

BRIEF BIO-DATA OF DR. VISHAL ACHARYA

- Present Post:** Senior Scientist, Functional Genomics & Complex System Lab, Biotechnology Division, CSIR-Institute of Himalayan Bioresource Technology (IHBT), Palampur-176061 (H.P.), India
- Email-id** vishal@ihbt.res.in, acharya.vishalacharya@gmail.com
- Awards**
- i) Indian Science Congress Association (ISCA) Young Scientist Award -2014 (New Biology)**
 - ii) Young Scientist Award for Best Paper Presentation (2014)** by Society of Plant Biochemistry and Biotechnology, New Delhi
 - iii) Bioclues Innovation, Research and Development (BIRD) Award-2016** from International Society for Computational Biology and Asia-Pacific Bioinformatics Network under the age of 35.
 - iv) Awarded for 2nd Position – Incentive Awards for Publications-2016** for publications in Year 2015, from BITSnet, Department of Biotechnology, Govt. of India (including my 5 out of total 8 papers).
 - v) Elected as "Associate" of National Academy of Agriculture Sciences (NAAS) under Social Sciences (Bioinformatics)-2021**
- Honours**
- i) Co-Chair of Bioclues organization** (an affiliate of International Society of Computational Biology (ISCB)) for the year 2017-2018.
 - ii) Chairperson and Invited speaker** for the "International Conference on Bioinformatics" held at Hans Raj Mahavidyalaya (HJV), Jalandhar, 2019.
 - iii) As a Co-co-ordinator** for “Establishment of Bioinformatics infrastructure for biology through bioinformatics (BTBI) under BTISnet”, Department of Biotechnology (DBT), Government of India.
- Fellowships Merits**
- i). ICAR’s JRF** for MSc Programme-2003
 - ii).DBT-Fellow (M.Sc), Gov. of India**, conducted by JNU-2003
 - iii). JRF (2005) for PhD** granted by **DBT, Gov. of India**
 - iv).Travel fellowship** by European Science Foundation (Availed)
- Supervisory Experience**
- i).Guided Three Phd students** through Academy of Scientific and Innovation Research (AcSIR) research program and one DBT-Research Associate (RA)
 - ii) Presently, guiding 7 (Seven) PhD** students through AcSIR-PhD program
- Computational Experience** Perl, Python, Awk, Linux Server Administrator, R Package, GNU, Matlab, Bioconductor, PHP
- Professional Memberships** 1.Life Member of the Indian Science Congress Association (ISCA)

2. Joint Secretary of Bioclues Organization affiliated with International Society for Computational Biology and Asia-Pacific Bioinformatics Network

Countries Visited: Germany; France; UAE (Dubai, Abu Dhabi)

Educational Qualifications

Examination	School/College	Year of Passing	Percentage/Remarks
PhD (Bioinformatics)	Center for DNA Fingerprinting & Diagnostics (CDFD), Hyderabad	2005- 2011	PhD Degree Awarded
M.Sc. (Biotechnology)	Madurai Kamaraj University, Madurai (T.N)	2003-2005	75.4%

Scientific Contributions:

- * Developed **artificial intelligence based software** (Support vector Machine) named “**Hansa**” (“<http://www.cdfd.org.in/HANSA/>) for discrimination of pathogenic from nonpathogenic missense mutations with 10% more accurate than best known methods (**Human Mutation, 2012; 2013**)
- * “**Hansa**” has been highlighted in annual virtual issue of Human Mutation entitled “**Evaluating Mutation Pathogenicity**” for the year 2012.
- * **The National Genetics Reference Laboratory (NGRL), Manchester, UK**, on analyzing popular missense prediction tools advised usage of “**Hansa**” as one of the three tools, thus emphasizing the importance of this software that will be highly beneficial to the interested biological community.
- * His **AI-based logistic regression modeling** method suggested plant derived molecules from Himalayas as anti-oral cancer agents (**BMC medical genomics, 2015, highly accessed article; Molecular BioSystems, 2015**)
- * His **stringent Hidden Markov model-based approach for prediction of disease-resistance** in *Malus x domestica* (apple) genome (**Plos One, 2014**) was being successfully applied in many **other plant sequenced genomes** supported by ≥ 80 publications.
- * Discovered **novel domain** (animal like defense regulator NACHT domain) for the first time related to immune response in **early green plants** (**Molecular genetics & Genomics, 2018; PloS One, 2016**)
- * His conceived developed pipeline on molecular adaptational analysis (<https://github.com/fqcs/Molecular-adaptational-analysis-cold>) can easily be applied to any sequenced genomes even by non-bioinformatics researchers (**Genomics, 2020**).
- * His another conceived **computational pipeline on prediction of transcription factors** (https://github.com/ShivalikaP/R_serpentina_transcriptome_annotation) led into the investigation and organization of secondary metabolites in *Rauvolfia serpentina* (**Plant Molecular biology reporter, 2015**) and abiotic stress (NAC) in potato (**DNA Research, 2013 (8th most read article)**).
- * His conceived pipeline on first ever implemented deep learning approach (DLNet) to understand the plant immune genes network response architecture using genomics data <https://gitlab.com/ravisaroch/dlnet-host-pathogen-interaction/> (**iScience, 2022, IF =6.1**)
- * His conceived pipeline <https://gitlab.com/neeraj-24/A-HIOT> on advanced Virtual Screening framework-**automated hit identification and optimization tool (A-HIOT)**-comprises chemical

space-driven stacked ensemble for identification and protein space-driven deep learning architectures for optimization of an array of specific hits for fixed protein receptors (**Journal of Cheminformatics, 2022, IF =8.48**)

* His conceived protocol for network and expression integration to identify potential defense gene in host-pathogen interactions <https://gitlab.com/ravisaroch/star-protocols> (**Star Protocols, 2023**)

* His conceived pipeline on clustering of protein molecule into active/inactive targets (<https://gitlab.com/neeraj-24/clustering-of-uncharacterised-data>) by applying unsupervised machine learning using atom pair, fingerprints and similarity indices as features (**Computers in Biology & Medicine, 2023, IF=6.698**)

Technology/Software Developed

Sl. No	Details of Product/Technology/Software* (Also write in one bullet point its impact in terms of adoption, commercialization and revenue generated)	List according to category (I,II,III,IV or V) as given in 2 of the guidelines for evaluation	Whether Nominee is a Developer, Co-developer or Associate
1.	Software: He conceived the novel method on first ever implementation of deep learning network algorithm named DLNet using genomics data to understand the plant network architecture in response to pathogens https://gitlab.com/ravisaroch/dlnet-host-pathogen-interaction/	I (Methodologies developed)	Developer
2.	Software: He conceived and developed the novel method on any protein molecule derived from medicinal plants clustered into active/inactive targets by applying unsupervised machine learning using atom pair, fingerprints and similarity indices as features for drug discovery https://gitlab.com/neeraj-24/clustering-of-uncharacterised-data	I (Methodologies developed)	Developer
3.	Software: He conceived and developed the novel approach on advanced Virtual Screening framework- automated hit identification and optimization tool (A-HIOT) -comprising chemical space-driven stacked ensemble from natural products for identification and protein space-driven deep learning architectures for optimization of an array of specific hits for fixed protein receptors https://gitlab.com/neeraj-24/A-HIOT	I (Methodologies developed)	Developer
4.	Software: He developed the novel machine learning protocol for integration of network and expression profiling to identify potential host defense genes in all	I (Methodologies developed)	Developer

	kind host-pathogen interaction datasets. https://gitlab.com/ravisaroch/star-protocols		
5.	Software: He conceived and developed the computational pipeline on prediction and identification of transcription factors regulating secondary metabolite in medicinal plants with <i>Rauvolfia serpentina</i> as a case study (https://github.com/ShivalikaP/R_serpentina_transcriptome_annotation)	I (Methodologies developed)	Developer
6.	Software: He conceived and developed pipeline on studying adaptive behavior of any genome (plant/microbes) adapting to cold conditions (https://github.com/fgcsl/Molecular-adaptational-analysis-cold)	I (Methodologies developed)	Developer
7.	Software: He developed AI based-software “Hansa” wherein novel biological-based features implemented (Gribskov’s probability score) has been applied for future prediction of disease-resistance genes on the basis of SNPs (http://www.cdfd.org.in/HANSA/)	I (Methodologies developed)	Developer
8.	Software: RicePathDLNet, online repository developed by him will aid the rice-focused researchers in understanding the distinct network levels in pattern-triggered immunity (PTI)- and effector triggered immunity (ETI)-based models of <i>Xanthomonas oryzae</i> and <i>Magnaporthe oryzae</i> (https://fgcsl.ihbt.res.in/RicePathDLNet/)	I (Methodologies developed)	Developer
9.	Software: Indian Himalayan metagenome database (IHM-DB) developed by him is a web-based database consisting of microbiome information on metagenomic datasets from various databases that are specifically reported from the Indian Himalayan Region (IHR) (https://fgcsl.ihbt.res.in/ihmdb)	I (Methodologies developed)	Developer

<p>10. Software: He conceived and developed an open-source 16S amplicon-based automated bioinformatics pipeline, AutoQii2, which will allow users to analyze the single-end and paired-end raw reads (https://github.com/fgcsl/autoqii2)</p>	<p>I (Methodologies developed)</p>	<p>Developer</p>
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Selected Publications

1. Ravi Kumar, **Vishal Acharya***, Effector protein structures: a tale of evolutionary relationship, Trends in Plant Science, 2023,ISSN 1360-1385, <https://doi.org/10.1016/j.tplants.2023.04.010> (IF =22.01)
2. Neeraj Kumar & **Vishal Acharya***, Machine intelligence-guided selection of optimized inhibitor for human immunodeficiency virus (HIV) from natural products. **Computers in Biology and Medicine** Volume 153, February 2023, 106525 (IF=6.698)
Software link: <https://gitlab.com/neeraj-24/clustering-of-uncharacterised-data>
3. Neeraj Kumar & **Vishal Acharya*** Machine intelligence-driven framework for optimized hit selection in virtual screening. **Journal of Cheminformatics** 2022 Jul 22;14(1):48. doi: 10.1186/s13321-022-00630-7. PMID: 35869511; PMCID: PMC9306080 (IF =8.48)
Software link: <https://gitlab.com/neeraj-24/A-HIOT>
4. Ravi Kumar, Abhishek Khatri & **Vishal Acharya*** Deep learning uncovers distinct behavior of rice network to pathogens response **iScience**, Volume 25, Issue 7, 104546 (IF =6.1)
Software link: <https://gitlab.com/ravisaroch/dlnet-host-pathogen-interaction/>
Database link: <https://fgcsl.ihbt.res.in/RicePathDLNet>
5. Meetal Sharma, Prince Anand, Yogender Padwad, Vivek Dogra, **Vishal Acharya*** DNA damage response proteins synergistically affect the cancer prognosis and resistance **Free Radical Biology & Medicine** 2021 Nov 27;S0891-5849 (21) 00831-5. doi:10.1016/j.freeradbiomed.2021.11.033 (IF=8.1)

Details of Publications is provided at the link: https://fgcsl.ihbt.res.in/fgcsl_lab/publication.php

Books Authored:

1. VijayKumar Muley & **Vishal Acharya** (2013) Genome-Wide Prediction and Analysis of Protein-Protein Functional Linkages in Bacteria, **Springer Briefs in Systems Biology** Volume 2,1-2, https://doi.org/10.1007/978-1-4614-4705-4_1 Online ISBN 978-1-4614-4705-4

Book Chapters:

1. Neeraj Kumar & **Vishal Acharya*** Metabolomics Resources: An Introduction of Databases and Their Future Prospective (2018) **Recent Trends and Techniques in Plant Metabolic Engineering** Springer DOI (Editors: Sudesh Kumar Yadav, Vinay Kumar, Sudhir P Singh) DOI: <https://doi.org/10.1007/978-981-13-2251-8> Online ISBN 978-981-13-2251-8

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