

## PROFILE

**Name:** Amal Kumar Bandyopadhyay

**Designation:** Assistant Professor



**Degree & Experience:**

BSc (Ag) Hons from BCKV Nadia, WB.

(Four and half years –specialization in Agril. Chemistry & Biochemistry & Soil Sciences)

MSc (Biochemistry) Department of Chemistry and Biochemistry, College of Basic Sciences and Humanities, CCS Haryana Agril. University.

**Thesis:** Effect of Naringenin and Nitrate on *Pisumsativum*L. - Rhizobium Symbiosis.

**Guide:** Professor H. S. Nainawati and Dr. Veena Jain 23

**Place of work:** Department of Chemistry and Biochemistry, CCSHAU, Hissar, Haryana

**Work Summary:** It was shown that rhizospheric application of naringenin a *nod* gene inducer increase: nodulation status, nodule efficiency as evidenced by increase in nodule number, weight; increase in nitrogenase, glutamine synthetase (GS), glutamine synthase (GOGAT) activities; increase in total nitrogen content and plant biomass. HPLC patterns of flavonoids support the contention that naringenin increase but the nitrate reduces nodulation status for the above cross nodulation group. The research work was supported by the award JRF to AKB from ICAR (Indian Council of Agricultural Research, Pusa, ND).

**Publication from Master's Research: Bandyopadhyay, AK, Jain, V. and Nainawatee, HS. (1996), Nitrate alters the flavonois profiles and nodulation status of pea (*Pisumsativum* L.) in *Biology and Fertility of Soils*, 21, 189-192.**

**PhD Course work** –Three semesters in the Department of Chemical Physics (presently: Department of Chemical Sciences (MBU)) Tata Institute of Fundamental Research, Mumbai)

**PhD** in Physical Chemistry (Degree awarded by the University of Mumbai).  
(5 years research work)

**Thesis:** Stabilization of Halophilic Proteins: [2Fe-2S] Ferredoxin from *Halobacterium salinarum* as a Paradigm.

**Guide:** Professor R. V. Hosur and Professor H. M. Sonawat

**Collaboration with:** Dr. Ananya Mazumdar, Professor G. Krishnamoorthy and Dr. L. C. Padhy

**Place of work:** Molecular Biophysics, Department of Chemical Sciences, Tata Institute of Fundamental Research, Mumbai, HomiBhabha Rd, 400 005.

**Discover for the first time on world basis that**

- a. **Halophilic ferredoxin indeed adapted in high salt and**
- b. **Mechanism of adaptation involve I. classical electrostatic II. Salt-solvent perturbation effect III. Specific electrostatic effect and IV. Post Hofmeister effect.**

**Work Summary during Doctoral period:** After completion of core courses and short-term experimental projects (three semesters), PhD work started. Two parallel projects: Theoretical work on development of analytical equation in TOCSY transfer and Purification and biophysical studies of halophilic ferredoxin was undertaken. Former was successfully completed in 2 years and later was then concentrated. Experimental structural studies on ferredoxin from *Halobacterium salinarum* involving spectroscopic (Absorbance, Fluorescence, Circular Dichroism, Stopped flow and NMR), kinetics and thermodynamics methods was carried out.

**Publications from Doctoral Research:**

- 1) Bandyopadhyay, A.K. and Sonawat, H.M., (2000), Salt Dependent Stability and Unfolding of [Fe<sub>2</sub>-S<sub>2</sub>] ferredoxin of *Halobacterium salinarum*: Spectroscopic Investigations, in **Biophysical Journal**, 79, 501-510.
- 2) Bandyopadhyay, A.K., Krishnamoorthy, G. and Sonawat, H.M., (2001), Structural Stabilization of [2Fe-2S] ferredoxin from *Halobacterium salinarum*, in **Biochemistry**, 20, 1284-1292.
- 3) Bandyopadhyay, A.K., Krishnamoorthy, G., Padhy, L.C. and Sonawat, H.M., (2007), Kinetics of Salt-Dependent Unfolding of [2Fe-2S] Ferredoxin of *Halobacterium salinarum*, in **Extremophiles**, 11, 615-625.

**Place of Research-** Molecular Biophysics Unit, Chemical Physic (Presently Department of Chemical Sciences) Tata Institute of Fundamental Research, Mumbai  
Mumbai)

**Post Doctoral Fellow:**

1. Department of Chemical Sciences (DCS), Tata Institute of Fundamental Research  
Mumbai, India

**Post Doctoral Research Associate**

2. Howard Hughes Medical Institute, Department of Chemistry, Rutgers, NJ, USA  
Joined the Department of Biotechnology, the University of Burdwan in 2006

Teaching in the Department of Biotechnology, The University of Burdwan:

**A. MSc**

1. Chemistry of Biomolecules,
2. Biochemistry (theory and practical),
3. Medical Biotechnology,
4. Proteomics
5. Molecular Techniques in Biotechnology (Q-PCR, NMR and X-ray)

## **B. PhD**

1. Structural Biology and
2. Biocomputing,
3. Molecular Dynamic Simulation for biological reactions.(theory and practice).

## **Research Interest**

Basic Research on Extreme and Mesophilic Proteins (Experimental Studies and database Analysis)

Analyses of Atomic Structure and Sequences of proteins for Understanding Protein Adaptation in Extreme Environments. Our preliminary studies on proteins show that

- a. Fundamental Matrices of amino acids deviate from Universal behavior
- b. Positional variation of amino acids play crucial role in structural Stabilization of extreme proteins w.r.t. its mesophilic counterparts
- c. Prediction inaccuracy in secondary structure of proteins seems to be an imposed law of natural evolution.
- d. Chromophore forming loop of some proteins shows strict selectivity in amino acids composition.

We are developing softwares using C-language, UNIX (C- & B- Shell), and Gawk for automated analysis of sequence and structure databases in these aspects.

Softwares developed in our Laboratory:

1. GSALT: automated salt bridge analysis using Crystal Structure as input
2. MSTRUCT: Secondary structural propensity and variability determination from crystal structure (Program has capability to Jump the chain discontinuity and to correct other errors in structure files)
3. PHYSICO: Physicochemical properties (25 kinds) and other 10 different sequence properties determination
4. MULTIBLOCK: Generation of BLOSUM Matrices from many (>2000) sequence blocks.
5. MULTIHENIK: Calculation and plotting of paired frequency, Obs. & Expected probability from sequence block
6. HAMBAs: Mass scale analysis of Local data bases of sequences
7. FSMD and VECNORM: together prepare crystal structure for Steered Molecular Dynamic Simulation in one step
8. PROTWATER: Make crystal structure ready for MD calculation in one step

## **Research activity from October, 2010 - 2013 (after research scholars join me)**

### **Research Scholars:**

- Shyamashree Banerjee (Full Time)
- Parth Sarthi Sengupta (part time)
- Pulak Das (part time)
- Arnab Nayek (part time)
- Sudipta Mondal (doing course work)
- Rifat Nawal Ul Islam (doing course work)
- Buddhadev Mondal (doing course work)

## Publication:

SEN GUPTA, PARTH SARTHI., MONDAL, BUDDHADEV., AND BANDYOPADHYAY AMAL KUMAR\*, IN SILICO CHARACTERIZATION OF HUMAN TYROSINASE USING COMPUTATIONAL TOOLS AND SERVERS, (2013), Int J Pharm Bio Sci , 4, 181 – 193.

Sen Gupta ParthSarthi, Banerjee Shyamashree and Bandyopadhyay Amal Kumar\*, Sequence, Structural and Functional Characterization of Homogentisate-1,2-dioxygenase of homo sapiens: An in silico Analysis, (2013), American Journal of Bioinformatics Research, 3, 42-61.

MondalSudipta, BandyopadhyayAmal Kumar\* and Islam Rifat Nawaz Ul, (2013), Protein structure determination of insulin of zebra fish (Daniorerio) by homology modeling and structure analysis. (2013), Journal of Pharmacy and Biological Sciences 5, 38-43.

MondalSudipta, MondalBuddhadev and Bandyopadhyay Amal Kumar\* HOMOLOGUE MODELING OF PHASEOLIN FROM KIDNEY BEAN (Phaseolus vulgaris L.): ENERGY MINIMIZATION AND STRUCTURE ANALYSIS, (2013), International Journal of Engineering Science and Technology, 5, 992-998.

Sen Gupta ParthSarthi, MondalBuddhadev. And Bandyopadhyay Amal Kumar\*, IN SILICO CHARACTERIZATION OF HUMAN CYCLOOXYGENASE USING COMPUTATIONAL TOOLS AND SERVERS, (2013), International Journal of Institutional Pharmacy and Life Sciences, (accepted).

Banerjee Shyamashree and Bandyopadhyay Amal Kumar\*, INVESTIGATION OF AMINO ACID PROPENSITY FOR THE LOOP REGION COVERING THE IRON-SULFUR CLUSTER FOR DIFFERENTIATING SALT DEPENDENT HALOPHILIC FERREDOXIN FROM MESOPHILIC ONES, (2013), International Journal of Institutional Pharmacy and Life Sciences, (accepted).

MondalSudipta, Banerjee Shyamashree, Sen Gupta ParthSarthi, MondalBuddhadev and Bandyopadhyay Amal Kumar\*, Sequence, structure analysis, homology modeling and epitope prediction of Japanese encephalitis virus (JEV) surface protein isolated from India: an in-silico analysis, (2013), (Submitted)

Banerjee Shyamashree, Sen Gupta ParthSarthi, MondalSudipta and BandyopadhyayAmal Kumar\*, Halophiles vs Thermophiles: An in silico Analyses of Sequence and Structure of Cytosolic Proteins, (2013), (Submitted).

Nayek, Arnab, Banerjee Shyamashree, Sen Gupta ParthSarthi and BandyopadhyayAmal Kumar\*, Salt-Bridge Energetics of halophilic Proteins using Adaptive Poison-Boltzmann Solver, (2013), (Submitted)

Sen Gupta ParthSarthi, Banerjee Shyamashree and Bandyopadhyay Amal Kumar\*, Insight into the Structure and Dynamics of Dioxigenase causing Alzimer, (2013), (Manuscript under Preparation).

Data Base Publication:

**Sequence**

Database: National Center for Biotechnology Information, USA

Sequence ID: KF285826

Authors: SenGupta,Parth.Sarthi., Das,Pulak., Banerjee,Shyamashree.  
andBandyopadhyay,Amal.Kumar\*.

Ties and Collaborations:

A. Dr. S. Chatterjee, ICMR, Virology Unit, Kolkata

B. Dr. S. Mukherjee, Department of Microbiology,  
The University of Burdwan

**Project from central DST:**