## BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Nicholas Noinaj

eRA COMMONS USERNAME (credential, e.g., agency login): noinajn

POSITION TITLE: Associate Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

| INSTITUTION AND LOCATION | DEGREE | Completion Date MM/YYYY | FIELD OF STUDY |
|---|---|---|---|
| Berea College, Berea, KY | BA/BA | 08/2003 | Chemistry/Mathematics |
| Univ of Kentucky College of Medicine, Lexington, KY | PhD | 08/2008 | Biochemistry |
| NIDDK, NIH, Bethesda, MD | Postdoc | 2008-2014 | Membrane protein crystallography |

### A. Personal Statement

Infectious diseases cause widespread sickness and death throughout the world each year and are the second leading cause of death, particularly in underdeveloped countries. And with the emergence of multidrug resistance strains of Gram-negative bacteria, the necessity for new, more effective, and more sustainable therapies is immediate and vital to protect against any future pandemics. **My lab focuses on studying membrane proteins and protein complexes that are promising targets for the development of new therapies (both antibiotics and vaccine) against these multidrug resistant pathogens**. In doing so, much of our attention lies in surface proteins found within the outer membranes of the bacteria, which often serve essential roles in mediating pathogenesis.

One major focus of my lab is the study of the biogenesis of membrane proteins in Gram-negative bacteria, where the outer membrane contains a host of beta-barrel proteins commonly called outer membrane proteins (OMPs). My lab has been instrumental in structurally and functionally characterizing the beta-barrel assembly machinery (BAM) which folds and inserts the new OMPs into the outer membrane. BAM is conserved across all Gram-negative bacteria and is essential for viability. Exactly how BAM is able to accomplish its function remains unknown, however, my lab has solved the structure of the fully assembled BAM complex from *E. coli*, which has revealed unprecedented conformational changes with the BamA protein. We have also solved a series of structures of BAM in complex with EspP, OmpT, and OmpA, revealing an unprecedented budding mechanism for OMP biogenesis. In unpublished studies, we have also determined the structure of fully assembled BAM from *N. gonorrhoeae*, alone and in complex with novel inhibitors.

Another focus of my lab are metal-acquisition systems, particularly in Neisseria, including the transferrin binding protein (Tbp) complex, the lactoferrin binding protein (Lbp) complex, and the calprotectin binding protein TdfH zinc transporter. Scavenging iron from transferrin, the Tbp complex consists of two receptors called TbpA and TbpB, both virulence factors mediating pathogenesis in Neisseria; with the Lbp system (scavenging from lactoferrin) being analogous to the Tbp system. As a postdoc, I determined the first structures of the related proteins TbpA and TbpB from *N. meningitidis*, both in complex with human transferrin. However, many critical mechanistic details about iron piracy remain unanswered. We aim to fill this long-standing gap in our understanding of the Tbp system, which will also better equip us on how to combat Neisserial infections. We are currently structurally characterizing complexes of TbpA and TbpB in complex with transferrin, having recently collected several important preliminary datasets of TbpA+TbpB complexes which serve as the basis for a new paradigm for how the Tbp/Lbp system function mechanistically. Our goal is to use our structural and functional studies to support current efforts at targeting these systems for therapeutics including new antibiotics and vaccines.

**B. Positions, Scientific Appointments, and Honors**

**Positions and Employment**

2019 – pres Associate Professor, Purdue University, Department of Biological Sciences
2014-2019 Assistant Professor, Purdue University, Department of Biological Sciences
2013-14 Research Fellow, NIDDK/NIH, Dr. Susan Buchanan

**Other Experience and Professional Memberships**

2020-pres Protein Society
2020-pres Biophysical Society
2008 Member of the Delta Epsilon Iota Academic Honor Society
2012 American Society for Microbiology
2006-pres American Crystallographic Association

**Honors**

2022 Team Award/Diversity Award, College of Science, Purdue University
2020 Excellence in Research Award, Purdue University
2019 Showalter Faculty Scholar, College of Science, Purdue University
2019 Mentoring Award, College of Science, Purdue University
2018 Excellence in Research Award, College of Science, Biological Sciences, Purdue University
2017 Team Award, College of Science, Purdue University
2013 Fellows Award for Research Excellence (FARE) Award Winner
2012 Fellows Award for Research Excellence (FARE) Award Winner
2008 Member of the Delta Epsilon Iota Academic Honor Society
2007 X-Ray Methods in Structural Biology, Cold Spring Harbor Laboratory (Full Scholarship)
2006 Best Poster - University of Kentucky Molecular and Cellular Biochemistry Symposium
2006 American Crystallographic Association Annual Meeting Travel Award
2004 National Institute on Drug Abuse (NIDA) Training Grant (2-years)
2006 National Institute on Drug Abuse (NIDA) Training Grant (2-years)
2003 Class of 1953 Chemistry Scholarship Award, Berea College 2004

**Conference/Meetings**

2023 BPS Annual Meeting: San Diego, CA (Selected talk)
2022 EMBO Workshop: Protein translocation across membranes, Girona, Spain (Selected talk)
2022 Dept. of Biochemistry Retreat, Univ. of Indiana (Invited talk)
2022 Hitchhiker's Guide to the Biomolecular Galaxy symposium, Purdue Univ.
2022 15th Annual Midwest Protein Folding, Assemblies symposium, Notre Dame
2022 Gordon Research Conference - Protein Transport Across Membranes (Invited talk)
2021 Hitchhiker's Guide to the Biomolecular Galaxy symposium, Purdue Univ. (Invited talk)
2020 Lorne Research Conference (45$^{th}$) on Protein Structure and Function, Lorne, Australia
2019 Hitchhiker's Guide to the Biomolecular Galaxy symposium, Purdue Univ.
2019 14th Annual Midwest Protein Folding symposium, Notre Dame
2019 Missouri Symposium in Molecular Biophysics, Univ. of Missouri
2018 Purdue CryoEM Symposium, Purdue Univ.
2018 Hitchhiker's Guide to the Biomolecular Galaxy symposium, Purdue Univ.
2018 13th Annual Midwest Protein Folding symposium, Notre Dame
2018 Gordon Research Conference - Protein Transport Across Membranes (Invited talk)
2017 American Crystallographic Association Meeting (Invited talk)
2017 Tessman symposium, Purdue Univ.
2017 Hitchhiker's Guide to the Biomolecular Galaxy symposium, Purdue Univ.
2017 12th Annual Midwest Protein Folding symposium, Notre Dame
2016 Zing Conference – Protein Secretion Across Membranes
2016 FASEB Meeting – Molecular Biophysics of the Membrane (Invited talk)
2016 11$^{th}$ Annual Midwest Protein Folding symposium, Notre Dame (Plenary talk)
2015 Membrane Proteins Symposium at APS/Argonne IL
2014 International Union of Crystallography (Invited talk)
2014 American Crystallographic Association (Invited talk)

2014 Gordon Research Conference - Protein Transport Across Membranes (Invited talk)
2014 44th Mid-Atlantic Macromolecular Crystallography meeting (Invited talk)
2013 Janelia Farm Symposium – Structure determination of membrane proteins (Invited talk)
2013 Annual ASBMB Meeting, Boston, MA
2013 MPIG/SBIG Postdoc Symposium (Invited talk)
2012 American Crystallographic Association (Two Invited talks)
2012 Gordon Research Conference – Protein Transport Across Membranes
2012 Gordon Research Conference – Ligand Recognition and Molecular Gating (Invited talk)

## C. Contributions to Science

1. During the first few years of my postdoctoral studies, I wanted to study membrane proteins using X-ray crystallography due to their importance in biology and since they are very challenging. Therefore, I began working on the receptor transferrin binding protein A (TbpA) from *Neisseria meningitidis* to determine how it interacts with human transferrin to mediate iron hijacking and pathogenesis. Here, I was able to determine the structure of TbpA bound with human transferrin, identifying residues important for receptor binding and iron extraction and import. I also determined the crystal structure of the Neisserial co-receptor TbpB and used SAXS analysis to determine the structure of the complex with human transferrin. Since being at Purdue, we have now solved additional structures of the Tbp system, and structure of other metal import machineries. These studies significantly advanced our understanding of how these receptors are able to specifically bind metal binding human proteins, extract their metals and import them across the Neisserial outer membrane for survival during infection within the human host.
    a. **Noinaj N**, Easley N, Oke M, Mizuno N, Gumbart JC, Boura E, Steere A, Zak O, Aisen P, Tajkhorshid E, Evans RW, Gorringe AR, Mason AB, Steven AC, and Buchanan SK. (2012). Structural basis for iron piracy in pathogenic Neisseria, *Nature* (Research Article), 483 (7387):53-8.
    b. Yadav R, **Noinaj N**, Ostan N, Moraes T, Stoudenmire J, Maurakis S, Cornelissen CN. (2020). Structural Basis for Evasion of Nutritional Immunity by the Pathogenic Neisseriae. *Front Microbiol*. 2020 Jan 10;10:2981.
    c. Yadav, R, Govindan, S, Daczkowski, C, Mesecar, A, Chakravarthy, S, and **Noinaj, N**. (2021). Structural Insight into the dual function of LbpB in mediating Neisserial pathogenesis. *eLife*. 10:e71683.
    d. Bera AK, Wu R, Harrison S, Cornelissen CN, Chazin WJ, **Noinaj N**. (2022). TdfH selectively binds metal-loaded tetrameric calprotectin for zinc import. *Commun Biol.* 2022 Jan 31;5(1):103.

2. Midway into my postdoctoral studies, I became involved in a project aimed at determining the crystal structure of neurotensin receptor 1 (NTS1), a GPCR that is the receptor for the neuropeptide neurotensin. I was able to determine the structure of NTS1 which was the first GPRC of its class, which revealed exactly how the peptide interacts with the receptor for downstream conformational changes and signaling. With many structures now available for different classes of GPCRs, we were able to contribute the first from this class which showed how the endogenous substrate binds.
    a. White JF, **Noinaj N**, Shibata Y, Love J, Kloss B, Xu F, Gvozdenovic-Jeremic J, Shah P, Shiloach J, Tate CG, Grisshammer R. (2012). Structure of the agonist-bound neurotensin receptor NTS1. *Nature* (Research Article), 490 (7421):508-513.

3. During the later stages of my postdoctoral studies, I began to make progress on my primary project, to determine the crystal structure of BamA, an essential outer membrane protein in Gram-negative bacteria required for the biogenesis of all outer membrane proteins, in particular, virulence factors for pathogenic strains. Over the course of several years, I was able to determine the crystal structure of BamA from *Neisseria gonorrhoeae* and *Haemophillius ducreyi*. These structures significantly advanced our knowledge of how it, as the core of a larger complex called the BAM complex, it is able to fold and insert nascent outer membrane proteins into the outer membrane. From the structures, we were able to propose a mechanism whereby a lateral opening into the membrane is required for direct insertion. Crosslinking experiments further verified this mechanism which has served as the basis for now testing how this folding/insertion occurs. Given the essential role of BamA, these studies have a huge impact on how these bacteria are able to survive and mediate pathogenesis. While at Purdue University, my lab has solved the structure of

the assembled BAM complex, providing high resolution details about the binding interfaces of the individual components with one another, and providing the first structure to suggest that binding of BamCDE may regulate BamA by inducing an unprecedented conformational change of the barrel domain of BamA, which primes the barrel in an activated state for insertion. Currently our lab studies BAM from E*. coli*, *Neisseria gonorrhoeae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Fucobacterium nucleatum*.

a. Lundquist K, Bakelar J, **Noinaj N**, Gumbart JC. (2018). C-terminal kink formation is required for lateral gating in BamA. *PNAS*. 115(34):E7942-E7949.
b. **Noinaj N**, Kuszak AJ, Gumbart JC, Lukacik P, Chang H, Easley NC, Lithgow T, and Buchanan SK. (2013). Structural insight into the biogenesis of β-barrel membrane proteins. *Nature* (Research Article), 501(7467):385-90.
c. Bakelar J, Buchanan SK, **Noinaj N**. (2015). The structure of the β-barrel assembly machinery complex. *Science* 351(6269):180-6.
d. Wu R, Bakelar JW, Lundquist K, Zhang Z, Kuo KM, Ryoo D, Pang YT, Sun C, White T, Klose T, Jiang W, Gumbart JC, **Noinaj N**. (2021). Plasticity within the barrel domain of BamA mediates a hybrid-barrel mechanism by BAM. *Nat Commun*. 2021 Dec 8;12(1):7131.

4. I continue to collaborate on another project to structurally characterize the Ton complex, which acts as an energy transducing machine within the inner membrane of Gram-negative bacteria to provide energy to drive ligand gating at the outer membrane. While here at Purdue, I was able to solve the structure of the complex which is the first of this complex, composed of a pentamer of ExbB and a single ExbD within the pore. We went on to fully characterize the fully assembled Ton complex with other methods including EM, DEER, crosslinking, and electrophysiology to show it consist of a pentamer of ExbB, a dimer of ExbD and a single TonB. My lab continues to collaborate on this project, working towards determining the full structure of the Ton complex bound with a TonB-dept transporter.
    a. Celia H[*], **Noinaj N[*1]**, Zakharov SD, Bordignon E, Botos I, Cramer WA, Lloubes R, and Buchanan SK. (2016). Structural insight into the role of the Ton complex in energy transduction. *Nature* 538(7623):60-65.
    b. Celia H, **Noinaj N**, Buchanan SK. (2020). Structure and Stoichiometry of the Ton Molecular Motor. Int J Mol Sci. 2020 Jan 7;21(2).

5. Protein trafficking across membranes is an essential function in cells; however, the exact mechanism for how this occurs is not well understood. In the endosymbionts, mitochondria and chloroplasts, the vast majority of proteins are synthesized in the cytoplasm as preproteins and then imported into the organelles via specialized machineries. In chloroplasts, protein import is accomplished by the TOC (translocon on the outer chloroplast membrane) and TIC (translocon on the inner chloroplast membrane) machineries in the outer and inner envelope membranes, respectively. TOC mediates initial recognition of preproteins at the outer membrane and includes a core membrane channel, Toc75, and two receptor proteins, Toc33/34 and Toc159, each containing GTPase domains that control preprotein binding and translocation. Progress in the field has been hindered by the lack of structural information on the Toc proteins. Our goal is to use X-ray crystallography and cryoEM to structurally and functionally characterize the full TOC complex. Recently, we determined the structure of the POTRA domains of Toc75, the core component of Toc75. And in more recent work, we can now isolate the TOC complex from plants and working to improve purity for structural studies using cryo-EM. Additionally, we just recently solved the structure of the soluble domain from Sam50 from *P. falciparum* (malaria) and working to isolate the full complex for structural studies.
    a. O' Neil P, Richardson LGL, Paila YD, Piszczek G, Chakravarthy S, **Noinaj N**, Schnell DJ. (2017). The POTRA domains of Toc75 exhibit chaperone-like function to facilitate import into chloroplasts. PNAS, 114(24):E4868-E4876.

Complete List of Published Work in My Bibliography:
http://www.ncbi.nlm.nih.gov/sites/myncbi/1redk8eN4_C5u/bibliography/47938167/public/?sort=date&direction=descending

## BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Dubey, Shubham

eRA COMMONS USER NAME (credential, e.g., agency login): DUBEY6

POSITION TITLE: Graduate Student

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

| INSTITUTION AND LOCATION | DEGREE *(if applicable)* | Start Date MM/YYYY | Completion Date MM/YYYY | FIELD OF STUDY |
|---|---|---|---|---|
| Banaras Hindu University (India) | B.Sc | 08/2013 | 05/2016 | Botany (Honors), Zoology, Chemistry and Geology |
| Indian Institute of Technology, Roorkee (India) | M.Sc. | 08/2016 | 05/2018 | Biotechnology |
| Purdue University | PHD | 08/2019 | In progress | Biological Sciences |

### A. Personal Statement

In my opinion, the most challenging and intriguing aspect of science is to understand the mechanism of the physiological process. It not only amazes us with the diversity which exists among the organism but also allows us to exploit them to cure deadly diseases. In particular, the structure of biomolecules has always been fascinating to me where I can see what is happening at the atomic scale. I started my research journey as an undergraduate research assistant in an ecology lab where derived an equation to calculate the below-ground biomass which can be used to calculate the carbon footprint of tropical forest. During this study, I realized the importance of mathematical equations in the real world and became more interested in the pragmatic aspect of biological sciences. So, I decided to pursue my master's degree in biotechnology. I was awarded the fellowship provided by 'The Department of Biotechnology (DBT, India)' to pursue my degree from IIT, Roorkee. Here I found my interest in biophysics courses which motivated me to join a structural biology lab. After joining the lab, I started following the big discoveries happening in the field and became acquainted with the work of Dr. Noinaj while I was preparing for a lab presentation. I completed my degree with the dream to continue in academia and decided to do research in the field of structural biology.

I joined the Ph.D. program at Purdue University in the structural and computational biology and biophysics cluster of the Department of Biological Sciences. In my first two years, I have taken various biophysics, structural biology, and computational biology core courses which will strengthen my base to pursue research in this field. After I finished my rotation, I joined the lab of Dr. Noinaj where I can implement my previous knowledge and learn new techniques to answer significant biological questions pertaining to bacterial pathogens. I am fortunate to be associated with the multicultural and internationally collaborative graduate program. I believe as an international student that T32 Molecular Biophysics and Training Program will strengthen and complement my current research conduit.

### B. Positions and Honors

**Positions and Employment**

2015 Undergraduate Research intern, Banaras Hindu University
2015 Undergraduate Research Assistant, Banaras Hindu University
2016 Summer Research intern, Indian Institute of Science.

2017 Graduate research assistant, Indian Institute of Technology
2018 Project Assistant, Regional Center for Biotechnology
2019- Graduate Researcher, Purdue University

**Professional Memberships**

2019-2020 Member, American Crystallographic Association

**Academic and Professional Honors**

2014 Gold medal in the college oratory competition.
2015 Excellence award for outstanding academic performance.
2016-2018 Department of Biotechnology Fellowship for Post-graduation studies
2017 Winner of cultural event, Biotechnology Day (IIT Roorkee)
2018 Junior Research Fellowship (RCB, UNESCO)
2018 Ph.D. fellowship at Umea University, Sweden
2019 P. T. Gilham award for excellent academic achievement, Purdue University
2019-2021 Teaching Assistant, Purdue University Department of Biological Sciences

**C. Contributions to Science**

1. **Previous Research and related experiences**: My undergraduate work has been slightly different from my current research field, but the basic knowledge of chemistry, microbiology, cell biology, and mathematics has helped me a lot to succeed in my biophysics research. In my master's I worked as a summer intern in a cancer research laboratory where I learned cell biology techniques. Through the multiple recombination and cloning techniques, we investigated the presence of homologous recombination (HR) in mitochondria which helps in maintaining its genomic integrity. The process is very important because mitochondrial DNA is exposed to oxidative damage very frequently, in comparison to nuclear DNA. Our work has been published in the peer journal of cell biology. For the partial fulfillment of my degree, I worked on a project where I was trying to characterize the enzyme Deoxyhypusine synthase from 'Cryptosporidium parvum' and I also proposed potent inhibitors against this enzyme through my *in silico* studies. I presented this work at the American Chemical society Seminar at IIT, Roorkee. I also attended and organized multiple workshops during this period hosted by the institute. After completing my master's worked as a project assistant in the Laboratory of Plant-Microbe Interactions where I learned next-generation sequencing and applied my computational skills in the project to propose a biological switch that helps sugar transporter protein-13 to acquire natural resistance from Powdery Mildew disease. This work has also been published international journal of plant physiology.
    a. Dahal S, **Dubey S**, Raghavan SC. Homologous recombination-mediated repair of DNA double-strand breaks operates in mammalian mitochondria. Cell Mol Life Sci. 2018
    b. **Dubey S**, and Chaudhary N. Pharmacophore modeling and virtual screening: search of new inhibitor for DHS in crypto disease. American Chemical Society, Seminar, IIT Roorkee, 2018
    c. Megha Gupta, **Dubey S**, Deepti Jain, Divya Chandran, The *Medicago truncatula* Sugar Transport Protein 13 and Its Lr67res-Like Variant Confer Resistance in Legumes via Defense Modulation, *Plant and Cell Physiology*, 2021

2. **Graduate Research and related experiences**: My current research work with Dr. Noinaj is focused on membrane proteins. My project requires a multidisciplinary approach to address the iron transport mechanism in *N. gonorrhoeae* and *N. meningitidis.* The iron transport is unique in this bacterium because it does not secrete siderophores, instead extract iron from the human proteins such as Transferrin (Tf), Lactoferrin (Lf), hemoglobin, etc. The hTf iron acquisition system is the most crucial for *Neisseria* because the knockout strains of this system show no infection in the mice model. I am looking forward to revealing the mechanism adopted by the bacteria to extract iron from the human protein. I will apply my structural and biophysical knowledge to answer the question. I am always interested in attending and presenting in seminars, and workshops. This will help me to develop my presentation skills. I am also looking forward to being part of organizing committees at the department events. This will improve my communication and network building skills.

**D. Additional Information: Research Support and/or Scholastic Performance**

| YEAR | COURSE TITLE | GRADE |
|---|---|---|
| | Banaras Hindu University | |
| 2013 | Cryptograms | A |
| 2013 | Lab Work based on Course: Cryptograms | S |
| 2013 | Structure, Bonding and Organic Chemistry | A |
| 2013 | Chemistry Practical I: Quantitative Analysis, Practical II: Qualitative Analysis | C |
| 2013 | Animal Diversity and Fundamentals of Cell Biology | B |
| 2013 | Lab exercises based on Course Animal Diversity and Fundamentals of Cell Biology | B |
| 2014 | Elements of Geology - I | A |
| 2014 | Microbiology, Plant Pathology, Cytology & Genetics | A |
| 2014 | Lab work based on Course: Microbiology, Plant Pathology, Cytology & Genetics | A |
| 2014 | Inorganic Chemistry - I & Physical Chemistry - I | A |
| 2014 | Chemistry Practical I & II | C |
| 2014 | Animal Form and Function & Elementary Biochemistry | A |
| 2014 | Exercises based on course: Animal Form and Function & Elementary Biochemistry | A |
| 2014 | Ecology and Physiology | A |
| 2014 | Lab work based on Course: Ecology and Physiology | A |
| 2014 | Basic Genetics & Evolution, Economic Zoology | A |
| 2014 | Lab exercises based on course: Basic Genetics & Evolution, Economic Zoology | B |
| 2014 | Organic Chemistry – II, Physical Chemistry - II | B |
| 2014 | Chemistry Practical – III: Quantitative Analysis, Practical IV: Qualitative Organic | A |
| 2015 | Elements of Geology - II | A |
| 2015 | Phanerogams | A |
| 2015 | Lab work based on course: Phanerogams | A |
| 2015 | Fundamental Endocrinology and Developmental Biology | B |
| 2015 | Lab work based on course: Fundamental Endocrinology and Developmental Biology | A |
| 2015 | Inorganic Chemistry – II, Organic Chemistry - III | A |
| 2015 | Practical – III: Quantitative Analysis/ IV: Qualitative Organic Analysis/ Preparations | B |
| 2015 | Comparative studies of Cryptograms | A |
| 2015 | Comparative studies of Phanerogams | A |
| 2015 | Plant Ecology and Toxicology | S |
| 2015 | Lab Work based on Course: Comparative studies of Cryptograms | S |
| 2015 | Lab Work based on Course: Comparative studies of Phanerogams | A |
| 2015 | Lab Work based on Course: Plant Ecology and Toxicology | S |
| 2015 | Field Study | A |
| 2016 | Plant Metabolism, Biochemistry and Biotechnology | A |
| 2016 | Microbiology and Plant Pathology | A |
| 2016 | Cytogenetics and Evolutionary Processes | B |
| 2016 | Lab work based on Course: Plant Metabolism, Biochemistry and Biotechnology | B |
| 2016 | Lab work based on Course: Microbiology and Plant Pathology | A |

| | | |
|---|---|---|
| 2016 | Lab work based on Course: Cytogenetics and Evolutionary Processes | C |
| 2016 | Dissertation Based on Review | S |

Indian Institute of Technology, Roorkee

| | | |
|---|---|---|
| 2016 | Computer Applications | B |
| 2016 | Biochemistry | B+ |
| 2016 | Biotechnology Laboratory I | B+ |
| 2016 | Applied Microbiology | B+ |
| 2016 | Genetics and Molecular Biology | B |
| 2016 | Cell and Developmental Biology | A |
| 2017 | Molecular Biophysics | A |
| 2017 | Immunology and Immunotechnology | B+ |
| 2017 | Biotechnology Laboratory - II | B+ |
| 2017 | Technical Communication | B+ |
| 2017 | Transgenic animal technology | B+ |
| 2017 | Research Methods in Bionanotechnology | A |
| 2017 | Biophysical Techniques | A |
| 2017 | Genetic Engineering | B+ |
| 2017 | Seminar | B+ |
| 2017 | Biotechnology Laboratory III | A |
| 2017 | Structural Biology | B+ |
| 2017 | Chemical Genetics and Drug Discovery | B |
| 2018 | Project | B+ |
| 2018 | Bioinformatics | B+ |

PURDUE UNIVERSITY

| | | |
|---|---|---|
| 2019 | Methods and Measurements in Biophysical Chemistry | A- |
| 2019 | Seminar Methods Prof Development I (Ethics in Research) | A |
| 2019 | Biological Research Methods (Rotation) | P |
| 2019 | Biological Research Methods (Rotation) | P |
| 2019 | Structural Biology Research Seminar | A |
| 2019 | Computing for Life Sciences | A |
| 2020 | CryoEM 3D Reconstruction | A+ |
| 2020 | X-Ray Crystallography | A- |
| 2020 | Seminar Methods Prof Development II (Professional Development) | A |
| 2020 | Biological Research Methods (Rotation) | P |
| 2020 | Biological Research Methods (Rotation) | P |
| 2020 | Research PhD Thesis | S |
| 2020 | Research PhD Thesis | S |
| 2020 | Grant Writing | A |
| 2020 | Microscopy for Life Scientists | A |
| 2020 | Research PhD Thesis | S |

Banaras Hindu University's undergraduate program and Indian Institute of Technology Master's program consider an "E" or above a passing grade and B+ as distinction in the subject. S represents the superlative grade with 100% marks.

The Department of Biological Sciences Graduate Program at Purdue considers a “B” or above to be a passing grade; however, a maximum of one C is allowed throughout the duration of the program. Rotations are evaluated as pass (P) or fail (F), and research credits are assessed as satisfactory (S) or unsatisfactory (U).