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PROFESSIONAL SUMMARY

A highly skilled and innovative scientist with a doctorate and eight years of dedicated experience in the field of Bioinformatics and computational biology. My expertise lies in the design and development of efficient analytical systems tailored for extracting valuable insights from vast datasets in genomics, transcriptomics, and proteomics. With a proven track record in machine learning, I bring a wealth of knowledge supported by numerous publications and contributions to open-source tools. As a dedicated team player, I possess exceptional analytical skills and an unwavering passion for unraveling complex biological enigmas.

EXPERIENCE

May 2021 - Present

POSTDOCTORAL FELLOW

National Cancer Institute - (NIH), Bethesda

- Investigated the molecular basis of Small Cell Lung Cancer, processing, analyzing and interpreting the large-scale clinical trial multi-omics data (RNA, WGS, WES, Chip-seq, ATAC-seq, scRNA, DRIP-seq, END-seq, OK-seq & spatial transcriptomics) from cancer patients, cell lines and PDX's.
- Employing computational tools like DeSeq2, Limma-Voom, NMF, Seurat, CIBERSORT, VIPER, AUCell, CellChat, MACS, SingleR and others to reveal insights into aberrant gene expression and tumor heterogeneity from transcriptomics, single cell, spatial, genomic and epigenomic dataset of SCLC.
- Developed a computational pipeline for identification of fusion genes from the transcriptomics datasets for immunotherapy and precision medicine.
- Identified novel hybrid subtype of SCLC by analyzing spatial transcriptomics dataset of patients and PDX's.
- Classified SCLC into novel molecular subtypes by integrating chromatin accessibility and transcriptomics.

Jan 2021 - Apr 2021

BIOINFORMATICS CONSULTANT

DeepKnomics Labs Bangalore, INDIA

- Worked on a "Computational vaccine development project" project as part of the IEDB, La Jolla, USA. My responsibilities included collect, curate, and maintain biological data for immunotherapy driven treatment from literature and databases; ensure that data adheres to the established standard and conventions of IEDB; generate reports and summaries of the datasets and highlight the key findings.

Aug 2015 - Aug 2020

RESEARCH FELLOW

CSIR-Institute of Microbial Technology, INDIA

- Developed public domain web resources, including 10 machine-learning based prediction servers for peptide-based vaccine design, identification of biomarkers for survival against Pancreatic, Hepatocellular and NSCLC carcinoma, 2 comprehensive tools for proteomics, genomics, and systems biology and 6 databases to optimize peptide properties, oncolytic viruses, fragile sites, and genomic signatures of different cancer types.
- Developed resources and tools to understand the genomic instability pattern in healthy and disease associated genomes by leveraging the power of CNV, fragile sites and non-coding enhancer elements.

- Conceptualized and led novel research projects, designing and execution of experiments to uncover insights using the CNV profile of enhancer element as a prognostic marker for TCGA cancer types.
- Worked with collaborators from multiple departments to efficiently achieve project goals in specified time resulting in publication of more than 25 research articles in international peer-reviewed journals.

EDUCATION

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| 2015-2021 | PhD (Bioinformatics) , CSIR-Institute of Microbial Technology, Chandigarh (under Jawaharlal Nehru University, New Delhi, INDIA) |
| 2012-2014 | Master of Science (Biotechnology) , Kurukshetra University, INDIA |
| 2009-2012 | Bachelor of Science (Biotechnology) , Kurukshetra University, INDIA |

TECHNICAL SKILLS

- **Operating system:** UNIX, Windows, MAC OS and LINUX environments, Biowulf and high-performance computing clusters
- **Programming languages:** Strong programming skills in R, Python, and Bash scripting
- **Machine learning/statistical techniques:** Expertise in implementing various popular machine-learning techniques like Support vector machine, linear regression, logistic regression, NaiveBayes, neural networks, random forest.
- **Public genomics data sources:** dbSNP, 1000 genomes, ENCODE, GTEx, UCSC Genome Browser, HapMap, Ensembl, ClinVar, TCGA, UniProt, GEO, cBioportal, SRA, dbGAP, COSMIC, FANTOM
- **Genomics software:** DeSeq2, STAR, STARFusion, BWA, circminer, BEDtools, SAMTools, VCFtools, RefSeq, LiftOver, PCA, GO analysis, Seurat, ORA, GSEA, gProfiler, CellChat, AUCcell, SingleR, CIBERSORT, VIPER, MACS, HOMER, ROSE, ChipSeeker, BAMScale, deepTools, Cytotrace, velocity, Monocle, t-SNE, UMAP, Diffbind
- **Data analysis and visualization tools:** dplyr, tidyverse, ggplot2, Pandas, NumPy, Sci-kit, Matplotlib, Bioconductor, NMF
- **Data mining tools:** Experience in data mining tools like WEKA
- **Motif/Profile search tools:** Knowledge of tools like MEME/MAST, MERCI, CD-Hit
- **Web Designing:** PHP, CGI-Perl, Javascript, jQuery, HTML, CSS
- **Database development:** Well versed with XAMPP (Apache, MySQL, PHP, Perl) package
- **Cheminformatics tools:** Open Babel, PaDEL, ChEMBL, PubChem, Gromacs, PyMol, AutoDock
- **Others:** Experience with common bioinformatics and cheminformatics methods (like QSAR, molecular dynamics, high performance cluster computing, Jupyter, Git), tools, websites and data resources. Excellent communication, writing, presentation, visualization, analytical and teaching skills. Team-oriented, adaptable, flexible, ability to handle multiple projects. Sound knowledge of biotechnology, cell biology, immunology and molecular biology.

ADDITIONAL SKILLS

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| • Data analysis & visualization | • Mentorship | • Effective communication |
| • Fast learner | • Problem solving | • Teamwork and collaboration |
| • Result-oriented | • Deadline-focused | • Strategic planning |
| • Project management | • Self-motivated | • Inventive and innovative |
| | • Time management | |

WEB SERVERS & DATABASES DEVELOPED

- **B3Pdb** (A repository of blood–brain barrier penetrating peptides) <https://webs.iitd.edu.in/raghava/b3pdb/>

- **OvirusTdb**(A Database of oncolytic viruses) <https://webs.iiitd.edu.in/raghava/ovirustdb/>
- **VLCvirus** (A Database of half-life of peptides) <https://webs.iiitd.edu.in/raghava/peplife/>
- **Antifp** (A web resource for designing antifungal peptides) <https://webs.iiitd.edu.in/raghava/antifp/>
- **HCCpred** (A method to predict hepatocellular carcinoma) <https://webs.iiitd.edu.in/raghava/hccpred/>
- **IL2pred** (A method to predict IL2 inducing peptides) <https://webs.iiitd.edu.in/raghava/il2pred/>
- **HemoPI-MOD** (Prediction of hemolytic potential of natural and modified peptides) <https://webs.iiitd.edu.in/raghava/hemopimod/>
- **CellPPD-MOD** (Webserver for predicting and designing of natural and modified cell-penetrating peptides) <https://webs.iiitd.edu.in/raghava/cellppdmod/>
- **CancerEnD** (A database of cancer-associated enhancers) <https://webs.iiitd.edu.in/raghava/cancerend/>
- **HumCFS** (A database of fragile sites in human chromosomes) <https://webs.iiitd.edu.in/raghava/humcfs/>
- **NAGbinder** (Webserver for identifying N-acetylglucosamine interacting residues of a protein from its primary sequence.) <https://webs.iiitd.edu.in/raghava/nagbinder/>
- **AntiTbPdb** (A knowledgebase of anti-tubercular peptides) <https://webs.iiitd.edu.in/raghava/antitbpdb/>
- **ccPDB 2.0** (A Compilation and Creation of datasets from PDB) <https://webs.iiitd.edu.in/raghava/ccpdb/>
- **DenvInd** (A Database of inhibitors of Dengue virus) <https://webs.iiitd.edu.in/raghava/denvind/>
- **CancerPDF** (A knowledgebase of cancer peptidome) <https://webs.iiitd.edu.in/raghava/cancerpdf/>
- **PEPlife** (A Database of half-life of peptides) <https://webs.iiitd.edu.in/raghava/peplife/>
- **Pfeature** (A web resource to compute the features of peptide sequences and their structures) <https://webs.iiitd.edu.in/raghava/pfeature/>
- **GPSRdocker** (A resource for Genomics, Proteomics and Systems biology) <https://webs.iiitd.edu.in/gpsrdocker/>

[GitHub \(https://github.com/imrjesh\)](https://github.com/imrjesh)

ACCOMPLISHMENTS

- 35+ research papers published in international peer-reviewed journals (10 papers as first-author) with 800+ citations.
- 15+ open-source databases and machine-learning prediction webserver to assist the global scientific community.
- Reviewed 20+ manuscripts for different peer-reviewed journals including Frontiers in Genetics, Genomics, Bioinformatics, Protein Science and Oxford journals.
- Received Junior and Senior Research Fellowship (CSIR) during PhD by the Council of Scientific and Industrial Research, Government of India (2015-2020).
- Qualified and recipient of fellowships from Department of Biotechnology and GATE-Biotechnology, Government of India.
- Recipient of Carl storm international diversity fellowship (\$1250) to attend GRC, DNA Damage and Repair conference at Ventura, California, USA, 2020.
- Editor of a book entitled “Computational Biology for Stem Cell Research”, in press by Elsevier.

PUBLICATIONS

- Schultz, C. W., Zhang, Y., Elmeskini, R., Zimmermann, A., Fu, H., Murai, Y., Wangsa, D., Kumar, S., Takahashi, N., Atkinson, D., Saha, L. K., Lee, C. F., Elenbaas, B., Desai, P., Sebastian, R., Sharma, A. K., Abel, M., Schroeder, B., Krishnamurthy, M., **Kumar, R.**, ... Thomas, A. (2023). ATR inhibition augments

the efficacy of lurbinectedin in small-cell lung cancer. *EMBO molecular medicine*, 15(8), e17313. <https://doi.org/10.15252/emmm.202217313>

- Abel, M. L., Takahashi, N., Peer, C., Redon, C. E., Nichols, S., Vilimas, R., Lee, M. J., Lee, S., Shelat, M., Kattappuram, R., Sciuto, L., Pinkiert, D., Graham, C., Butcher, D., Karim, B., Sharma, A. K., Malin, J., **Kumar, R.**, Schultz, C. W., Goyal, S., ... Thomas, A. (2023). Targeting Replication Stress and Chemotherapy Resistance with a Combination of Sacituzumab Govitecan and Berzosertib: A Phase I Clinical Trial. *Clinical cancer research : an official journal of the American Association for Cancer Research*, OF1–OF9. Advance online publication. <https://doi.org/10.1158/1078-0432.CCR-23-0536>
- Pongor, L. S., Schultz, C. W., Rinaldi, L., Wangsa, D., Redon, C. E., Takahashi, N., Fialkoff, G., Desai, P., Zhang, Y., Burkett, S., Hermoni, N., Vilks, N., Gutin, J., Gergely, R., Zhao, Y., Nichols, S., Vilimas, R., Sciuto, L., Graham, C., Caravaca, J. M., **Kumar, R.**, ... Thomas, A. (2023). Extrachromosomal DNA Amplification Contributes to Small Cell Lung Cancer Heterogeneity and Is Associated with Worse Outcomes. *Cancer discovery*, 13(4), 928–949. <https://doi.org/10.1158/2159-8290.CD-22-0796>
- Thomas, A., Fontaine, S. D., Diolaiti, M. E., Desai, P., **Kumar, R.**, Takahashi, N., Sciuto, L., Nichols, S., Ashworth, A., Feng, F. Y., Ashley, G. W., Nguyen, M., Pommier, Y., & Santi, D. V. (2022). PLX038: A Long-Acting Topoisomerase I Inhibitor With Robust Antitumor Activity in ATM-Deficient Tumors and Potent Synergy With PARP Inhibitors. *Molecular cancer therapeutics*, 21(11), 1722–1728. <https://doi.org/10.1158/1535-7163.MCT-22-0217>
- Takahashi, N., Hao, Z., Villaruz, L., Zhang, J., Ruiz, J., Petty, W., Mamdani, H., Riess, J., Nieva, J., Pacheco, J., Fuld, A., Shum, E., Chauhan, A., Nichols, S., Shimellis, H., McGlone, J., Sciuto, L., Pinkiert, D., Graham, C., Shelat, M., Kattappuram, R., Abel, M., Schroeder, B., Upadhyay, D., Krishnamurthy, M., Sharma, K. A., **Kumar, R.**, Malin, J., Schultz, C., Goyal, S., Redon, C., Pommier, Y., Aladjem, M., Gore, S., ... Thomas, A. (2023). Efficacy of Berzosertib plus Topotecan or Topotecan Alone in Patients with Relapsed Small Cell Lung Cancer: A Randomized Clinical Trial. *JAMA Oncology*.
- Kumar, V., Patiyal, S., **Kumar, R.**, Sahai, S., Kaur, D., Lathwal, A., & Raghava, G. P. S. (2021). B3Pdb: an archive of blood-brain barrier-penetrating peptides. *Brain structure & function*, 226(8), 2489–2495. <https://doi.org/10.1007/s00429-021-02341-5>
- Dwivedi, V. D., Arya, A., Yadav, P., **Kumar, R.**, Kumar, V., & Raghava, G. P. S. (2021). DenvInD: dengue virus inhibitors database for clinical and molecular research. *Briefings in bioinformatics*, 22(3), bbab098. <https://doi.org/10.1093/bib/bbaa098>
- Lathwal, A., **Kumar, R.**, & Raghava, G. P. S. (2021). In-silico identification of subunit vaccine candidates against lung cancer-associated oncogenic viruses. *Computers in biology and medicine*, 130, 104215. <https://doi.org/10.1016/j.compbiomed.2021.104215>
- Lathwal, A., **Kumar, R.**, Arora, C., & Raghava, G. P. S. (2020). Identification of prognostic biomarkers for major subtypes of non-small-cell lung cancer using genomic and clinical data. *Journal of cancer research and clinical oncology*, 146(11), 2743–2752. <https://doi.org/10.1007/s00432-020-03318-3>
- Lathwal, A., **Kumar, R.**, & Raghava, G. P. S. (2020). OvirusTdb: A database of oncolytic viruses for the advancement of therapeutics in cancer. *Virology*, 548, 109–116. <https://doi.org/10.1016/j.virol.2020.05.016>
- **Kumar, R.**, Lathwal, A., Kumar, V., Patiyal, S., Raghav, P. K., & Raghava, G. P. S. (2020). CancerEnD: A database of cancer associated enhancers. *Genomics*, 112(5), 3696–3702. <https://doi.org/10.1016/j.ygeno.2020.04.028>
- Kumar, V., **Kumar, R.**, Agrawal, P., Patiyal, S., & Raghava, G. P. S. (2020). A Method for Predicting Hemolytic Potency of Chemically Modified Peptides From Its Structure. *Frontiers in pharmacology*, 11, 54. <https://doi.org/10.3389/fphar.2020.00054>
- Kaur, H., Dhall, A., **Kumar, R.**, & Raghava, G. P. S. (2020). Identification of Platform-Independent Diagnostic Biomarker Panel for Hepatocellular Carcinoma Using Large-Scale Transcriptomics Data. *Frontiers in genetics*, 10, 1306. <https://doi.org/10.3389/fgene.2019.01306>
- Patiyal, S., Agrawal, P., Kumar, V., Dhall, A., **Kumar, R.**, Mishra, G., & Raghava, G. P. S. (2020). NAGbinder: An approach for identifying N-acetylglucosamine interacting residues of a protein from its primary sequence. *Protein science : a publication of the Protein Society*, 29(1), 201–210. <https://doi.org/10.1002/pro.3761>
- Raghav, P. K., **Kumar, R.**, Kumar, V., & Raghava, G. P. S. (2019). Docking-based approach for identification of mutations that disrupt binding between Bcl-2 and Bax proteins: Inducing apoptosis in cancer cells. *Molecular genetics & genomic medicine*, 7(11), e910. <https://doi.org/10.1002/mgg3.910>

- **Kumar, R.**, Patiyl, S., Kumar, V., Nagpal, G., & Raghava, G. P. S. (2019). In Silico Analysis of Gene Expression Change Associated with Copy Number of Enhancers in Pancreatic Adenocarcinoma. *International journal of molecular sciences*, 20(14), 3582. <https://doi.org/10.3390/ijms20143582>
- **Kumar, R.**, Nagpal, G., Kumar, V., Usmani, S. S., Agrawal, P., & Raghava, G. P. S. (2019). HumCFS: a database of fragile sites in human chromosomes. *BMC genomics*, 19(Suppl 9), 985. <https://doi.org/10.1186/s12864-018-5330-5>
- Agrawal, P., Patiyl, S., **Kumar, R.**, Kumar, V., Singh, H., Raghav, P. K., & Raghava, G. P. S. (2019). ccPDB 2.0: an updated version of datasets created and compiled from Protein Data Bank. *Database : the journal of biological databases and curation*, 2019, bay142. <https://doi.org/10.1093/database/bay142>
- Kumar, V., Agrawal, P., **Kumar, R.**, Bhalla, S., Usmani, S. S., Varshney, G. C., & Raghava, G. P. S. (2018). Prediction of Cell-Penetrating Potential of Modified Peptides Containing Natural and Chemically Modified Residues. *Frontiers in microbiology*, 9, 725. <https://doi.org/10.3389/fmicb.2018.00725>
- Agrawal, P., Bhalla, S., Chaudhary, K., **Kumar, R.**, Sharma, M., & Raghava, G. P. S. (2018). In Silico Approach for Prediction of Antifungal Peptides. *Frontiers in microbiology*, 9, 323. <https://doi.org/10.3389/fmicb.2018.00323>
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- Bhalla, S., Verma, R., Kaur, H., **Kumar, R.**, Usmani, S. S., Sharma, S., & Raghava, G. P. S. (2017). CancerPDF: A repository of cancer-associated peptidome found in human biofluids. *Scientific reports*, 7(1), 1511. <https://doi.org/10.1038/s41598-017-01633-3>
- Mathur, D., Prakash, S., Anand, P., Kaur, H., Agrawal, P., Mehta, A., **Kumar, R.**, Singh, S., & Raghava, G. P. (2016). PEPlife: A Repository of the Half-life of Peptides. *Scientific reports*, 6, 36617. <https://doi.org/10.1038/srep36617>

SUBMITTED MANUSCRIPTS

- Desai, P., Takahasi, N., **Kumar, R.**, ... Thomas, A. Microenvironment shape cell state, plasticity, heterogeneity of small cell lung cancer. (Cancer Discovery) 2nd author
- F, Gavriel., Takahasi, N., Sharika, I., Gutin, J., Pongor, L., Rajan, A., **Kumar, R.**, ... Thomas, A. Subtyping of small cell lung cancer using plasma cell-free nucleosome. (Nature Genetics)
- Lathwal, A., **Kumar, R.**, Kaur, D., Raghava, G.P.S. In silico model for predating the IL-2 inducing peptides in human (<https://www.biorxiv.org/content/10.1101/2021.06.20.449146v1.abstract>). co-1st author
- Agrawal, P., **Kumar, R.**, Usmani, S., Dhall, A., ... Raghava, G.P.S. GPSRdocker: a docker based resource for genomic proteomic and system based biology. co-1st author
- **Kumar, R.**, Lathwal, A., Raghava, G.P.S. Prediction of pancreatic adenocarcinoma patient risk status using alternative splicing events.

REVIEWS & BOOK CHAPTERS

- Kaur, H., **Kumar, R.**, Lathwal, A., & Raghava, G. P. S. (2021). Computational resources for identification of cancer biomarkers from omics data. *Briefings in functional genomics*, 20(4), 213–222. <https://doi.org/10.1093/bfpg/elab021>
- **Kumar, R.**, Lathwal, A., Nagpal, G., Kumar, V., & Raghava, P. K. (2021). Impact of chemoinformatics approaches and tools on current chemical research. *Chemoinformatics and Bioinformatics in the Pharmaceutical Sciences*, <https://doi.org/10.1016/B978-0-12-821748-1.00001-4>
- Lathwal, A., **Kumar, R.**, & Raghava, G. P. S. (2020). Computer-aided designing of oncolytic viruses for overcoming translational challenges of cancer immunotherapy. *Drug discovery today*, 25(7), 1198–1205. <https://doi.org/10.1016/j.drudis.2020.04.008>

- Usmani, S. S., **Kumar, R.**, Bhalla, S., Kumar, V., & Raghava, G. P. S. (2018). In Silico Tools and Databases for Designing Peptide-Based Vaccine and Drugs. *Advances in protein chemistry and structural biology*, 112, 221–263. <https://doi.org/10.1016/bs.apcsb.2018.01.006>

CONFERENCES ABSTRACT

- Distint immunosuppressive tumor microenvironment modulates small cell lung carcinoma neuroendocrine phenotypic plasticity and heterogeneity. https://aacrjournals.org/cancerres/article/83/7_Supplement/5828/721665
- Dissecting small cell lung cancer subtypes with cell-free DNA fragmentomes. https://ascopubs.org/doi/pdf/10.1200/JCO.2023.41.16_suppl.8592?role=tab

REFERENCES

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