बसु विज्ञान मंदिर
कोलकाता

(विज्ञान एंव प्रौद्योगिकी विभाग, भारत सरकार के अधीन एक स्वायत्त संस्था)

विज्ञापन संख्या : BI/NET-JRF/01/2024-25

पीएचडी कार्यक्रम के लिए भर्ती
वसंत 2024

बसु विज्ञान मंदिर, कोलकाता भारत सरकार के विज्ञान और प्रौद्योगिकी मंत्रालय के विज्ञान और प्रौद्योगिकी विभाग के तहत एक स्वायत्त विज्ञान और प्रौद्योगिकी संस्थान है, जिसे भारत सरकार से 100% सहायता अनुदान प्राप्त होता है। विभिन्न शैक्षणिक अनुसंधान गतिविधियों के विवरण के लिए, कृपया संस्थान की वेबसाइट http://www.jcbose.ac.in पर जाएँ।

भारतीय उपमहाद्वीप में आधुनिक विज्ञान के संस्थापक आचार्य जे.सी. बोस ने 1917 में बसु विज्ञान मंदिर की स्थापना की थी। संस्थान को एशिया के पहले अंतःविषय अनुसंधान केंद्र के रूप में स्थापित किया गया था और यह अनुसंधान में उत्कृष्टता की एक सदी पुरानी परंपरा को दर्शाता है।

संस्थान वर्ष में दो बार अपने पीएचडी कार्यक्रम के लिए छात्रों को प्रवेश देना चाहता है। इस सत्र के लिए साक्षात्कार अपेक्षाकृत जून 2024 के द्वितीय सप्ताह के दौरान आयोजित किए जाएंगे।

अनुसंधान के क्षेत्र: पृथ्वी और वायुमंडलीय विज्ञान, रासायनिक विज्ञान, जीवन विज्ञान और भौतिक विज्ञान।

● उम्मीदवारों को अधिकतम दो परियोजनाओं का चयन करना होगा जिनमें वे काम करने के इच्छुक होंगे और निर्धारित प्रारूप में परियोजना को चुनने के लिए एक उपयुक्तता प्रस्तुत करना होगा।

फ़ेलोशिप: यूजीसी/सीएसआईआर/डीबीटी/डीएसटी/आईसीएमआर आदि द्वारा प्रदान किए गए भारत सरकार के नियमों के अनुसार स्वीकार्य।

कुल रिक्तियों की संख्या: 50 (अनारक्षित-22, ओबीसी-13, एससी-7, एसटी-3, ईडब्ल्यूएस-5)

आयु सीमा: 30 वर्ष से कम (आयु में छूट भारत सरकार के नियमों के अनुसार लागू है)।

पीएचडी साक्षात्कार के लिए पात्रता:

(1) उम्मीदवारों को जेआरएफ (सीएसआईआर-यूजीसी जेआरएफ / डीबीटी-जेआरएफ / आईसीएमआर-जेआरएफ / डीएसटी- इंस्पायर / डीबीटी-बीआईएनसी या समकक्ष) उत्तीर्ण होना चाहिए, जिसकी वैधता की अंतिम तिथि **30 सितंबर, 2024** से पहले नहीं होनी चाहिए। यदि उम्मीदवार, जो अपने मास्टर डिग्री प्रोग्राम के अंतिम वर्ष में हैं और उनके पास जेआरएफ उत्तीर्ण है, का चयन किया जाता है, तो उन्हें शामिल होने के समय अपना अंतिम डिग्री प्रमाणपत्र जमा करना होगा।

(2) निम्नलिखित में से किसी भी क्षेत्र में मास्टर डिग्री या समकक्ष: सामान्य उम्मीदवारों के लिए कम से कम 55% अंकों के साथ इंजीनियरिंग/विज्ञान/प्रौद्योगिकी/मेडिकल, जबकि एससी/एसटी/ओबीसी (नॉन-क्रीमी लेयर) के लिए 50% अंक आवश्यक हैं / अलग रूप से सक्षम और अन्य श्रेणियों के उम्मीदवार, यूजीसी मानदंडों के अनुसार।

(3) डीएसटी-इंस्पायर उम्मीदवारों को केवल अनंतिम रूप से प्रवेश दिया जा सकता है। बसु विज्ञान मंदिर के पीएचडी कार्यक्रम में उनके प्रवेश की पुष्टि डीएसटी द्वारा इंस्पायर फेलोशिप के अंतिम उत्तीर्ण होने के अधीन है। यदि उम्मीदवार अंततः डीएसटी द्वारा इंस्पायर फेलोशिप उत्तीर्ण नहीं कर पाता है, तो संस्थान द्वारा उसका अनंतिम प्रवेश रद्द कर दिया जा सकता है। डीएसटी इंस्पायर फेलोशिप के मामले में, बसु विज्ञान मंदिर में पीएचडी कार्यक्रम में विचार किए जाने के लिए उम्मीदवार को नेट-एलएस/गेट/समान राष्ट्रीय स्तर की परीक्षा में उत्तीर्ण होना चाहिए।

(4) जिन अभ्यर्थियों ने जीएटीई/जेईएसटी/जेजीईई बीआईएलएस/एनईटी (एलएस) आदि में अर्हता प्राप्त की है, लेकिन जिनके पास ऊपर (1) में उल्लिखित जेआरएफ या समकक्ष योग्यता नहीं है, वे आवेदन करने के लिए पात्र नहीं हैं।

(5) आईसीएआर फेलोशिप के लिए सम्मानित कोई भी छात्र बसु विज्ञान मंदिर में पीएचडी कार्यक्रम में भाग लेने के लिए पात्र नहीं होगा।

आवेदन प्रक्रिया:

आवश्यक पात्रता पूरी करने वाले इच्छुक उम्मीदवार यूआरएल http://www.jcbose.ac.in/applications/PHD-ADMISSION/ पर ऑनलाइन आवेदन करें ।

ऑनलाइन आवेदन की अंतिम तिथि: 20.05.2024 पर 23:59 बजे

ऑनलाइन आवेदन पत्र सफलतापूर्वक जमा करने के बाद एक **पावती रसीद** उत्पन्न की जाएगी। उम्मीदवारों को भविष्य में संदर्भ के लिए यह रसीद अपने पास रखनी चाहिए। यदि साक्षात्कार के लिए बुलाया जाता है, तो उम्मीदवारों को यह **पावती रसीद प्रस्तुत करनी होगी।** इस रसीद के बिना किसी भी उम्मीदवार को साक्षात्कार में शामिल होने की अनुमति नहीं दी जाएगी।

ऑनलाइन आवेदन से संबंधित किसी भी कठिनाई के लिए कृपया ईमेल भेजें:
bosephdadmission@gmail.com

1. उम्मीदवारों को सलाह दी जाती है कि वे ऑनलाइन आवेदन सावधानीपूर्वक भरें और आवश्यकतानुसार जानकारी प्रदान करें। उम्मीदवारों से अनुरोध है कि वे अपडेट के लिए नियमित रूप से संस्थान की वेबसाइट (http://www.jcbose.ac.in) देखते रहें। किसी भी अभ्यर्थी को अलग से कोई सूचना नहीं भेजी जाएगी।

2. उम्मीदवारों को ऑनलाइन आवेदन पत्र में आयु, शैक्षणिक योग्यता, वैध सामुदायिक प्रमाणपत्रों का विवरण आदि सहित सभी आवश्यक विवरण सावधानीपूर्वक भरना चाहिए, क्योंकि आवेदन जमा होने के बाद विवरण में बदलाव के संबंध में कोई पत्राचार पर विचार नहीं किया जाएगा। यदि उनका कोई भी दावा झूठा या गलत पाया गया तो उनकी उम्मीदवारी खारिज कर दी जाएगी।

3. बताई गई निर्धारित आवश्यक योग्यताएं न्यूनतम हैं और इनके पास होने मात्र से ही उम्मीदवार साक्षात्कार के लिए बुलाए जाने का हकदार नहीं हो जाएगा।

4. सत्यापन के लिए साक्षात्कार में उपस्थित होने के समय उम्मीदवारों को अपनी आयु, आरक्षण श्रेणी, शैक्षिक योग्यता के समर्थन में सभी मूल दस्तावेजों/प्रमाणपत्रों के साथ-साथ उनकी स्व-सत्यापित प्रतियों के एक सेट का प्रस्तुत करना होगा, अन्यथा उसे साक्षात्कार में शामिल होने की अनुमति नहीं दी जाएगी।

5. संस्थान के पास योग्यता के आधार पर साक्षात्कार के पहले दौर के लिए बुलाए गए उम्मीदवारों की संख्या को उचित सीमा तक सीमित करने का अधिकार सुरक्षित है। संस्थान उन उम्मीदवारों को दूसरे दौर के साक्षात्कार के लिए न बुलाने का अधिकार भी सुरक्षित रखता है जिनका साक्षात्कार के पहले दौर में स्कोर एक निश्चित कट-ऑफ से नीचे आता है।

6. शॉर्टलिस्ट किए गए उम्मीदवारों के नाम, साक्षात्कार की तारीख और समय के साथ संस्थान की वेबसाइट पर प्रदर्शित किए जाएंगे
   - यह ध्यान दिया जाना चाहिए कि केवल शॉर्टलिस्ट में उपस्थिति का मतलब प्रवेश नहीं है
   - साक्षात्कार ऑफ़लाइन मोड में आयोजित किया जाएगा। ऑनलाइन साक्षात्कार तभी लिया जाएगा जब:
     (i) उम्मीदवार का निवास स्थान बसु विज्ञान मंदिर के एकीकृत शैक्षणिक परिसर से 100 किमी से अधिक है (उम्मीदवार को निवास का प्रमाण प्रस्तुत करना होगा)
     (ii) उम्मीदवार उसी तिथि को किसी अन्य संस्थान में साक्षात्कार के लिए उपस्थित होंगे (उम्मीदवार को संस्थान की वेबसाइट पर बसु विज्ञान मंदिर के साक्षात्कार कार्यक्रम के प्रकाशन से पहले दिनांकित साक्षात्कार पत्र की एक प्रति प्रस्तुत करनी होगी, जिसमें साक्षात्कार का तिथि का उल्लेख है)

   ऐसे मामलों में उम्मीदवार को बसु विज्ञान मंदिर वेबसाइट पर **साक्षात्कार कार्यक्रम के प्रकाशन के दो दिनों के भीतर** ईमेल (bosephdadmission@gmail.com) के माध्यम से अनुरोध प्रस्तुत करना होगा।

7. दो-चरणीय स्क्रीनिंग प्रक्रिया का पालन किया जाएगा, जिसमें पहले चरण में मुख्य विषय में ज्ञान का मूल्यांकन किया जाएगा और दूसरे चरण में पीएचडी गाइड-उम्मीदवार मिलान को अंतिम रूप देने के साथ-साथ बसु विज्ञान मंदिर में वैज्ञानिक अनुसंधान करने के लिए उम्मीदवार की उपयुक्तता का मूल्यांकन किया जाएगा। आवेदन के समय, उम्मीदवारों को उद्देश्य का विवरण जमा करना होगा, जिस पर स्क्रीनिंग के दूसरे दौर के दौरान विचार किया जाएगा।
8. संस्थान के पास शॉर्ट लिस्टिंग और चयन के लिए आवेदनों की स्क्रीनिंग का तरीका तय करने का अधिकार सुरक्षित है।
9. ऊपरी आयु सीमा सहित पात्रता मानदंड की गणना आवेदन जमा करने की अंतिम तिथि पर की जाएगी।
10. केवल शॉर्टलिस्ट किए गए उम्मीदवारों को साक्षात्कार की तारीख केवल आवेदन पत्र में दिए गए संबंधित ईमेल पते पर ईमेल के माध्यम से सूचित की जाएगी (उम्मीदवारों को नियमित आधार पर अपना ईमेल जांचने की सलाह दी जाती है)। सूची www.jcbose.ac.in पर भी उपलब्ध होगी।
11. आवेदन करने से पहले, आवेदकों को यह सुनिश्चित करना चाहिए कि उनके पास विज्ञापन में निर्दिष्ट कम से कम आवश्यक योग्यताएं और अन्य शर्तें हैं। यदि कोई उम्मीदवार अयोग्य पाया जाता है, तो साक्षात्कार प्रक्रिया के किसी भी चरण में उसकी उम्मीदवारी रद्द कर दी जाएगी। यह ध्यान दिया जा सकता है कि यदि कोई उम्मीदवार साक्षात्कार में उत्तीर्ण हो जाता है और बाद में यह पाया जाता है कि वह पात्रता मानदंडों को पूरा नहीं करता है, तो भी उसकी उम्मीदवारी रद्द कर दी जाएगी।
12. सभी सहायक दस्तावेजों को अपलोड करना आवश्यक है और इसलिए, उम्मीदवारों को सलाह दी जाती है कि वे ऑनलाइन आवेदन प्रक्रिया शुरू करने से पहले आवश्यक दस्तावेजों की पीडीएफ फाइलें तैयार कर लें।
13. साक्षात्कार में उपस्थित होने के लिए कोई टीए/डीए स्वीकार्य नहीं है।
14. साक्षात्कार के संबंध में विशिष्ट निर्देश केवल शॉर्टलिस्ट किए गए उम्मीदवारों को सूचित किए जाएंगे।
15. चयनित उम्मीदवारों की अंतिम सूची संस्थान की वेबसाइट पर प्रदर्शित की जाएगी।
16. संस्थान प्राधिकरण बिना कोई कारण बताए किसी भी या सभी आवेदनों को अस्वीकार करने का अधिकार सुरक्षित रखता है।
17. संस्थान के पास विज्ञापित सभी पदों को न भरने और बिना कारण बताए किसी भी या सभी आवेदनों को अस्वीकार करने का अधिकार सुरक्षित है।
18. किसी भी संशोधन के लिए उम्मीदवारों को संस्थान की वेबसाइट पर नजर रखनी होगी।
19. किसी भी रूप में कोई अंतरिम प्रश्न पर विचार नहीं किया जाएगा।
20. प्रचार करना या किसी भी रूप में प्रभाव डालना उम्मीदवारी को अयोग्य घोषित कर देगा।
21. योग्य उम्मीदवारों को भारत सरकार के दिशानिर्देशों के अनुसार आयु में छूट दी जाएगी।
22. एससी/एसटी/ओबीसी/ईडब्ल्यूएस को आरक्षण के लिए यूजीसी द्वारा अधिसूचित आरक्षण नियम लागू होंगे।
23. एससी/एसटी/ओबीसी श्रेणी में आरक्षण का दावा करने के लिए संबंधित उम्मीदवार को जाति प्रमाण पत्र प्रस्तुत करना होगा।
24. ओबीसी से संबंधित होने का दावा करने वाले किसी भी उम्मीदवार को किसी भी निर्दिष्ट प्राधिकारी द्वारा हस्ताक्षरित निर्धारित प्रपत्र में एक प्रमाण पत्र प्रस्तुत करना होगा। कोई अन्य प्रमाणपत्र स्वीकार नहीं किया जाएगा. जाति प्रमाण पत्र जारी करने वाले प्राधिकारी को यह भी प्रमाणित करना चाहिए कि उम्मीदवार किसी भी क्रीमी लेयर (बसु विज्ञान मंदिर वेबसाइट में दिया गया प्रारूप) से संबंधित नहीं है।
25. सभी विवाद कोलकाता न्यायालय क्षेत्राधिकार के अंतर्गत आएंगे।

महत्वपूर्ण तिथियाँ:

- ऑनलाइन आवेदन की अंतिम तिथि: 20.05.2024 को 23:59 बजे।

सभी जानकारी के लिए हमारी वेबसाइट www.jcbose.ac.in को फॉलो करें
संपर्क करना: bosephdadmission@gmail.com

Sd/-
Registrar (Officiating)
Bose Institute

Annexure – I

Areas of Research: Physical Sciences

Name of Faculty	Research Project	Desired Master's Background
Dr. Abhijit Chatterjee	**Title :** India's Air Quality: Long-term variability, sources and future prediction **Project Code:** AC1 **Description:** Air pollution is one of the most critical threats to the Indians at the current scenario. The proposed study would be on an in-depth understanding of air pollution and air quality across the country through a long-term analysis. The major sources of poor air quality for different sectors will be addressed based on both the ground based and satellite-based observation. Source apportionment studies will be conducted for quantitative source contribution for each sources of air pollution over different sectors in India using a suitable source-receptor model. Future prediction would also be conducted based on long-term data for each of the sectors	Physical Science/ Chemical Sciences/ Earth and Atmospheric Sciences/ Environmental Sciences
Prof. 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	Physical Sciences
Prof. 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	Physical Sciences
Prof. Achintya Singha	**Title :** Surface Enhanced Raman Spectroscopy based diagnostic tool **Project Code:** AS **Description:** The broad interest of this project would be: a) To develop SERS based new generation quantum sensors using 2D materials b) To understanding the quantum effects in the SERS process. c) To check the sensitivity of the SERS sensor using reference molecules d) To fabricate ultra-sensitive biomolecules sensor	Physical Sciences
Prof. Achintya Singha	**Title :** Optoelectronics properties of Janus / alloy Transition metal transition metal dichalcogenides **Project Code:** AS4 Description: The broad interest of this project would be: a) To develop strategy for the fabrication of Janus / alloy transition metal dichalcogenides b) To characterize the prepared sample using optical and vibrational spectroscopy. c) To fabricated optoelectronic devices	Physical Sciences

	d) Optoelectonics study	
Prof. 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, 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, 3He and 4He 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 8Li 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 br+eakup. 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.	Physical Sciences
Prof. 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	Physical Sciences

	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.	
Prof. 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(β+ν)^{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 17MeV/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.	Physical Sciences
Prof. Dhruba Gupta	**Title :** Scattering of protons from the radioactive nucleus 7Be **Project Code:** DG4 **Description:** Proton scattering of exotic unstable nuclei in inverse kinematics is used to study such nuclei. A systematic pscattering 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 an enhancement of the total reaction crosssection. 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	Physical Sciences

	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.	
Dr. 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.	Physical Sciences
Dr. 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×ZM) and T^6/Z_N. Superstring compactifications on such backgrounds lead to some fourdimensional 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.	Physical Sciences
Dr. 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 nongeometric extensions) using some concrete CY fourfolds. The second part of the project aims to study the Ftheory uplifts of the type IIB global models with open-string moduli. These two aspects are very	Physical Sciences

	significant in the area of superstring/F-theory phenomenology in order to construct realistic models.	
Prof. Rajarshi Ray	**Title :** Polyakov Quark-Hadron Model **Project Code:** RR1 **Description:** One of the most promising models describing the thermodynamics of strongly interacting matter is the Polyakov Quark-Hadron models. Among the several varieties of this model our group has developed expertise in dealing with both the Polyakov (effective gluon) potential as well as the hadronic potential contributions. Further development in this direction is necessary to obtain quantitative evaluation of a number of observables in a strongly interacting system.	Physical Sciences
Prof. Rajarshi Ray	**Title :** Hadron Resonance Gas Model **Project Code:** RR2 **Description:** One of the most promising models describing the abundance of hadronic matter formed in heavy-ion collision experiments is the Hadron Resonance Gas Model. With ever increasing advances in the detection techniques as well as statistics it is a real challenge to establish if hadronic matter formed were in chemical equilibrium or not. Either way a lot of exciting physics could be uncovered. Our group has developed expertise in dealing with the hadronic model alongside the experimental data. Further development in this direction is necessary to obtain quantitative evaluation of a number of observables in a strongly interacting system.	Physical Sciences
Dr. 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.	Physical Sciences, Electronics
Dr. 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. However, the selected candidate will mostly be stationed at the cosmic ray laboratory in the Darjeeling campus of Bose Institute.	Physical Sciences, Electronics

Dr. Saikat Biswas	**Title :** Research and development of Gas Electron Multiplier detector for the high-rate heavy ion experiment **Project Code:** SB3 **Description:** Micro Pattern Gaseous Detector (MPGD) is one of the best choices for the ongoing and upcoming high rate heavy-ion experiments because of its good rate handling capability and spatial resolution. The Gas Electron Multiplier (GEM) detector is one of the most advanced members of the MPGD group. The proposed project aims at the detailed investigation of the GEM detector which will include the understanding of the behaviour of the chamber under high irradiation (~ 10 MHz/cm2), the effect of the geometry of the chamber on its performance under high irradiation and also Monte Carlo based simulation studies to give an insight on the possible modification in the detector technology to improve its performance for the high rate heavy-ion experiments (e.g. FAIR in Germany). The work will consist of hardware activities and the development of a simulation framework for the GEM detector. As a part of a large collaboration, the student needs to collaborate in several experiments in India as well as abroad.	Physical Sciences, Electronics
Prof. Supriya Das	**Title :** Study of nuclear matter at high baryonic densities. **Project Code:** SD1 **Description:** During the last few decades Ultrarelativistic Heavy-Ion Collisions has become the most frontline research area in the field of high-energy nuclear physics. The goal of these experiments is to study the nature of matter under extreme conditions such as high temperature as existed after a few microseconds after the big bang and/or high densities that exist inside the astrophysical objects such as neutron stars. Quantum Chromodynamics (QCD) predicts that the phase of matter changes from normal confined phase to deconfined quark gluon plasma (QGP) phase under these extreme conditions. The aim of this project is to characterize the matter created under high baryonic densities through the study of the charged hadrons created in the heavy-ion collisions at the collision energy range that has been proposed at the upcoming multipurpose Facility for Antiproton and Ion Research (FAIR). The successful candidate will work towards the development and fabrication of particle detectors, analysis/simulation software and study of detector performance as well as analysis of data from prototype tests of the detectors. Knowledge of programming along with basic courses on nuclear and particle physics in masters level will be advantageous for this project.	Physical Sciences
Prof. Suman Kumar Banik	**Title :** Role of feedback loop in the quorum sensing network **Project Code:** SKB1 **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	Physical Sciences/ Chemical Sciences

	inhibition and amplification of information processing along the quorum sensing network.	
Prof. Suman Kumar Banik	**Title :** Signal transduction in mixed feed-forward loop motif **Project Code:** SKB2 **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.	Physical Sciences/ Chemical Sciences
Dr. Sanat Kumar Das	**Title :** Quantification of Impact of Carbonaceous aerosols on the recent acceleration of 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 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 effects to quantify their contribution in enhanced atmospheric temperature over the Himalayas. The most challenging part of this work is to identify the dominating type and amount of carbonaceous aerosols with their source identification responsible for the Himalayan glacier melting, and find out a 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.	Physical Sciences/ Earth and Atmospheric Sciences
Dr. Sidharth Kumar Prasad	**Title :** Understanding the dynamics of small collision systems **Project Code:** SPK1 **Description:** One of the main goals of the relativistic nucleus-nucleus (A-A) collisions is to produce and characterize a system of strongly interacting deconfined quarks and gluons known as Quark Gluon Plasma (QGP). Proton-proton (p-p) and proton-nucleus (p-A) collisions at same centre of mass energies are performed to provide a baseline measurements for making final conclusions about the QGP formation in A-A collisions. Conventionally formation of QGP is not expected in p-p and p-A collisions due to small achieved energy densities in these collisions. However, in recent experimental measurements, some of the observables in high multiplicity events for these collision systems are found to resemble features similar to that in A-A collisions hinting towards the possible formation of medium in these collisions. Some of the other observables related to the phenomena of jet quenching (one of the most important signatures of QGP) in contrary, do not show the effect of presence of medium in these collisions. Whether the QGP like effect seen in small collision systems is really a final state effect due to QGP formation or it is a manifestation of some initial state effects or both is not yet conclusive. As a part of this research project we plan to investigate and study the particle production mechanism in small collision systems (p- p and p-A) at LHC energies by the measurements of hard probes and distributions of multiplicity, transverse momentum and energy of the	Physical Sciences

	produced particles in these collisions	
Dr. Sidharth Kumar Prasad	**Title :** Study of relativistic nuclear collisions using photons **Project Code:** SKP2 **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 photons at high transverse momentum.	Physical Sciences
Prof. Soumen Roy	**Title :** Statistical physics **Project Code:** SR1 **Description:** 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 theorems precisely quantify this probability. Our general understanding of phase transitions and critical phenomena is that there are (discontinuous) firstorder 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. 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. Our lab is interested in the application of statistical physics to diverse problems cutting across disciplines. Some of them are in the areas of inference, machine learning and artificial intelligence. We look forward to students who are eager to work in any or all of the above areas. If they wish, selected candidates are welcome to pursue this project with other projects/ of their choice conducted in our lab.	Physical Sciences/ Applied mathematics/ All engineering streams/ Computer Science
Prof. 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 nonlocal 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. We look forward to students who are eager to work in the above areas.	Physical Sciences/ Applied mathematics/ All engineering streams/ Computer Science

	If they wish, selected candidates are welcome to pursue this project with other projects/ of their choice conducted in our lab.	

Areas of Research: Chemical Sciences

Name of Faculty	Research Project	Desired Master's Background
Prof. Anirban Bhunia	**Title :** Unravelling the molecular mechanism of Amyloid fibril formation and designing of inhibitors **Project Code:** AB1 **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.	Chemical Sciences/ Life Sciences/ Biotechnology/ Microbiology/ Zoology/ Biochemistry/ Biophysics
Prof. Ajit Bikram Datta	**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:** Modification of proteins with ubiquitin is an important post-translational modification in eukaryotes. It has been frequently observed that aberrant ubiquitination leads to diverse pathological conditions that include neurological disorders as well as various types of cancers. Ubiquitination takes place via a concerted action of E1, E2 and E3 enzymes. 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 a second ubiquitin molecule significantly enhances their activity though the precise molecular events behind this phenomenon is yet to be understood. In this project we intend to understand the molecular basis of this activity enhancement by the second ubiquitin moiety.	Chemical Sciences/ Life Sciences
Prof. Ajit Bikram Datta	**Title :** Understanding the topology and functional diversity of branched ubiquitin chains **Project Code:** ABD2 **Description:** Ubiquitination is one of the most crucial post-translational mechanisms found conserved across all eukaryotes. Research have revealed that despite its primary role in proteostasis, ubiquitination also play diverse cellular roles in signaling, localization, transcription regulation etc. These diverse roles arise not only out of diverse substrate proteins that are modified by ubiquitin but also by differences in ubiquitin chain topologies. Initially though only homotypic ubiquitin chains were studied and characterized, recent research have shown various roles of mixed and branched	Chemical Sciences/ Life Sciences

	ubiquitin chains as well. In this project, we aim to look into topological differences of various such Ub chains that lead to differences in their function.	
Prof. Ajit Bikram Datta	**Title :** Understanding regulatory mechanism of RING E3 ligases **Project Code:** ABD3 **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 RING E3 ligases that are implicated in cancer.	Chemical Sciences/ Life Sciences
Dr. Abhijit Chatterjee	**Title :** India's Air Quality: Long-term variability, sources and future prediction **Project Code:** AC1 **Description:** Air pollution is one of the most critical threats to the Indians at the current scenario. The proposed study would be on an in-depth understanding of air pollution and air quality across the country through a long-term analysis. The major sources of poor air quality for different sectors will be addressed based on both the ground based and satellite-based observation. Source apportionment studies will be conducted for quantitative source contribution for each sources of air pollution over different sectors in India using a suitable source-receptor model. Future prediction would also be conducted based on long-term data for each of the sectors	Physical Science/ Chemical Sciences/ Earth and Atmospheric Sciences/ Environmental Sciences
Prof. Anup Kumar Misra	**Title :** Chemical synthesis 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.**	Chemical Sciences
Dr. Basudeb Maji	**Title :** Design and synthesis of small molecules and their anticancer application in triple negative breast cancer **Project Code:** BM1 **Description:** Synthetic small molecules are the most promising drug candidates for various human diseases. Small molecule anticancer drug covers more than 90% of the anticancer drugs. Despite the availability of promising and effective anticancer small molecule	Chemical Sciences

	drugs, triple negative breast cancer therapy is a huge challenge. Through systematic design and optimization, the molecule demonstrates selective targeting of cancer cells, inducing apoptosis and inhibiting tumor growth. In vitro and in vivo studies reveal its efficacy across diverse cancer types, with minimal impact on normal cells. The molecule's mechanism involves disrupting key signaling pathways critical for cancer survival. This breakthrough offers a promising avenue for the development of a new class of anticancer therapeutics, showcasing the potential for targeted, synthetic small molecules in advancing precision medicine for cancer treatment. We are working on developing a new approach for treating triple negative breast cancer with the help of synthetic small molecules. While most of the anticancer drugs inhibits biomolecular function, our strategy will not only inhibit the biomolecule like onco-proteins but will degrade them inside cancer cells. Thus, our strategy will have amplified activity compared to the conventional anticancer drugs. The candidate will get a chance to design and synthesize small molecule and test them for their biological activities in collaboration with the other members in the lab.	
Prof. 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.	Chemical Sciences (Preferably Organic Chemistry)
Prof. Debaraj Mukherjee	**Title :** Development of novel analogs of 3'-5'-linkedc-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	Chemical Sciences (Preferably Organic Chemistry/ Biochemistry)

	available starting materials, the role of these compounds in CDNs signaling will be investigated.	
Prof. Debaraj Mukherjee	**Title :** Rational design and synthesis of engineered Proteolysis-targeting chimeras for Yes-associated protein (YAP)/ transcriptional co-activator PDZ-binding motif (TAZ) degraders as anti-cancer agent **Project Code:** DM3 **Description:** Cancer contributes a broad spectrum of genetic disorders that can originate in nearly any organ or tissue in the body and is accompanied by abnormal cell growth (tumor) with the potential to proliferate out of control and metastasize to distant organs. YAP and TAZ have been identified as important regulators of tumorigenesis. In aggressive human cancers, YAP/TAZ is frequently upregulated and inhibition of YAP/TAZ by small molecules can be a good strategy to mitigate broad-spectrum cancers. These above molecules/ drugs sometimes bind irreversibly with target proteins, thus affecting conformational changes with mutation. Targeted protein degradation (TPD) is an area that has captured the attention of drug developers in recent years. A class of molecules that may enable such proteins to be modulated through TPD is known as PROTAC protein degraders. PROTAC can target multiple proteins for degradation in a catalytic manner with the help of ligase. Design and synthesis of PROTAC molecules against YAP/TAZ proteins is the objective of the project. Successful implementation of these experiments will not only prove the inhibitory activity of PROTAC but also establish it as a novel regulator of the YAP/TAZ signaling axis.	Chemical Sciences (Preferably Organic Chemistry/ Biochemistry)
Prof. Debaraj Mukherjee	**Title :** Role of Directing groups toward the metal-free stereoselective synthesis of 1-3 and 1-1 disaccharides **Project Code:** DM4 **Description:** 1-1 and 1-3 *O*/*S*-linked disaccharides have great importance in the field of glycobiology. In particular, 1-3 S-linked disaccharides have been extensively explored as mimetics of biologically active *O*-glycosides and act as a powerful tool to probe various biological processes. Besides 1-3 linked thiodisaccharides, 1-1 linked *O*-disaccharides were also found to have great potential in various biologically active compounds including anti-bacterial, anti-microbial active components, and various natural products such as maradolipids, trehalosamine, everninomicins, tunicamycin V, avilamycin A. Chemical synthesis of 1-1 O-linked disaccharide-like trehalose derivatives is more challenging as the stereochemistry of both the anomeric centers need to be controlled out of four possible diastereomers. It is always desirable if we can have a common donor and mild metal-free condition to access above mentioned glycosidic linkages stereo-selectively. Synthesis of C3-thio glycosylation is always difficult.The objective of the present project will be the development of the stereoselective synthesis of more challenging ax-eq 1-3 and eq-eq 1-1 *S* and *O* linked disaccharides under metal-free mild basic conditions at room temperature using directing group at C-2 position of sugar enol ether.	Chemical Sciences (Preferably Organic Chemistry)
Prof. Shubhra Ghosh Dastidar	**Title :** Investigating allostery and its thermodynamics of a,ß-tubulin, to develop drugs using molecular simulations and machine learning **Project Code:** SGD1 **Description:** The biological processes are outcome of the molecular level changes and those biomolecules are large composed of thousands of atoms. These macromolecules (e.g. proteins) experience continuous fluctuations of the atoms, go through conformational changes, bind with each other, dissociate form assemblies, pass	Chemical Sciences

	through membrane etc. Due to advancement of computing power it is possible to simulate such events in computer using the fundamental principles of Chemistry, in combinations of Biophysics and Biochemistry. Such large scale computational data, using high-performance computing facilities, can offer molecular mechanism of biological events. The latest methods like, machine learning, deep learning have been helping this work tremendously to understand how these macromolecules functions and how small molecule drugs could be planned and designed in order to interfere with their functions to treat a disease which might arise due to the malfunction of any such biomolecules. More specifically we will focus on a,ß-tubulin dimers and their assemblies, whose conformational dynamics have high significance in cancer therapy. The objectives of the work will be to obtain mechanistic insights into the molecular processes and for possible applications to develop ligands as promising drugs.	
Prof. Shubhra Ghosh Dastidar	**Title :** Designing allosteric inhibitors of Kinases using Molecular simulations and Machine learning. **Project Code:** SGD2 **Description:** Kinases are enzymes and are involved in numerous cellular pathways. The key of its functions is its transition from inactive to active conformations, which have only a subtle difference. The thermodynamic of this switch is a frontier area of investigation and that understanding can form the basis of designing drug molecule which can interfere with this inactive-active transfer process and ultimately can control a cellular machinery to cure a disease. Also, some ligands could be suitably designed to target sites on the kinases which are away from its ATP binding pocket and yet can remotely disturb the binding resulting the activity of the kinase to stop. Such remote site inhibitors are called allosteric inhibitors and could be kinase specific with least side effects. Such allosteric changes of the kinase could be predicted using the concept of normal model calculations. So, Kinase allostery itself is a laboratory for the chemists and Biophysicists to use their concept of to understand mechanism and for possible applications in drug design. In this project we will do this using large scale computer simulations and machine learning methods.	Chemical Sciences
Prof. Suman Kumar Banik	**Title :** Role of feedback loop in the quorum sensing network **Project Code:** SKB1 **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.	Physical Sciences/ Chemical Sciences
Prof. Suman Kumar Banik	**Title :** Signal transduction in mixed feed-forward loop motif **Project Code:** SKB2 **Description:** Small RNAs (sRNAs) controls gene regulation in bacteria via post-transcriptional modification of mRNAs. The	Physical Sciences/ Chemical Sciences

	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.	

Areas of Research: Life Sciences

Name of Faculty	Research Project	Desired Master's Background
Prof. Anirban Bhunia	**Title :** Unravelling the molecular mechanism of Amyloid fibril formation and designing of inhibitors **Project Code:** AB1 **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.	Chemical Sciences/ Life Sciences, Biotechnology, Microbiology/ Zoology/ Biochemistry/ Biophysics
Prof. Ajit Bikram Datta	**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:** Modification of proteins with ubiquitin is an important post-translational modification in eukaryotes. It has been frequently observed that aberrant ubiquitination leads to diverse pathological conditions that include neurological disorders as well as various types of cancers. Ubiquitination takes place via a concerted action of E1, E2 and E3 enzymes. 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 a second ubiquitin molecule significantly enhances their activity though the precise molecular events behind this phenomenon is yet to be understood. In this project we intend to understand the molecular basis of this activity enhancement by the second ubiquitin moiety.	Chemical Sciences/ Life Sciences
Prof. Ajit Bikram Datta	**Title :** Understanding the topology and functional diversity of branched ubiquitin chains **Project Code:** ABD2 **Description:** Ubiquitination is one of the most crucial post-translational mechanisms found conserved across all eukaryotes. Research have revealed that despite its primary role in proteostasis, ubiquitination also play diverse cellular roles in signaling, localization, transcription regulation etc. These diverse roles arise not only out of diverse substrate proteins that are modified by	Chemical Sciences/ Life Sciences

	ubiquitin but also by differences in ubiquitin chain topologies. Initially though only homotypic ubiquitin chains were studied and characterized, recent research have shown various roles of mixed and branched ubiquitin chains as well. In this project, we aim to look into topological differences of various such Ub chains that lead to differences in their function.	
Prof. Ajit Bikram Datta	**Title :** Understanding regulatory mechanism of RING E3 ligases **Project Code:** ABD3 **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 RING E3 ligases that are implicated in cancer.	Chemical Sciences/ Life Sciences
Dr. Abhrajyoti Ghosh	**Title :** Development of Genetic toolbox for plant growth promoting rhizobacteria Bacillus aryabhattai AB211 **Project Code:** ABG1 **Description:** *Bacillus aryabhattai* AB211 is a plant growth promoting, Gram-positive firmicute, isolated from the rhizosphere of tea (Camellia sinensis), one of the oldest perennial crops and a major non-alcoholic beverage widely consumed all over the world. The whole genome of B. aryabhattai AB211 was previously sequenced, annotated, and evaluated with special focus on genomic elements related to plant microbe interaction. Genome sequence comparisons between strain AB211 and other related environmental strains of *B. aryabhattai*, identified about 3558 genes conserved among all *B. aryabhattai* genomes. Most of the common genes involved in plant growth promotion activities were found to be present within core genes of all the genomes used for comparison, illustrating possible common plant growth promoting traits shared among all the strains of *B. aryabhattai*. Functional annotation of the genes predicted in the strain AB211 revealed the presence of genes responsible for mineral phosphate solubilization, siderophores, acetoin, butanediol, exopolysaccharides, flagella biosynthesis, surface attachment/biofilm formation, and indole acetic acid production, most of which were experimentally verified in our previous study. Genome analysis and experimental evidence suggested that AB211 has robust central carbohydrate metabolism implying that this bacterium can efficiently utilize the root exudates and other organic materials as an energy source. Based on the genome sequence information and experimental evidence as presented in previous study, strain AB211 appears to be metabolically diverse and exhibits tremendous potential as a plant growth promoting bacterium. In the present work we intend to develop a genetic toolbox for *B. aryabhattai* AB211. For this purpose, we would like to use an integration shuttle vector pHBintE (Shuttle vector E. coli/B.meg.), carrying a temperature sensitive origin of replication for *Bacillus megaterium* group of organisms, and selection marker erythromycin. Development of genetic toolbox for this organism will allow us to investigate the intricate interactions between AB211 and its host at the genetic and molecular levels.	Life Sciences

Dr. Abhrajyoti Ghosh	**Title :** Temperature-driven oligomeric dynamics of archaeal group II chaperonin: insights into protein homeostasis under extreme conditions **Project Code:** ABG2 **Description:** *Sulfolobus acidocaldarius*, a thermoacidophilic crenarchaeon, thrives in an extreme environment with temperatures of 75ºC and pH levels ranging from 2-3. In this harsh setting, maintaining protein homeostasis becomes a significant challenge due to the susceptibility of proteins to thermal stress-induced denaturation. Notably, Sulfolobus relies on only one group II chaperonin, Hsp60, *comprising* three subunits: α, β, and γ, to cope with these challenging conditions. The intriguing aspect lies in the dynamic nature of oligomeric complex formation among these subunits, which is temperature-dependent. At native temperatures, α and β subunits create a hetero-oligomeric complex. As the temperature decreases, a hetero-oligomeric complex involving α, β, and γ subunits forms, while at higher temperatures, only the β subunit assembles into a homooligomeric complex. This temperature-dependent variation prompts questions regarding the necessity of different oligomeric complexes within a single organism. Unravelling the mechanism behind oligomer formation raises key inquiries: How is this process regulated? What triggers the shift between complexes? Are there specific substrate recognition properties associated with each complex? Investigating these questions will not only shed light on the adaptability of *Sulfolobus* to extreme conditions but also contribute to our understanding of the broader cellular responses to thermal and environmental stress.	Life Sciences
Dr. Anupama Ghosh	**Title :** Investigating the virulence function of extracellular lipases in *Ustilago maydis* **Project Code:** AG1 **Description:** *Ustilago maydis* is a biotrophic plant pathogen that causes smut disease in maize recognized by formation of tumors on all the aerial parts of the plant. It uses a repertoire of secreted proteins to gain control over the host defense responses. This group of secreted proteins is broadly called pathogen effector proteins. In *U. maydis* the effector proteins can be categorized into two major classes based on whether they exhibit any specific functional domain or not. Majority of the secreted proteins belong to uncharacterized protein classes with no known domains and motifs. However, a relatively smaller population does exist with members showing specific enzymatic activity domains. This project aims to investigate the biological function of one of such enzymatic classes of *U. maydis* effector proteins, the lipases. Lipases are the enzymes that catalyse the hydrolysis of fats and release free fatty acids. Individual fatty acids in plants play important role in response against varied stress conditions including biotic stress. Through this project the contribution of *U. maydis* secreted lipases in regulating the fatty acid mediated stress response in maize plants during smut disease will be evaluated. Molecular techniques that will be applied for the study will include mostly recombinant DNA technology and Cell Biology techniques with some Biophysical techniques.	Life Sciences
Prof. Atin Kumar Mandal	**Title :** Praja1 ubiquitin ligase: Function and regulation in maintaining cellular proteostasis **Project Code: AKM1** **Description:** Ubiquitin ligases maintain balance of cellular	Life Sciences

	proteome by tagging ubiquitin to both normal and misfolded proteins for their clearance by the degradation machinery. Aberrant function or regulation of ubiquitin ligases are the roots of developmental disorders, cancer, and neurodegeneration. Praja1 (PJA1), a RING finger ubiquitin ligase promotes ubiquitination and degradation of polyQ proteins, Ataxin-3 and Huntingtin and reduces polyQ-associated pathogenesis. PJA1 also controls the turnover of aggregation-prone proteins such as TDP43, α-Synuclein, SOD1, and FUS. PJA1 ligase is highly enriched in brain tissue and acts as a mitigator of proteotoxic stress and serves as a crucial ubiquitin ligase of the brain proteome. Hence, dysfunction of PJA1 ligase might result in pathogenesis and onset of neurodegeneration. Therefore, identifying the function and regulation of PJA1 ligase in maintaining proteostasis network is crucial in defining strategies for therapeutic interventions against such debilitating diseases. Notably, PJA1 is upregulated in glioblastomas and gastrointestinal cancer and has been implicated in osteoblast differentiation and myogenesis.	
Prof. Jayanta Mukhopadhyay	**Title :** Mapping the interaction of d factor with RNA polymerase of *B. subtilis* **Project Code:** JM1 **Description:** Most bacterial RNA polymerases (RNAP) contain five conserved subunits viz. 2α, β, β' and ω. However, in many gram positive bacteria, especially in fermicutes, RNAP is associated with an additional factor, called δ. Over three decades since its identification, it had been thought that δ functioned as a subunit of RNAP to enhance the level of transcripts by recycling RNAP. In support of the previous observations, we also find that d is involved in recycling of RNAP by releasing the RNA from the ternary complex. However, we decipher a new function of d. Performing biochemical and mutational analysis we show that *Bacillus subtilis* δ binds to DNA immediately upstream of the promoter element at A-rich sequences on the *abrB* and *rrnB1* promoters and facilitates open complex formation. Our observations that δ does not bind to RNAP holo enzyme but is required to bind to DNA upstream of the -35 promoter element for transcription activation, suggest that δ functions as a transcriptional regulator. In this project, we aim to map the interaction of δ factor with RNA polymerase in the context of the holoenzyme and the elongation complex.	Life Sciences
Dr. Nirmalya Sen	**Title :** Role of Mitochondrial Dynamics in Cancer **Project Code:** NS1 **Description:** Mitochondria, often termed as the 'powerhouse' of the cells, plays important multifunctional roles in relation to cancer. Previous assumptions regarding dysfunctional mitochondria, aerobic glycolysis bias or impaired nuclear coded mitochondrial genes have been challenged repeatedly with evidence of i) non-mitochondrial driver gene mutations of K-ras, Myc, Pten or p53 up-regulating glycolysis, ii) retained mitochondrial respiration and ATP generating functions in various tumors and iii) decreased tumorigenesis upon dysregulation of core mitochondrial genes responsible for mitochondrial replication. The functionality of mitochondria in cancer cells beyond energy production ranges from redox homeostasis, cell death susceptibility, oxidative stress regulation, and amino acid metabolism, demarcating them as targets of the next-generation cancer therapeutics. Mitochondrial fusion and fission constitute mitochondrial dynamics in a cell. Paradoxically, Mito fusion/fission genes are often variably regulated in cancers. Various transcription factors and their	Life Sciences/ Molecular Biology/ Biochemistry/ Biotechnology and Allied subjects

	cofactors, like myc, Ras and PGC1-α/β, can act as master regulators of mitochondrial dynamics in specific cancer types. However, a universal transcriptional master regulator of mitochondrial dynamics in cancers is unknown. This project will focus on the following objectives: i) Study the role of transcription factors in regulating mitochondrial fusion and fission events during cancer progression ii) Identifying intervention strategies that alters mitochondrial dynamics during chemoresistance	
Prof. Shubho Chaudhury	**Title :** Change in phosphoprotein profile during pollen development in Arabidopsis **Project Code:** SC1 **Description:** We have investigated the role of plant specific HMG-box protein AtHMGB15 in pollen development. Our result indicated that athmgb15 mutant plants have defective pollen morphology and retarded pollen tube germination. Comparative transcriptomic study to decipher the role of AtHMGB15 in pollen development shows repression of JA biosynthesis and signalling in athmgb15 flowers. Further, preliminary analysis shows that AtHMGB15 acts as an transcriptional activator for the expression of two important master regulators of JA signalling, MYB21 and MYB24. MYBs are known to be the positive regulator of JA signalling for stamen and pollen development. However, JA signalling needs to be attenuated by regulating the transcriptional activity of MYBs. It is believed that additional stamen -specific factors plays an important role in regulating JA signalling. One way to identify the key signalling events (early signal components) may be to look for phosphoprotein profiling. This is the objective of the present study.	Life Sciences (Preferences: Biochemistry/ Microbiology/ Botany)
Dr. Subhash Haldar	**Title:** Role Of NLRP3 Mediated Inflammasome In Chemotherapy Drug Resistant Prostate Cancer. **Project Code:** SH1 **Description:** As per the worldwide cancer statistics in men, the second most cause of death due to malignancy is prostate cancer (PCa). In PCa, metastasis issue can be addressed by androgen deprivation therapy initially but over time patient may develop castrate-resistant PCa (CRPC) which have no curative treatment to date. It is very common practice of using chemotherapeutic agents to handle a wide variety of malignant cancers. While effective, some chemotherapeutic agents pose significant toxicity and patients gradually develop resistance against the drugs during the treatment period, as a result tumor relapse takes place. It is well established that inflammation is associated with the progression of tumorigenesis and carcinogenesis. Inflammasomes consist of certain multi-protein complexes which produces numerous inflammatory reactions inside the cells that is perilous for maintaining homeostasis. NOD like receptor protein 3 (NLRP3) binds and activates caspase-1 that triggers the maturation of inflammatory cytokines including IL-1β and IL-18, which are responsible for initiation of inflammatory response. Inflammasome components and pathways may provide novel targets to treat inflammation and associated cancer. As a result of chemotherapeutic treatment, cancer cells secret many factors through the activation of the inflammasome, where IL-1β and IL-18 play important role. Because of their pro-inflammatory nature, they share certain pro-proliferating signaling responsible for cancer progression. So, it would be important to examine the signaling pathways involved during chemotherapy resistant prostate cancer progression in connection with inflammasome activation.	Life Sciences

Dr. Subhash Haldar	**Title :** Epigenetic Regulation, Aging, And Cancer Risk **Project Code:** SH2 **Description:** Aging is a universal biologic process accompanied by a series of prominent hallmarks, including genetic and epigenetic alterations in cells. The aging-associated epigenetic changes include DNA methylation, histone modifications, and chromatin remodeling, which can affect the accessibility of DNA to transcription factors and RNA polymerase, ultimately leading to changes in gene expression and these alterations can contribute to the development of diseases including cancer. However, very limited studies available regarding epigenetic alteration mediated aging factors involved in different chemotherapy resistant cancers. To find out epigenetic alterations mediated aging factors involved in tumor progression, metastasis, and in chemotherapy-resistant cancer, it is pertinent to identify the epigenetically silenced/activated genes involved after and before the treatment with chemotherapeutic drugs and to check the mechanisms involved in such silencing/activation of genes expression. Understanding the factors involved in epigenetic changes in both cultured cells and patient's samples will provide a therapeutic strategy against chemotherapy-resistant cancer.	Life Sciences
Prof. Soumen Roy	**Title :** Systems biology of macromolecular interactions **Project Code:** SR3 **Description:** 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. Many of our theoretical predictions have been experimentally verified. Our research is strongly guided by theoretical (mathematical and computational) investigations. The ideal candidate is expected to use both theoretical and experimental techniques in course of his research. Experiments would 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
Prof. Soumen Roy	**Title :** Microbial systems biology **Project Code:** SR4 **Description:** Recently published and ongoing projects in our lab are in the areas of: (1) phage-bacteria interactions and dynamics, and, (2) antimicrobial resistance. In the recent past, we have unraveled the phenomenon of secondary host lethality in mycobateria, which has a strong bearing for phage therapy. Further, emplying both experimental and theoretical techniques in conjunction, we have formulated a rigorous mathematical approach to mutations and mutagenesis, and how phenotypes are influenced as a result of mutations. Our research is strongly guided by theoretical (mathematical and computational) investigations. The ideal candidate is expected to use both theoretical and experimental techniques in course of his research. Experiments would 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

Prof. Srimonti Sarkar	**Title :** Understanding the Assembly of the Proteasomal Lid of the Human Pathogen *Giardia Lamblia* **Project Code:** SRS1 **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 the substrate's access to the CP. RP assembly is well-coordinated, with the formation of intermediate subcomplexes. Previous results indicate that *Giardia*'s RP assembly process differs from its human host's. 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
Dr. Wriddhiman Ghosh	**Title :** Geomicrobiology of the minerologically peculiar hot springs of the Indian Trans-Himalayas **Project Code:** WG1 **Description:** Our Geomicrobiology Group is engaged in revealing the in situ metabolisms, ecosystem constraints and opportunities, and geochemical manifestations, of microorganisms within ecosystems having extreme physicochemical conditions. One major habitat explored in that direction is the geochemically-special (pH-neutral, silica-poor, but boron-, sulfide-, sulfate- and thiosulfate-rich) hot spring systems of the Trans-Himalayan regions of eastern Ladakh, India. Methodologically, our investigations at the cross-roads of microbiology and geochemistry are conducted at various organizational levels of life ranging from biomacromolecules, genes/proteins, metabolic pathways, genomes and cell systems, to populations, metagenomes, communities and ecosystems. Outcomes of our studies have implications for understanding early metabolism, ancient ecosystems, origin of life, and habitability of biophysically-extreme biomes on Earth, as well as potential extra-terrestrial locations.	Life Sciences

Areas of Research: Environmental Sciences

Name of Faculty	Research Project	Desired Master's Background
Dr. Abhijit Chatterjee	**Title :** India's Air Quality: Long-term variability, sources and future prediction **Project Code:** AC1 **Description:** Air pollution is one of the most critical threats to the Indians at the current scenario. The proposed study would be on an in-depth understanding of air pollution and air quality across the country through a long-term analysis. The major sources of poor air quality for different sectors will be addressed based on both the ground based and satellite-based observation. Source apportionment studies will be conducted for quantitative source contribution for each sources of air pollution over different sectors in India using a suitable source-receptor model. Future prediction would also be conducted based on long-term data for each of the sectors	Physical Science/ Chemical Sciences/ Earth and Atmospheric Sciences/ Environmental Sciences

Dr. Sanat Kumar Das	**Title :** Quantification of Impact of Carbonaceous aerosols on the recent acceleration of 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 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 effects to quantify their contribution in enhanced atmospheric temperature over the Himalayas. The most challenging part of this work is to identify the dominating type and amount of carbonaceous aerosols with their source identification responsible for the Himalayan glacier melting, and find out a 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.	Physical Sciences/ Earth and Atmospheric Sciences