

PH.D. BIOTECHNOLOGY

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Bioinformatics, Bacteriology, Molecular Biology, Biotechnology, Protein Biochemistry

Research Interests

Highly efficient molecular biologist, with focus on Protein Biochemistry and Infection Biology • Adept at *in-silico* characterization of proteins (phylogenetic analysis, homology modeling, drug discovery, molecular docking and simulations etc.) • Knowledge and experience of Genomics, metagenomics and RNA-Seq data analyses tools and software • Efficient at the techniques in the context of drug discovery against infectious pathogens

Technical Skills

Molecular biology techniques (DNA and RNA isolation and quantitation, PCR, RT-PCR, AGE, genomic strain variation, SNPs detection, Cloning, expression and purification of proteins (using various plasmids, *E.coli* cell types (BL21, C41, C43, Rosetta))), Microbiology techniques (experience of handling pathogenic organisms i.e. *Brucella malitensis*, *Mycobacterium tuberculosis*, *Treponema pallidum* (causes sexually transmitted disease (STD) Syphilis), *T. denticola* and Oomycetes, including their culture, isolation and maintenance, diagnosis from clinical samples), Protein biochemistry (Affinity chromatography, PAGE, WB, Blue Native PAGE, Protein folding, Circular Dichroism (CD), Biochemical assays, enzyme kinetics, ELISA, spectrophotometry, Antibody production in rats, Fluorescent microscopy (DAPI, antibodies), Protein crystallography (From setting plates, growing crystals, diffraction, data analysis using CCP4 and phoenix), Drug discovery (Sequence based matching with DrugBank, Large scale docking and simulations), Bioinformatics (Pharmaceutical Bioinformatics, Genomic and Metagenomics data analysis, Anti Microbial Resistance (AMR), Homology modeling, Docking), Programing (R, Python, bash. Adept user of UNIX), Microsoft office tools (Word, PowerPoint, Excel)

Research Experience

Division of Glycoscience, School of Biotechnology, KTH Royal Institute of Technology *Researcher*, Oomycetes Biology

Stockholm, Sweden August 2017 - Present

As a researcher with the Vaibhav Srivastava's Lab, I am responsible for the development and implementation of research strategy towards novel anti-infectives against Oomycete pathogens. Including following roles: • Expression, purification and biochemical characterization of proteins involved in cell-wall biogenesis from Oomycete pathogens, Horizon 2020 project • Cell wall linkage analysis of various Oomycete pathogens, Horizon 2020 project • Identification and characterization of protein targets and inhibitors important for disease control strategies against *Saprolegnia parasitica* and their *in-vitro* assessment.

Justin Radolf Lab at University of Connecticut Health Center

Post-Doctoral Fellow, Infectious Biology

Connecticut, USA April 2015 - August 2017

As a Post-Doctoral Fellow at UConn Health, I was involved with the characterization of rare Outer Membrane Proteins (OMPs) from *Treponema pallidum*, which causes sexually transmitted disease (STD) Syphilis. Including 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 at Indian Institute of Science Education and Research, Bhopal (IISER-B)

**Bhopal, India Post-Doctoral Fellow, 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. Some of the roles were: • 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, Institute of Genomics and Integrative Biology

Junior Research Fellow, Genomics and Integrative Biology

New Delhi, India December 2007 - February 2015

As a Junior Research Fellow, I was responsible for the identification of novel adhesins from *Mycobacterium tuber-culosis*, including • Identification of novel potential adhesins of *M. tuberculosis* H37RV and their experimental vali-

dation • 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)

Supervised Persons_

Magnus Olsson, Masters Student, (2021), KTH Royal Institute of Technology, as Secondary supervisor • Mari C. Villacañas, Masters Student, (2020), KTH Royal Institute of Technology, as Secondary supervisor, • Saad Saeed, Masters Student, (2020), KTH Royal Institute of Technology, as Secondary supervisor, • Sara Giancristofaro, Trainee, (2019), KTH Royal Institute of Technology, as Secondary supervisor

Education

Institute of Genomics and Integrative Biology (CSIR-IGIB)

Ph.D. in Biotechnology, Savitribai Phule Pune University, Maharashtra

Delhi, India 2014

Lala Lajpat Rai University of Veterinary and Animal Sciences

Masters in Veterinary Sciences (M.V.Sc.), Veterinary Microbiology

Haryana, India 2007

Veterinary College, KVAFS University

Bachelor of Veterinary Sciences & Animal Husbandry (B.V.Sc. & A.H.)

Bangalore, Karnataka, India 2004

Training

Pharmaceutical Bioinformatics, Grade: **VG**, Uppsala University, *Uppsala, Sweden, Aug. 31 - Nov. 01, 2020* [Credential], **Applied Pharmaceutical Structural Bioinformatics**, Grade: **VG**, Uppsala University, *Uppsala, Sweden, Aug. 31 - Oct. 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

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, Apr. 2019 [Credential], Introduction to R Course, DataCamp, Nov. 2017 [Credential]

Publications

For a updated list of publications please visit My Google Scholar Profile.

First Author Peer-Reviewed Publications – 6 • Total Peer-Reviewed Publications – 19 • Popular Science Articles – 1.

- 1. 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*. [ScienceDirect]
- 2. **Kumar, S.**, Mandal, R.S., 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]
- 3. Murugan, N.A., **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. [Scientific Reports]
- 4. Yadav, S., Srivastava, A., Biswas, S., Chaurasia, N., Singh, S.K., **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. [PubMed]

- 5. Mittal, P., PK, V.P., Dhakan, D.B., **Kumar, S.** & Sharma, V.K. (**2019**) Metagenome of a polluted river reveals a reservoir of metabolic and antibiotic resistance genes. *Environmental Microbiome*, 14: 5. [BioMed Central]
- 6. 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]
- 7. **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]
- 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]
- 9. 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. [PubMed]
- 11. 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]
- 12. 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]
- 13. 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]
- 14. 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]
- 15. **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]
- 16. 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]
- 17. 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]
- 18. 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]
- 19. **Kumar S**, Puran C. (**2006**) Molecular diagnosis of brucellosis using polymerase chain reaction. *Journal of Immunology and Immunopathology*. 8(2):0972-561. [IndianJournals]

References_

Dr. Vaibhav Srivastava, Researcher,

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