

Curriculum vitae

Name	Dr. Shiekh Nadeem
Gender	Male
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Teaching Experience

Teaching	University/college	Year
Assistant Professor	Government Degree College Handwara Kashmir	Mar2018-Dec2021

Courses taught to B.Sc Biotechnology: Transcription regulation in prokaryotes and eukaryotes, Developmental Biology Structural Biology & Endocrinology, Protein structure & Chemistry, Cell Biology & Genetics , Biochemistry and Molecular Biology Microbiology & Immunology, Biotechniques & Biostatistics, cell Cycle, Signalling and Cancer, Environmental Biotechnology, Microbial and Industrial Biotechnology Plant Biotechnology & Tissue Culture, Recombinant DNA technology, Enzymology & Hybridoma technology, Time and space in biology, Biological rhythms, Bioinformatics, Evolutionary Biology

Educational Qualification:

Post-Doctoral Experience: Three years Postdoctoral experience from Institute of Genomics and Integrative Biology

Ph.D: CSIR-IGIB India (March 2009-Oct 2014)

PhD research experience in

- Expression and purification of Normal and expanded human TBP (TATA Binding Protein) which causes SCA17 disorder in its expanded form.

- Change in the Kinetics and thermodynamics of TBP-DNA interactions with the change in (polyQ) domain present in the N-terminal region of TATA binding protein.
- Whole human genome annotation for CAG-CTG repeats in human genome and prediction of novel genes as candidates for neurodegenerative disorders using gene ontology based classification utilizing DAVID tool and microarray.
- Analysis of microarray expression pattern of CAG repeat containing genes.
- Localization and distribution of human TBP variants in Transfected neuronal cell lines and study of protein interaction partners in normal versus SCA17 mutant protein expressed cell lines via coimmunoprecipitation.
- Prediction of miRNA mediated regulation of TATA Binding Protein, which harbours the causative mutation in the neurodegenerative disorder, SCA17.
- Genome wide search for Identification of RNA localization signals in neuronally expressed genes.

M.Sc in Biotechnology from University of Kashmir.

M.Sc Project “Protective effects of *Rumex dentatus* on membrane lipid peroxidation” carried out at University of Kashmir.

Technical Skills

- Protein expression, Purification, Protein estimation (BCA assay) and protein concentration and dialysis and ELISA.
- Chromatographic techniques. Affinity, Immunoaffinity, size exclusion, ion exchange chromatography.
- Plasmid isolation, competent cell preparation and bacterial transformation.
- Native PAGE, SDS PAGE, Silver staining and Western blotting.
- Electrophoretic Mobility shift Assay (EMSA).
- Fluorescence Resonance Energy transfer (FRET) for detecting DNA protein interactions.
- Isothermal titration calorimetry.
- Stem cell culture, Neuronal cell culture, Transfection, Microarray, DNA and RNA purification and estimation, PCR and RT-PCR, Northern Blotting.
- Mouse Model.
- Microarray analysis, Coimmunoprecipitation. Immunotechniques.
- Quantitative and qualitative estimation of carbohydrates, proteins and lipids.

Computer and bioinformatics knowledge : Basics in computer operations, Microsoft Excel, Microsoft Word, PowerPoint and experience to handle bioinformatics data and use of various bioinformatic tools and softwares. Like DAVID, GENECODIS, GENEKO,

NCBI Unigene: - mRNA collection database, GenBank- data collection **UCSC Genome Browser** for Blat

NCBI PubMed: - Papers and Review Database

UTR resource:- 3'UTR and 5'UTR database

Blast (diff types) –

nucleotide-nucleotide : - align two nucleotide sequences

Align 2 seq : - align any two sequences

Genome blast : - align your sequence with genomic DNA

Protein blast :- compare protein sequences and align protein-protein sequences chromosomal map

ExPASy Tool - Translated tool to convert nucleotide sequence to protein sequence

Clustalw - multiple alignment of input sequences

MultiAlin - multiple alignment of input sequences

Motif searching tool – biobase :- Takes an input Motif and searches the motif in different databases

Several miRNA prediction tools such as **miRanda, RNAhybrid and Target Scan** were used to predict miRNA

Fellowships/ Awards/ Achievements:

Qualified national level examination that grants university level **Assistant Professorship** across all Indian Universities.

Qualified CSIR JRF 1/6/2004 under Roll No: 313973

Qualified CSIR JRF 1/12/2004 under Roll No: 301388

Qualified CSIR JRF 1/6/2005 under Roll No: 301932

Granted Junior research fellowship (**JRF**) and Senior research fellowship (**SRF**) from **Council of Scientific and Industrial Research (CSIR) India.**

Granted Department of Biotechnology (DBT) fellowship for M.Sc

Conferences/Seminars/ Symposium/Workshops.

Presentations:

Oral Presentation: Transcription regulation by PolyQ domain of human TBP in neurodegeneration, XXIX Annual conference of Indian Academy of Neurosciences 30th October- 1st November 2011, DRDO Delhi.

Oral Presentation: Protein aggregation and neurodegeneration, Biosparks
2013/11th Annual conference from School of Life Sciences 15- 16 February 2013,
JNU New Delhi.

**Oral Presentation: Bioinformatics bases Genome wide search for Identification of
RNA localization signals across phyla,** NextGen Genomics & Bioinformatics
Technologies (NGBT) Conference 17th -19th November 2014, NIMHANS, Bangalore India

Posters:

Nadeem.S. Transcription dysregulation in neurodegeneration, 19th Biennial
Meeting hosted by the Tata Institute of Fundamental Research 11-14 January 2012.

Nadeem.S. CAG- CTG distribution in Human Genome, 8th Annual Research
Festival, SLS, Biosparks 11-12 March 2010 JNU, New Delhi.

Workshops/ Saminars

Attended International Symposium on “Frontier in Molecular Medicine” 13th -14th Feb.
2009, SCMM,JNU, India.

Attended AIIMS Delhi CSIR-IGIB Joint Workshop on Exome Sequence Analysis
and Interpretation 25-26 July 2018

Attended 3rd Certificate Course on Laboratory Animal Science
(CCLAS) Dec. 5th – 16th, 2016 CSIR- Institute of Genomics and
Integrative Biology, New Delhi, India

Publications

1. CAG repeat distribution in human genome and prediction of genes as candidates for neurodegenerative disorders. (manuscript under preparation).
2. Transcription regulation by PolyQ domain of human TBP in neurodegeneration. (manuscript under preparation).

Referee

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