

## **BRIEF BIO-DATA OF DR. VISHAL ACHARYA**

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

**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  $\geq 60$  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](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 (8<sup>th</sup> most read article)**).

## 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.	<b>Products:</b> By means of the integrated Artificial intelligence- and system biology- approaches, <b>novel animal-like defense apoptosis/cell death regulator gene “NACHT NTPase”</b> discovered for the first time in the <b>early green plant lineages</b> (green algae and lycophyte) can be used for the enhancement of disease-resistance genes in many crop plants by transgenic approaches ( <b>Molecular Genetics and Genomics, 2017; PloS One, 2016</b> )	Developer
2.	<b>Software:</b> His conceived computational pipeline on prediction of transcription factors ( <a href="https://github.com/ShivalikaP/R_serpentina_transcriptome_annotation">https://github.com/ShivalikaP/R_serpentina_transcriptome_annotation</a> ) led into the investigation and organization of secondary metabolites in <i>Rauvolfia serpentina</i> ( <b>Plant Molecular biology reporter, 2015</b> ) and abiotic stress (NAC) in potato ( <b>DNA Research, 2013 (8<sup>th</sup> most read article)</b> )	Developer
3.	<b>Software:</b> His conceived developed pipeline on molecular adaptational analysis ( <a href="https://github.com/fgcsl/Molecular-adaptational-analysis-cold">https://github.com/fgcsl/Molecular-adaptational-analysis-cold</a> ) can easily be applied to any sequenced genomes even by non-bioinformatics researchers ( <b>Genomics, 2020</b> ).	Developer
4.	<b>Software:</b> HNHdb database ( <a href="http://bicmku.in:8081/hnh">http://bicmku.in:8081/hnh</a> .) 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 ( <b>Bioinformation, 2009</b> )	Developer
5.	<b>Software &amp; Technology:</b> AI based-software “Hansa” <a href="http://www.cdfd.org.in/HANSA/">http://www.cdfd.org.in/HANSA/</a> ( <b>Human Mutation,2012; 2013</b> ) wherein novel biological-based features implemented (Gribskov’s probability score) has been applied for <b>future prediction of disease-resistance genes</b>	Developer
6.	<b>Products:</b> Developed novel computational pipeline for screening available Himalayan plant-derived molecules by means of the advanced Artificial Intelligence <b>AI-based logistic regression modeling</b> method suggested plant derived molecules from Himalayas ( <b>Molecular BioSystems, 2015; BMC medical genomics, 2015,</b>	Developer

highly accessed article). for pharmaceutical discovery as an anti-oral cancer agents
--------------------------------------------------------------------------------------

## Best Five Publications

1. Srijana Mukhia#, Abhishek Khatri#, **Vishal Acharya\***, Rakshak Kumar\* Comparative genomics and molecular adaptational analysis of *Arthro bacter* 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=6.205)
2. Supriya Sharma#, Meetal Sharma#, Anil Kumar Rana, Robin Joshi, Mohit Swarnkar, **Vishal Acharya\***, Damanpreet Singh\* Deciphering key regulators involved in epilepsy-induced cardiac damage through whole transcriptome and proteome analysis in a rat model **Epilepsia (2020)** DOI: **10.1111/epi.16794** (IF=6.04)
3. Preeti Arya & **Vishal Acharya\*** (2018) Plant STAND P-loop NTPases: A current perspective of genome distribution, evolution and function. **Molecular Genetics and Genomics** **293** <https://doi.org/10.1007/s00438-017-1368-3> (IF = 2.797)
4. 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 BioSystems, 2015**, 3362-3377 DOI: 10.1039/C5MB00468C (IF= 3.336)
5. Vinay Randhawa & **Vishal Acharya\*** (2015) Integrated network analysis and logistic regression modeling identify stage-specific genes in Oral Squamous Cell Carcinoma **BMC Medical Genomics** 8:39, DOI: 10.1186/s12920-015-0114-0 (IF = 2.57) (**Highly Accessed Article**)

Details of Publications is provided at the link:

[https://fgcs.iibt.res.in/fgcs\\_lab/publication.php](https://fgcs.iibt.res.in/fgcs_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](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

\*Corresponding author