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 Mahavidalaya (HMV), 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 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 adapatational analysis (https://github.com/fgcsl/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, 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, IF =8.48)**

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)	Main role as a Developer, Co-developer or Associate
1.	**Software:** 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, IF =8.48)**	Developer
2.	**Software:** His conceived pipeline on plant-pathogen interactions can be used to investigate network responses in various stress/plant situations https://gitlab.com/ravisaroch/dlnet-host-pathogen-interaction/ **(iScience, IF =6.1)**	Developer
3.	**Software:** His 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)**	Developer
4.	**Software:** His conceived developed pipeline on molecular adapatational analysis (https://github.com/fgcsl/Molecular-adaptational-analysis-cold) can easily be applied to any sequenced genomes even by non-bioinformatics researchers **(Genomics,** 2020**).**	Developer
5.	**Software:** HNHdb database (http://bicmku.in:8081/hnh.) associated with a range of DNA binding proteins domain HNHc (SMART id: SM00507) which performs a variety of binding and cutting functions especially used in CRISPR/Cas9 system (**Bioinformation,** 2009**)**	Developer
6.	**Software & Technology: AI based-software** *"Hansa"* http://www.cdfd.org.in/HANSA/ (**Human Mutation,2012; 2013)** wherein novel biological-based features implemented (Gribskov's probability score) has been	Developer

	applied for **future prediction of disease-resistance genes**	
7.	**Products:** Developed novel computational pipeline for screening available Himalayan plant-derived molecules by means of the advanced Artificial Intelligence **AI-based logistic regression modeling** method suggested plant derived molecules from Himalayas (**Molecular BioSystems, 2015; BMC medical genomics**, 2015, **highly accessed article**). for pharmaceutical discovery as an anti-oral cancer agents	Developer
8.	**Products:** By means of the integrated Artificial intelligence- and system biology- approaches, **novel animal-like defense apoptosis/cell death regulator gene** "**NACHT NTPase"** discovered for the first time in the **early green plant lineages** (green algae and lycophyte) can be used for the enhancement of disease-resistance genes in many crop plants by transgenic approaches **(Molecular Genetics and Genomics, 2017; PloS One, 2016)**	Developer

Selected Publications

1. 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
2. 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
3. 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)**
4. Srijana Mukhia#, Abhishek Khatri#, **Vishal Acharya*,** Rakshak Kumar* Comparative genomics and molecular adaptational analysis of Arthrobacter from Sikkim Himalaya provided insights into its survivability under multiple high-altitude stress **Genomics (2020)** https://doi.org/10.1016/j.ygeno.2020.12.001 **(IF=4.31)**
5. Vinay Randhawa, Anil Kumar Singh & **Vishal Acharya*** (2015) A systematic approach to prioritize drug targets using machine learning, a molecular descriptor-based classification model, and high-throughput screening of plant derived molecules: a case

study in oral cancer ***Molecular Omics, 2015,*** 3362-3377 **DOI:** 10.1039/C5MB00468C **(IF= 4.212)**

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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