

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: Christina R. Bourne

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

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 (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
University of Oklahoma, Norman OK	BS	05/1997	Biochemistry
Oklahoma Medical Research Foundation and OU Health Sciences Center, Oklahoma City OK	PhD	10/2003	Biochemistry, Mol Biol and Structural Biology
OU Health Sciences Center, Oklahoma City OK	Postdoctoral Fellow	10/2007	Structural Virology

A. Personal Statement

I have more than 20 years of experience in biochemistry and structural biology, including 15 years working in microbiology and antibacterial development. My research interests focus on targeting drug-resistant and chronic bacterial infections, and I am especially motivated to develop innovative new methods and novel targets to control bacterial growth.

I have built my independent research program to study Toxin Antitoxin systems (publications a-c), including a strong mentoring philosophy that shapes a productive team. These are challenging proteins to produce and work with, and my team has gained significant expertise. We have identified a protective effect to anti-gyrase antibiotics, including fluoroquinolones, mediated by a chromosomal ParE-type toxin (publication a). An important finding from this work was the concentration-dependence of toxin phenotypes, introducing a new concept in the field - that toxin effects can be attenuated by concentration and exposure time. This strongly suggests that chromosomally-encoded TA systems could be integrated into pro-survival pathways in bacterial cell physiology. We have also compared the toxicities of different ParE toxins following over-expression in *E. coli*. This has allowed for the first time a direct comparison within the family (publication b). We have also focused on the interaction of the ParE toxin with its cognate ParD antitoxin, and recently identified a key position that can greatly weaken the kinetics of interaction (publication c). This demonstrates a feasible strategy for manipulation of these systems to impact bacterial cell growth.

Our current investigations build from our previously funded work in relating structure to function of ParE toxins, and has expanded through our current funding from the Department of Defense to formulate a central hypothesis of the structure-function relationship of how different sequence motifs found in ParE toxins differentially interact with and inhibit DNA gyrase.

- Muthuramalingam M, White JC, Murphy, T., Ames, J.R., **Bourne C.R.** The toxin from a ParDE toxin-antitoxin system found in *Pseudomonas aeruginosa* offers protection to cells challenged with anti-gyrase antibiotics. Mol. Microbiol. 2019 Feb; 111(2):441-54. PMID: [30427086](#); PMCID: [PMC6368863](#).
- Ames, J.R., Muthuramalingam M, Murphy, T., Najar F.Z., **Bourne C.R.** Expression of different ParE toxins results in conserved phenotypes with distinguishable classes of toxicity. Microbiol. Open. 2019 July; e902. PMID: [31309747](#); PMCID: [PMC6813445](#).
- Snead, K.S., Moore, L., **Bourne, C.R.** ParD antitoxin hotspot alters a disorder-to-order transition upon binding to its cognate ParE toxin, lessening its interaction affinity and increasing its protease degradation kinetics. ACS Biochemistry 2022 Jan; PMID: [34914378](#); PMCID: *in progress*.

Ongoing and completed projects that I would like to highlight:

d. U.S. Army, Department of Defense W81XWH2010121 (PI: C. Bourne)

02/20 – 02/23

“Unlocking the potential of bacterial ParE toxins: developing a blueprint for co-opting molecular time bombs that impact bacterial cell survival”

This project is examining the phenotypic outcomes for four human bacterial pathogens when their native chromosomal ParE toxins are over-expressed within the native host cells. A proof-of-concept study design will assess the efficiency of antitoxin removal from these ParE systems in an *E. coli* host.

e. Oklahoma Center for the Advancement of Science HR17-099 (PI: C. Bourne)

07/17 – 3/21

“Targeting bacterial cell metabolism by manipulating toxin-antitoxin systems”

The goal of this project was to identify a strategy to interrupt the interactions of a chromosomally encoded ParE gyrase-inhibiting toxin with its cognate ParD antitoxin. We characterized a novel mechanism of weakening the interaction of toxin with antitoxin by perturbing the dynamics of antitoxin association and increasing the off-rate of interaction by 1000-fold. This proof-of-principle study demonstrated that increased off-rates could promote greatly increased antitoxin degradation, thereby providing a novel therapeutic intervention strategy.

B. Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments

2021 - *current* Associate Professor, U. of Oklahoma, Dept. of Chemistry and Biochemistry, Norman, OK
2021 – (2023) U. of Oklahoma, Dept. of Chemistry and Biochemistry, Executive Committee Member (elected) Member, User Review Committee, National Center for CryoEM Access and Training (NCCAT)
2021 - *current*
2017 - *current* Member (Chair, effective 2021), Advisory Committee, OU Biomolecular Structure Core Facility
2015 - *current* Member, OU Institutional Biosafety Committee
2014 - 2021 Assistant Professor, U. of Oklahoma, Dept. of Chemistry and Biochemistry, Norman, OK
2011 - 2013 Member (Chair, 2012-2013) BEI Resources Scientific Focus Group for Biodefense and High Containment Bacteria
2007 – 2013 Associate Research Scientist, Oklahoma State University, Center for Veterinary Health Sciences, Stillwater, OK
2005 – 2007 American Cancer Society Mary Horton Postdoctoral Fellow, University of Oklahoma Health Sciences Center, Oklahoma City, OK
2003 Adjunct Instructor, Oklahoma City Community College, Science Division, Oklahoma City, OK
1997 - 1998 Associate Research Technician, Oklahoma Medical Research Foundation, Dept. of Crystallography, Oklahoma City, OK

Other Experience and Professional Memberships

Ad Hoc manuscript reviewer (limited to the previous 4 years): *ACS Medicinal Chemistry*, *ACS Omega*, *Frontiers in Microbiology*, *Frontiers in Genetics*, *Genes*, *Journal of Biochemistry*, *mBio*, *Medicinal Research Reviews*, *Microorganisms*, *Molecular Microbiology*, *Nature Reviews in Microbiology*, *Nucleic Acids Research*, *Protein Science*, *Structure*, *Toxins*

Proposal reviews (limited to previous 4 years): French National Research Agency, BBSRC, US Army Research Office, NIH Special Emphasis Panel ZRG1 BST-M, University of Missouri Research Board, University of Central Oklahoma

Member, American Crystallographic Association (2001-present), American Society for Biochemistry and Molecular Biology (2003-present), American Society for Microbiology (2008-present), American Association for the Advancement of Science(2017-present)

2021 - *current* Member, Editorial Board, *Frontiers in Microbiology* specialty section Microbial Physiology and Metabolism
2014 - 2017 Member, Editorial Board, *Scientific Reports*
2011 - 2017 Member, Editorial Advisory Board, *Journal of Molecular Recognition*
2015 Tech to Trek guest promoting science careers to young women, Southwestern Okla State Uni.
2015 Participant, BioCAT Advanced SAXS Training Course, Argonne National Laboratory
2000, 2014 Participant, RapiData X-ray Diffraction Data Collection and Structure Solving at Brookhaven National Laboratory, Upton, NY
2012 - 2013 Mentor, Oklahoma State University Women’s Mentorship Program

- 2010 Guest Scientist, Community outreach program "Born To Do Science"
- 2009 Participant, MolSoft2009 Workshop on Modern Drug Target Crystallography and Structure Based Drug Discovery, San Diego, CA

Honors

- 2020 Nancy L. Mergler Faculty Mentor Award for Undergraduate Research
- 2020 Peggy Cotter Branch Travel Award, American Society of Microbiology
- 2018 OK - Louis Stokes Alliance for Minority Participation (LSAMP) Outstanding Faculty Mentor Award (Norman campus)
- 2014, 2015 VPR Summer Faculty Fellowship, University of Oklahoma
- 2005 Mary Horton Postdoctoral Fellowship, American Cancer Society
- 2005 Travel Grant, US National Committee for Crystallography
- 2003 Pauling Poster Prize, American Crystallographic Association
- 2001 Ludo Frevel Crystallography Scholarship, International Centre for Diffraction Data

C. Contributions to Science

1. **Toxin Antitoxin systems as targets to control bacterial growth:** I joined the field of Toxin Antitoxin (TA) systems when I started my independent position at OU. My team has worked to characterize and compare the extensive interaction interfaces between the toxin and antitoxin proteins with an aim of manipulating them to alter bacterial growth. An early contribution was a critical assessment of antitoxin half-life, culminating in a review article examining the evidence for protease degradation of these molecules (publication f). The shortened half-life of antitoxins also appears relevant to purified samples, and we have deduced an intrinsic degradation specifically at the toxin-binding region (g). Through our studies we also characterized RNase-type toxins, and identified a promiscuous nuclease activity and species-specific toxicity for the YoeB type (h, i).
 - f. Muthuramalingam M, White JC, **Bourne CR**. Toxin-Antitoxin Modules Are Pliable Switches Activated by Multiple Protease Pathways. *Toxins* (Basel). 2016 Jul 9;8(7)PubMed PMID: [27409636](#); PubMed Central PMCID: [PMC4963847](#).
 - g. Snead, K.J., **Bourne C.R**. Intrinsic degradation of the Type-II antitoxin ParD from *Pseudomonas aeruginosa*. *bioRxiv* 2021 March; doi: [10.1101/2021.03.29.437564](#).
 - h. Ames, J.R., McGillick, J., Murphy, T., Reddem, E., **Bourne, C.R**. Identifying a molecular mechanism that imparts species-specific toxicity to YoeB toxins. *Front. Micro.* 2020 May; 11:(article)959. PMID: [32528435](#); PMCID: [PMC7256200](#).
 - i. McGillick, J., Ames, J.R., Murphy, T., **Bourne C.R**. A YoeB toxin cleaves both RNA and DNA. 2021 *Sci. Reports* 11:3592. PMID: [33574407](#) PMCID: [PMC7878887](#).
2. **New inhibitors of bacterial biosynthetic folate pathway:** I carried out screening, biochemical assays, and structural biology for inhibitors of whole bacterial (including Select Agent) cell growth, and I expanded a commercial screening platform by developing novel analysis methodology (publication j). I crystallized and solved the structures of the dihydrofolate (DHFR) from three different bacteria (publication k, l). I carried out extensive SAR studies to characterize a series of inhibitors derived from the structure of the antibiotic trimethoprim, including whole cell MIC measurements, *in vitro* enzyme activity inhibition, and three-dimensional structure determinations. These studies have been continued and expanded in my independent lab at OU (publication m).
 - j. **Bourne CR**, Wakeham N, Bunce RA, Nammalwar B, Berlin KD, Barrow WW. Classifying compound mechanism of action for linking whole cell phenotypes to molecular targets. *J Mol Recognit.* 2012 Apr;25(4):216-23. PubMed PMID: [22434711](#); PubMed Central PMCID: [PMC3703735](#).
 - k. **Bourne CR**, Wakeham N, Nammalwar B, Tseitin V, Bourne PC, Barrow EW, Mylvaganam S, Ramnarayan K, Bunce RA, Berlin KD, Barrow WW. Structure-activity relationship for enantiomers of potent inhibitors of *B. anthracis* dihydrofolate reductase. *Biochim Biophys Acta.* 2013 Jan;1834(1):46-52. PubMed PMID: [22999981](#); PubMed Central PMCID: [PMC3530638](#).
 - l. **Bourne CR**, Wakeham N, Webb N, Nammalwar B, Bunce RA, Berlin KD, Barrow WW. The structure and competitive substrate inhibition of dihydrofolate reductase from *Enterococcus faecalis* reveal

- restrictions to cofactor docking. *Biochemistry*. 2014 Feb 25;53(7):1228-38. PubMed PMID: [24495113](#); PubMed Central PMCID: [PMC3985486](#).
- m. Muddala, P.N., White, J.C., Nammalwar, B., Pratt, I., Thomas, L.M., Bunce, R.A., Berlin, K.D., **Bourne, C.R.** Inhibitor design to target a unique feature in the folate pocket of *Staphylococcus aureus* dihydrofolate reductase. 2020 *Eur. J. Med. Chem.* 200:112412. Pubmed PMID: [32502861](#).
3. **A new strategy for antiviral therapy using misdirection of capsid assembly:** As a post-doc I contributed to validating a novel approach to anti-viral therapies by altering the assembly pathway of the Hepatitis B virus capsid assembly. Using biophysical measurements and biochemical assays, we determined this compound mis-directed HBV assembly (publication n) and I identified a lab-derived genotype that could mimic these effects (publication o). I was awarded a fellowship from the American Cancer Society to pursue structural studies, and these resulted in identifying the binding pocket for these compounds, contributed to structure-guided compound modifications, and subsequently tested derivatized compounds to validate the compound orientation (publications p, q). This work is on-going in the lab and start-up company (Assembly Biosciences) of Dr. Adam Zlotnick (postdoc supervisor).
- n. Stray SJ, **Bourne CR**, Punna S, Lewis WG, Finn MG, Zlotnick A. A heteroaryldihydropyrimidine activates and can misdirect hepatitis B virus capsid assembly. *Proc Natl Acad Sci U S A*. 2005 Jun 7;102(23):8138-43. PubMed PMID: [15928089](#); PubMed Central PMCID: [PMC1149411](#).
- o. **Bourne CR**, Katen SP, Fulz MR, Packianathan C, Zlotnick A. A mutant hepatitis B virus core protein mimics inhibitors of icosahedral capsid self-assembly. *Biochemistry*. 2009 Mar 3;48(8):1736-42. PubMed PMID: [19196007](#); PubMed Central PMCID: [PMC2880625](#).
- p. **Bourne CR**, Finn MG, Zlotnick A. Global structural changes in hepatitis B virus capsids induced by the assembly effector HAP1. *J Virol*. 2006 Nov;80(22):11055-61. PubMed PMID: [16943288](#); PubMed Central PMCID: [PMC1642186](#).
- q. **Bourne C**, Lee S, Venkataiah B, Lee A, Korba B, Finn MG, Zlotnick A. Small-molecule effectors of hepatitis B virus capsid assembly give insight into virus life cycle. *J Virol*. 2008 Oct;82(20):10262-70. PubMed PMID: [18684823](#); PubMed Central PMCID: [PMC2566253](#).
4. **Structure and function of human antibodies:** My graduate work focused on mechanisms of protein crystal growth and their application to the structural properties of human antibodies. I participated in studies conducted on flight missions STS-95 and STS-107 to evaluate the effect of microgravity on protein crystal quality (publication r). One sample produced a very large crystal, and the subsequent structure determination revealed improved diffraction properties (publication s). Other work identified an inherent proteolytic capacity of a subset of neoplastic-derived human IgM antibodies (publications t, u), a revolutionary finding that is still an active area of research, for example in the Ramsland lab at RMIT, Melbourne, AU.
- r. Alverado UR, **DeWitt CR**, Shultz BB, Ramsland PA, Edmundson AB. A method for growing protein crystals in capillary tubes. *J Cryst Growth* 2001; 233:407-414.
- s. Terzyan SS, **Bourne CR**, Ramsland PA, Bourne PC, Edmundson AB. Comparison of the three-dimensional structures of a human Bence-Jones dimer crystallized on Earth and aboard US Space Shuttle Mission STS-95. *J Mol Recognit*. 2003 Mar-Apr;16(2):83-90. PubMed PMID: [12720277](#).
- t. Ramsland PA, Upshaw JL, Shultz BB, **DeWitt CR**, Chissoe WF, Raison RL, Edmundson AB. Interconversion of different crystal forms of Fabs from human IgM cryoglobulins. *J Cryst Growth* 2001; 232:204-214.
- u. Ramsland PA, Terzyan SS, Cloud G, **Bourne CR**, Farrugia W, Tribbick G, Geysen HM, Moomaw CR, Slaughter CA, Edmundson AB. Crystal structure of a glycosylated Fab from an IgM cryoglobulin with properties of a natural proteolytic antibody. *Biochem J*. 2006 May 1;395(3):473-81. PubMed PMID: [16422668](#); PubMed Central PMCID: [PMC1462693](#).

Complete List of Published Work in MyBibliography:

<http://www.ncbi.nlm.nih.gov/sites/myncbi/10usXwuC15FAk/bibliography/47974641/public/?sort=date&direction=descending>

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
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NAME: Avishek Mitra, Ph.D.

eRA COMMONS USER NAME (credential, e.g., agency login): MITRA2020

POSITION TITLE: Assistant Professor of Microbiology and Molecular Genetics

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)	Completion Date MM/YYYY	FIELD OF STUDY
University of South Florida, FL	B.S.	12/2008	Biomedical Sciences
University of South Florida, FL	Ph.D.	05/2014	Cell & Molecular Biology
University of Alabama at Birmingham, AL	Research Associate	04/2014-07/2020	Microbiology
Oklahoma State University	Assistant Professor	08/2020 -	Microbiology

A. Personal Statement

My research interests have always involved studying bacterial pathogens. During my undergraduate and graduate programs, I studied regulation of pathogenic mechanisms in *Staphylococcus aureus* and Enterohemorrhagic *Escherichia coli*. Currently I work with *Mycobacterium tuberculosis* (Mtb), which is the causative agent of tuberculosis and was the leading cause of human deaths until the pandemic. Over the last six years my research has focused on studying mechanisms of iron acquisition in Mtb because iron is an essential nutrient for Mtb survival and virulence. My background in molecular biology techniques gained during my graduate studies allowed me to develop a novel selection assay to screen for Mtb heme uptake components. More specifically, we synthesized a toxic heme analog and I selected for resistant mutants, identifying novel Mtb membrane proteins that play crucial roles in heme uptake. I made two consequential discoveries. First, I discovered that Mtb uses unique outer membrane channel proteins, exclusively found in mycobacteria, for nutrient uptake. Second, I discovered that Mtb acquires heme iron by two independent pathways, which contrasts all known heme acquisition systems in bacteria. The main goal in our lab is to elucidate the fundamental mechanisms by which Mtb transports heme into the cell.

I have always been committed to research and education at all stages of my career. Mentoring, training and working with students has always been important to me and has been a crucial part of my own development. As an assistant professor at Oklahoma State University (OSU), I have brought together a diverse group of graduate and undergraduate students and trained them to perform hypothesis driven scientific research. Our group (<https://mitralab.okstate.edu/>) works in teams under my supervision to identify novel components of the Mtb heme acquisition system. The recent progresses made by my lab at OSU not only forms the basis of our proposal but also allowed us to independently secure pilot project funding. In conclusion, I have the expertise, training, and support to perform the research described in our proposal.

Ongoing project that I would like to highlight include:

P20 GM103648

Mitra (PI)

07/01/21-01/31/24

Mechanisms of hemoglobin utilization by *Mycobacterium tuberculosis*.

B. Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments

2020 - Present Assistant Professor, Oklahoma State University, Stillwater, OK.
2020 - Present Member, Institutional Biosafety Committee, Oklahoma State University
2020 - Present Vice-Chair (Microbiology), Oklahoma Academy of Sciences
2020 - Present Member, American Society of Microbiology
2020 - Present Member, Missouri Valley American Society of Microbiology

Honors

2018 University of Alabama at Birmingham (UAB) Microbiology Award of Excellence
2017 6th Southeastern Mycobacterium Meeting (Second Place - Oral)
2016 UAB Department of Microbiology Award of Excellence
2015 UAB Department of Microbiology Award of Excellence
2014 UAB Department of Microbiology Award of Excellence
2013 Wind River Conference Travel Award
2012 Verocytotoxin Producing *Escherichia coli* (VTEC) Infections Conference Travel Award
2012 ASM Annual SE Regional Meeting Travel Award
2011 Fred L. and Helen M. Tharp Scholarship Fund Graduate Award
2011 ASM Annual SE Regional Meeting Travel Award
2011 Wind River Conference Travel Award

Mentoring

2020 - Present	OSU (Mitra Lab)	Graduate Student	Mamie Kannon
2020 - Present	OSU (Mitra Lab)	Graduate Student	Haley Merrick
2020 - Present	OSU (Mitra Lab)	Undergraduate Student	Jessica Arlington
2020 - Present	OSU (Mitra Lab)	Undergraduate OK-LSAMP Scholar	November Sankey
2020 - Present	OSU (Mitra Lab)	Undergraduate Honors Student	Genesis Valero
2020 - Present	OSU (Mitra Lab)	Undergraduate Wentz Research Student	Chandler Dean
2020 - Present	OSU (Mitra Lab)	Undergraduate Student	David Steichen
2020 - Present	OSU (Mitra Lab)	Undergraduate Student	Aneisha White
2017-2018	UAB	Graduate Student	Jonathan Zhang
2017-2018	UAB	Graduate Student	Gillian Holder
2016-2019	UAB	Undergraduate Student	Bjorn Sunde
2016-2018	UAB	Graduate Student	Joshua Huffines
2016-2017	UAB	Undergraduate Student	Diane Rojas
2016	UAB	Graduate Student	Rachel Andrews
2012-2014	USF	Undergraduate Student	Riley Bednar
2012-2013	USF	Undergraduate Student	Carly Harro
2011-2014	USF	Undergraduate Student	Zimrisha Alla
2010-2014	USF	Undergraduate Student	Khoury Vendura
2010-2012	USF	Undergraduate Student	Salvatore Versaggi
2010-2011	USF	Undergraduate Student	Cesar Tabora
2010-2011	USF	Undergraduate Student	Leonardo Estevez
2010-2011	USF	Undergraduate Student	Mayenna Greuerre

C. Contributions to Science

Current contributions in bacterial pathogenesis

Identifying the molecular mechanisms of heme iron acquisition in *Mycobacterium tuberculosis* (Mtb). I used a combination of genetics and biochemical methods to demonstrate that mycobacterial PPE (proline-proline-glutamate) family of proteins are involved in acquisition of heme iron which is an essential micronutrient for Mtb survival and virulence. Our studies were the first to demonstrate that PPE proteins are outer membrane proteins (OMP) of Mtb that are functional homologs of beta-barrel OMPs found in gram-negative diderm bacteria. I also demonstrated that a dipeptide ABC (Dpp) transporter is required for heme uptake across the inner membrane of Mtb.

1. **Mitra, A.,** Speer, A., Lin, K., Ehrt, S., and Niederweis, M. **(2017).** PPE surface proteins are required for heme utilization by *Mycobacterium tuberculosis*. **Mbio.** **8(1): e01720 (PMID 28119467)** <https://pubmed.ncbi.nlm.nih.gov/28119467/>
2. **Mitra, A.,** Ko, Y.H., Cingolani, G., and Niederweis, M. **(2019).** Heme and hemoglobin utilization by *Mycobacterium tuberculosis*. **Nature Communications.** **10(8): 4260 (PMID 31534126)** <https://pubmed.ncbi.nlm.nih.gov/31534126/>

Previous contributions in bacterial pathogenesis

Identifying the regulatory mechanisms through which alternative sigma factor N (σ^N) controls virulence in Enterohemorrhagic *Escherichia coli* (EHEC). In this early stage of my career I identified the regulatory pathway through which σ^N regulates type III secretion (required for intestinal colonization) and extreme acid resistance (required for survival in stomach) in EHEC. The results of our study demonstrated that a complex network of regulation of these systems by σ^N both at the post-transcriptional level and at the biochemical level and identified σ^N as a major regulator of EHEC virulence.

1. Riordan, J.T. and **Mitra A. (2017).** Regulation of *Escherichia coli* pathogenesis by alternative sigma factor N. **EcoSal (PMID 28635589)** <https://pubmed.ncbi.nlm.nih.gov/28635589/>
2. **Mitra, A.,** Fay, P., Vendura, K., Alla, Z., Carroll, R., Shaw, L., and Riordan, J. T. **(2014)** σ^N -dependent control of acid resistance and the locus of enterocyte effacement in enterohemorrhagic *Escherichia coli* is activated by acetyl phosphate in a manner requiring flagellar regulator FlhDC and the σ^S antagonist FliZ. **MicrobiologOpen.** **3(4): 497 (PMID 24931910)** <https://pubmed.ncbi.nlm.nih.gov/24931910/>
3. **Mitra, A.,** Fay, P., Morgan, J., Vendura, K., Versaggi, S., and Riordan, J. T. **(2012)** Sigma factor N, liaison to an *ntnC*- and *rpoS*-dependent regulatory pathway controlling acid resistance and LEE expression in enterohemorrhagic *Escherichia coli*. **PLoS One.** **7(9): e46288 (PMID 23029465)** <https://pubmed.ncbi.nlm.nih.gov/23029465/>
4. Neupane, M.S., Abu-Ali, G. S., **Mitra, A.,** Manning, S. D., and Riordan, J. T. **(2011)** Shiga toxin 2 overexpression in *Escherichia coli* O157:H7 strains associated with severe human disease. **Microb. Pathog.** **51(6): 466. (PMID 21864671)** <https://pubmed.ncbi.nlm.nih.gov/21864671/>

Other Peer reviewed journal articles

1. Neyrolles, O., Wolschendorf, F., **Mitra, A.,** and Niederweis, M. **(2015)** Mycobacteria, metals and the macrophage. **Immunol. Rev.** **264(1): 249 (PMID 25703564)** <https://pubmed.ncbi.nlm.nih.gov/25703564/>
2. V. Meikle, A. Mossberg, **A. Mitra,** A. Hakansson, and M. Niederweis **(2018).** A protein complex from human milk enhances the activity of antibiotics and drugs against *Mycobacterium tuberculosis*. **AAC.** **63(2): e01846 (PMID 30420480)** <https://pubmed.ncbi.nlm.nih.gov/30420480/>