Bose Institute
Kolkata

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

Advertisement No. : BI/NET-JRF/06/2023-24

Admission for PhD Programme
Spring 2023

Bose Institute, Kolkata is an Autonomous S&T Institute under Department of Science & Technology, Ministry of Science & Technology, Govt. of India, receiving 100% Grant-in-Aid from Government of India. For details of various academic research activities, please visit Institute's website at http://www.jcbose.ac.in.

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. Interviews for this session will be held tentatively during early August 2023.

Areas of research: Environmental Sciences, Chemical Sciences, Life Sciences & Physical Sciences.

- Candidates are required to provide a **Statement of Purpose** (SOP), in prescribed format.

Fellowship: Admissible as per Govt. of India rules as provided by UGC/CSIR/DBT/DST/ICMR etc.

Total number of vacancies: **45 (UR-20, OBC-11, SC-7, ST-3, EWS-4)**

Age limit: Below 28 years (relaxation of age is applicable as per Government of India 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 **30th September, 2023**. If candidates, who are in the final year of their Master's degree programme **and** are in possession of an award of a JRF, are selected, they 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 candidates, while 50% marks is necessary for SC/ST/OBC (non-creamy layer)/ differently-abled and other categories of candidates, as per UGC norms.

(3) 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. If the candidate is finally not awarded the INSPIRE fellowship by DST, his/her provisional admission is liable to be cancelled by the Institute. In case of DST Inspire Fellowship, the candidate must be qualified NET-LS/GATE/similar National Level Test, for being considered in the Ph.D. Programme in Bose Institute.

(4) 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**.

(5) No student awarded for ICAR Fellowship will be eligible for participating in the Ph.D. Programme in Bose Institute.

Application Process:

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

Deadline for online application: 23:59 Hrs. on 20.08.2023

An acknowledgement receipt will be generated following successful submission of the online application form. Candidates **should retain this receipt** for future reference. If called for the interview, candidates **must** produce this acknowledgement receipt. No candidate will be allowed to appear for the interview without this receipt.

For any difficulties pertaining to online application, please send email to: bosephdadmission@gmail.com

1. Candidates are advised to fill up the online application carefully and provide the information as required. Candidates are requested to visit the Institute website (http://www.jcbose.ac.in) regularly for updates. No separate intimation will be sent to any candidate.

2. Candidates should carefully fill up all the details required in the online application form including age, educational qualification, details of valid community certificates, etc., as no correspondence regarding change of details will be entertained once the applications is submitted. If any of their claims is found to be false or incorrect, it will lead to rejection of their candidature.

3. The prescribed essential qualifications indicated are bare minimum and mere possession of same will not entitle the candidate to be called for interview.

4. Candidates shall have to produce all the original documents/certificates in support of at their age, reservation category, educational qualifications along with one set of a self-attested copies of the same, at the time appearing for interview for verification, failing which he/she will not be allowed to appear for interview.

5. The Institute reserves the right to restrict the number of candidates called for the 1st round of interview to a reasonable limit on the basis of qualifications. The Institute also reserves the right to not call for the 2nd round of interview those candidates whose score in the 1st round of interview fall below a certain cut-off.

6. Names of the shortlisted candidates, along with the date and time of interview will be displayed on the Institute website
   - It should be noted that mere appearance on the shortlist does not imply admission
   - The interview will be conducted in offline mode. Online interview will be taken only if :
     (i) The candidate's place of residence is beyond 100 km from the Unified Academic Campus of Bose Institute (candidate must furnish proof of residence)
     (ii) The candidate will be appearing for an interview at another institution on the same date (candidate must furnish a copy of interview letter, dated prior to the publication of the interview schedule of Bose Institute on the Institute website, which mentions the date of interview)

     In such cases candidate must submit request via email (bosephdadmission@gmail.com) **within two days of publication of interview schedule** on Bose Institute website.

7. A two-step screening process will be followed, with knowledge in core subject being assessed in the first step and suitability of the candidate for conducting scientific research at Bose Institute, along with finalization of Ph.D. guide-candidate matching, being assessed in the second step. At the time of application, candidates will be required to submit a Statement of Purpose, which will be taken into consideration during the second round of screening.
8. The Institute reserves the right to decide the mode of screening the applications for short listing and selection.
9. Eligibility criteria including upper age limit will be reckoned on the last date of submission of application.
10. Only shortlisted candidates will be intimated the date of interview only via email to the respective email addresses provided in the application forms (candidates are advised to check their email on a regular basis). The list will also be available at www.jcbose.ac.in.
11. Before applying, the applicants should ensure that they possess at least the essential qualifications and other conditions specified in the advertisement. If a candidate is found ineligible, his/her candidature will be cancelled at any stage of interview process. It may be noted that even if a candidate qualified in the interview and subsequently it is found that he/she does not fulfill the eligibility criteria, his/her candidature will be cancelled.
12. All supporting documents are required to be uploaded and therefore, candidates are advised to prepare the PDF files of the required documents before starting the online application process.
13. No TA/DA is admissible for appearing for the interview.
14. Specific instructions regarding the interview will be communicated to the shortlisted candidates only.
15. The final list of selected candidates will be displayed on the Institute website
16. The Institute Authority reserves the right to reject any or all applications without assigning any reason thereof.
17. The Institute reserves the right not to fill all the posts advertised and to reject any or all applications without assigning reason.
18. The candidates must keep a watch at Institute's website for any amendment.
19. No interim queries in any form whatsoever will be entertained.
20. Canvassing or bringing influence in any form will disqualify the candidature.
21. Age relaxation will be given to the eligible candidates as per Govt. of India guidelines.
22. Reservation rules, as notified by UGC for reservation to SC/ST/OBC/EWS, shall be applicable.
23. Caste Certificate shall be furnished by the respective candidate to claim reservation in SC/ST/OBC category.
24. Any candidate claiming to belong to the OBC shall furnish a certificate in the prescribed form signed by any of the specified authorities. No other certificate will be accepted. The caste certificate issuing authority should also certify that the candidate does not belong any of the Creamy Layers (format given in Bose Institute website).
25. All disputes shall come under the Kolkata jurisdiction.

Important Dates:

- Last Date for online application: 23:59 Hrs. on 20.08.2023
- For all information to follow our website at www.jcbose.ac.in

Annexure – I

Areas of Research: Physical Sciences

Name of Faculty	Research Project	Desired Master's Background
Achintya Singha	**Title:** Raman and Photoluminescence Spectroscopy of Two-Dimensional Materials and their Heterostructures **Project Code: AS1** **Description:** The broad interest of this project would be: • To fabricate 2D layered materials with varying layer thickness and their heterostructures • Probing vibrational and optical properties of the 2D materials and their heterostructures varying temperature, pressure and electric filed. • Understanding fundamental of the quantum interactions in the 2D materials and their heterostructures	Physics
Achintya Singha	**Title:** Optoelectronics Properties of Two-Dimensional Materials and their Heterostructures **Project Code: AS2** **Description:** The broad interest of this project would be: • To fabricate 2D layered materials and their heterostructures based optoelectronic devices • Investigating optical and vibrational properties of the materials • Study of photo-response behavior of the fabricated devices	Physics
Basudeb Maji	**Title:** Chemogenetic Therapy Development against Epithelial-Mesenchymal Transition (EMT) in Triple-Negative Breast Cancer **Project Code: BM** **Description:** The incidence of breast cancer (BC) is increasing and might be a leading cause of death in the future in women. In India, the incidence rate of breast cancer is increasing in metropolitan and urban areas, and it is almost three times higher compared to rural regions. Statistical analysis reveals that India contributes to 7% of breast cancer cases globally, and the disease has become the second most common cancer among women in the subcontinent. Molecular classification defines BC as ER+, PR+, Her2+, and basal type of Triple-negative breast cancer (TNBC) having high proliferation index (Ki-67), expressing EGFR and basal cytokeratins. Among all, PR+ shows a poor prognosis compared to ER+ while Her2-enriched and TNBCs have worse outcomes in BC patients. Targeted therapy is one of the most effective ways to treat diseases minimizing the side effects. Unfortunately, due to the absence of all three cell surface markers (ER, PR, and Her), targeted therapy is not possible in TNBC incidents. We are developing synthetic small molecule probes that can selectively target TNBC cells and induce targeted degradation of oncoproteins. We envision designing small molecules for the CRISPR-based gene editing method and coupling them with chemopreventives toward developing chemogenetic methods for TNBC.	Physics/ Organic Chemistry
Dhruba Gupta	**Title:** Breakup of the ^{9}Li nucleus in the context of nuclear astrophysics **Project Code: DG1** **Description:** Considerable attention has been paid to the possibility that the early universe might have been rather inhomogeneous,	Physics

	consisting of high-density 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/u and take advantage of higher ^{9}Li beam intensity offered by HIE-ISOLDE at CERN. We 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, Switzerland.	
Dhruba Gupta	**Title:** Breakup of the ^{7}Be nucleus in the context of nuclear astrophysics **Project Code: DG2** **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 with a heavy target like ^{208}Pb, 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 ^{7}Be with ^{208}Pb, 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 ^{3}He + ^{4}He $\rightarrow$ ^{7}Be + γ. Monte Carlo simulations of proposed experiments would be carried out using the NPTool package, based on CERN Root and Geant4 framework. The successful candidate will be involved in all aspects of experiments namely, simulations, experimental design and setup, data analysis, and	Physics

	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, Switzerland.	
Dhruba Gupta	**Title:** Coulomb dissociation of ^{14}O in the context of the hot CNO cycle **Project Code: DG3** **Description:** In nuclear astrophysics, the study of p + ^{13}N radiative capture reaction is important in determining the transit from the Carbon-Nitrogen-Oxygen (CNO) cycle to the hot CNO cycle, occuring in supermassive stars, novae etc. In standard stellar atmosphere, the hydrogen burning in massive stars proceeds largely through CNO cycle. The observed ^{15}N/^{14}N ratio is 100 times more than we calculate from the cold CNO cycle and the introduction of hot CNO cycle accounts for that deficiency. At the higher temperatures characteristic of explosive hydrogen burning in red giants and in novae and supernovae explosions, the ^{13}N(p,γ)^{14}O reaction rate exceeds the temperature independent ^{13}N($\beta^+\nu$)^{13}C rate. This causes the conversion of CNO cycle to the hot CNO cycle, resulting in an increased energy production rate. The turning point is directly dependent on the cross section of the above radiative capture reaction and thus its rate and cross section is of significant interest. The measurement of direct reaction is difficult because of very low cross section. On the contrary, Coulomb dissociation of ^{14}O to study this radiative capture reaction is an established method. However, to address the present discrepancies of 20-30% in both theoretical estimates and experimental data, new measurements with highly efficient detector systems like MUST2 are required. We propose to study Coulomb dissociation of ^{14}O at 17 MeV/u with ^{208}Pb target using MUST2 and VAMOS, at the GANIL rare isotope beam facility in France, to detect the protons and ^{13}N respectively. We expect an order of magnitude improvement in the accuracy of the radiative width of the 5.173 MeV state of ^{14}O. This would help to conclude if the hot CNO cycle may be ignited at lower densities to prevent collapse of supermassive stars. Monte Carlo simulations of the proposed experiment would be carried out using the NPTool package, based on CERN 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, Switzerland and GANIL, France.	Physics
Dhruba Gupta	**Title:** Scattering of protons from the radioactive nucleus ^{7}Be **Project Code: DG4** **Description:** Proton scattering of exotic unstable nuclei in inverse kinematics is used to study such nuclei. A systematic p- scattering study of a loosely bound stable nucleus and its radioactive mirror counterpart throws light on the change in reaction dynamics as we move towards the driplines. The elastic scattering is known to be affected by the coupling to reaction channels, which usually results in	Physics

	an enhancement of the total reaction cross- section. Several works on proton elastic and inelastic scattering with the stable weakly bound ^{6,7}Li nuclei at near barrier energies have been carried out in this regard. We plan to carry out similar studies on ^{7}Be, the radioactive mirror counterpart of ^{7}Li, at energies < 10 MeV. The Monte Carlo simulations for experiments are carried out using the NPTool package, based on CERN Root and Geant4 framework. The relevant continuum discretized coupled channel calculations would be carried out using the code FRESCO. 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, Switzerland.	
Pramod Kumar Shukla	**Title:** String Phenomenology with Open-string moduli **Project Code: PKS1** **Description:** In the context of model building in String Phenomenology, moduli stabilization has been among the most crucial and challenging aspects to deal with. In the last two decades, a tremendous amount of effort has been put in this direction which has resulted in mainly two schemes (and a few of their variants) for fixing the moduli in a dynamical manner. This is done via using some effective four-dimensional scalar potential arising from a set of possible sources, e.g. background fluxes and other (non-)perturbative effects. These two popular schemes, namely the KKLT framework and the LARGE volume scenario (LVS) framework, mainly deal with the so-called closed-string moduli which form only a subset of the types of moduli that can possibly enter in a given realistic construction. In this regard, the D7-brane fluctuations and Wilson line moduli have been found to be crucially important, especially for models which attempt to combine particle physics and cosmological aspects in a single framework. Studying the dynamics of these moduli along with their implications for addressing interesting issues such as de-Sitter realization and embedding inflationary models in some explicit global constructions are some of interesting prime goals which we plan to achieve in this project.	Physics
Pramod Kumar Shukla	**Title:** A Non-geometer's Toolkit to String Phenomenology **Project Code: PKS2** **Description:** Toroidal orbifolds have been used as playgrounds for checking many simple ideas and conjectures due to the possibility of performing explicit computations in such backgrounds. The main goal of this project is to present some concrete non-geometric constructions for all the classified toroidal orbifolds of the type T^6/(Z_N×Z_M) and T^6/Z_N. Superstring compactifications on such backgrounds lead to some four- dimensional effective theories which can be subsequently used for addressing a variety of issues related to realistic model building; for example analysis of flux vacua, moduli stabilization and de-Sitter/inflationary possibilities in the lights of swampland conjectures.	Physics

Pramod Kumar Shukla	**Title:** Aspects of F-theory Phenomenology **Project Code: PKS3** **Description:** The four-dimensional effective theories arising from F-theory compactifications using Calabi-Yau (CY) fourfolds have been explored for realizing MSSM-like models in some good detail. However, moduli stabilization and other related phenomenological aspects have not been studied much so far, except for a couple in recent initiatives being taken in this direction. In this regard, the first part of this project aims to study and classify the vast landscape of F-theory flux vacua arising from the G4-flux (and its possible non-geometric extensions) using some concrete CY fourfolds. The second part of the project aims to study the F- theory uplifts of the type IIB global models with open-string moduli. These two aspects are very significant in the area of superstring/F-theory phenomenology in order to construct realistic models.	Physics
Saikat Biswas	**Title:** Research and development of Resistive Plate Chamber for the high-rate heavy ion experiment **Project Code: SB1** **Description:** The Resistive Plate Chambers (RPC) are widely used in High Energy Physics (HEP) Experiments for timing and tracking purposes. With the ever-increasing requirement of high luminosity in heavy-ion experiments (e.g. FAIR in Germany, CERN at Switzerland), detectors with good rate handling capability are needed. The goal of the proposed project is to address the issues like limited rate handling (~ 10 kHz/cm2) capability of the RPC detector, effect of electrode materials on the rate handling capability of the detector, effect of gas mixtures and treatment of the electrodes (e.g. oil coating) on the performance of the chamber at higher rates. The work will consist of hardware and simulation of the RPC detector. As a part of a large collaboration, the student needs to participate actively in several experiments in India as well as abroad.	Physics/ Electronics
Saikat Biswas	**Title:** Research and Development of detectors for imaging and study of cosmic ray **Project Code: SB2** **Description:** Several R&D on the societal application of the gas-filled detectors, developed for the High Energy Physics (HEP) experiments are ongoing across the globe. The proposed work is aimed to understand the possibility and applicability of gas-filled detectors such as Resistive Plate Chamber (RPC), Gas Electron Multiplier (GEM) etc. as an imaging device. We are also doing R&D of scintillation detectors for the study of cosmic rays. This will include detection of muon, gamma ray and neutrons. Both the work will require dedicated involvement for the hardware activities and in the development of the software framework. The R&D on the proposed project can be carried out at the operational detector laboratory at Bose Institute, Kolkata and the cosmic ray laboratory at the Darjeeling campus of Bose Institute.	Physics/ Electronics
Sanat Kumar Das	**Title:** Carbonaceous aerosols and their radiative warming effect on Himalayan glacier melting **Project Code: SKD1** **Description:** Our nation is going to face severe drinking water crisis in future due to day-by-day reduction of input water from the Himalayan glaciers to the glacier-fed rivers. This project is for a student who is ready to accept the challenge to pin- point the reason	Physics / Computer Science

	and establish the cause-&-effect relation in between aerosols and climate change. Our earlier research works discovered various types of carbonaceous aerosols present in the atmosphere from our observations at Darjeeling since last 10 years. This research project is to quantify these various types of carbonaceous aerosols and simulate their radiative effect, which warms up the atmosphere over the Himalayas. 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.	
Sanat Kumar Das	**Title:** Study on Fog-induced changes of Aerosol properties and its impact on Fog Forecasting **Project Code: SKD2** **Description:** This research work is a part of the 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 programming languages. The selected student will participate in on-field group work to collect atmospheric observational data from in-situ experiments using monochromatic lasers, carry out lab-based measurements using modern sophisticated instruments and perform data analysis and simulation work for pursuing PhD.	Physics / Environmental Science / Atmospheric Science / Computer Science / Geoinformatics
Smarajit Polley	**Title:** Regulation by phosphorylation: Structure-function relationship of protein kinases and their substrates **Project Code: SP** **Description:** Majority of the Eukaryotic Protein Kinases (EPKs) are Ser/Thr/Tyr kinases (STYKs) that phosphorylate those residues on the substrates. Residue-level specificities of STYKs are considered to group them as Ser/Thr Kinases, Tyr Kinases or dual specificity that phosphorylate Ser/Thr, Tyr or Ser/Thr as well as Tyr residues, respectively. One of the remarkable features of the HKs in TCSs is the stringent specificity wherein a specific HK primarily phosphorylate a single cognate RR, though exceptions are also reported. Many STYKs on the other hand are often known to phosphorylate a plethora of substrates. Despite such pleotropic assertion at the substrate level, some of the STYKs are so crucial at a certain context that they show exquisite specificity for a distinct substrate down to the specific residue(s) level thereby ensuring activation and fidelity of a particular signaling cascade. Using biochemical, genetic, biophysical and structural biology tools (CryoEM and X-ray crystallography) we ask a) how some of the EPKs maintain exquisite specificity in a particular signaling context	Physics/ Chemistry/ Life Sciences/ Biotechnology/ Microbiology/ Zoology/ Botany/ Biochemistry/ Biophysics/ Computer Science/ B. Tech.

	b) how EPKs achieve signaling modularity by phosphorylating different sets of substrates in a different signaling context	
Soumen Roy	**Title:** Statistical physics **Project Code: SR1** **Description:** 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. A lot of exciting developments are revisiting the second law of thermodynamics and entropy through the machinery of the recently proposed fluctuation theorems. The second law of thermodynamics informs us that the entropy of an isolated system tends to increase. However, from statistical mechanics we know that this law is only statistical, implying that there is always a nonzero probability that the entropy of an isolated system might spontaneously decrease. The recent fluctuation theorem precisely quantifies this probability. Our general understanding of phase transitions and critical phenomena is that there are (discontinuous) first- order transitions, and (continuous) second-order transitions exhibiting critical behavior. However, recent research suggests the so-called mixed-order transitions, which combine features of both types, like discontinuity accompanied by the exhibition of diverging correlation length. We look forward to students who are eager to work in the above areas. If they wish, selected candidates are welcome to pursue this project with other projects/ of their choice conducted in our lab.	Physics/ Computer Science/ Engineering/ Applied mathematics/ Electronics/ Statistics
Soumen Roy	**Title:** Quantum entanglement and quantum information **Project Code: SR2** **Description:** 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 other project/s of their choice conducted in our lab. We look forward to students who are eager to work in the above areas. If they wish, selected candidates are welcome to pursue this project with other projects/ of their choice conducted in our lab.	Physics/ Computer Science/ Engineering/ Applied mathematics/ Electronics/ Statistics
Soumen Roy	**Title:** Systems Biology (Theory and Experiments) **Project Code: SR3** **Description:** **Macromolecular interactions:** Most interactions defining molecular recognition and cell signaling are macromolecular in nature. Recently published and ongoing projects are in the areas of amino acid residue interaction networks, protein-protein interaction networks, protein-	Life Sciences/ Biotechnology/ Microbiology/ Zoology/ Biochemistry/ Biophysics/ Computer Science

	nucleic acid complexes, as well as protein- small molecule interactions. **Microbial systems:** Recently published and ongoing projects in our lab are in the areas of: (1) phage-bacteria interactions and dynamics, and, (2) antimicrobial resistance. Our research is strongly guided by theoretical (mathematical and computational) investigations. The ideal candidate is expected to use both theoretical techniques and obtain their experimental validation. Experiments could be conducted in our own lab as well as in the labs of our collaborators. If they wish, selected candidates are welcome to pursue this project in conjunction with other project/s of their choice conducted in our lab.	
Sudipto Saha	**Title:** Studying interactions between the lung microbiome and host immunity in pulmonary diseases **Project Code: SS** **Description:** • To study how microbial metabolites interact to host immune cells (macrophages and T-cells) in obstructive lung diseases. • To study the role of antibiotic-resistant bacteria (commensals and pathogens) in the lung microbiome • Metagenomics, metabolomics, transcriptomics and proteomics-based approaches will be used to address these questions.	Chemistry/ Microbiology/ Zoology/ Computer Science
Suman Kumar Banik	**Title:** Signal transduction in mixed feed-forward loop motif **Project Code: SKB1** **Description:** Small RNAs (sRNAs) controls gene regulation in bacteria via post-transcriptional modification of mRNAs. The interaction between sRNA and mRNA constitutes diverse regulatory circuits, e.g., mixed feed-forward loop (FFL) motif. Using theoretical and computational tools we aim to model signal transduction in diverse mixed FFL structures. The central goal of the project is to identify the contribution of different types of sRNA-mRNA interactions in the overall process of signal propagation.	Physics/ Chemistry/ Biotechnology / Biophysics/ Computer Science
Suman Kumar Banik	**Title:** Role of feedback loop in the quorum sensing network **Project Code: SKB2** **Description:** Quorum sensing in bacteria is a signal transduction mechanism through which regulation of gene expression takes place in response to change in cell density. During quorum sensing, generation, secretion and detection of autoinducers are executed by an individual cell. The concentration of autoinducer, which depends upon the local cell density, when exceeds a threshold value significant expression of quorum sensing regulated genes takes place. The multitude of genes are responsible for several phenotypes, e.g., bioluminescence, biofilm formation and secretion of virulence factors, which in turn depends on the local cell density. Recent studies show that quorum sensing network of *Vibrio harveyi* has multiple feedback loops that regulates precise gene expression. Using theoretical and computational tools we aim to model information processing in quorum sensing network of *Vibrio harveyi*. The central goal is to identify the role of feedback loops in the inhibition and amplification of information processing along the quorum sensing network.	Physics/ Chemistry/ Biotechnology / Biophysics/ Computer Science

Areas of Research: Biological Sciences

Name of Faculty	Research Project	Desired Master's Background
Ajit Bikram Data	**Title:** Understanding the residues that regulate the activity of Ubiquitin conjugating E2 U enzymes upon "back-binding" of the allosteric ubiquitin **Project Code: ABD1** **Description:** Ubiquitin conjugating E2s share a common UBC fold domain that harbors the catalytic cysteine residue. Many of the E2s also harbor a second ubiquitin binding site distal to the active site that is referred as the "back- binding site". It has been demonstrated that for a subset of E2s binding of this second ubiquitin molecule distal to the catalytic cysteine significantly enhances their catalytic efficiency though the precise molecular events behind this phenomenon is yet to be understood. We have serendipitously stumbled upon a few E2 residues that play an important role in determining the catalytic activity of an E2, most likely via the back-binding though many of these residues are away from either the catalytic or the or the backbinding site. This project shall involve biochemical studies on pinpointing the exact roles of these residues.	Chemistry/ Life Sciences/ Biotechnology/ Microbiology/ Zoology/ Biochemistry/ Biophysics
Ajit Bikram Data	**Title:** Understanding regulatory mechanism of RING E3 ligases **Project Code: ABD2** **Description:** Conjugation of ubiquitin to substrate proteins occur via a three-step mechanism requiring sequential action of E1, E2 and E3 enzymes. E3 ligases carry out the final step of ubiquitin transfer to the substrate and the largest subfamily of these proteins are called as RING E3 ligases due to the presence of a RING domain in those proteins. In fact as RING E3 ligases confer substrate specificity, eukaryotic genomes code for a large number of these proteins exceeded by only kinases. The activity of RING E3s also needs to be regulated spatio-temporally to regulate ubiquitination of substrates for proper physiological response. In this project, we shall look into diverse mechanisms of regulation of few model RING E3 ligases.	Chemistry/ Life Sciences/ Biotechnology/ Microbiology/ Zoology/ Biochemistry/ Biophysics
Ajit Bikram Data	**Title:** Molecular basis of differential E2 recognition by ubiquitin activating enzyme Uba6 **Project Code: ABD3** **Description:** All higher vertebrates, unlike lower organisms such as yeast, code for two ubiquitin activating enzymes, referred as Uba1 and Uba6. Out of these two, Uba6 was discovered and characterized about a decade ago and is referred as the non-canonical E1. Uba6 is also unique amongst all UbL activating E1 enzymes due to the fact that it can activate two UbLs, Ubiquitin and FAT10. This non-canonical E1 transfers the activated ubiquitin to only a subset of E2s, some of which, but not all, are also capable of accepting ubiquitn from Uba1. Interestingly, though the C-terminal Ufd domain of E1s is thought to impart their E2 specificity, swapping of the Ufd domain of Uba1 with that of Uba6 does not make Uba1 to transfer ubiquitin to Ube2Z, an Uba6 specific E2. This observation emphasized that other E1 domains apart from the Ufd also takes part in E2 recognition. To understand the basis of this, we aim to utilize the recently published atomic resolution structure of Uba6 and carry out biochemical and mutational analyses on these protein as well as Uba1 to understand	Chemistry/ Life Sciences/ Biotechnology/ Microbiology/ Zoology/ Biochemistry/ Biophysics

	the basis of their E2 specificity. We further aim to understand the biological implications of these specificity altering mutations in cultured cell lines.	
Anirban Bhunia	**Title:** Unravelling the molecular mechanism of Amyloid fibril formation and designing of inhibitors **Project Code: AB** **Description:** In biology, protein aggregation is a fatal event. More than 20 diseases (e.g., Alzheimer's disease, Parkinson's disease, type-II diabetes etc.) including neuronal disorders happen due to misfolding and aggregation of many important proteins. However, the complex nature of biomolecules limits the comprehensive understanding of the factors controlling the mis-folding and self-assembling properties. The aggregation of amyloidogenic proteins e.g., Alzheimer's and other devastating diseases has led to intense interest in developing approaches to inhibit this aggregation. However, success in implementing such approaches has been limited, in part due to the complexity of the aggregation process and also in part because the mechanisms and targets of the inhibitors are poorly defined. Our *in vitro* study proposes to eliminate some of these gaps in our knowledge by identifying and characterizing the targets of protein aggregation inhibitors and defining the mechanism of interaction at the atomic level.	Chemistry/ Life Sciences/ Biotechnology/ Microbiology/ Zoology/ Biochemistry/ Biophysics
Debaraj Mukherjee	**Title:** Development of novel analogs of 3'-5'-linked c-di-nucleotides (CDNs) as a potential vaccine candidate for mycobacteria tuberculosis **Project Code: DM2** **Description:** Recent research revealed that CDNs play a significant role in the pathogenesis of Mycobacterium tuberculosis (MTB). The CDNs play two roles in the control of MTB. By increasing the concentration of CDN and activating the stimulator of interferon genes (STING) in the HOST, phosphodiesterase inhibition (PDE) can operate as an immunostimulant. DisA inhibition inhibits DNA repair, fatty acid synthesis, and other processes that are necessary for bacterial survival. Researchers also showed that the aforementioned pathways can be inhibited by CDN analogues. The synthesis of 3'-5'-linked CDNs derivatives and c-di-nucleotide MK-1454 is quite challenging and requires multistep procedures, starting with advanced expensive materials and using costly enzymes. Therefore, there is an unmet need for the discovery of novel routes to access these privileged scaffolds in good amounts so that their role in MTB can be explored. With the help of our experience synthesis CDNs (phosphate backbone is replaced with a biosimilar) analogs from readily available starting materials, the role of these compounds in CDNs signaling will be investigated.	Chemistry/ Biochemistry (desirable Interest in Medicinal Chemistry)
Jayanta Mukhopadhyay	**Title:** Study the interaction of δ factor of *B. subtilis* with RNAP **Project Code: JM** **Description:** The αCTD (C-terminal domain of the α subunit) of RNA polymerase (RNAP) is a target for transcriptional regulators. In the transcription activation at Class I and Class II promoters of *E. coli*, the transcriptional regulator, CAP (catabolite activator protein) binds to DNA at different sites and interacts with the αCTD to stabilize the RNAP at the promoter. This 'simple recruitment mechanism' of the transcriptional machinery at the promoter is responsible for the activation of transcription. Strikingly, in *B. subtilis*	Chemistry/ Life Sciences/ Biochemistry/ Biophysics

	the binding of RNAP at the promoter stabilizes the transcriptional regulator, δ at the -41 site of the promoter DNA through an interaction with its αCTD and successively facilitates the open complex formation. Two residues R293 and K294 of αCTD (equivalent to K297 and K298 of *E. coli*) are involved in the interactions with δ and essential for the activation of transcription. R293 is responsible for the stabilization of δ, while K294 is responsible for facilitating the open complex formation. Based on our data we propose a new model of transcription activation by δ of *B. subtilis* that is distinct from the models for Class I and Class II promoters in *E. coli*. We further like to investigate the detailed interaction of αCTD of RNAP with δ and DNA to get a complete picture of the model.	
Nirmalya Sen	**Title:** Regulation of ETS transcription factors in refractory cancers **Project Code: NS** **Description:** ETS transcription factors are aberrantly over-expressed and mediate cancer progression through altered transcription of their target genes such as FLI1 in hematological malignancies, ERG in prostate cancer. We speculate that the regulatory post translational modifications of the ETS factors modulating their oncogenic functions might remain conserved and can serve as drug targets. Our lab will be studying posttranslational modifications (PTMs like phosphorylation, ubiquitination, acetylation, etc) within the ETS proteins that are crucial for the stability and function of these protein and can provide excellent therapeutic targets. Currently, we are using various cancer to model our studies. We are using the latest molecular biological techniques ranging from mass spectroscopy to sequencing as well as mouse based studies to figure out the role of these ETS factors during progression of cancer. The project tends to capture various aspects of resistance cancer including metabolic reprogramming, clinical intervention, DNA damage and drug resistance.	Life Sciences/ Biotechnology/ Zoology/ Biochemistry
Pallob Kundu	**Title**: Enigmatic roles of novel miRNAs in shaping tomato thermal stress-response **Project Code: PK1** **Description:** MicroRNAs are a class of small regulatory RNA molecules that play key roles in fine-tuning a wide range of biological processes, including stress responses, by binding to mRNAs and either preventing their translation into proteins or promoting their degradation. The response of tomato plants to a variety of stresses, including drought, salt, heat, cold, and pathogen infections, has been shown to include miRNAs. Targeting and regulating the expression of stress-related genes is one way miRNAs impact stress responses. They regulate gene expression in either a positive or negative fashion, depending on the miRNA in question and the genes it binds to. Stress-responsive processes such as signaling, transcriptional control, hormone production, and antioxidant defense can all be influenced by miRNAs by altering the expression of target genes. Long non-coding RNAs (lncRNAs) are another type of non-coding RNA that have been demonstrated to be regulated by miRNAs also. The number of miRs that have been reported in tomato is quite low compared to similar plant species. In our lab we have different ultradeep NGS data of tomato from various biotic and abiotic stress conditions which uncovered novel miRNAs, their target genes, and other regulatory components in tomato stress- response pathways.	Life Sciences/ Biotechnology/ Microbiology/ Botany/ Biochemistry/ Agriculture/ Horticulture/ Genetics and plant breeding

	However, their exact significance in stress-signaling is still enigmatic. Incorporating a wide range of omics technologies, molecular biology tools and transgenic procedures, the researcher will decipher the intricate molecular pathways governed by the novel miRNAs for stress adaptation in tomato. Therefore, the study will be paving the way for the creation of strategies to increase stress-tolerance in this crucial crop.	
Pallob Kundu	**Title:** Activating metacaspase during immune response in plants: structure-function analysis **Project Code: PK2** **Description:** Genetic and biochemical evidence have established the role of metacaspases, a family of conserved cell death-related cysteine proteases, in the immune signaling of several plants. Transcript profiling in tomato, a dicotyledonous model crop plant, has demonstrated that the metacaspase landscape undergoes dynamic changes in expression when challenged with pathogens. The onset of infection is coupled with massive upheavals in the host cytoplasmic ion and pH gradients. Computational studies have indicated that such physiological alterations influence the structure of the metacaspase zymogens, which in turn leads to their functional activation, and modulates their interaction with other proteins. Unwarranted progression of cell death compromises the fitness of the plant, whereas controlled cell death can assist the plant in restricting the spread of the pathogen. In this line, identification of the upstream activators as well as the downstream substrate degradome of metacaspases, becomes imperative to exercise greater control over metacaspase activity. To achieve this, a combination of advanced proteomics approaches and molecular biology techniques needs to be adopted. Control over metacaspase expression can also be brought about by specific targeting of the ion channels which maintain the redox balance in the cell, hence limiting the changes in the cellular environment which drives metacaspase activation. Furthermore, stable overexpressing or knockdown/loss-of-function transgenics can be developed, employing the CRISPR-Cas9-based genome editing technology to assess the pathophysiological role of the metacaspases or their biological targets.	Life Sciences/ Biotechnology/ Microbiology/ Botany/ Biochemistry/ Agriculture/ Horticulture/ Genetics and plant breeding
Smarajit Polley	**Title:** Regulation by phosphorylation: Structure-function relationship of protein kinases and their substrates **Project Code: SP** **Description:** Majority of the Eukaryotic Protein Kinases (EPKs) are Ser/Thr/Tyr kinases (STYKs) that phosphorylate those residues on the substrates. Residue-level specificities of STYKs are considered to group them as Ser/Thr Kinases, Tyr Kinases or dual specificity that phosphorylate Ser/Thr, Tyr or Ser/Thr as well as Tyr residues, respectively. One of the remarkable features of the HKs in TCSs is the stringent specificity wherein a specific HK primarily phosphorylate a single cognate RR, though exceptions are also reported. Many STYKs on the other hand are often known to phosphorylate a plethora of substrates. Despite such pleotropic assertion at the substrate level, some of the STYKs are so crucial at a certain context that they show exquisite specificity for a distinct substrate down to the specific residue(s) level thereby ensuring activation and fidelity of a particular signaling cascade. Using biochemical, genetic, biophysical and structural biology tools (CryoEM and X-ray crystallography) we ask a) how some of the EPKs maintain exquisite specificity in a particular signaling context	Physics/ Chemistry/ Life Sciences/ Biotechnology/ Microbiology/ Zoology/ Botany/ Biochemistry/ Biophysics/ Computer Science/ B. Tech.

	b) how EPKs achieve signaling modularity by phosphorylating different sets of substrates in a different signaling context	
Soumen Roy	**Title:** Systems Biology (Theory and Experiments) **Project Code: SR3** **Description:** **Macromolecular interactions:** Most interactions defining molecular recognition and cell signaling are macromolecular in nature. 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. **Microbial systems:** Recently published and ongoing projects in our lab are in the areas of: (1) phage-bacteria interactions and dynamics, and, (2) antimicrobial resistance. Our research is strongly guided by theoretical (mathematical and computational) investigations. The ideal candidate is expected to use both theoretical techniques and obtain their experimental validation. Experiments could be conducted in our own lab as well as in the labs of our collaborators. If they wish, selected candidates are welcome to pursue this project in conjunction with other project/s of their choice conducted in our lab.	Life Sciences/ Biotechnology/ Microbiology/ Zoology/ Biochemistry/ Biophysics/ Computer Science
Srimonti Sarkar	**Title:** Understanding the assembly of the proteasomal lid of the human pathogen *Giardia Lamblia* **Project Code: SRS** **Description:** Regulated protein degradation by the 26S proteasome is responsible for protein quality control in eukaryotes. The multi-subunit proteasome consists of the 20S core particle (CP) and the 19S regulatory particle (RP). The RP plays an important role in controlling substrate's access to the CP. RP assembly is well-coordinated, with formation of intermediate subcomplexes. Previous results indicate that the RP assembly process in Giardia is different from that of its human host. This project aims to understand this pathogen's RP assembly process with the aim of uncovering avenues for therapeutic targeting of this important cellular machinery.	Life Sciences/ Biotechnology/ Microbiology/ Zoology/ Botany/ Biochemistry/ Biophysics
Subhrangsu Chatterjee	**Title:** Deciphering a combined immuno-therapeutic approach utilizing non coding RNAs and immune checkpoints in breast cancer **Project Code: SC1** **Description:** Tumor micro-environments are generally heterogeneous, not only by the type of cells which are present but also by the phenotype of the cancer cells which are present in a single metastatic cluster at a particular stage. A single immuno-therapeutic dose, may kill many tumorigenic cells at each stage of metastasis, but on the other hand it may leave many cells in their reduced phenotype, such cells still have a lot of potency to undergo rounds of mutations to gain back its proliferation and differentiation properties. Based on this, in this work it would be great to test the hypothesis of a novel molecular approach into combination therapy involving the immune checkpoints which may wipe out the entire cluster of the therapeutic molecule based lncRNA down-regulated cancer cells (phenotype reduced cancer cells). This shall open a new dimension of a therapeutic window, where a combination therapy can be used to treat this metastatic disease.	Life Sciences/ Biotechnology/ Microbiology/ Zoology/ Biochemistry

Subhrangsu Chatterjee	**Title:** Targeting G-quadruplex structures in the impediment of Glioblastoma Multiform **Project Code: SC2** **Description:** Glioblastoma multiform (GBM) is a debilitating disease that is associated with poor prognosis, short median patient survival and a very limited response to therapies. It is the most frequently occurring malignant Central Nervous System tumour (malignant of all glial tumours). GBM has a very complex pathogenesis that involves mutations and alterations of several key cellular pathways that are involved in cell proliferation, survival, migration and angiogenesis. Therefore, efforts that are directed towards better understanding of GBM pathogenesis are essential to the development of efficient therapies that provide hope and extend patient survival. G quadruplex interference in GBM can help us to enlighten about the genomic landscape dictating the functional aspects of oncogenic proteins and progression of malignancy. Understanding the genetic fine tuning can help us to decipher the molecular mechanisms behind the progression of GBM.	Life Sciences/ Biotechnology/ Microbiology/ Zoology/ Biochemistry/ Biophysics
Sudipto Saha	**Title:** Studying interactions between the lung microbiome and host immunity in pulmonary diseases **Project Code: SS** **Description:** • To study how microbial metabolites interact to host immune cells (macrophages and T-cells) in obstructive lung diseases. • To study the role of antibiotic-resistant bacteria (commensals and pathogens) in the lung microbiome. • Metagenomics, metabolomics, transcriptomics and proteomics-based approaches will be used to address these questions.	Chemistry/ Microbiology/ Zoology/ Computer Science
Suman Kumar Banik	**Title:** Signal transduction in mixed feed-forward loop motif **Project Code: SKB1** **Description:** Small RNAs (sRNAs) controls gene regulation in bacteria via post-transcriptional modification of mRNAs. The interaction between sRNA and mRNA constitutes diverse regulatory circuits, e.g., mixed feed-forward loop (FFL) motif. Using theoretical and computational tools we aim to model signal transduction in diverse mixed FFL structures. The central goal of the project is to identify the contribution of different types of sRNA-mRNA interactions in the overall process of signal propagation.	Physics/ Chemistry/ Biotechnology/ Biophysics/ Computer Science
Suman Kumar Banik	**Title:** Role of feedback loop in the quorum sensing network **Project Code: SKB2** **Description:** Quorum sensing in bacteria is a signal transduction mechanism through which regulation of gene expression takes place in response to change in cell density. During quorum sensing, generation, secretion and detection of autoinducers are executed by an individual cell. The concentration of autoinducer, which depends upon the local cell density, when exceeds a threshold value significant expression of quorum sensing regulated genes takes place. The multitude of genes are responsible for several phenotypes, e.g., bioluminescence, biofilm formation and secretion of virulence factors, which in turn depends on the local cell density. Recent studies show that quorum sensing network of *Vibrio harveyi* has multiple feedback loops that regulates precise gene expression.	Physics/ Chemistry/ Biotechnology/ Biophysics/ Computer Science

	Using theoretical and computational tools we aim to model information processing in quorum sensing network of *Vibrio harveyi*. The central goal is to identify the role of feedback loops in the inhibition and amplification of information processing along the quorum sensing network.	

Areas of Research: Chemical Sciences

Name of Faculty	Research Project	Desired Master's Background
Ajit Bikram Data	**Title:** Understanding the residues that regulate the activity of Ubiquitin conjugating E2 U enzymes upon "back-binding" of the allosteric ubiquitin **Project Code: ABD1** **Description:** Ubiquitin conjugating E2s share a common UBC fold domain that harbors the catalytic cysteine residue. Many of the E2s also harbor a second ubiquitin binding site distal to the active site that is referred as the "back- binding site". It has been demonstrated that for a subset of E2s binding of this second ubiquitin molecule distal to the catalytic cysteine significantly enhances their catalytic efficiency though the precise molecular events behind this phenomenon is yet to be understood. We have serendipitously stumbled upon a few E2 residues that play an important role in determining the catalytic activity of an E2, most likely via the back-binding though many of these residues are away from either the catalytic or the or the backbinding site. This project shall involve biochemical studies on pinpointing the exact roles of these residues.	Chemistry/ Life Sciences/ Biotechnology/ Microbiology/ Zoology/ Biochemistry/ Biophysics
Ajit Bikram Data	**Title:** Understanding regulatory mechanism of RING E3 ligases **Project Code: ABD2** **Description:** Conjugation of ubiquitin to substrate proteins occur via a three-step mechanism requiring sequential action of E1, E2 and E3 enzymes. E3 ligases carry out the final step of ubiquitin transfer to the substrate and the largest subfamily of these proteins are called as RING E3 ligases due to the presence of a RING domain in those proteins. In fact as RING E3 ligases confer substrate specificity, eukaryotic genomes code for a large number of these proteins exceeded by only kinases. The activity of RING E3s also needs to be regulated spatio-temporally to regulate ubiquitination of substrates for proper physiological response. In this project, we shall look into diverse mechanisms of regulation of few model RING E3 ligases.	Chemistry/ Life Sciences/ Biotechnology/ Microbiology/ Zoology/ Biochemistry/ Biophysics
Ajit Bikram Data	**Title:** Molecular basis of differential E2 recognition by ubiquitin activating enzyme Uba6 **Project Code: ABD3** **Description:** All higher vertebrates, unlike lower organisms such as yeast, code for two ubiquitin activating enzymes, referred as Uba1 and Uba6. Out of these two, Uba6 was discovered and characterized about a decade ago and is referred as the non-canonical E1. Uba6 is also unique amongst all UbL activating E1 enzymes due to the fact that it can activate two UbLs, Ubiquitin and FAT10. This non-canonical E1 transfers the activated ubiquitin to only a subset of E2s, some of which, but not all, are also capable of accepting ubiquitn from Uba1. Interestingly, though the C-	Chemistry/ Life Sciences/ Biotechnology/ Microbiology/ Zoology/ Biochemistry/ Biophysics

	terminal Ufd domain of E1s is thought to impart their E2 specificity, swapping of the Ufd domain of Uba1 with that of Uba6 does not make Uba1 to transfer ubiquitin to Ube2Z, an Uba6 specific E2. This observation emphasized that other E1 domains apart from the Ufd also takes part in E2 recognition. To understand the basis of this, we aim to utilize the recently published atomic resolution structure of Uba6 and carry out biochemical and mutational analyses on these protein as well as Uba1 to understand the basis of their E2 specificity. We further aim to understand the biological implications of these specificity altering mutations in cultured cell lines.	
Anirban Bhunia	**Title:** Unravelling the molecular mechanism of Amyloid fibril formation and designing of inhibitors **Project Code: AB** **Description:** In biology, protein aggregation is a fatal event. More than 20 diseases (e.g., Alzheimer's disease, Parkinson's disease, type-II diabetes etc.) including neuronal disorders happen due to misfolding and aggregation of many important proteins. However, the complex nature of biomolecules limits the comprehensive understanding of the factors controlling the mis-folding and self-assembling properties. The aggregation of amyloidogenic proteins e.g., Alzheimer's and other devastating diseases has led to intense interest in developing approaches to inhibit this aggregation. However, success in implementing such approaches has been limited, in part due to the complexity of the aggregation process and also in part because the mechanisms and targets of the inhibitors are poorly defined. Our *in vitro* study proposes to eliminate some of these gaps in our knowledge by identifying and characterizing the targets of protein aggregation inhibitors and defining the mechanism of interaction at the atomic level.	Chemistry/ Life Sciences/ Biotechnology/ Microbiology/ Zoology/ Biochemistry/ Biophysics
Anup Kumar Misra	**Title:** Chemical synthesis of bacterial cell wall oligosaccharides for their use in the preparation of anti-bacterial glycoconjugate derivatives **Project Code: AKM1** **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. The project will be dealing with synthetic organic chemistry. Desirable academic background of the student: **M.Sc. in Organic Chemistry**	Chemistry

Anup Kumar Misra	**Title:** Design and synthesis of glycomimetics and carbohydrate derived biodynamic molecules **Project Code: AKM2** **Description:** Carbohydrates are the most abundant natural products. Besides their role in metabolism and as structural building blocks, they are fundamental constituents of every cell surface, where they are involved in vital cellular recognition processes. Advances in the functional understanding of carbohydrate–protein interactions have enabled the development of a new class of small-molecule drugs, known as glycomimetics. Glycomimetics are chemical entities that mimic the biological essence of carbohydrates and behave as pharmacologically useful molecules. Common structural changes to carbohydrate structures include replacement of the ring oxygen or substitution of the glycosidic oxygen, with nitrogen, sulfur or carbon. Such substitutions are usually made to impart a degree of metabolic or biological stability into the compounds being developed or to generate compounds that mimic transition-state structures from glycohydrolase reactions. We will design and synthesize a variety of glycomimetics to evaluate their biological potential to develop possible therapeutics. Objective: Chemical synthesis of glycomimetics and carbohydrate derived molecules of biological importance. The project will be dealing with synthetic organic chemistry. Desirable academic background of the student: **M.Sc. in Organic Chemistry**	Chemistry
Basudeb Maji	**Title:** Chemogenetic Therapy Development against Epithelial-Mesenchymal Transition (EMT) in Triple-Negative Breast Cancer **Project Code: BM** **Description:** The incidence of breast cancer (BC) is increasing and might be a leading cause of death in the future in women. In India, the incidence rate of breast cancer is increasing in metropolitan and urban areas, and it is almost three times higher compared to rural regions. Statistical analysis reveals that India contributes to 7% of breast cancer cases globally, and the disease has become the second most common cancer among women in the subcontinent. Molecular classification defines BC as ER+, PR+, Her2+, and basal type of Triple-negative breast cancer (TNBC) having high proliferation index (Ki-67), expressing EGFR and basal cytokeratins. Among all, PR+ shows a poor prognosis compared to ER+ while Her2-enriched and TNBCs have worse outcomes in BC patients. Targeted therapy is one of the most effective ways to treat diseases minimizing the side effects. Unfortunately, due to the absence of all three cell surface markers (ER, PR, and Her), targeted therapy is not possible in TNBC incidents. We are developing synthetic small molecule probes that can selectively target TNBC cells and induce targeted degradation of oncoproteins. We envision designing small molecules for the CRISPR-based gene editing method and coupling them with chemopreventives toward developing chemogenetic methods for TNBC.	Physics/ Organic Chemistry

Debaraj Mukherjee	**Title:** Development of the methods for the synthesis of C-glycosides of medicinal Importance **Project Code: DM1** **Description:** C-oligosaccharides are the carbon counterparts of naturally existing O-oligosaccharides that bear an atom of carbon instead of the interglycosidic oxygen, the most straightforward class being the C-disaccharide. C-saccharides are much more stable towards the chemical hydrolysis and enzymatic degradation, enabling them to act as preferred chemotherapeutics & subsequently, as synthetic targets. Many naturally occurring bio-active molecules embody interglycosidic C-C bond linkages with or without the spacer in their structural framework such as dodecadaiulose (analog of trehalose), hikizimycin (antihelminthic), maitotoxin (neurotoxic), tunicamycine (antibiotics). Some of the C-aryl glycosides are now FDA-approved drugs like Dapagliflozins. C-disaccharide synthesis is much more challenging than O-disaccharides due to the inertness of two coupling sugar molecules. The project's objective will be developing novel versatile methods to access medicinally important C- glycosides using easily available chiral building blocks obviating the use of harsh conditions.	Chemistry (desirable Organic Chemistry)
Debaraj Mukherjee	**Title:** Development of novel analogs of 3'-5'-linked c-di-nucleotides (CDNs) as a potential vaccine candidate for mycobacteria tuberculosis **Project Code: DM2** **Description:** Recent research revealed that CDNs play a significant role in the pathogenesis of Mycobacterium tuberculosis (MTB). The CDNs play two roles in the control of MTB. By increasing the concentration of CDN and activating the stimulator of interferon genes (STING) in the HOST, phosphodiesterase inhibition (PDE) can operate as an immunostimulant. DisA inhibition inhibits DNA repair, fatty acid synthesis, and other processes that are necessary for bacterial survival. Researchers also showed that the aforementioned pathways can be inhibited by CDN analogues. The synthesis of 3'-5'-linked CDNs derivatives and c-di-nucleotide MK-1454 is quite challenging and requires multistep procedures, starting with advanced expensive materials and using costly enzymes. Therefore, there is an unmet need for the discovery of novel routes to access these privileged scaffolds in good amounts so that their role in MTB can be explored. With the help of our experience synthesis CDNs (phosphate backbone is replaced with a biosimilar) analogs from readily available starting materials, the role of these compounds in CDNs signaling will be investigated.	Chemistry/ Biochemistry (desirable Interest in Medicinal Chemistry)
Jayanta Mukhopadhyay	**Title:** Study the interaction of δ factor of *B. subtilis* with RNAP **Project Code: JM** **Description:** The αCTD (C-terminal domain of the α subunit) of RNA polymerase (RNAP) is a target for transcriptional regulators. In the transcription activation at Class I and Class II promoters of *E. coli*, the transcriptional regulator, CAP (catabolite activator protein) binds to DNA at different sites and interacts with the αCTD to stabilize the RNAP at the promoter. This 'simple recruitment mechanism' of the transcriptional machinery at the promoter is responsible for the activation of transcription. Strikingly, in *B. subtilis* the binding of RNAP at the promoter stabilizes the transcriptional regulator, δ at the -41 site of the promoter DNA through an interaction with its αCTD and	Chemistry/ Life Sciences/ Biochemistry/ Biophysics

	successively facilitates the open complex formation. Two residues R293 and K294 of αCTD (equivalent to K297 and K298 of *E. coli*) are involved in the interactions with δ and essential for the activation of transcription. R293 is responsible for the stabilization of δ, while K294 is responsible for facilitating the open complex formation. Based on our data we propose a new model of transcription activation by δ of *B. subtilis* that is distinct from the models for Class I and Class II promoters in *E. coli*. We further like to investigate the detailed interaction of αCTD of RNAP with δ and DNA to get a complete picture of the model.	
Smarajit Polley	**Title:** Regulation by phosphorylation: Structure-function relationship of protein kinases and their substrates **Project Code: SP** **Description:** Majority of the Eukaryotic Protein Kinases (EPKs) are Ser/Thr/Tyr kinases (STYKs) that phosphorylate those residues on the substrates. Residue-level specificities of STYKs are considered to group them as Ser/Thr Kinases, Tyr Kinases or dual specificity that phosphorylate Ser/Thr, Tyr or Ser/Thr as well as Tyr residues, respectively. One of the remarkable features of the HKs in TCSs is the stringent specificity wherein a specific HK primarily phosphorylate a single cognate RR, though exceptions are also reported. Many STYKs on the other hand are often known to phosphorylate a plethora of substrates. Despite such pleotropic assertion at the substrate level, some of the STYKs are so crucial at a certain context that they show exquisite specificity for a distinct substrate down to the specific residue(s) level thereby ensuring activation and fidelity of a particular signaling cascade. Using biochemical, genetic, biophysical and structural biology tools (CryoEM and X-ray crystallography) we ask a) how some of the EPKs maintain exquisite specificity in a particular signaling context b) how EPKs achieve signaling modularity by phosphorylating different sets of substrates in a different signaling context	Physics/ Chemistry/ Life Sciences/ Biotechnology/ Microbiology/ Zoology/ Botany/ Biochemistry/ Biophysics/ Computer Science/ B. Tech.
Sudipto Saha	**Title:** Studying interactions between the lung microbiome and host immunity in pulmonary diseases **Project Code: SS** **Description:** • To study how microbial metabolites interact to host immune cells (macrophages and T-cells) in obstructive lung diseases. • To study the role of antibiotic-resistant bacteria (commensals and pathogens) in the lung microbiome • Metagenomics, metabolomics, transcriptomics and proteomics-based approaches will be used to address these questions.	Chemistry/ Microbiology/ Zoology/ Computer Science
Suman Kumar Banik	**Title:** Signal transduction in mixed feed-forward loop motif **Project Code: SKB1** **Description:** Small RNAs (sRNAs) controls gene regulation in bacteria via post-transcriptional modification of mRNAs. The interaction between sRNA and mRNA constitutes diverse regulatory circuits, e.g., mixed feed-forward loop (FFL) motif. Using theoretical and computational tools we aim to model signal transduction in diverse mixed FFL structures. The central goal of the project is to identify the contribution of different types of sRNA-mRNA interactions in the overall process of signal propagation.	Physics/ Chemistry/ Biotechnology/ Biophysics/ Computer Science

Suman Kumar Banik	**Title:** Role of feedback loop in the quorum sensing network **Project Code: SKB2** **Description:** Quorum sensing in bacteria is a signal transduction mechanism through which regulation of gene expression takes place in response to change in cell density. During quorum sensing, generation, secretion and detection of autoinducers are executed by an individual cell. The concentration of autoinducer, which depends upon the local cell density, when exceeds a threshold value significant expression of quorum sensing regulated genes takes place. The multitude of genes are responsible for several phenotypes, e.g., bioluminescence, biofilm formation and secretion of virulence factors, which in turn depends on the local cell density. Recent studies show that quorum sensing network of *Vibrio harveyi* has multiple feedback loops that regulates precise gene expression. Using theoretical and computational tools we aim to model information processing in quorum sensing network of *Vibrio harveyi*. The central goal is to identify the role of feedback loops in the inhibition and amplification of information processing along the quorum sensing network.	Physics/ Chemistry/ Biotechnology/ Biophysics/ Computer Science