BIOGRAPHICAL SKETCH

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NAME: Lauren Parker Jackson

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

POSITION TITLE: Assistant Professor of Biological Sciences & Biochemistry

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
Vanderbilt University	B.S.	05/2003	Chemistry
MRC Laboratory of Molecular Biology & Trinity College, University of Cambridge	Ph.D.	01/2008	Molecular Biology/ Structural Biology
Cambridge Institute for Medical Research	Postdoctoral	11/2013	Biochemistry

A. Personal Statement

The goal of my laboratory is to understand the cellular roles of important protein complexes that initiate cellular trafficking pathways by forming coats around vesicles or tubules at specific membranes. We focus on the retromer, adaptor protein 4 (AP4), and coat protein complex I (COPI) complexes and the roles they undertake in both fundamental cell biology and human disease. Each coat functions as a "hub" to coordinate large protein networks that drive the regulated formation of vesicles or tubules at precise locations. We use biochemical, biophysical, and structural methods to address at the molecular level how coats interact with protein and lipid partners to regulate coat assembly and to sort important cargoes to different destinations. We use our mechanistic data to address functional relevance of coat protein complexes in cultured cell lines or in model systems, including budding yeast. Ultimately, we aim to characterize molecular mechanisms of coat protein assembly and regulation in order to understand fundamental cell biology and how coats drive human diseases, including cancers and brain disorders.

A. Frazier MN and **Jackson LP**. (2017). Spotlight: Watching real-time endocytosis in living cells. *J Cell Biol* 216, 9-11.

B. **Jackson LP**. (2014). Structure and mechanism of COPI vesicle biogenesis. *Curr Opin Cell Biol* **29C**, 67-73. PMCID not available.

C. **Jackson LP**†, Kümmel D†, Reinisch K, and Owen DJ. (2012). Structures and mechanisms of vesicle coat components and multisubunit tethering complexes. *Curr Opin Cell Biol* **24,** 475-483. (†corresponding authors). PMCID: PMC3425711.

B. Employment, Honors, & Service

Employment

2014-present Assistant Professor, Dept. of Biological Sciences, Vanderbilt University, Nashville, TN, USA
2016-present Assistant Professor, Dept. of Biochemistry, Vanderbilt University School of Medicine
2009-2013 Postdoctoral Research Associate, Cambridge Institute for Medical Research, Cambridge, UK
2009-2013 Supervisor, Natural Sciences Part IA, Jesus College, Cambridge, UK (teaching experience)
2007-2009 Junior Consultant, The Boston Consulting Group, London, UK

Honors

2019 Nordhaus Award for Excellence in Undergraduate Teaching, Vanderbilt College of Arts & Sciences
2016 Pew Scholar
2016 Provost Research Studio for faculty development, Vanderbilt University
2016 Littlejohn Faculty Fellow, Vanderbilt Undergraduate Summer Research Program
2013 Gordon Research Conference travel award (Molecular Membrane Biology)
2012 Keystone Symposia Future of Science Fund Scholarship (Structural Biology of Cellular Processes)
2011 Protein Society Young Investigator Travel Grant/Finn Wold Travel Award
2010 Gordon Research Conference travel award (Lysosomes and Endocytosis)
2004 Academy of Achievement International Achievement Summit, Chicago, IL
2003 MRC Laboratory of Molecular Biology Student Scholarship
2003 Trinity College Honorary External Research Studentship
2003 National Science Foundation Fellowship (declined)
2003 Gates Cambridge Scholarship (declined)
2003 Founder's Medalist, College of Arts & Science, Vanderbilt University
2003 Phi Beta Kappa, Vanderbilt University
2003 Joel Tellinghuisen Award for Undergraduate Research, Phi Beta Kappa, Vanderbilt University
2003 Outstanding Senior in Chemistry, Vanderbilt University Dept. of Chemistry
2003 Donald E Pearson Award for Undergraduate Research, Vanderbilt University Dept. of Chemistry

Professional Service & Memberships

Discussion leader, GRC Lysosomes & Endocytosis, June 2020 (canceled due to COVID-19 outbreak)
Editorial board member, *Traffic*, 2017-present
Guest Editor, *Traffic* structural biology review series ("Traffic at Atomic Resolution"), July 2019
Member, Planning Committee, 2018 Pew Annual Meeting
Chair, Science Session I, 2018 Pew Annual Meeting
F1000 contributing faculty member, Cell Signaling & Trafficking Structures, 2018-present
Ad hoc reviewer, NIH Membrane Biology & Protein Processing (MBPP) study section
Ad hoc reviewing for *Nature Struct Mol Biol, eLife, J Cell Biology*, *Structure*, *PNAS*, *Nat Chem Biology*
Ad hoc reviewer, book chapter in "Biomolecular and Bioanalytical Techniques: Theory, Methodology and Applications", Wiley (UK)
Ad hoc reviewing for Stanford Synchrotron Radiation Light Source (SSRL)
Ad hoc reviewing for Deutsche Forschungsgemeinschaft (DFG) funding body
Member, American Society for Cell Biology, 2015-present
Member, Biophysical Society, 2017-present

C. Contributions to Science

1. Molecular mechanisms of vesicular and tubular coat assembly

My work on coat protein complexes has provided insight into how vesicular and tubular coats form at specific membranes. Clathrin-mediated endocytosis at the plasma membrane has long served as a paradigm for understanding coated vesicle formation. My postdoctoral work revealed how AP2 is recruited to membranes by a specific phosphoinositide, where it then undergoes a substantial conformational change to bind linear motifs found in the C-termini of cargo molecules. Subsequent work by other groups showed how this conformational change is required for clathrin recruitment and is likely conserved in related coats (AP1, COPI). More recent work in my independent laboratory focuses on the related AP4 coat. We provided the first mechanistic glimpse into how AP4 interacts with its accessory protein, tepsin, and we determined structures and evolutionary history of the tepsin ENTH and VHS-like domains. Our work provides a foundation for understanding AP4 coat assembly and ultimately how AP4 impacts brain function. Finally, on endosomes, retromer sorts cargoes to at least two destinations, the plasma membrane and *trans*-Golgi network (TGN). A major question is how retromer can specifically sort protein cargoes to distinct destinations. As a postdoc, I showed VARP binds retromer directly and links it to an ancestral SNARE protein, VAMP7. In my independent laboratory, we determined the first single particle cryo-EM structures of mammalian retromer and showed how it can form multiple oligomers *in vitro.* This paves the way for understanding mechanisms of coated tubule assembly and regulation

A. **Jackson LP***, Kelly BT*, McCoy AJ, Gaffry T, James LC, Collins BM, Höning S, Evans PR, Owen DJ. (2010). A large scale conformational change couples membrane recruitment to cargo binding in the AP2 clathrin adaptor complex. *Cell* 141, 1220-29, (*joint first authors), PMCID: PMC3655264.

B. Frazier MN, Davies AK, Voehler M, Kendall AK, Borner GHH, Chazin WJ, Robinson MS, and **Jackson LP**. (2016). Molecular basis for the interaction between Adaptor Protein Complex 4 (AP4) β4 and its accessory protein, tepsin. *Traffic* 17, 400-415. PMCID: PMC4805503.

C. Archuleta TL*, Frazier MN*, Monken A, Kendall AK, Harp J, McCoy AJ, Creanza N, and **Jackson LP**. (2017). Structure and evolution of ENTH and VHS/ENTH-like domains in tepsin. *Traffic* 18, 590-603. (*joint first authors), PMCID: PMC5567745.

D. Kendall AK, Xie B, Xu P, Wang J, Burcham B, Frazier MN, Binshtein E, Wei H, Graham TR, Nakagawa T, **Jackson LP**. (2020). Mammalian retromer is an adaptable scaffold for cargo sorting from endosomes. *Structure* 28, 393-405. PMCID: PMC7145723. (Featured on cover and in Preview article)

2. Cargo recognition by vesicle coat proteins

The identification and sorting of protein cargoes to specific destinations lie at the heart of membrane trafficking. Recognition of linear motifs by the clathrin coat machinery was well-understood in the field, but there were no molecular data on how the COPI coat interacted with any of its important cargoes in the retrograde pathway. Our structural work elucidated how two COPI subunits could interact with dilysine motifs found in retrograde cargoes, which in turn implied COPI coats assemble differently from clathrin-based coats. A second major question was how SNARE proteins are sorted as cargo back to their steady-state destination following a fusion event. Our work on the lysosomal SNARE protein, VAMP7, provided one of the first two structural examples of how coats package SNAREs into forming vesicles in a non-competitive way. Instead of linear motifs, SNAREs instead use folded structural domains to interact specifically with a single adaptor protein, and loss of important residues in these domains have important implications for mis-sorting. My independent work at Vanderbilt has built upon and combined these two interests. In collaboration with Todd Graham's lab, we uncovered the biochemical basis for recognition of a ubiquitinated SNARE protein by COPI. This work highlighted that ubiquitin can act as a retrieval signal for a SNARE. Finally, we collaborated with Margaret Robinson's lab to demonstrate how new AP4 coat protein

A. **Jackson LP**†, Lewis M, Kent HM, Edeling MA, Evans PR, Duden R, and Owen DJ†. (2012). Molecular basis for recognition of dilysine trafficking motifs by COPI. *Dev Cell* **23**, 1-8 (†corresponding authors), PMCID: PMC3521961.

B. Pryor PR, **Jackson LP**, Gray SR, Edeling MA, Thompson A, Sanderson CM, Evans PR, Owen DJ, Luzio JP. (2008). Molecular basis for the sorting of the SNARE VAMP7 into endocytic clathrin-coated vesicles by the ArfGAP Hrb. *Cell* 134, 817-27, PMCID: PMC2648964.

C. Xu P, Hankins HM, Macdonald C, Erlinger SJ, Frazier MN, Diab NS, Piper RC, **Jackson LP**, MacGurn JA, and Graham TR. (2017). COPI mediates recycling of an exocytic SNARE from endosomes by recognition of a ubiquitin sorting signal. *eLife* 2017; 6:e28342. DOI:10.7554/eLife.28342.

D. Davies AK, Itzhak DN, Edgar JR, Archuleta TL, Hirst J, **Jackson LP**, Robinson MS, and Borner GHH. (2018). AP-4 vesicles contribute to spatial control of autophagy via RUSC-dependent peripheral delivery of ATG9A. *Nature Communications* 27: 3958.

3. Structural studies of filamentous plant viruses

Filamentous plant viruses are important models for understanding helical virus assembly and in agricultural disease; potyviruses alone account for more than half the viral crop damage world-wide. Because of their filamentous nature, these viruses do not crystallize. As an undergraduate, I helped develop methods for making filamentous virus samples of the potexvirus, potato virus X (PVX), and the potyvirus, wheat streak

mosaic virus (WSMV). Our fiber diffraction data on PVX provided the first estimates of helical symmetry for the virus, while our work on WSMV was one of the first examples of potyvirus fiber diffraction. Subsequently, the combination of structural techniques like EM and STEM was used together with our fiber diffraction data to produce a more detailed analysis of PVX structure.

A. **Parker L**, Kendall A, Berger, PH, Shiel, PJ, and Stubbs, G. (2005). Wheat streak mosaic virus—Structural parameters for a *Potyvirus*. *Virology* 340, 64-69. (featured on cover)

B. Stubbs G, **Parker L**, Junn J, and Kendall, A. (2005). Flexible filamentous virus structures from fiber diffraction. *Fiber Diffraction Review* 13, 38-42.

C. **Parker L**, Kendall A, and Stubbs, G. (2002). Surface Features of Potato Virus X from Fiber Diffraction. *Virology* 300, 291-29. (featured on cover)

Full publication list
https://www.ncbi.nlm.nih.gov/myncbi/10O8lSLY-fBAo/bibliography/public/

D. Research Support

Current funding

1. NIH/NIGMS R35GM119525 09/01/2016 – 05/31/2021 Role: PI
"Molecular mechanisms of coat protein assembly and regulation in membrane trafficking"

The major goal of this project is to determine the molecular mechanisms by which vesicular and tubular coat protein complexes assemble and are regulated on cellular membranes.

2. Pew Charitable Trusts, Pew Scholars Award 08/01/2016 – 07/31/2020 Role: PI
"Coat protein function in membrane trafficking and human disease"

The major goal of this project is to elucidate molecular structures and functions of important non-clathrin coat protein complexes that initiate trafficking pathways at the Golgi and endosomes.

3. NIH/NIGMS R01GM1184532 (PI: Todd Graham) 05/01/2016 – 04/30/2020 Role: Collaborator
"Mechanisms of protein transport between Golgi and endosomes"

The major goal of this project is to define the function of COPI and ubiquitin in recycling a SNARE protein from early endosomes to the Golgi.

4. NIH/NCI 1R01 CA224188-01A1 07/01/2020-06/30/2025 Role: Collaborator
(PI: Yashi Ahmed, Dartmouth; Vanderbilt PI: Ethan Lee)
"Inhibition of the Wnt Receptor Complex by the Tumor Suppressor Adenomatous Polyposis Coli"

The long-term objective of this study is to investigate how the tumor suppressor Adenomatous polyposis coli inhibits the Wnt signal transduction pathway by regulating the Wnt receptor complex (signalosome) and to demonstrate how this can be exploited to target APC mutant colorectal cancers

BIOGRAPHICAL SKETCH

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NAME: Kendall, Amy

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

POSITION TITLE: Laboratory Manager

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)	END DATE MM/YYYY	FIELD OF STUDY
Vanderbilt University, Nashville, TN	BS	05/1993	Elementary Education / Natural Sciences
Vanderbilt University, Nashville, TN	MS	05/2000	Biological Sciences

A. Personal Statement

Beginning with my graduate work in the mid-nineties, I have always worked at the intersection of structural methods that have included x-ray fiber diffraction, xray crystallography, and negative stain and cryo-electron microscopy. My studies of flexible filamentous plant viruses eventually led to studies of disordered amyloid and prion filaments, and this work has prepared me well for structural studies of malleable membrane trafficking proteins including retromer. As a senior staff scientist, I have helped to drive the adoption of negative stain and cryoEM methods by our laboratory, and have served as the EM "point person" for more than 20 years. I have trained students in microscopy methods and written protocols for sample preparation, instrument use, image processing and validation, and publication production. I have attended workshops and conferences in order to remain up-to-date on current topics in microscopy, and have disseminated this information to our laboratory and others at Vanderbilt.

1. Kendall AK, Xie B, Xu P, Wang J, Burcham R, Frazier MN, Binshtein E, Wei H, Graham TR, Nakagawa T, Jackson LP. Mammalian Retromer Is an Adaptable Scaffold for Cargo Sorting from Endosomes. Structure. 2020 Apr 7;28(4):393-405.e4. PubMed PMID: 32027819; PubMed Central PMCID: PMC7145723.
2. Tuttle MD, Comellas G, Nieuwkoop AJ, Covell DJ, Berthold DA, Kloepper KD, Courtney JM, Kim JK, Barclay AM, Kendall A, Wan W, Stubbs G, Schwieters CD, Lee VM, George JM, Rienstra CM. Solid-state NMR structure of a pathogenic fibril of full-length human α-synuclein. Nat Struct Mol Biol. 2016 May;23(5):409-15. PubMed PMID: 27018801; PubMed Central PMCID: PMC5034296.
3. Kendall A, Williams D, Bian W, Stewart PL, Stubbs G. Barley stripe mosaic virus: structure and relationship to the tobamoviruses. Virology. 2013 Sep 1;443(2):265-70. PubMed PMID: 23725818.
4. Kendall A, McDonald M, Bian W, Bowles T, Baumgarten SC, Shi J, Stewart PL, Bullitt E, Gore D, Irving TC, Havens WM, Ghabrial SA, Wall JS, Stubbs G. Structure of flexible filamentous plant viruses. J Virol. 2008 Oct;82(19):9546-54. PubMed PMID: 18667514; PubMed Central PMCID: PMC2546986.

B. Positions and Honors

Positions and Employment

1999 - 2002 Research Assistant II, Vanderbilt University, Nashville , TN
2002 - 2005 Research Assistant III, Vanderbilt University, Nashville, TN
2005 - Laboratory Manager, Vanderbilt University, Nashville, TN

Other Experience and Professional Memberships

Honors

C. Contribution to Science

1. Structural studies of membrane trafficking proteins

   The diverse pathways of membrane trafficking are essential to maintaining cellular homeostasis and function. We have used a combination of biochemical and structural methods to determine details of the interaction between AP4 and its accessory protein tepsin, and have explored the range of conformations adopted by the endosomal trafficking protein retromer by cryoEM and disrupted its function in yeast. Continued study of these and other trafficking proteins will allow us to characterize the mechanisms by which transport is executed within the cell and to describe the associated proteins that make this transport possible.

   a. Kendall AK, Xie B, Xu P, Wang J, Burcham R, Frazier MN, Binshtein E, Wei H, Graham TR, Nakagawa T, Jackson LP. Mammalian Retromer Is an Adaptable Scaffold for Cargo Sorting from Endosomes. Structure. 2020 Apr 7;28(4):393-405.e4. PubMed PMID: 32027819; PubMed Central PMCID: PMC7145723.
   b. Archuleta TL, Frazier MN, Monken AE, Kendall AK, Harp J, McCoy AJ, Creanza N, Jackson LP. Structure and evolution of ENTH and VHS/ENTH-like domains in tepsin. Traffic. 2017 Sep;18(9):590-603. PubMed PMID: 28691777; PubMed Central PMCID: PMC5567745.
   c. Frazier MN, Davies AK, Voehler M, Kendall AK, Borner GH, Chazin WJ, Robinson MS, Jackson LP. Molecular Basis for the Interaction Between AP4 β4 and its Accessory Protein, Tepsin. Traffic. 2016 Apr;17(4):400-15. PubMed PMID: 26756312; PubMed Central PMCID: PMC4805503.

2. Structural studies of amyloid and prion proteins.

   Structural studies of self-propagating amyloids (prions) are essential to understand the mechanism of prion self-propagation and molecular toxicity, and structural studies of both prion and non-prion amyloids are required for the rational design of drugs to treat these diseases. We used x-ray fiber diffraction in combination with solid state NMR and negative stain electron microscopy to determine low resolution structures of Aβ, the amyloid implicated in Alzheimer's disease, and α-synuclein, the amyloid implicated in Parkinson's disease. We also used x-ray fiber diffraction to compare a number of different types of natural and synthetic PrP prions.

   a. Barran-Berdon AL, Ocampo S, Haider M, Morales-Aparicio J, Ottenberg G, Kendall A, Yarmola E, Mishra S, Long JR, Hagen SJ, Stubbs G, Brady LJ. Enhanced purification coupled with biophysical analyses shows cross-β structure as a core building block for Streptococcus mutans functional amyloids. Sci Rep. 2020 Mar 20;10(1):5138. PubMed PMID: 32198417; PubMed Central PMCID: PMC7083922.
   b. Tuttle MD, Comellas G, Nieuwkoop AJ, Covell DJ, Berthold DA, Kloepper KD, Courtney JM, Kim JK, Barclay AM, Kendall A, Wan W, Stubbs G, Schwieters CD, Lee VM, George JM, Rienstra CM. Solid-state NMR structure of a pathogenic fibril of full-length human α-synuclein. Nat Struct Mol Biol. 2016 May;23(5):409-15. PubMed PMID: 27018801; PubMed Central PMCID: PMC5034296.
   c. Wan W, Wille H, Stöhr J, Kendall A, Bian W, McDonald M, Tiggelaar S, Watts JC, Prusiner SB, Stubbs G. Structural studies of truncated forms of the prion protein PrP. Biophys J. 2015 Mar 24;108(6):1548-1554. PubMed PMID: 25809267; PubMed Central PMCID: PMC4375555.
   d. Wille H, Bian W, McDonald M, Kendall A, Colby DW, Bloch L, Ollesch J, Borovinskiy AL, Cohen FE, Prusiner SB, Stubbs G. Natural and synthetic prion structure from X-ray fiber diffraction. Proc Natl Acad Sci U S A. 2009 Oct 6;106(40):16990-5. PubMed PMID: 19805070; PubMed Central PMCID: PMC2761340.

3. Structural studies of filamentous plant viruses.

Filamentous plant viruses have long been used as models for viral structure and assembly. Using a combination of x-ray fiber diffraction and cryo-electron microscopy, we determined the low resolution structures of a number of different flexible filamentous plant viruses including potato virus X and soybean mosaic virus, and the low resolution structure of a rigid filamentous plant virus, barley stripe mosaic virus. These low resolution structures allowed us to speculate about the relationships between the filamentous plant viruses and provided information that might be used to design modified coat proteins for peptide expression and conferral of resistance on host plants.

a. Stubbs G, Kendall A. Fibre diffraction in the analysis of filamentous virus structure. Crystallography Reviews. 2016; 22:84-101.
b. Kendall A, Williams D, Bian W, Stewart PL, Stubbs G. Barley stripe mosaic virus: structure and relationship to the tobamoviruses. Virology. 2013 Sep 1;443(2):265-70. PubMed PMID: 23725818.
c. Kendall A, McDonald M, Bian W, Bowles T, Baumgarten SC, Shi J, Stewart PL, Bullitt E, Gore D, Irving TC, Havens WM, Ghabrial SA, Wall JS, Stubbs G. Structure of flexible filamentous plant viruses. J Virol. 2008 Oct;82(19):9546-54. PubMed PMID: 18667514; PubMed Central PMCID: PMC2546986.

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

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
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NAME: Mintu Chandra

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

POSITION TITLE: Post Doctoral Research Scholar

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
Jadavpur University, Kolkata, India	M.Sc.	06/2010	Life Science and Biotechnology
Indian Institute of Science Education and Research (IISER) Bhopal, Madhya Pradesh, India	Ph.D.	02/2016	Structural Biology
Institute for Molecular Biosciences (IMB), University of Queensland, St. Lucia, Australia	Postdoctoral	12/2018	Structural Biology
Department of Biological Sciences & Biochemistry, Vanderbilt University, Nashville, TN, USA	Postdoctoral	Ongoing	Structural Biology

A. Personal Statement

My long-standing interest has been in the protein-protein and protein-small molecule interactions with the help of protein biochemistry, biophysics, X-ray crystallography and Cryo-EM. We all have evolved highly sophisticated protein machineries to control the flow of trans-membrane molecules and lipids between different organelles. Any disruption of these processes are linked to numerous diseases including neurodegenerative disorders and cancer. Using cutting-edge structural, molecular and cellular approaches I aim to determine how these trafficking machineries are assembled and regulated at the molecular level. My future goal is to uncover the details of the architecture of the functional membrane-associated complex, Retromer-Varp and Retromer-SNXs (SNX27 and SNX-BAR), assembled in the presence of PI3P-enriched nanodiscs. This will provide a molecular foundation for identifying target sites and rational design for developing potential therapeutics.

- ***Chandra M**, Chin YK, Mas C, Feathers JR, Paul B, Datta S, Chen KE, Jia X, Yang Z, Norwood SJ, Mohanty B, Bugarcic A, Teasdale RD, Henne WM, Mobli M, Collins BM. Classification of the human phox homology (PX) domains based on their phosphoinositide binding specificities. **Nat Commun.** 2019 Apr 4;10(1):1528. doi: 10.1038/s41467-019-09355-y.*
- *Ugrankar R, Bowerman J, Hariri H, **Chandra M**, Chen KE, Bossanyi MF, Datta S, Rogers S, Eckert KM, Vale G, Victoria A, Fresquez J, McDonald JG, Jean S, Collins BM, and Henne WM. Drosophila Snazarus regulates a lipid droplet sub-population at plasma membrane-droplet contacts in fat body adipocytes. **Developmental Cell**. 2019 Aug 15; doi: 10.1016/j.devcel.2019.07.021.*

- *Chen KE, Tillu VA, **Chandra M**, Collins BM. Molecular basis for membrane recruitment by the PX and C2 domains of class II phosphoinositide 3-kinase-C2α. **Structure.** 2018 Dec 4;26(12):1612-1625.e4. doi: 10.1016/j.str.2018.08.010. Epub 2018 Oct 4.*
- ***Chandra M**, Collins BM. The Phox Homology (PX) Domain. **Adv Exp Med Biol.** 2018 Mar 23. doi: 10.1007/5584_2018_185. [Epub ahead of print].*

- *Yang Z, Follett J, Kerr MC, Clairfeuille T, **Chandra M**, Collins BM, Teasdale RD. Sorting Nexin 27 (SNX27) regulates the trafficking and activity of the glutamine transporter ASCT2. **J Biol Chem**. 2018 Mar 21. pii: jbc.RA117.000735. doi: 10.1074/jbc.RA117.000735. [Epub ahead of print].*

- *Clairfeuille T, Mas C, Chan AS, Yang Z, Tello-Lafoz M, **Chandra M**, Widagdo J, Kerr MC, Paul B, Mérida I, Teasdale RD, Pavlos NJ, Anggono V, Collins BM. A molecular code for endosomal recycling of phosphorylated cargos by the SNX27–retromer complex. **Nature Structural & Molecular Biology** (2016) doi:10.1038/nsmb.3290.*

B. Employment, Honors, & Service

Employment

February, 2019 - Present	Post Doctoral Research Scholar, Dept. of Biological Sciences, Vanderbilt University, Nashville, TN, USA.
May, 2016 – December, 2018	Post Doctoral Research Officer, Institute for Molecular Biosciences (IMB), University of Queensland, St. Lucia, Australia.

Honors

2019	**William N Pearson Fellowship Award 2019** in Nutritional Science and Metabolism, Vanderbilt University, Nashville, TN, USA.
2015	**Best Poster Award** at the 13th Conference of the Asian Crystallography Association (AsCA), Science City, Kolkata, India, December 05-08th, 2015.
2015	**International Travel Grant from Department of Science and Technology (DST) -** To attend the Biophysical Society conference November 16-20th, 2015 at Spier Wine Estate, Stellenbosch, Western Cape, South Africa.

C. Contributions to Science

Publication list

https://www.ncbi.nlm.nih.gov/pubmed/?term=mintu+chandra

1. To understand the retromer coat assembly and regulation on endosomes and to provide a fundamentally improved understanding of the role of endosomal membrane recycling in cellular homeostasis.

My recent work on PX domain for their phospholipid preferences has provided insight into the molecular basis of membrane trafficking mediated by the Phox Homology (PX) domains. The systematic screening of all human PX domains for their phospholipid preferences and the PX domain structures revealed two distinct binding sites that explain their lipid specificities, providing a basis for defining and predicting the functional membrane interactions of the entire PX domain protein family. This work has recently been published in Nature Communications journal.
Currently, I am trying to understand the molecular mechanisms by which the Retromer complex (VPS26/VPS35/VPS29 subunits) interacts with SNX27. Retromer plays a fundamental role in nutrition. In metazoans, the Retromer/SNX27 complex recycles a number of critical nutrient receptors, including glucose transporter type 1 (GLUT1) and the iron transporter DmtI. Although SNX27 appears to facilitate cargo specificity of Retromer, regulatory mechanisms for SNX27/Retromer assembly during receptor recycling remain elusive. I aim to identify novel regulators associated with SNX27/Retromer assembly and investigate their role in GLUT1 recycling to the plasma membrane. Subsequently, I will

pursue the structural studies of the complex on its own and assembled in the presence of PI3P-enriched nanodiscs. This work will provide critical insight into how retromer assembles in the presence of cargo. In order to get insights into the complex assembly of SNX27-retromer, I have successfully reconstituted the retromer-SNX27 complex at the highest purity level and currently obtaining initial 2D class averages.

- ***Chandra M**, Chin YK, Mas C, Feathers JR, Paul B, Datta S, Chen KE, Jia X, Yang Z, Norwood SJ, Mohanty B, Bugarcic A, Teasdale RD, Henne WM, Mobli M, Collins BM. Classification of the human phox homology (PX) domains based on their phosphoinositide binding specificities. **Nat Commun.** 2019 Apr 4;10(1):1528. doi: 10.1038/s41467-019-09355-y.*
- *Ugrankar R, Bowerman J, Hariri H, **Chandra M**, Chen KE, Bossanyi MF, Datta S, Rogers S, Eckert KM, Vale G, Victoria A, Fresquez J, McDonald JG, Jean S, Collins BM, and Henne WM. Drosophila Snazarus regulates a lipid droplet sub-population at plasma membrane-droplet contacts in fat body adipocytes. **Developmental Cell**. 2019 Aug 15; doi: 10.1016/j.devcel.2019.07.021.*
- *Chen KE, Tillu VA, **Chandra M**, Collins BM. Molecular basis for membrane recruitment by the PX and C2 domains of class II phosphoinositide 3-kinase-C2α. **Structure.** 2018 Dec 4;26(12):1612-1625.e4. doi: 10.1016/j.str.2018.08.010. Epub 2018 Oct 4.*
- ***Chandra M**, Collins BM. The Phox Homology (PX) Domain. **Adv Exp Med Biol.** 2018 Mar 23. doi: 10.1007/5584_2018_185. [Epub ahead of print].*
- *Yang Z, Follett J, Kerr MC, Clairfeuille T, **Chandra M**, Collins BM, Teasdale RD. Sorting Nexin 27 (SNX27) regulates the trafficking and activity of the glutamine transporter ASCT2. **J Biol Chem**. 2018 Mar 21. pii: jbc.RA117.000735. doi: 10.1074/jbc.RA117.000735. [Epub ahead of print].*
- *Clairfeuille T, Mas C, Chan AS, Yang Z, Tello-Lafoz M, **Chandra M**, Widagdo J, Kerr MC, Paul B, Mérida I, Teasdale RD, Pavlos NJ, Anggono V, Collins BM. A molecular code for endosomal recycling of phosphorylated cargos by the SNX27–retromer complex. **Nature Structural & Molecular Biology** (2016) doi:10.1038/nsmb.3290.*

2. Biochemical and X-ray crystallographic studies on *Eh*RabX3, a novel GTPase from *Entamoeba histolytica* with tandem G-Domains

My doctoral dissertation was focused on biochemical and structural studies of *Eh*RabX3, a unique and catalytically inefficient tandem Rab GTPase from *Entamoeba histolytica*. I identified how the conventional GTP/GDP cycle is regulated in *Eh*RabX3 and what is the molecular basis of low catalytic efficiency of this atypical Rab protein. The biochemical, structural and functional investigation carried out on EhRabX3 would allow us to design potential inhibitors for the better treatment of intestinal amebiasis.

- ***Chandra M**[#], Srivastava VK[#], Saito-Nakano Y, Nozaki T and Datta S. Crystal Structure analysis of wild-type and fast hydrolyzing mutant of EhRabX3, a tandem Ras superfamily GTPase from Entamoeba histolytica. **J Mol Biol**. 2015 Nov 7. pii: S0022-2836(15)00624-5. doi: 10.1016/j.jmb.2015.11.003). (# Co-first authors).*
- ***Chandra M**[#], Srivastava VK[#] and Datta S. Crystallization and preliminary X-ray analysis of RabX3, a tandem GTPase from Entamoeba histolytica. **Acta Crystallographica Section F**: Structural Biology Communications, Acta Cryst. (2014). F70, 933–937. (# Co-first authors).*
- ***Chandra M**, Mukherjee M, Srivastava VK, Saito-Nakano Y, Nozaki T, Datta S. Insights into the GTP/GDP Cycle of RabX3, a Novel GTPase from Entamoeba histolytica with Tandem G-Domains. **Biochemistry**, January 28, 2014 (Article), DOI: 10.1021/bi401428f.*
- ***Chandra M**, Datta S. Role of cysteine residues in the redox-regulated oligomerization and nucleotide binding to EhRabX3. **Mol Biochem Parasitol**. 2016 Aug;208(2):84-90. doi: 10.1016/j.molbiopara.2016.06.009. Epub 2016 Jul 30.*

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"Molecular mechanisms of SNX27/retromer assembly in receptor homeostasis"

The major goal of this project is to determine the molecular mechanisms by which by which the retromer complex (VPS26/VPS35/VPS29 subunits) interacts with SNX27 on its own and assembled in the presence of PI3P-enriched nanodiscs. This work will provide critical insight into how retromer assembles in the presence of cargo.