclinPred: A SVM-based method for predicting cyclin protein sequences. ***PLoS ONE***. 3(7):e2605. [PMID: 18596929]

11. **Kumar, M.**, Thakur, V. and Raghava, G.P.S. (**2008**). COPid: Composition based protein identification. ***Insilico Biology*** 8(2):121-8. [PMID: 18928200]

10. **Kumar, M.**, Gromiha, M.M. and Raghava, G.P.S. (**2007**). Identification of DNA-binding proteins using support vector machines and evolutionary profiles. ***BMC Bioinformatics***. 8(1):463. [PMID: 17932917]

9. **Kumar, M.**, Gromiha, M.M. and Raghava, G.P.S. (**2008**). Prediction of RNA binding sites in a protein using SVM and PSSM profile. ***Proteins*** 71(1):189-94. [PMID: 17932917]

8. Mishra, N.K., **Kumar, M.** and Raghava, G.P.S. (**2007**). Support vector machine based prediction of glutathione S-transferase proteins. ***Protein & Peptide Letters.*** 14(6):575-80.

[PMID: 17627599]

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

6. **Kumar, M.**, Bhasin, M., Natt, N.K. and Raghava, G.P.S. (**2005**). BhairPred: prediction of beta-hairpins in a protein from multiple alignment information using ANN and SVM techniques. *Nucleic Acids Research*. 33:W154-9. [PMID: 15988830]

CONFERENCE PAPERS/POSTERS

5. 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.

4. 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.

3. Kernel based machine learning (SVM) for predicting cyclins. 5th International Conference on Bioinformatics 18th-20th December 2006. New Delhi- India.

OTHER REPORTS

2. Harbi, D, Parthiban, M, Gendoo, D, Ehsani, S, **Kumar, M**, Schmitt-Ulms, G, Sowdhamini, R, and Harrison, P. PrionOme: A database of prions and other sequences relevant to prion phenomena. *Nature Procedings* <http://hdl.handle.net/10101/npre.2011.6430.1> (2011).

1. **Kumar M**, Verma R and Raghava GPS. Mitpred2: An improved method for predicting mitochondrial proteins using SVM and HMM. *Nature Protocols* (DOI: 10.1038/nprot.2007.488).

HONORS AND AWARDS

1.   2017: Selected for participation with full financial support in **Summer School in Computational Biology for Infectious Disease** at Quy Nhon Vietnam (16-24 September). Organized by Pasteur Institute and NIH.

2.   2014: **Long Term HRD Fellowship in Foreign Institute** from Department of Health Research, Government of India, New Delhi (not availed).

3.   2014 to till date: Editorial Board Member of **'Scientific Reports'**, Nature Publishing Group.

4.   2007: Travel award by Swiss Proteomic Society to attend **2007 congress of the Swiss Proteomics Society** held at Lausanne, Switzerland.

5.   2005: **Senior Research Fellowship**, Council of Scientific and Industrial Research, Govt. of India.

6.   2003: **Junior Research Fellowship**, Council of Scientific and Industrial Research, Govt. of India.

7.   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).

8.   2002: Scored 93.50 percentile (All India Rank 163) in '**Graduate Aptitude Test in Engineering (GATE)**' conducted by Indian Institute of Science.

9.   2002: Qualified **UGC/NET (National Eligibility Test)** conducted jointly by the Council of Scientific and Industrial Research (CSIR) and University Grants Commission (UGC).

10. 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).

11. 2000: Qualified **All India Entrance Examination for M.Sc. in Biotechnology** at Department of Biotechnology (Government of India) funded centers.

INVITED TALKS

1. 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).

2. 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).

3. 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)

4. Introduction to Perl programing language for biologists during 7-13 November 2016. Pt. J. N. M. Medical College, Raipur (C.G.), India.

5. National workshop on Bioinformatics-based Genomic & Proteomic Data Analysis in Microbial Domain during March 04-09, 2016. ICAR-National Bureau of Agriculturally Important Microorganism, Mau (Uttar Pradesh), India.

6. Annual Microbiology Festival "Microquest-16" on 16th March 2016. Sukshmjeev Society of Microbiology Department, Bhaskaracharya College of Applied Sciences, University of Delhi, New Delhi.

7. Computational Approach to Understand Proteomes and Antibiotics Resistance (5th National Science Day Symposium 27-28 Feb, 2015. University of Delhi South Campus, New Delhi)

8. Title: Combating Infectious Disease by Bioinformatics Approach. International Conference IC LIFE 2014 JIIT Noida 29-30 August 2014 (Session Chair). 29 Aug 2014 (30 min)

9. Protein Sequence-Structure-Function Relationship. Protein sequence-structure-function relationship. (3rd National Science Day Symposium 27-28 Feb, 2013. University of Delhi South Campus, New Delhi).

10. Next Generation Sequencing: A new challenge for both biology and computer science. (Inter University Accelerator Center, Aruna Asaf Ali Marg, New Delhi. 25 May 2011)

11. Discovering new members of prion gene family. (1st National Science Day Symposium 28 Feb, 2011. University of Delhi South Campus, New Delhi).

12. A quest to predict protein function. (Indian Institute of Chemical Biology, Kolkata. 27 Nov 2009).

CONFERENCES / WORKSHOPS ATTENDED

1. ASM CME on "Antibiotic Resistance: Renewed Fears". September 10, 2016. India International Center, New Delhi India

2. ICMR-NIAID workshop on systems biology of antimicrobial resistance. January 20-21, 2016. New Delhi.

3. National Conference on 'New Trends in Bioinformatics'. July 30-31st 2012 at the Supercomputing Facility for Bioinformatics and Computational Biology, Indian Institute of Technology Delhi, New Delhi.

4. PrP Canada 2010: On The Horizon. March 8-10, 2010. Ottawa, Ontario, Canada.

5. PrP Canada 2009: Navigating the Risks. March 1-3, 2009. Edmonton, Alberta, Canada.

6. 7th Swiss Proteomics Society Congress (SPS07: Pushing the limits), 3rd-5th December, 2007: Presented a poster entitled "Mitpred 2.0: An Improved Method of Mitochondrial Protein Prediction".

7. 5th International Conference on Bioinformatics 18th-20th December 2006. Presented a poster on "Kernel based machine learning (SVM) for predicting cyclins".

8. South East Asian Training Course on Bioinformatics Applied to Tropical Diseases 28th September 2004–11th October 2004 conducted by WHO, at International Center for Genetic Engineering and Biotechnology (ICGEB), New Delhi.

9. Participated in 91st session of Indian Science Congress Association which was held on January 3rd-7th 2004 at Punjab University and Institute of Microbial Technology, Chandigarh.

ADMINISTRATIVE RESPONSIBILITES

1. Resident Tutor of Saramati PG Men's Hostel, University of Delhi South Campus (09 July 2010 to till date).

2. Member of Departmental Research Committee of Department of Biophysics, University of Delhi South Campus (01-June-2010 to till date).

3. Member of Board of Research, Faculty of Inter-disciplinary and Applied Sciences (25-Sept-2013 to 24-Sept-2015).

4. Member of Faculty of Inter-disciplinary and Applied Sciences (04-April-2014 to 03-April-2017).

5. Member of Grievance Redressal Cell of South Campus Students Union Election 2014-15.

6. Member of NAAC peer review team of South Campus, Delhi University.