# Sanjiv Kumar

PH.D. BIOTECHNOLOGY

+46 076 057 62 08 | drsanjivk@gmail.com | 0000-0003-3514-8999 | sanjiv856 | sanjiv-kumar-b246b44a

*Computational Biology, Bioinformatics, Biotechnology, Bacteriology, Molecular Biology*

## Profile

Harnessing data science to drive innovation in biotech and pharmaceuticals, I specialize in applying machine learning, statistical modeling, and AI-driven analytics to extract insights from complex biological and multi-omics data. With over a decade of experience in bioinformatics and computational biology, I optimize R&D pipelines, accelerate drug discovery, and advance precision medicine. By integrating cutting-edge data science methodologies with deep domain expertise, I enhance decision-making and deliver measurable business impact. Known for my analytical mindset, problem-solving skills, and collaborative approach, I excel in fast-paced, data-driven environments where innovation and strategic execution are critical.

## Technical Skills

• Programming: `Python`, `R`, `SQL`, `Bash` • Machine Learning & AI: `Scikit-Learn`, `TensorFlow`, `PyTorch`, `XGBoost` • Data Visualization: `Matplotlib`, `Seaborn`, `Plotly`, `ggplot` • LLM Stack: Ollama, LM Studio, Open WebUI, HuggingFace, Gradio • Statistical Analysis: Hypothesis Testing, Regression Models • Python-based Image Analysis: Image Segmentation, OpenCV, scikit-image, PIL • Bioinformatics & Computational Biology: Genomics, Metagenomics, RNA-Seq, Molecular Dynamics Simulations (GROMACS), Structural Bioinformatics • Docker • Business & Industry Applications: Biomarker Discovery, Drug Target Identification, Predictive Analytics, • Scientific & Technical Communication: Technical Writing, Data Storytelling, Cross-Functional Collaboration

## Career goal

I aim to leverage my expertise in data science, bioinformatics, and AI to drive innovation in the biotech, pharmaceutical, and healthcare industries. My focus is on developing scalable, data-driven solutions that accelerate drug discovery, improve patient outcomes, and enhance precision medicine. By integrating machine learning, big data analytics, and computational biology, I seek to bridge the gap between data science and business strategy, ensuring that complex biological insights translate into tangible industry impact. Long-term, I aspire to take on leadership roles where I can mentor teams, influence data-driven decision-making, and contribute to the development of next-generation therapeutics and healthcare solutions. I am committed to lifelong learning, fostering innovation, and driving measurable results in an evolving biotech landscape.

## Research Experience

**BrainZell AB in association with Jobbsprånget** ***Stockholm, Sweden***

BrainZell Trainee, Data Scientist – Multimodal Data Integration & Analysis November 2024 - February 2025

I was responsible for the following roles:

- Developed and fine-tuned customer reports in RMarkdown for the data and statistical analysis.
- Optimized image segmentation methods for detection and differentiation of brain organoids.
- Developed a pipeline for image-based-analysis in Python for screening of compounds.
- Developed CNN based model in Python to differentiate empty-wells from organoids.

**Torbjörn Group, Faculty of Medicine and Health, Örebro University, Sweden.** ***Örebro, Sweden***

Researcher, Bioinformatics and Microbial Proteogenomics *August 2021 - August 2023*

Here, I was responsible for the understanding of the mechanism of action of anti-microbial peptides (AMPs) against bacterial and viral pathogens using MD Simulations (GROMACS). With following roles:

- Understanding interactions of Plantaricin NC8 αβ with lipid bilayer model using MD simulations.
- Identification of interaction of AMPs with the viral proteins using docking and simulations.

**Srivastava Lab, Dept. of Chemistry, KTH Royal Institute of Technology** ***Stockholm, Sweden***

Researcher, Bioinformatics, Oomycetes Biology *August 2017 - August 2021*

I was responsible for the development and implementation of research strategy towards novel anti-infectives against Oomycete pathogens, Horizon 2020 project. With following roles:

- Expression, purification and biochemical characterization of proteins from Oomycetes
- Identification and characterization of protein targets and inhibitors for *S. parasitica*

**Justin Radolf Lab, University of Connecticut Health Center** ***Connecticut, USA***
Post-Doctoral Fellow, Bioinformatics, Infectious Biology *April 2015 - August 2017*

As a Post-Doctoral Fellow at UConn Health, I was involved with the characterization of rare Outer Membrane Proteins (OMPs) in *Treponema pallidum*. With following roles:

- Consensus computational framework to identify rare OMPs in *T. pallidum*
- Biophysical and experimental characterization of BAM – complex in *T. pallidum*
- Identification and analysis of sequence variations in *T. pallidum* from clinical samples

**Vineet Sharma Lab, Indian Institute of Science Education and Research, Bhopal (IISER-B)** ***Bhopal, India***
Post-Doctoral Fellow, Bioinformatics, Metagenomics and Systems Biology *December 2013 - February 2015*

As a Post-Doctoral Fellow at MetaBioSys lab, I was responsible for the Metagenomic analysis of human gut and polluted river microbiomes. With following roles:

- Reconstruction of bacterial and viral genomes from multiple human gut metagenomes
- Development of prediction tool for peptidoglycan hydrolases from bacterial genomes
- De novo assembly of genomes from human gut metagenomic data

**S. Ramachandran Lab, CSIR-Institute of Genomics and Integrative Biology** ***New Delhi, India***
Junior Research Fellow, Bacteriology *December 2007 - February 2015*
I was responsible for the identification of novel adhesins from *Mycobacterium tuberculosis*, including:
• Characterization of novel adhesins of *M. tuberculosis* H37RV and their experimental validation
• Characterization of a novel N-acetylmuramoyl-L-alanine amidase Rv3717 from *M. tuberculosis* H37Rv

## Patent Filed

- Vaibhav Srivastava, **Sanjiv Kumar**, and Vincent Bulone (2020). "Treatment of saprolegniasis." International Patent Application No.PCT/SE2020/050468, Filing date: May 7, 2020. [Link]

## Awards

KTH Innovation Challenge Tech for the Global Goals award of 50000 SEK, jointly shared with Vaibhav Srivastava, awarded by KTH Royal Institute of Technology, Stockholm, Sweden (May 2018) • Senior Research Fellowship from CSIR, New Delhi, India (March 2009 – February 2012) • Junior Research Fellowship from CSIR, New Delhi, India, (March 2007 – February 2009) • Defense Scholarship during graduation (B. V. Sc. & A. H.) (1998-2003)

## Education

**Institute of Genomics and Integrative Biology (CSIR-IGIB)** *Delhi, India*
Ph.D. in Biotechnology *2014*

**Lala Lajpat Rai University of Veterinary and Animal Sciences** *Haryana, India*
Masters in Veterinary Sciences (M.V.Sc.), Veterinary Microbiology *2007*

**Veterinary College, KVAFS University** *Bangalore, India*
Bachelor of Veterinary Sciences & Animal Husbandry (B.V.Sc. & A.H.) *2004*

## Training

**Regulatory Affairs (RA) and Good Distribution Practice (GDP)**, Svensk Medicin AB, *Stockholm, Sweden*, *Feb. 8-9, 2024* [Credential] • **Good Manufacturing Practice (GMP)**, Svensk Medicin AB, *Stockholm, Sweden*, *Jan. 24 2024* [Credential] • **Statistical analyses and visualization in R: I**, Södertörn University, *Stockholm, Sweden*, *Aug. 31 2021 - Jan. 31, 2022* [Credential] • **Applied Pharmaceutical Bioinformatics**, Uppsala University, *Uppsala, Sweden*, *Aug. 31*

*2021 - Jan. 31, 2022* [Credential] • **Pharmaceutical Bioinformatics**, Uppsala University, *Uppsala, Sweden*, *Aug. 31 - Nov. 01, 2020* [Credential] • **Applied Pharmaceutical Structural Bioinformatics**, Uppsala University, *Uppsala, Sweden*, *Aug. 31 - Oct.r 15, 2020* [Credential] • **RNA-Seq Data Analysis**, Workshop by National Bioinformatics Infrastructure Sweden (**NBIS**) and **SciLifeLab**, *Uppsala, Sweden*, *May 13 - 15, 2019* [Credential].

## Independent Coursework

**Google Data Analytics Specialization**, Google, *Feb. 2024* [Credential] • **Intro to Machine Learning**, Kaggle, *Mar. 2021* [Credential] • **Python**, Kaggle, *Mar. 2021* [Credential] • **Automate the Boring Stuff with Python Programming**, Udemy, *Jun. 2019* [Credential] • **Python Programming Bootcamp**, Udemy, *Jun. 2019* [Credential] • **Python for Absolute Beginners**, Udemy, *Jun. 2019* [Credential] • **Introduction to Python**, DataCamp, *April 2019* [Credential] • **Introduction to R Course**, DataCamp, *Nov. 2017* [Credential].

## Publications

For the complete list of publications please visit *My Google Scholar Profile* : `https://scholar.google.com/citations?user=ML7X29AAAAAJ`.

First Author Peer-Reviewed Publications – **6** • Total Peer-Reviewed Publications – **24** • Popular Science Articles – **1**.

**24**. Abubakr AM Omer, **Sanjiv Kumar**, Robert Selegård, Torbjörn Bengtsson, Hazem Khalaf (**2025**). Characterization of Novel Plantaricin-Derived Antiviral Peptides Against Flaviviruses. ***International Journal of Molecular Sciences*** . [MDPI IJMS].
**23**. Abubakr AM Omer, **Sanjiv Kumar**, Bo Söderquist, Wessam Melik, Torbjörn Bengtsson, Hazem Khalaf (**2024**). PLNC8 αβ Potently Inhibits the Flavivirus Kunjin and Modulates Inflammatory and Intracellular Signaling Responses of Alveolar Epithelial Cells. ***Viruses*** . [MDPI Viruses].
**22**. Ajay Kumar, Rajni Sharma, Muskan Bokolia, Riyapi Das, **Sanjiv Kumar**, Ravindresh Chhabra, Baljinder Singh* (**2024**). Impact of microplastics, fluoride, and mancozeb on tomato plant growth and rhizosphere microbial dynamics: A metagenomic analysis. ***Pedosphere*** . [In Press].
**21**. Kumar R, **Kumar S**, Bulone V, Srivastava V. (**2022**). Biochemical characterization and molecular insights into substrate recognition of pectin methylesterase from *Phytophthora infestans*. ***Computational and Structural Biotechnology Journal*** 20:6023-32. [ScienceDirect]
**20**. Srivastava, A., Biswas, S., Yadav, S., **Kumar, S**., Srivastava, V., & Mishra, Y. (**2021**). Acute cadmium toxicity and post-stress recovery: Insights into coordinated and integrated response/ recovery strategies of *Anabaena sp.* PCC 7120. ***Journal of Hazardous Materials*** 411:124822. [ScienceDirect]
**19**. **Kumar S**, Mandal RS, Bulone V, Srivastava V. (2020). Identification of growth inhibitors of the fish pathogen *Saprolegnia parasitica* using in silico subtractive proteomics, computational modelling, and biochemical validation. ***Frontiers in Microbiology*** 11, 2533. [PubMed]
**18**. Murugan NA, **Kumar S**, Jeyakanthan J, Srivastava V. (2020). Searching for target-specific and multi-targeting organics for COVID-19 in the Drugbank database with a double scoring approach. ***Scientific Reports*** 10(1), 19125. doi: 10.1038/s41598-020-75762-7. [Scientific Reports]
**17**. Srivastava A, Biswas S, Yadav S, **Kumar S**, Srivastava V, Mishra Y. (2020). Acute cadmium toxicity and post-stress recovery: Insights into coordinated and integrated response/ recovery strategies of *Anabaena sp.* PCC 7120. ***Journal of Hazardous Materials***. [ScienceDirect]
**16**. Yadav S, Srivastava A, Biswas S, Chaurasia N, Singh SK, **Kumar S**, Srivastava V, Mishra Y. (2020) Comparison and optimization of protein extraction and two-dimensional gel electrophoresis protocols for liverworts. ***BMC Research Notes*** 13, 60. `https://doi.org/10.1186/s13104-020-4929-1`. [PubMed]
**15**. Mittal P, Prasoodanan PK V, Dhakan DB, **Kumar S**, Sharma VK. (2019) Metagenome of a polluted river reveals a reservoir of metabolic and antibiotic resistance genes. ***Environmental Microbiome***, 14: 5. [BioMed Central]
**14**. Kaur, S., Srivastava, A., **Kumar, S.**, Srivastava, V., Ahluwalia, A.S. and Mishra, Y., (2019). Biochemical and proteomic analysis reveals oxidative stress tolerance strategies of *Scenedesmus abundans* against allelochemicals released by *Microcystis aeruginosa*. ***Algal Research***, 41, p.101525. [ScienceDirect]
**13**. **Kumar, S.**, Caimano, M. J., Anand, A., Dey, A., Hawley, K. L., LeDoyt, M., La Vake, C., Cruz, A. R., Ramirez, L. G., Pastekova, L., Bezsonova I, Smajs D, Salazar J. C., Radolf J. D. (2018) Sequence variation of rare outer membrane protein β-barrel domains in clinical strains provides insights into the evolution of *Treponema pallidum* subsp. pallidum, the syphilis spirochete. ***mBio*** 9(3): e01006-18.[PubMed]
**12**. Radolf J., **Kumar S.**, Smajs, D., Dey, A., Anand, A., Ledoyt, M., Karanian, C., Cruz, A., Ramirez, L., and Caimano, M. (2017). Insights into the evolution of syphilis spirochetes within at-risk populations: sequence variation of outer membrane protein β-barrel domains in clinical samples. ***Sexually Transmitted Infections*** 93:A41. [BMJ]

**11**. Puthenveetil, R., **Kumar S.**, Caimano, M. J., Dey, A., Anand, A., Vinogradova, O., and Radolf, J. D. (2017) The major outer sheath protein forms distinct conformers and multimeric complexes in the outer membrane and periplasm of *Treponema denticola*. ***Scientific Reports*** 7, 13260. [Scientific Reports]
**10**. Radolf J.D., **Kumar S**. The *Treponema pallidum* Outer Membrane. In: ***Current Topics in Microbiology and Immunology***, 2017. Springer, Berlin, Heidelberg. doi:10.1007/82_2017_44. [PubMed]
**9**. Gupta A+, **Kumar S+**, Prasoodanan VP, Harish K, Sharma AK, Sharma VK. (2016) Reconstruction of bacterial and viral genomes from multiple metagenomes. (+equal contribution). ***Frontiers in Microbiology***.[Frontiers]
**8**. Sharma AK, **Kumar S**, Harish K, Dhakan DB, Sharma VK. (2016) Prediction of peptidoglycan hydrolases-a new class of antibacterial proteins. ***BMC Genomics***. 17(1):411. [PubMed]
**7**. Sharma AK, Gupta A, **Kumar S**, Dhakan DB, Sharma VK. (2015) Woods: A fast and accurate functional annotator and classifier of genomic and metagenomic sequences. ***Genomics***.106(1):1-6. [ScienceDirect]
**6**. Puniya BL, Kulshreshtha D, Verma SP, **Kumar S**, Ramachandran S. (2013) Integrated gene co-expression network analysis in the growth phase of *Mycobacterium tuberculosis* reveals new potential drug targets. ***Molecular BioSystems***. 9(11):2798-815. [PubMed]
**5**. **Kumar S**, Puniya BL, Parween S, Nahar P, Ramachandran S. (2013) Identification of novel adhesins of *M. tuberculosis* H37Rv using integrated approach of multiple computational algorithms and experimental analysis. ***PloS One***. 8(7): e69790.[PubMed]
**4**. Kumar A+, **Kumar S+**, Kumar D, Mishra A, Dewangan RP, Shrivastava P, et al. (2013) The structure of Rv3717 reveals a novel amidase from *Mycobacterium tuberculosis*. (+equal contribution). ***Acta Crystallographica Section D***: Biological Crystallography. 69(12):2543-54. PDB ID: **4LQ6**. [PubMed]
**3**. Kumar N, Shukla S, **Kumar S**, Suryawanshi A, Chaudhry U, Ramachandran S, et al. (2008) Intrinsically disordered protein from a pathogenic mesophile *M. tuberculosis* adopts structured conformation at high temperature. ***Proteins****: Structure, Function, and Bioinformatics*. 71(3):1123-33. [PubMed]
**2**. Sindhu N, Sharma A, **Kumar S**, Jain V. (2007) Polymerase chain reaction assay for detection of *Staphylococcus aureus* in buffalo milk. ***Italian Journal of Animal Science***. 6(sup2):862-4. [TandFonline]
**1**. **Sanjiv K**, Puran C. (2006) Molecular diagnosis of brucellosis using polymerase chain reaction. ***Journal of Immunology and Immunopathology***. 8(2):0972-561. [IndianJournals]

## Publications in Progress

**1**. **Sanjiv Kumar**, Rajender Kumar, Dayanand C. Kalyani, Sara Giancristofaro, Loguprasanth Kanagaraj, Natrajan Arul Murugan, Michael Melzer, Martin Moche, Vincent Bulone and Vaibhav Srivastava*. Characterization of inhibition mechanism of enoyl-acyl carrier protein reductase from the oomycete pathogen Saprolegnia parasitica.*
***2. Sanjiv Kumar****, Per Eugen Kristiansen, Elisa Zattarin, Daniel Aili, Hazem Khalaf, Torbjörn Bengtsson*. Understanding interactions of Plantaricin NC8 α and β with lipid bilayer model membranes using molecular dynamics (MD) simulations.
**3**. **Sanjiv Kumar**, Amisha Panda, Ravindresh Chhabra, B. Hareramadas, Ilmas Naqvi, Anannya Bandyopadhyay. Computational Identification of Outer Membrane Proteins in Borrelia burgdorferi : Structural Models, Functional Predictions, and Sequence Variation Analysis. Currently under review in PROTEINS: Structure, Function, and Bioinformatics. (**As co-corresponding author**).
**4**. Amisha Panda, Ravindresh Chhabra, B. Hareramadas, Ilmas Naqvi, **Sanjiv Kumar**, Anannya Bandyopadhyay. Identification and characterization of novel Outer Membrane Proteins of Brachyspira pilosicoli. (**As co-corresponding author**).

## References

Available upon request.