Curriculum Vitae

Venkatesh Ramakrishnan
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PERSONAL DETAILS

Nationality	:	Indian
Sex & Marital Status	:	Male, unmarried
Age	:	28

ACADEMIC RECORD

1. July 2005 to present:

Associate Scientist in **Aurigene Discovery Technologies Limited, Bangalore, India** leading a protein-NMR group.

2. August 2001 to July 2005:

Ph.D. in Prof. Griesinger's lab at the **Max-Planck Institute for Biophysical Chemistry, Göttingen, Germany.**
Title:: **"Structural Analysis of a Transactivation Domain Co-Factor Complex."**

3. August 1995 to May 2000:

M. Sc. in **Life Sciences** (a 5 years integrated research oriented master's degree program in life sciences) at the School of Life Sciences, **Bharathidasan University, Tiruchirappalli, India**, with distinction (75% aggregate marks).

FELLOWSHIPS

1.	**Sept. 2004 - May. 2005**	E.U. Proteomics Initiative Graduate Fellowship, Univ. of Frankfurt
2.	**Aug. 2001 – Aug. 2004**	Max Planck Ph. D. Fellowship, MPG, Munich.
3.	**Aug. 1994 – May 2000**	National Merit Scholarship, Govt. Of India.

SHORT TERM TRAINING /SUMMER SCHOOLS

Summer 1998

Fellow of the Rajiv Gandhi National Summer Research Program, 1998, at the Jawaharlal Nehru Center for Advanced Scientific Research, Bangalore, India.
Project: ***"Computer simulation of prey-predator populations in a tropical rain forest."***

Winter 1998

Inter-University consortium of Atomic Energy- Dept. of Atomic Energy, Government of India, Calcutta, orientation course in atomic physics for university students.

Summer 1999

Indian Institute for Chemical Biology, Calcutta, trainee in molecular biology methods.

August 2002

EMBO Practical Course in Protein NMR Methods at Il-Ciacco resort, Lucca, Italy.

SUMMARY OF RESEARCH WORK:

(a) Signal Transducers and Activators of Transcription (STAT proteins) are involved in regulating a number of biological processes. STAT6, in particular, has a transactivation domain (TAD), apart from its DNA binding region, that interacts with regulatory proteins like CBP and NCoA-1 (Nuclear Receptor Co-activator). The latter interaction is essential in the regulation of genetic response to stimuli like IL-4 and IL-13. This Ph.D. work aims to have an understanding of the structural basis of the interaction between a transactivation domain and its co-factor, by NMR, crystallography and other complementary biophysical techniques. The complex between NCoA-1 and the STAT6 transactivation domain has been studied by crystallography and it is now known that NCoA-1 (257-385) is a canonical PAS domain when bound to the STAT6 TAD. NMR showed that the NCoA-1 (257-370) might have a different structure in its free form.

(b) An attempt was made to study the process of misfolding of the Syrian hamster prion protein, using NMR. A semi-synthetic prion protein was made, where a recombinantly expressed, N terminal domain was chemically ligated *in vitro*, to a synthetic C terminal peptide with N-glycosylation at two key cysteine residues, in order to facilitate novel NMR studies. The protein: peptide ratio required for the ligation was established to be 1:20.

PUBLICATIONS

Razeto A, **Ramakrishnan V**, Litterst CM, Giller K, Griesinger C, Carlomagno T, Lakomek N, Heimburg T, Lodrini M, Pfitzner E, Becker S. Structure of the NCoA-1/SRC-1 PAS-B domain bound to the LXXLL motif of the STAT6 transactivation domain. *J Mol Biol.* 2004 Feb13;336(2):319-29.

TECHNICAL EXPERTISE

Biophysics

1. Measurement of two and three dimensional spectra using Bruker/Varian spectrometers, including 600 and 900 MHz (+ cryoprobe).
2. Mass spectroscopic analysis of proteins.
3. Crystal screens of proteins for obtaining crystals.
4. Analysis of protein-ligand interactions by isothermal titration calorimetry, including the estimation of binding parameters.
5. Analysis of protein folding using circular dichroism.
6. Fluorescence anisotropy studies of protein-peptide interaction where the peptide in attached to a fluorescent probe.
7. Preparation and testing of novel alignment media for measuring residual dipolar couplings.

Biochemistry & Molecular Biology

1. Cloning of mammalian protein domains into *E. coli*
2. Expression of proteins in isotope labeled media using *E. coli*
3. Purification of proteins by affinity based methods like ion exchange and size exclusion chromatography.
4. Synthesis of peptides by solid phase synthesis.
5. Purification of peptides by HPLC.
6. Agrobacterium mediated transformation and plant tissue culture.

Bioinformatics & NMR software

1. Processing of NMR data using NMRPipe, Felix.
2. Analysis including resonance assignment of protein backbones using softwares like Sparky, NMRView, Felix etc.
3. Programming knowledge in Java, Python, C/C++.
4. 3D homology modeling, docking small molecules to protein structures.

RESEARCH INTERESTS

Signal Transduction, Cell Biology, Biochemistry and Biophysics.

ENGLISH PROFICIENCY

Secured 623 in TOEFL in Jan. 2000

REFEREES

Prof. Dr. Christian Griesinger
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Max Planck Institute for Biophysical Chemistry
030, NMR Based Structural Biology
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