Bose Institute
Kolkata

(An autonomous research institute of Dept. of Science & Technology, Govt. of India)

Advertisement No. : BI/NET-JRF/04/2021-22

Admission for PhD Programme Autumn 2021

http://www.jcbose.ac.in/applications/PHD-ADMISSION/

Acharya J.C. Bose, the founder of modern science in the Indian subcontinent, established Bose Institute in 1917. The Institute was set up as Asia's first interdisciplinary research centre and bears a century old tradition of excellence in research.

The Institute desires to admit students for its Ph.D. programme twice a year, for sessions beginning tentatively in January and July. Interviews for this session will be held tentatively during 3rd week of December, 2021 in online/hybrid mode.

Broad areas of research: Atmospheric Sciences, Chemical Sciences, Life Sciences, Physical Sciences and Applied Biosciences.

- Candidates can apply simultaneously to maximum of two positions as mentioned in **Annexure - I**.
- Candidates are required to provide a **Statement of Purpose** (SOP), in prescribed format, for **each of the positions** she/he applies for.

Fellowship: Admissible as per Govt. of India rules.

Reservation : Reservation quota will be adhered to the standard GoI rules.

Eligibility for PhD Interview:

(1) Candidates should have an award of JRF (CSIR-UGC JRF/ DBT-JRF/ ICMR-JRF/ DST-INSPIRE/ DBT-BINC or equivalent), whose last date of validity should not be earlier than 31st March 2022 Candidates, who are in the final year of their Master's degree and are in possession of an award of a JRF, if selected, will have to submit their final degree certificate at the time of joining.

(2) Master's degree or equivalent in any of the following fields: Engineering/ Science/ Technology with at least 55 %of marks for general, while for SC/ST/OBC (non-creamy layer) / Differently abled and other categories 50% marks is necessary

(3) Age limit: 28 years as on the day of application and relaxation of age is applicable as per Government of India rule.

(4) DST-INSPIRE candidates can only be admitted provisionally. Confirmation of their admission to the PhD programme of Bose Institute is subject to the final award of INSPIRE fellowship by DST. Subsequently, in case, the candidate is not finally awarded the INSPIRE fellowship by DST, his/her provisional admission is liable to be cancelled by the Institute.

(6) Candidates who have qualified in GATE/ JEST/ JGEEBILS/ NET (LS) etc. but who do not have a valid award of JRF mentioned in (1) above or equivalent are ineligible to apply.

Registration for PhD Interview:

- Interested candidates fulfilling required eligibility should register online at the URL – http://www.jcbose.ac.in/applications/PHD-ADMISSION/

  Deadline for online Registration: 6 PM of November 30th, 2021

- An online acknowledgement receipt will be generated on successful registration. Candidates should retain this receipt for future reference. Candidates must produce this acknowledgement receipt for the interview. No candidates will be entertained for interview without this receipt.
- In case of any difficulty during online registration, please send email to phdadmission@jcbose.ac.in

Shortlisting for Interview:

- A shortlisting will be done based on 50% weightage on past academic records and 50% weightage on SOP.
- List of shortlisted candidates, along with the date and time of interview will be displayed at the Institute website
  Note: Candidates applying for more than one discipline may be called for separate interviews.

PhD interview:

- The interview will be conducted online/hybrid mode. Specific instructions for the interview will be communicated to the candidates at a later date.
- The medium of the interviews is English.

Shortlist and selection:

- The shortlist of candidates selected for the interviews, will be posted on the Institute website.
- It should be noted that mere appearance on the shortlist does not imply admission.
- Once the shortlist of candidates is posted on the Institute website, information on the future course of action and the timelines thereof, will be mentioned on the Institute website or will be communicated to the candidates.
- The Institute Authority reserves the right to reject any or all applications without assigning any reason thereof.

Important Dates:

- Last Date for online Registration: 18:00 hrs. November 30th, 2021
- Date of display of short-listed candidates and instructions on the Institute website: December 10th, 2021
- Tentative date of interview: 3rd week of December, 2021. The final dates of interview will be confirmed when the list of short-listed candidates is displayed on the BI website.

Annexure -I

Broad Area of Research: Atmospheric Sciences

Position Code	Name of Faculty	Research Area	Desired Master's Background
AS01	Abhijit Chatterjee	**Title:** Spatio-temporal variabilities of atmospheric aerosols over different atmospheric environments in India **Description:** The broader objective of the study would be addressing the issues of "Air Pollution and Climate Change" in India. The ground based and the satellite-based observation would be made in order to the study the spatio-temporal variabilities of atmospheric aerosols over different atmospheric environments in India. Chemical analysis and the re-analysis data would be used for identifying the major source types of aerosols and the quantitative contribution of each of the sources would be made using some suitable source-receptor model. The study would be focused on several strategic locations like tropical urban metropolis, tropical coastal stations and high altitude Himalayan stations etc.	Atmospheric Science/ Environmental Science/
AS02	Abhijit Chatterjee	**Title:** Microphysical properties of clouds: Impact of anthropogenic aerosols **Description:** The broader objective of the study would be addressing the issues of "Air Pollution and Climate Change" in India. The ground based and the satellite-based observation would be made in order to the study the microphysical properties of clouds and their spatio-temporal variabilities induced by the rapidly changing aerosols properties. The locally generated and transported pollution plumes bear immense potential in changing the aerosol potential to act as cloud condensation nuclei. Such observation would be made over high altitude Himalayan station. In addition, satellite based monitoring of microphysical properties of clouds and their long-term changes would be studied with the changes in aerosols chemistry and physics.	Atmospheric Science/ Environmental Science/

AS03	Sanat Kumar Das	**Title:** Carbonaceous aerosols and their radiative warming effect on Himalayan glacier melting **Description:** Our nation is going to face severe drinking water crisis in future due to day-by-day reduction in input water of glacier-fed rivers. However, at present there is no known solution for this problem. This project is for a student who is ready to accept this challenge to find out a plausible solution. My earlier research work discovered various types of carbonaceous aerosols present in the atmosphere. This research project is to quantify these various types of carbonaceous aerosols and simulate their radiative effect that warms up the atmosphere over the Himalayas, However, the most challenging part of this work is to identify the dominating type of carbonaceous aerosols responsible for the Himalayan glacier melting and find out the possible solution to remove them from the atmosphere. The selected student should have an understanding of basic physics and knowledge of basic programing languages. The student should be able to work in-group to take atmospheric observations using modern sophisticated instruments over the Himalayas and perform data analysis and simulation works for pursuing PhD.	Atmospheric Science/ Environmental Science
AS04	Sanat Kumar Das	**Title:** Study on alteration of hygroscopic properties of aerosols during Fog and impact on forecasting **Description:** This research work is a part of my project funded by CSIR, Govt. of India. The work is on improvement of fog forecast system, which is important for navigation, agriculture, human health etc., and thereby plays a significant role in national economy. Forecast of fog is a big challenge for atmospheric scientists as it is very difficult to reduce the uncertainty present in the output of forecast models. The uncertainty comes from lack of on-field observational data of alteration of hygroscopic properties of aerosols during foggy period. This research work includes not only challenging field experiments to obtain time-series of aerosol optical and physical properties, but also run the atmospheric models. Therefore, the work is very demanding and includes fieldwork. The student should have a good understanding of basic physics and knowledge of basic programing languages. The selected student will participate in on-field group work to collect	Atmospheric Science/ Environmental Science

		atmospheric observational data from in-situ experiments using monochromatic lasers, carry out labbased measurements using modern sophisticated instruments and perform data analysis and simulation work for pursuing PhD.	
AS05	Sanat Kumar Das	**Title:** Atmospheric microbial loading and their role in cloud formation **Description:** This research work is a part of my project approved by the Ministry of Earth Science (MoES), Govt. of India that comprises of several research cruises including Sagar Tara, Sagar Anveshika for on-board experiments over the Bay of Bengal and the Indian Ocean. There are varieties of continental air-borne microbiomes transported from the mainland of India to its surrounding oceanic regions. This project is to identify the different types of air-borne microbiomes and the reason behind their presence and survival in the marine environment using different types of on-board insitu experiments. The objective is to find their role in cloud formation processes. The student should have a basic understanding of microbiology. Additional knowledge in basic meteorology is preferable. The selected student should be able to work in a group for on-board ship experiments, carry out lab-based measurements using modern sophisticated instruments and perform data analysis and simulation work for pursuing PhD.	Environmental Science
AS06	Soumen Roy	**Title:** Competition, Cooperation, and Communication in microbes **Description:** Brief description of the Research Project: Recently published and ongoing projects are in the areas of: (1) phage-bacteria interactions and dynamics, and, (2) antimicrobial resistance. Our research here is strongly guided by theoretical (rigorous mathematical and computational) investigations which can be validated by experimental studies conducted in our own lab. The former includes but is not limited to network science, game theory, nonlinear dynamics, statistical physics, and information theory. If they wish, selected candidates are welcome to pursue this project in conjunction with other lab project/s of their choice.	Environmental Science

AS07	Soumen Roy	**Title :**Systems Biology of macromolecular interactions **Description:** Brief description of the Research Project: Macromolecular interactions define molecular recognition and cell signaling. Recently published and ongoing projects are in the areas of amino acid residue interaction networks, protein-protein interaction networks, protein-nucleic acid complexes, as well as protein-small molecule interactions. Here we strongly focus on the theoretical (rigorous mathematical methods and computational) aspects of intra-macromolecular and inter-macromolecular interactions. Validation of our theoretical predictions can be carried out through our experimental collaborators as well as our in-house setup. If they wish, selected candidates are welcome to pursue this project in conjunction with other lab project/s of their choice.	Environmental Science

Broad Area of Research: Chemical Sciences

Position Code	Name of Faculty	Research Area	Desired Master's Background
CS01	Samarjit Polley	**Title:** Understanding the Structure-Function Relationship of IKK1 in Regulating NF-kB Activation and Beyond. **Description:** More than 500 protein kinases are encoded in the human genome. Protein kinases provide the regulatory framework for most signaling pathways in eukaryotic cells. Stringent regulation of their activities is critical to proper functioning of cellular processes, and consequently they act as important drug targets. Indiscriminate inhibition of kinase activities often has deleterious effect on healthy being of cells. Signaling modularity is dictated by choice of substrates, cognate-binding partners, subcellular localization and post-translational modifications of the kinase itself. It is important to investigate the mechanistic details of their activation and spatio-temporal regulations to fully realize the scope of modulating them in a manner beneficial for the	Chemistry

		organism. We aim to study structure-function relationship of, Inhibitor of kappaB Kinase 1/a (IKK1/a) and its close partner NIK (NF-kB Inducing Kinase also known as MAP3K14); and how they regulate each other's function. Primary function of IKK1 in cells is to activate NF-kB thorough the non-canonical/alternative pathway in response to an array of ligands and developmental cues. IKK1 is also known to regulate gene expression by directly modifying the epigenome --- it phosphorylates Ser10 of histone H3. Interestingly, IKK1 is dependent on NIK for its NF-kB-activating function but not for its epigenome modifying activity.	
CS02	Anup Kumar Misra	**Title:** Synthesis of complex oligosaccharides corresponding to the cell wall polysaccharides of pathogenic bacterial strains **Description:** Development in the glycobiology research amplified the demands for well-defined oligosaccharide motifs for various biological studies. Naturally derived bacterial capsular polysaccharides have been the basis for effective anti-bacterial vaccines, but little is known about the protective glycotopes for many serotypes. Since natural source cannot provide the large quantity of oligosaccharides with homogeneity and adequate purity, it is essential to develop chemical synthetic approaches for getting access to the complex oligosaccharides. Stereoselective glycosylation reaction is the key component for assembling of monosaccharides towards the synthesis of complex oligosaccharides. Cell wall oligosaccharides corresponding to the repeating units and sub-units of polysaccharides, differing in chain length and monosaccharide composition help to identify antigenic determinants for the creation of semi-synthetic glycoconjugate vaccine candidates. Objective: Chemical synthesis of complex oligosaccharides corresponding to the cell wall of bacterial polysaccharides	Chemistry

CS03	Anup Kumar Misra	**Title:** Synthesis of complex oligosaccharides corresponding to the cell wall polysaccharides of pathogenic bacterial strains **Description:** Naturally derived bacterial capsular polysaccharides have been the basis for effective anti-bacterial vaccines. Since natural source cannot provide the large quantity of oligosaccharides with homogeneity and adequate purity, it is essential to develop chemical synthetic approaches for getting access to the complex oligosaccharides. Stereoselective glycosylation reaction is the key component for assembling of monosaccharides towards the synthesis of complex oligosaccharides. Cell wall oligosaccharides corresponding to the repeating units and sub-units of polysaccharides help to identify antigenic determinants for the creation of semi-synthetic glycoconjugate vaccine candidates. Objective: Development of novel reaction methodologies for the synthesis of glycomimetics for their use in the medicinal chemistry.	Chemistry
CS04	Soumen Roy	**Title:** Competition, Cooperation, and Communication in microbes **Description:** Brief description of the Research Project: Recently published and ongoing projects are in the areas of: (1) phage-bacteria interactions and dynamics, and, (2) antimicrobial resistance. Our research here is strongly guided by theoretical (rigorous mathematical and computational) investigations which can be validated by experimental studies conducted in our own lab. The former includes but is not limited to network science, game theory, nonlinear dynamics, statistical physics, and information theory. If they wish, selected candidates are welcome to pursue this project in conjunction with other lab project/s of their choice.	Chemistry

CS05	Soumen Roy	**Title:** Systems Biology of macromolecular interactions **Description:** Brief description of the Research Project: Macromolecular interactions define molecular recognition and cell signaling. Recently published and ongoing projects are in the areas of amino acid residue interaction networks, protein-protein interaction networks, protein-nucleic acid complexes, as well as protein-small molecule interactions. Here we strongly focus on the theoretical (rigorous mathematical methods and computational) aspects of intra-macromolecular and inter-macromolecular interactions. Validation of our theoretical predictions can be carried out through our experimental collaborators as well as our in-house setup. If they wish, selected candidates are welcome to pursue this project in conjunction with other lab project/s of their choice.	Chemistry
CS06	Achintya Singha	**Title:** Surface-Enhanced Raman Scattering (SERS) based bio-sensor **Description:** Surface-Enhanced Raman Scattering (SERS) combines molecular fingerprint specificity with single-molecule detection, which is the ultimate sensitivity required in chemical analysis, trace detection and bio-sensing. Two-dimensional transition metal dichalcogenides (TMDs)/plasmon nanostructure (Au, Ag, etc) integrate the superior light-solid interaction and therefore are promising for surface-enhanced Raman Spectroscopy (SERS). The present work aims to develop TMDc-plasmon hybrid structures to detect and study a single molecule using the SERS technique.	Chemistry

Broad Area of Research: Life Sciences

Position Code	Name of Faculty	Research Area	Desired Master's Background
LS01	Sanat Kumar Das	**Title :**Atmospheric microbial loading and their role in cloud formation **Description:** This research work is a part of my project approved by the Ministry of Earth Science (MoES), Govt. of India that comprises of several research cruises including Sagar Tara, Sagar Anveshika for on-board experiments over the Bay of Bengal and the Indian Ocean. There are varieties of continental air-borne microbiomes transported from the mainland of India to its surrounding oceanic regions. This project is to identify the different types of air-borne microbiomes and the reason behind their presence and survival in the marine environment using different types of on-board insitu experiments. The objective is to find their role in cloud formation processes. The student should have a basic understanding of microbiology. Additional knowledge in basic meteorology is preferable. The selected student should be able to work in a group for on-board ship experiments, carry out lab-based measurements using modern sophisticated instruments and perform data analysis and simulation work for pursuing PhD.	Zoology/ Microbiology
LS02	Anupama Ghosh	**Title :** Investigating the extracellular ribonucleases of Ustilago maydis and their role in targeting cell-cell communication through apoplastic RNA in maize **Description:** Effector proteins from phytopathogenic fungi are secreted proteins that are exclusively expressed during infection and contribute to the fungal pathogenicity. Ustilago maydis is a biotrophic phytopathogen that causes smut disease in maize. During infection U. maydis secretes a huge repertoire of effector proteins within the maize apoplast. In this project we are exploring the possible biological	Zoology / Microbiology / Botany

		functions of a group of such effector proteins that possess ribonuclease activity and can successfully degrade RNAs in the extracellular milieu. The project also explores a pool of apoplstic RNA in maize and its possible functions. The project would use various molecular biology and cell biology techniques including genetic manipulations in Ustilago maydis. In addition a considerable part of the study would also include experiments involving different forms of microscopy.	
LS03	Anupama Ghosh	**Title:** Role of small heat shock proteins in the pathogenic mechanisms of Ustilago maydis **Description:** Ustilago maydis is a biotrophic plant pathogen that causes smut disease in maize. During infection the pathogen experiences a number of defence responses from the host plant that it needs to overcome to establish infection. This project deals with the biological role of a group of small heat shock proteins from Ustilago maydis in establishing infection by the pathogen. Besides, in Ustilago maydis the pathogenic development is linked to morphological transitions from sporidia to filament and finally to spores within the host plants. The project also includes investigations on the involvement of the small heat shock proteins in the pathogenic development of Ustilago maydis in-planta. The project would use various molecular biology and cell biology techniques including genetic manipulations in Ustilago maydis. In addition a considerable part of the study would also include experiments involving different forms of microscopy.	Zoology / Microbiology / Botany
LS04	Shubho Chaudhuri	**Title :** Exploring the interactome associated with chromatin remodeler AtHMGB15 during pollen development. **Description:**This project deals with Arabidopsis protein AtHMGB15 , which is a nuclear architectural protein belonging to ARID-HMG family. The	Microbiology / Botany /

		main function of nuclear architectural proteins is to prepare the right environment for the DNA so that many nuclear processes like transcription, replication and repair, can be facilitated. In higher eukaryotes, these group of protein remodel the higher order chromatin structure for facilitating many nuclear processes; thus can function as chromatin remodeller. Recent work from our group has shown that ARID-HMG can bind different DNA topological forms, can bend DNA backbone and can also induce DNA supercoiling to facilitating nuclear processes [Roy et al, (2016) Plant Molecular Biology 92 (3), 371-388]. We have also identified the genome wide targets and DNA binding motif of ARID-HMG [Mallik et al, (2020). BBA-Gene Regulatory Mechanisms 1863 (12), 194644]. Presently we have identified its role in pollen development pathway. Using the knock-out mutant, we have observed alteration in pollen morphology, pollen growth and development. In continuation of this project, we will be looking for genome-wide targets of AtHMGB15 during pollen development using ChIP-sequencing. We are also interested to know the interacting partners of AtHMGB15 protein during flower development, which involves high-through put proteome analysis. Hypothesis: many nuclear architectural proteins are the part of chromatin remodelling complex because of their unique DNA binding and bending property. Thus, it is believe that they act as transcription activators and interact with many transcription factors and chromatin remodellers.	
LS05	Shubho Chaudhuri	**Title :** Investigating the recruitment of ARID-HMG protein AtHMGB15, to the nucleosome and its effect on the accessibility of nucleosomal DNA for nuclear processes **Description:** The compaction of the eukaryotic genome into chromatin makes DNA accessibility a rate limiting step during essential nuclear processes like transcription, replication, repair and	Microbiology

		recombination. To facilitate these processes, multi-subunit protein complexes/machineries often need access to regions of the genome packaged into dense chromatin. The dynamic nature of chromatin allows targeted alteration of local chromatin structure at genomic regions which need to be accessed. The nuclear machineries are assisted by multiple chromatin binding proteins to regulate the dynamics of local chromatin structure and increase DNA accessibility. Many of these proteins are chromatin readers or modifiers which work in combinations and in tandem with chromatin remodelers to allow localised nucleosomal dynamics. Apart from these, there are DNA binding proteins that bind, stabilise or change various topological structures of DNA that are formed by the multi-subunit machineries in the intermediate steps of the nuclear processes. One such superfamily of proteins is the High Mobility Group (HMG) of proteins, which are indeed highly mobile and abundant within the nucleus where they are part of a dynamic network of architectural components that modulate the structure of chromatin and, thereby, affect multiple DNA-dependent activities The HMG-box containing ARID-HMG protein binds DNA through its ARID domain and promotes supercoiling of plasmid DNA through its HMG-box domain. Considering that ARID domains are found in transcription factors and HMG-box containing proteins are capable of nucleosomal interactions, the presence of both these domains in AtHMGB15 indicate the possibility that this protein by direct interaction with the DNA may mediate interactions between general transcription factors and chromatin remodelers to promote inducible gene expression. To investigate this possibility, it is important to analyse if indeed AtHMGB15 interacts with nucleosomal DNA and if so the mechanism and effects of its interaction with the nucleosome. Hypothesis: Unique ARID-HMG protein AtHMGB15	

		interacts with nucleosomal DNA in a manner antagonistic to linker histone H1 such that its recruitment stabilises a locally open chromatin conformation and increases DNA accessibility	
LS06	Shubho Chaudhuri	**Title :** Understanding the effect of histone modifications on chromatin dynamicity during cold stress response in indica rice **Description:** Previous studies suggest that histone modifications and DNA methylation play an important role in inducing stress responsive loci in rice under environmental stress. In plants, although extensive work has been done on genome wide scale during salinity and drought stress, the epigenome dynamicity under cold stress remains completely unexplored (19). Although we have identified regions of genome which shows change from repressive H3K27me3 mark to H3K27acetylation activation mark during cold stress response; it is not clear how this epigenetic switch regulate the chromatin conformational change to regulate stress induced transcription. The current study entails a comprehensive analysis of the epigenomic landscape and chromatin conformation, with respect to the status of H3K27, associated with cold stress response in rice. PcG (Polycomb) group mediated repression (H3K27me3 enriched) is the default state of most inducible genes, which are activated upon Trx (Trithorax) group mediated H3K27 acetylation (20). Trimethylation of histone H3 lysine 4 (H3K4me3) is an important intermediate step in the switch of H3K27me3 to H3K27ac (21). The SET1/COMPASS domain of Trx (Trithorax complex responsible for H3K27ac) group trimethylates H3K4 residue which provides a recognition and docking site for the H3K27 acetylation components of the Trx complex (22). Since, the Trx and PcG complexes have been reported to be colocalized on chromatin for various genes (active/inactive) (23-25), the question remains how is the decision	Microbiology / Botany

		made for the locus activation/repression or the switch, i.e., which are the triggering factor. Objectives: In this work, we intend to address this question at three different levels: 1. The status of H4K3 trimethylation associated with H3K27ac and H3K27me3 enriched regions under early cold stress. 2. How these histone modifications regulate the nucleosome dynamicity with reference to differentially expressed genes during cold stress response. 3. How these histone modifications high-resolution three-dimensional genome organization i.e. the chromatin conformation for contiguous enriched regions under early cold stress.	
LS07	Abhrajyoti Ghosh	**Title :** Understanding the role of type II toxin-antitoxin in the survival of thermoacidophilic archaeon Sulfolobus acidocaldarius **Description:** Toxin-Antitoxin (TA) system are important stress-response elements widespread in bacteria and archaea. Toxins operate in diverse mechanisms leading to cell death, reversible growth stasis and are involved directly in inhibiting essential cellular processes, while the antitoxin blocks the effect of toxins. Several cellular functions of the TA system have been proposed in case of bacteria, however their exact role in archaeal cell physiology still remains elusive. TA modules are important in several events in cellular physiology such as plasmid maintenance, formation of persister cells, stress resistance, protection from bacteriophages and regulation of biofilm formation, acting on crucial cellular processes including translation, replication, cytoskeleton formation and membrane integrity. Our group is mainly interested in characterization of the different TA gene systems identified in hyperthermophilic crenarcheon Sulfolobus acidocaldarius, exploiting various biochemical and biophysical techniques. Gene expression analysis revealed differential expression of	Microbiology/Life Sciences

		plethora of TA genes, in response to different stress. We are keen to understand the role and regulation of the different TA system in stress adaptation from our model organism, Sulfolobus acidocaldarius. In addition, our recent venture is to manipulate the genetic system of this extremophile, in order to generate TA deleted strains for efficient understanding of their function in cellular physiology. Candidates having interest in protein biochemistry, biotechnology, cell biology and genomics are suitable for this position.	
LS08	Abhrajyoti Ghosh	**Title:** Understanding the molecular players involved in the survival of model haloarchaea in fluctuating salinity of Sundarbans **Description:** Archaea remain important players in global biogeochemical cycles worldwide, including in the highly productive mangrove estuarine ecosystems. In the present study, we have explored the diversity, distribution, and function of the resident archaeal community of the Sundarban mangrove ecosystem, using both culture-independent and culture-dependent approaches. Our results showed that haloarchaea are the dominant archaeal group in hydrocarbon polluted sediments, of Sundarbans. We have successfully isolated eleven p-hydroxybenzoic acid degrading haloarchaeal species. These isolates could survive in different salinity of Sundarban. Genome sequencing of selected haloarchaeal isolates revealed that they possibly employ multiple mechanisms to cope with the changes in salinity. In this project, we would like to study the molecular players involved in the survival of these haloarchaeal species in different saline conditions. Candidates having interest in archaeal biology, biochemistry, high throughput sequencing analysis and biotechnology are suitable for this position.	Microbiology/ Life Sciences
LS09	Samarjit Polley	**Title:** Understanding the Structure-Function Relationship of IKK1 in Regulating NF-kB Activation and	Zoology/ Microbiology

		Beyond. **Description:** More than 500 protein kinases are encoded in the human genome. Protein kinases provide the regulatory framework for most signaling pathways in eukaryotic cells. Stringent regulation of their activities is critical to proper functioning of cellular processes, and consequently they act as important drug targets. Indiscriminate inhibition of kinase activities often has deleterious effect on healthy being of cells. Signaling modularity is dictated by choice of substrates, cognate-binding partners, subcellular localization and post-translational modifications of the kinase itself. It is important to investigate the mechanistic details of their activation and spatio-temporal regulations to fully realize the scope of modulating them in a manner beneficial for the organism. We aim to study structure-function relationship of, Inhibitor of kappaB Kinase 1/a (IKK1/a) and its close partner NIK (NF-kB Inducing Kinase also known as MAP3K14); and how they regulate each other's function. Primary function of IKK1 in cells is to activate NF-kB thorough the non-canonical/alternative pathway in response to an array of ligands and developmental cues. IKK1 is also known to regulate gene expression by directly modifying the epigenome --- it phosphorylates Ser10 of histone H3. Interestingly, IKK1 is dependent on NIK for its NF-kB-activating function but not for its epigenome modifying activity.	
LS10	Soumen Roy	**Title :** Competition, Cooperation, and Communication in microbes **Description:** Brief description of the Research Project: Recently published and ongoing projects are in the areas of: (1) phage-bacteria interactions and dynamics, and, (2) antimicrobial resistance. Our research here is strongly guided by theoretical (rigorous mathematical and computational)	Zoology/ Microbiology/ Botany

		investigations which can be validated by experimental studies conducted in our own lab. The former includes but is not limited to network science, game theory, nonlinear dynamics, statistical physics, and information theory. If they wish, selected candidates are welcome to pursue this project in conjunction with other lab project/s of their choice.	
LS11	Soumen Roy	**Title :** Systems Biology of macromolecular interactions **Description:** Brief description of the Research Project: Macromolecular interactions define molecular recognition and cell signaling. Recently published and ongoing projects are in the areas of amino acid residue interaction networks, protein-protein interaction networks, protein-nucleic acid complexes, as well as protein-small molecule interactions. Here we strongly focus on the theoretical (rigorous mathematical methods and computational) aspects of intra-macromolecular and inter-macromolecular interactions. Validation of our theoretical predictions can be carried out through our experimental collaborators as well as our in-house setup. If they wish, selected candidates are welcome to pursue this project in conjunction with other lab project/s of their choice.	Zoology/ Microbiology/ Botany

Broad Research Area: Applied Biosciences

Position Code	Name of Faculty	Research Area	Desired Master's Background
AB01	Anupama Ghosh	**Title:** Investigating the extracellular ribonucleases of Ustilago maydis and their role in targeting cell-cell communication through apoplastic RNA in maize **Description:** Effector proteins from	Biotechnology / Biochemistry / Biophysics

		phytopathogenic fungi are secreted proteins that are exclusively expressed during infection and contribute to the fungal pathogenicity. Ustilago maydis is a biotrophic phytopathogen that causes smut disease in maize. During infection U. maydis secretes a huge repertoire of effector proteins within the maize apoplast. In this project we are exploring the possible biological functions of a group of such effector proteins that possess ribonuclease activity and can successfully degrade RNAs in the extracellular milieu. The project also explores a pool of apoplstic RNA in maize and its possible functions. The project would use various molecular biology and cell biology techniques including genetic manipulations in Ustilago maydis. In addition a considerable part of the study would also include experiments involving different forms of microscopy.	
AB02	Anupama Ghosh	**Title:** Role of small heat shock proteins in the pathogenic mechanisms of Ustilago maydis **Description:** Ustilago maydis is a biotrophic plant pathogen that causes smut disease in maize. During infection the pathogen experiences a number of defence responses from the host plant that it needs to overcome to establish infection. This project deals with the biological role of a group of small heat shock proteins from Ustilago maydis in establishing infection by the pathogen. Besides, in Ustilago maydis the pathogenic development is linked to morphological transitions from sporidia to filament and finally to spores within the host plants. The project also includes investigations on the involvement of the small heat shock proteins in the pathogenic development of Ustilago maydis in-planta. The project would use various molecular biology and cell biology techniques including genetic manipulations in Ustilago maydis. In addition a considerable part of the study would also include experiments involving different forms of microscopy.	Biotechnology / Biochemistry / Biophysics
AB03	Shubho	**Title :** Exploring the interactome	Biochemistry

	Chaudhuri	associated with chromatin remodeler AtHMGB15 during pollen development. **Description:** This project deals with Arabidopsis protein AtHMGB15 , which is a nuclear architectural protein belonging to ARID-HMG family. The main function of nuclear architectural proteins is to prepare the right environment for the DNA so that many nuclear processes like transcription, replication and repair, can be facilitated. In higher eukaryotes, these group of protein remodel the higher order chromatin structure for facilitating many nuclear processes; thus can function as chromatin remodeller. Recent work from our group has shown that ARID-HMG can bind different DNA topological forms, can bend DNA backbone and can also induce DNA supercoiling to facilitating nuclear processes [Roy et al, (2016) Plant Molecular Biology 92 (3), 371-388]. We have also identified the genome wide targets and DNA binding motif of ARID-HMG [Mallik et al, (2020). BBA-Gene Regulatory Mechanisms 1863 (12), 194644]. Presently we have identified its role in pollen development pathway. Using the knock-out mutant, we have observed alteration in pollen morphology, pollen growth and development. In continuation of this project, we will be looking for genome-wide targets of AtHMGB15 during pollen development using ChIP-sequencing. We are also interested to know the interacting partners of AtHMGB15 protein during flower development, which involves high-through put proteome analysis. Hypothesis: many nuclear architectural proteins are the part of chromatin remodelling complex because of their unique DNA binding and bending property. Thus, it is believe that they act as transcription activators and interact with many transcription factors and chromatin remodellers.	
AB04	Shubho Chaudhuri	**Title :** Investigating the recruitment of ARID-HMG protein AtHMGB15, to the nucleosome and its effect on the accessibility of nucleosomal DNA for nuclear processes	Biochemistry

		Description: The compaction of the eukaryotic genome into chromatin makes DNA accessibility a rate limiting step during essential nuclear processes like transcription, replication, repair and recombination. To facilitate these processes, multi-subunit protein complexes/machineries often need access to regions of the genome packaged into dense chromatin. The dynamic nature of chromatin allows targeted alteration of local chromatin structure at genomic regions which need to be accessed. The nuclear machineries are assisted by multiple chromatin binding proteins to regulate the dynamics of local chromatin structure and increase DNA accessibility. Many of these proteins are chromatin readers or modifiers which work in combinations and in tandem with chromatin remodelers to allow localised nucleosomal dynamics. Apart from these, there are DNA binding proteins that bind, stabilise or change various topological structures of DNA that are formed by the multi-subunit machineries in the intermediate steps of the nuclear processes. One such superfamily of proteins is the High Mobility Group (HMG) of proteins, which are indeed highly mobile and abundant within the nucleus where they are part of a dynamic network of architectural components that modulate the structure of chromatin and, thereby, affect multiple DNA-dependent activities The HMG-box containing ARID-HMG protein binds DNA through its ARID domain and promotes supercoiling of plasmid DNA through its HMG-box domain. Considering that ARID domains are found in transcription factors and HMG-box containing proteins are capable of nucleosomal interactions, the presence of both these domains in AtHMGB15 indicate the possibility that this protein by direct interaction with the DNA may mediate interactions between general transcription factors and chromatin remodelers to promote inducible gene expression. To investigate this possibility, it is important to analyse if indeed AtHMGB15 interacts with nucleosomal DNA and if so the mechanism and effects of its interaction with the nucleosome. Hypothesis:	

		Unique ARID-HMG protein AtHMGB15 interacts with nucleosomal DNA in a manner antagonistic to linker histone H1 such that its recruitment stabilises a locally open chromatin conformation and increases DNA accessibility	
AB05	Shubho Chaudhuri	**Title :** Understanding the effect of histone modifications on chromatin dynamicity during cold stress response in indica rice **Description:** Previous studies suggest that histone modifications and DNA methylation play an important role in inducing stress responsive loci in rice under environmental stress. In plants, although extensive work has been done on genome wide scale during salinity and drought stress, the epigenome dynamicity under cold stress remains completely unexplored (19). Although we have identified regions of genome which shows change from repressive H3K27me3 mark to H3K27acetylation activation mark during cold stress response; it is not clear how this epigenetic switch regulate the chromatin conformational change to regulate stress induced transcription. The current study entails a comprehensive analysis of the epigenomic landscape and chromatin conformation, with respect to the status of H3K27, associated with cold stress response in rice. PcG (Polycomb) group mediated repression (H3K27me3 enriched) is the default state of most inducible genes, which are activated upon Trx (Trithorax) group mediated H3K27 acetylation (20). Trimethylation of histone H3 lysine 4 (H3K4me3) is an important intermediate step in the switch of H3K27me3 to H3K27ac (21). The SET1/COMPASS domain of Trx (Trithorax complex responsible for H3K27ac) group trimethylates H3K4 residue which provides a recognition and docking site for the H3K27 acetylation components of the Trx complex (22). Since, the Trx and PcG complexes have been reported to be colocalized on chromatin for various genes (active/inactive) (23-25), the question remains how is the decision made for the locus activation/repression or the switch, i.e., which are the triggering factor. Objectives: In this work, we intend to	Biochemistry

		address this question at three different levels: 1. The status of H4K3 trimethylation associated with H3K27ac and H3K27me3 enriched regions under early cold stress. 2. How these histone modifications regulate the nucleosome dynamicity with reference to differentially expressed genes during cold stress response. 3. How these histone modifications high-resolution three-dimensional genome organization i.e. the chromatin conformation for contiguous enriched regions under early cold stress.	
AB06	Abhrajyoti Ghosh	**Title:** Understanding the role of type II toxin-antitoxin in the survival of thermoacidophilic archaeon Sulfolobus acidocaldarius **Description:** Toxin-Antitoxin (TA) system are important stress-response elements widespread in bacteria and archaea. Toxins operate in diverse mechanisms leading to cell death, reversible growth stasis and are involved directly in inhibiting essential cellular processes, while the antitoxin blocks the effect of toxins. Several cellular functions of the TA system have been proposed in case of bacteria, however their exact role in archaeal cell physiology still remains elusive. TA modules are important in several events in cellular physiology such as plasmid maintenance, formation of persister cells, stress resistance, protection from bacteriophages and regulation of biofilm formation, acting on crucial cellular processes including translation, replication, cytoskeleton formation and membrane integrity. Our group is mainly interested in characterization of the different TA gene systems identified in hyperthermophilic crenarcheon Sulfolobus acidocaldarius, exploiting various biochemical and biophysical techniques. Gene expression analysis revealed differential expression of	Biotechnology/ Biochemistry/ Biophysics

		plethora of TA genes, in response to different stress. We are keen to understand the role and regulation of the different TA system in stress adaptation from our model organism, Sulfolobus acidocaldarius. In addition, our recent venture is to manipulate the genetic system of this extremophile, in order to generate TA deleted strains for efficient understanding of their function in cellular physiology. Candidates having interest in protein biochemistry, biotechnology, cell biology and genomics are suitable for this position.	
AB07	Abhrajyoti Ghosh	**Title :** Understanding the molecular players involved in the survival of model haloarchaea in fluctuating salinity of Sundarbans **Description:** Archaea remain important players in global biogeochemical cycles worldwide, including in the highly productive mangrove estuarine ecosystems. In the present study, we have explored the diversity, distribution, and function of the resident archaeal community of the Sundarban mangrove ecosystem, using both culture-independent and culture-dependent approaches. Our results showed that haloarchaea are the dominant archaeal group in hydrocarbon polluted sediments, of Sundarbans. We have successfully isolated eleven p-hydroxybenzoic acid degrading haloarchaeal species. These isolates could survive in different salinity of Sundarban. Genome sequencing of selected haloarchaeal isolates revealed that they possibly employ multiple mechanisms to cope with the changes in salinity. In this project, we would like to study the molecular players involved in the survival of these haloarchaeal species in different saline conditions. Candidates having interest in archaeal biology, biochemistry, high throughput	Biotechnology/ Biochemistry/ Biophysics

		sequencing analysis and biotechnology are suitable for this position.	
AB08	Samarjit Polley	**Title:** Understanding the Structure-Function Relationship of IKK1 in Regulating NF-kB Activation and Beyond. **Description:** More than 500 protein kinases are encoded in the human genome. Protein kinases provide the regulatory framework for most signaling pathways in eukaryotic cells. Stringent regulation of their activities is critical to proper functioning of cellular processes, and consequently they act as important drug targets. Indiscriminate inhibition of kinase activities often has deleterious effect on healthy being of cells. Signaling modularity is dictated by choice of substrates, cognate-binding partners, subcellular localization and post-translational modifications of the kinase itself. It is important to investigate the mechanistic details of their activation and spatio-temporal regulations to fully realize the scope of modulating them in a manner beneficial for the organism. We aim to study structure-function relationship of, Inhibitor of kappaB Kinase 1/a (IKK1/a) and its close partner NIK (NF-kB Inducing Kinase also known as MAP3K14); and how they regulate each other's function. Primary function of IKK1 in cells is to activate NF-kB thorough the non-canonical/alternative pathway in response to an array of ligands and developmental cues. IKK1 is also known to regulate gene expression by directly modifying the epigenome --- it phosphorylates Ser10 of histone H3. Interestingly, IKK1 is dependent on NIK for its NF-kB-activating function but not for its epigenome modifying activity.	Biotechnology/ Biochemistry/ Biophysics
AB09	Soumen Roy	**Title :** Competition, Cooperation, and Communication in microbes **Description:** Brief description of the Research Project: Recently published and ongoing projects are in the areas of: (1) phage-bacteria interactions and dynamics, and, (2) antimicrobial resistance. Our research here is strongly guided by theoretical (rigorous mathematical and computational)	Biotechnology/ Computer Science/ Biochemistry/ Biophysics/ Mathematics/ Statistics/ Engineering

		investigations which can be validated by experimental studies conducted in our own lab. The former includes but is not limited to network science, game theory, nonlinear dynamics, statistical physics, and information theory. If they wish, selected candidates are welcome to pursue this project in conjunction with other lab project/s of their choice.	
AB10	Soumen Roy	**Title :** Systems Biology of macromolecular interactions **Description:** Brief description of the Research Project: Macromolecular interactions define molecular recognition and cell signaling. Recently published and ongoing projects are in the areas of amino acid residue interaction networks, protein-protein interaction networks, protein-nucleic acid complexes, as well as protein-small molecule interactions. Here we strongly focus on the theoretical (rigorous mathematical methods and computational) aspects of intra-macromolecular and inter-macromolecular interactions. Validation of our theoretical predictions can be carried out through our experimental collaborators as well as our in-house setup. If they wish, selected candidates are welcome to pursue this project in conjunction with other lab project/s of their choice.	Biotechnology/ Computer Science/ Biochemistry/ Biophysics/ Mathematics/ Statistics/ Engineering
AB11	Zhumur Ghosh	**Title of the project:** Understanding the role of noncoding RNAs in axonal degeneration **Description:** **Axonal degeneration** is the destruction of axons which can occur as an effect of sudden Traumatic Brain injury (TBI) as in the case of Diffuse axonal injury(DAI) or can occur **gradually** at the early stages of neurodegenerative conditions like Alzheimer's disease(AD), Amyotrophic lateral sclerosis(ALS), and Parkinson's disease(PD). Despite differences in the	Biotechnology/ Computer Science/ Biochemistry/ Bioinformatics

		rate of degeneration, axon loss in neurodegenerative diseases like AD or ALS share many morphological features with those in acute injuries like DAI. Long noncoding RNAs (lncRNAs) are a group of novel noncoding RNAs which has a profound role in neuronal development and disorders. In this proposal, we shall specifically focus on the cases of DAI for sudden axonal degeneration and AD and ALS for gradual axonal degeneration and shall probe into the role of microglia shared common gene regulatory circuits orchestrated by lncRNAs in both the cases of sudden and gradual axonal degeneration.	

Broad Area of Research: Physical Sciences

Position Code	Name of Faculty	Research Area	Desired Master's Background
PS01	Achintya Singha	**Title:** 2D-0D coupled nanostructures for photon harvesting **Description:** The efficient manipulation and conversion of absorbed photons into free carriers is the key to achieve high-performance optoelectronic devices. Due to the large surface area semiconducting two-dimensional (2D) materials have attracted a great deal for light harvesting. However, their applications are hampered by the low photon absorption of the atomically thin layer. The present research proposal aims to achieve amplification of light collection in the atomically thin layers by coupling the 2D semiconductor to engineered noble metal nanoclusters. The samples will be prepared by Chemical Vapour Deposition (CVD) method and optical Spectroscopy and optoelectronic techniques will be used to study the materials.	Physics
PS02	Achintya Singha	**Title :** Surface-Enhanced Raman Scattering (SERS) based bio-sensor **Description:** Surface-Enhanced Raman Scattering (SERS) combines molecular	Physics

		fingerprint specificity with single-molecule detection, which is the ultimate sensitivity required in chemical analysis, trace detection and bio-sensing. Two-dimensional transition metal dichalcogenides (TMDs)/plasmon nanostructure (Au, Ag, etc) integrate the superior light-solid interaction and therefore are promising for surface-enhanced Raman Spectroscopy (SERS). The present work aims to develop TMDc-plasmon hybrid structures to detect and study a single molecule using the SERS technique.	
PS03	Dhruba Gupta	**Title:** Breakup of the ^{7}Be nucleus in the context of nuclear astrophysics **Description:** Breakup reactions involving loosely bound nuclei are extensively used to study nuclear reactions and astrophysics. While stable nuclei having prominent cluster structures have been studied a lot, breakup studies of the radioactive nuclei have been very difficult due to the low beam intensities. The breakup nuclear reaction leads to a minimum three body final state with a broad continuum in the energy spectra. The reaction may occur as a direct breakup, or a sequential breakup through resonance states in the breakup continuum of the nuclei. Both Coulomb and nuclear forces can contribute to the breakup processes. Coulomb breakup reactions are often used to derive information on the time reversed, astrophysically relevant, radiative capture reactions, whose direct measurements are almost impossible due to extremely low yield. We plan to study both the direct and sequential breakup of 7Be over a wide angular range. The relative contribution of the direct and sequential breakup would throw light on the reaction dynamics as we move from stable to unstable nuclei. The breakup fragments detected at very forward angles would help in deriving astrophysical information in the context of the radiative capture reaction 3He + 4He → 7Be + γ. Monte Carlo simulations of proposed experiments would be carried out using the NPTool package, based on CERN	Physics

		Root and Geant4 framework. The successful candidate will be involved in all aspects of experiments namely, simulations, experimental design and setup, data analysis, and publication of scientific results. The candidate will also participate in other research endeavors of the group. We offer the opportunity to work in a stimulating environment on cutting edge research. The PhD work may involve experimental activity in leading international research facilities like HIE-ISOLDE at CERN.	
PS04	Dhruba Gupta	**Title :** Breakup of the ^{9}Li nucleus in the context of nuclear astrophysics **Description:** Considerable attention has been paid to the possibility that the early universe might have been rather inhomogeneous, consisting of highdensity proton rich regions along with low-density regions, which were comparatively neutron-rich. This was the natural consequence of neutron's longer mean free path, for which it could diffuse out of the high-density zones. Although D, ^{3}He and ^{4}He are produced in the observed relative abundances, there may also be non-negligible production of A >12 isotopes. It is difficult to evaluate the merits of inhomogeneous nucleosynthesis versus standard big-bang nucleosynthesis, because the rates of several important reactions are either not measured or not well established. For example, only few reactions involving ^{8}Li have been measured and thus any conclusions regarding A>6 nucleosynthesis must be regarded as tentative. Previous attempts to study the neutron capture ^{8}Li(n, γ)^{9}Li reaction were mostly through (d,p) reaction with only a couple of experiments where direct (n, γ) was studied through Coulomb breakup. The main constraint in the previous measurements was low beam intensity and the difficulty to separate Coulomb and nuclear breakup contributions. In the proposed experiment we plan to separate these two contributions using low beam energy of 7 MeV/A and take advantage of higher ^{9}Li beam intensity offered by HIE-ISOLDE at CERN. We	Physics

		plan to use the scattering chamber and SAND array at the third beamline of HIE-ISOLDE. The successful candidate will be involved in all aspects of experiments namely, simulations, experimental design and setup, data analysis, and publication of scientific results. The candidate will also participate in other research endeavors of the group. We offer the opportunity to work in a stimulating environment on cutting edge research. The PhD work may involve experimental activity in leading international research facilities like HIE-ISOLDE at CERN.	
PS05	Soumen Roy	**Title :** Quantum entanglement and Quantum information **Description:** Brief description of the Research Project: Quantum entanglement reexamines the concept of locality and reality in quantum mechanics. It allows non-local connections between two or more distant objects. This enables us to explore several useful information processing protocols such as quantum teleportation, quantum cryptography, quantum dense coding, etc. On the other hand, quantum information helps us in exploiting the principles of quantum mechanics in information processing. The study of quantum information is necessary for quantum computation and also in quantum communication. Though quantum entanglement can be implemented in various quantum algorithms, the effect of quantum entanglement in quantum information needs further scrutiny. We intend to study various problems in both quantum entanglement and quantum information separately and possibly in conjunction. Another aim is to study how entanglement influences the flow of information between quantum states towards the secure establishment of long-range quantum communication. If they wish, selected candidates are welcome to pursue this project in conjunction with	Physics

		other lab project/s of their choice.	
PS06	Soumen Roy	**Title :**Interdisciplinary statistical physics: games, networks, economies, and living systems **Description:** Brief description of the Research Project: The interdisciplinary potential of statistical physics was foreseen over a century ago by Ludwig Boltzmann. Today, statistical physics is widely regarded as one of the most interdisciplinary areas in modern science. The following is a brief summary of recently published and ongoing projects in our lab. We remain perennially interested in finding new measures to investigate the structure, function and dynamics of complex networks as well as its innovative applications in diverse systems. A range of phenomena in life sciences ranging from the level of individual proteins to microbes are studied in the lab. Of late, we have scrutinised the effect of topology in evolutionary games on networks. Our recent interests include the physics of wealth distribution. If they wish, selected candidates are welcome to pursue this project in conjunction with other lab project/s of their choice.	Physics
PS07	Soumen Roy	**Title :** Competition, Cooperation, and Communication in microbes **Description:** Brief description of the Research Project: Recently published and ongoing projects are in the areas of: (1) phage-bacteria interactions and dynamics, and, (2) antimicrobial resistance. Our research here is strongly guided by theoretical (rigorous mathematical and computational) investigations which can be validated by experimental studies conducted in our own lab. The former includes but is not limited to network science, game theory, nonlinear dynamics, statistical physics, and information theory. If they wish, selected candidates are welcome to pursue this project in conjunction with other lab	Physics

		project/s of their choice.	
PS08	Soumen Roy	**Title :** Systems Biology of macromolecular interactions **Description:** Brief description of the Research Project: Macromolecular interactions define molecular recognition and cell signaling. Recently published and ongoing projects are in the areas of amino acid residue interaction networks, protein-protein interaction networks, protein-nucleic acid complexes, as well as protein-small molecule interactions. Here we strongly focus on the theoretical (rigorous mathematical methods and computational) aspects of intra-macromolecular and inter-macromolecular interactions. Validation of our theoretical predictions can be carried out through our experimental collaborators as well as our in-house setup. If they wish, selected candidates are welcome to pursue this project in conjunction with other lab project/s of their choice.	Physics
PS09	Sidharth Kumar Prasad	**Title:** Study of relativistic hadronic and nuclear collisions using hard probes and photons at LHC **Description:** At the Large Hadron Collider (LHC) at CERN two beams of heavy ions are made to collide at relativistic energies. A new form of matter of free quarks and gluons known as Quark-Gluon-Plasma (QGP) is produced in these collisions. One of the main goals of experiments at LHC is to study and characterize the properties of the produced matter. Both in theoretical and experimental fronts there are various observables that are defined using the properties of the produced particles in these collisions and used to characterize the QGP. As a part of this research project we plan to explore and study the QGP properties using produced charged particles at high momentum (hard probes) and photons.	Physics

PS10	Saikat Biswas	**Title:** R&D on Micro-Pattern Gaseous Detectors for radiation measurements **Description:** The research will be dedicated to the study of properties of Micro-Pattern Gaseous Detectors (MPGD) such as Gas Electron Multiplier (GEM) for physics experiments. The research program will include both simulation and hardware activities. Progress in the property of GEM detector is the key point of this particular project. Characteristics of GEM detector will be studied with radioactive sources in the laboratory. A large fraction of time of the selected student will be dedicated in the hardware activities in the laboratory. Development of electronics will also be a key point.	Physics