CURRICULUM VITAE

Lokesh Kumar

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PERMANENT ADDRESS:-VILLAGE-SOHANJANI JATAN,
POST-ALIPUR KHERI, DISTIC- MUZAFFARNAGAR,
UTTAR PRADESH PIN CODE-251301



EDUCATION

- **Ph.D.** with **Biotechnology** from H.N.B.G. University Srinagar Garhwal Uttarakhand India in 2023
- **Master of Science (M.Sc.)** with **Biotechnology** from H.N.B.G. University Srinagar Garhwal Uttarakhand India in 2017 with 73.8%
- **Bachelor of Science (B.Sc.)** with **Biotechnology** from CSJMU University Kanpur in 2014 with 66.75%
- **Intermediate** with **Biology, Chemistry, Physics, English, and Hindi** from UP Board Allahabad in 2009 with 54.2%
- **High school** with **Science** from UP Board Allahabad in 2005 with 56%

Qualified Entrance Exam

- **GATE 2021** have been Qualified in Biomedical Engineering(BM) with Gate Score-437, All India Rank -119
- **GATE 2020** have been Qualified in Biotechnology(BT)- with Gate Score-408, all Indian Rank 1117
- **GATE 2017** have been qualified in Biotechnology(BT) with Gate score-405, All India Rank:895
- **DBT-JRF2017** have been Qualified in Biotechnology

MAJOR EXPERIENCE

- Having sound experience of running **Gromacs, Rosetter, Modeller, Mastro, Autodock vina, Modeller, Descovery studio, chimera,** other molecular engineering software.
- Nation skill Development and hands on Training Programme on quality control og Biologicals fromNational Institute of Biological NOIDA time(14th Feb-4th March 2017).
- Having 6 years sound experience of teaching in Biotechnology in HNBG University IBT 1-10 semester and 1-4 semester of M.Sc. Biotechnology.

PUBLICATIONS

- **Kumar, L**., Joshi, S., Rauthan, K., & Kumar, S. (2023). Annotation of a probable ATPase family AAA domain containing protein 3 (ATAD3) from human parasitic nematode *Loa loa.* Biochemical and Cellular Archives, 23(2): 855-862. https://doi.org/10.51470/bca.2023.23.2.855
- Rauthan, K., Joshi, S., **Kumar, L**., & Kumar, S. (2023). Functional and structural annotation of an uncharacterized protein A0A077Z4I5 from ***Trichuris trichiura.*** Biochemical and Cellular Archives, 23(2): 1253-1256. ***https://doi.org/10.51470/bca.2023.23.2.1253***

- Rauthan, K., Joshi, S., **Kumar, L**., Goel, D., & Kumar, S. (2023). Functional annotation of uncharacterized proteins from *Fusobacterium nucleatum*: identification of virulence factors. Genomics & Informatics, 21(2). https://doi.org/10.5808/gi.22065
- Joshi, S., **Kumar, L**., Rauthan, K., & Kumar, S. (2022). Comparative analyses of the complete mitochondrial genomes of the two filarial worms *Wuchereria bancrofti* & *Brugia malayi* with *Caenorhabditis elegans*. Journal of Integrated OMICS, 12(1). https://doi.org/10.5584/jiomics.v12i1.212

Language Known: Speak: Read: Write: Hindi, English

Key Skills:Operating System : Linux, Kali, Ubuntu, Windows

Bioinformatics Software: Rosetta,Gromacs, Mastro, Autodock vina, Other molecular dynamics and analysis software grace,pymol,etc.

Software package: visual studio,MS-Office2019 (Word, Excel, PowerPoint etc)

Computer Language: Java, python, C++, html, R, etc

Personal Details: DOB: 02/01/1991, Sex: Male, Nationality: India, Religion: Hindu, Marital status: Married

Declaration:

I do hereby confirm that the information furnished above is true to the best of my Knowledge and belief.

Date: 14/01/2024

Place: Muzaffarnagar **LOKESH KUMAR**

(Candidate Name)

References

Dr. Sudhir Kumar(Assistent Professor)
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H.N.B. Garhwal University (a central University),
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Research Summary

(Ph.D. work)

Nematoda, a phylum of worms, has over 25,000 documented species, including parasitic nematodes like hookworms, pinworms, and filarial worms infecting humans, animals, plants and even insects. These diseases cause severe pain, harm, and loss of agricultural production, with a significant global impact. The ATAD3 protein, a mitochondrial protein, plays a crucial role in mitochondrial functions like fusion, fission, lipid metabolism, DNA maintenance, and protein import. However, its structural details are not fully explored. This research aims to identify a suitable structural model for ATAD3 and its active sites, aiming to develop effective drugs for nematode control. The work involves *in silico* characterization, structural analysis, ligand docking, and evolutionary analysis.

ATAD3 protein sequences from nematodes were retrieved from WormBase database and subjected to physicochemical characterization, localization, signal peptide identification and transmembrane helix prediction. Further, *ab initio* structural modelling was performed using trRosetta software. Structural models were refined, and energy minimized using Gromacs package. ATP binding residues were predicted, and docking was performed. Docking was also done with the several ATP analogues. Phylogenetic and comparative analysis was performed to understand the relation of ATAD3 proteins in nematodes.

About 100 ATAD3 proteins form nematode worms were identified and characterized using in silico tools in this study. Most sequences were localized in mitochondria, with no specific signal peptide detected. Domain analysis identified ATAD3 specific N and C-terminal domains in all sequences. The structural model of ATAD3 protein from the human parasitic nematode *Strongyloides stercoralis* was prepared using trRosetta scripts and subjected to molecular dynamics simulation. The full-length model showed two distinct domains: a conserved, globular-like C-terminal domain and an extended, fibrous type N-terminal domain. The dimeric and hexameric conformation was visualized by generating a six-fold symmetry of the ATAD3 monomer revealing a probable structural model of ATAD3 role in the mitochondria. Similar

A docking analysis was conducted on the *Strongyloides stercoralis* ATAD3 protein, using Autodock Vina and the ATP structure from DrugBank. The ATP was found to be situated within the ATPase domain at the C-terminal, with adenine components in pockets formed by Gly352, Ser525, His564, and Leu571. The study identified three distinct groups of interactors: mitochondrial ribosomal proteins, Prohibitin 2 and Prohibitin 1, and V-type protein subunits. The core structure of ATAD3 proteins from five other nematode worms belonging to different classes was also validated and analyzed.

The study analyzed ATP analogues of ATAD3 proteins, including Cangrelor, Citicoline, Metixene, Valganciclovir, and Protoporphyrin IX. Cangrelor, a platelet receptor antagonist, is used in cardiac

procedures to reduce heart attacks and stent clotting showed maximum binding energy which is even more than ATP. Several such potential ligands were identified based on their binding energy.

MegaX software analyzed 102 ATAD3 protein sequences from free-living nematodes, animal, human, and plant parasitic nematodes. The study found that sequence-level variations in ATAD3 proteins were observed in each of these organisms, with the C-terminal domain being the most consistent. Both the N-terminal and C-terminal sequences were found to influence diversity in nematodes, with most aligning based on their parasitic nature. The C-terminal domain exhibited enough diversity to categorize various nematodes by class. Heatmap analysis was also done to visualize the sequential relationship of ATAD3 proteins in all organisms under study and provided a comprehensive understanding of ATAD3 diversity in nematodes. In conclusion, we present the first full-length structural model of the ATAD3 protein in native as well as ATP bound form and identified several probable ATAD3 specific ligands.